

Alzheimer's Disease

Cover image: White matter atrophy in AD. See page 125, chapter 8 for details.

Alzheimer's Disease

Edited by

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Codon Publications
Brisbane, Australia

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ISBN: 978-0-6468096-8-7

DOI: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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Published by

Codon Publications
Brisbane, Australia

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First Published in November 2019

Printed in Australia

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FOREWORD

Alzheimer's disease (AD) is the sixth leading cause of death in the USA. Globally about 50 million individuals have AD or related dementias. With the increasing average age of humans worldwide, the total number of people with dementia is projected to reach 82 million by 2030 and 152 million by 2050. Despite its prevalence, AD is the only cause of death among the top 10 causes of death globally for which no effective pharmaceutical agents exist to halt or slow down the disease progression. By some estimates, AD and related dementias are the single most expensive medical condition. In 2019, direct costs of AD in the USA will be ~\$290 billion, which is expected to rise to ~\$1.1 trillion by 2050 if no treatments are developed. Hence, there is a tremendous imperative to gain a better understanding of the pathogenesis of AD and to develop effective treatments. AD is a complex, multifactorial disease, which is unique to humans. AD is defined neuropathologically by the accumulation of amyloid β ($A\beta$) into extracellular plaques in the brain parenchyma and in the vasculature (known as congophilic amyloid angiopathy [CAA]), and abnormally phosphorylated tau that accumulates intraneuronally forming neurofibrillary tangles (NFTs). Pathological aggregation of phosphorylated tau and $A\beta$ occurs in a sequential process. Monomers first aggregate into oligomers intraneuronally that then further aggregate into the fibrils observed in amyloid plaques and NFTs. This pathology then spreads in a characteristic brain topography that is distinct for NFTs and plaques. This process develops over many years, with a preclinical period of two to three decades, the onset of which is modulated by apolipoprotein E (apoE) genotype, as well as other genetic and environmental risk factors.

This book integrates considerable expertise from a wide range of authors from different disciplines. It includes clinicians through to translational and basic scientists. In aggregate, this book provides a comprehensive and up-to-date overview of AD. It covers the heterogeneous underlying AD pathology, with a review of genetic and proteomic approaches to better understand the disease. In addition, there is an extensive review of various potential contributing factors to the emergence of AD, as well as a discussion of novel biomarkers and potential effective therapeutic approaches. I trust that these reviews will be of value to clinicians and health professionals caring for patients with AD, and will provide a comprehensive and thought-provoking introduction to young investigators interested in translational aspects of the AD and related dementias field.

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.f>

PREFACE

Alzheimer's disease (AD) is the most common cause of dementia. The term "dementia" is derived from the Latin word *demens*, meaning "being out of one's mind," and has been used since the 13th century. AD has been recognized as a distinct entity since the publication of Alzheimer's description of a patient with presenile dementia in 1906. The first biochemical identification of amyloid beta (A β) as the major component of amyloid plaques, a key neuropathological lesion in AD, was published in 1984 with the seminal work of Dr. George Glenner. The latter discovery led to the amyloid cascade hypothesis of AD, with a focus on developing amyloid directed therapeutic approaches. The latter have all failed in clinical trials thus far. More recently, there is growing body of genetic, transcriptomic, and proteomic data pointing to the complexity of AD pathogenesis. This has resulted in a greater diversity of therapeutic approaches being attempted—in effect, resulting in "more shots on goal," with the prospect that at least some of these approaches will be efficacious. Hence, despite the many failures of AD therapeutic clinical trials, this is a hopeful time in AD research. There is a growing anticipation that our greater understanding of the underlying multifactorial pathogenesis of AD will result in effective therapeutic interventions in the near future.

In this book, we present reviews with the most current information on several critical aspects of AD, providing the readers with a broad picture of the underlying neuropathology, genetics, proteomics, risk factors, novel biomarkers, and potential interventions. Chapters 1–5 discuss the underlying AD pathogenesis using genomic and proteomic approaches, linking diverse pathways that can lead to complex metabolic dysfunction. Chapter 6 reviews the potential role of trace metals in AD, while Chapter 7 examines the diversity of A β species involved in AD pathology. Chapter 8 discusses the contributions of white matter degeneration in AD. Chapter 9 examines the potential intriguing role of the brain-gut-microbiota axis in mediating AD. Chapters 10 and 11 discuss potential biomarkers for AD, such as deficits in ocular exploration and early language impairments, respectively. Chapters 12–15 examine possible novel preventative and/or therapeutic methodologies such as exercise, optimizing depression therapy, and diverse psychosocial interventions.

We would like to thank all the authors for their diligent work in contributing toward this book. The 15 chapters review diverse facets of AD, which together paint a comprehensive picture of the pathogenesis, associated risk factors, novel biomarkers, and potential therapeutic targets. We believe that this book will encourage readers to delve deeper into this field and take up the critical challenge of working toward effective treatments for AD and related dementias.

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.cont>

A New Perspective on Alzheimer's Disease as a Brain Expression of a Complex Metabolic Disorder

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch1>

Abstract: Alzheimer's disease (AD) is an irredeemable chronic neurodegenerative disorder and the predominant cause of dementia. The disease progression is associated with the deposition of amyloid plaques and formation of neurofibrillary tangles in the brain, yet clinical dementia is the end and culminating stage of the enduring pathology. Recent evidence suggests that AD is characterized by distinctive abnormalities apparent on systemic, histological, macromolecular, and biochemical levels. Besides the well-described characteristic profuse neurofibrillary tangles, dystrophic neurites, and A β deposits, the AD pathology includes substantial neuronal loss, inflammation, extensive DNA damage, considerable mitochondrial malfunction, impaired energy metabolism, and chronic oxidative stress. Moreover, severe metabolic dysfunction leading to oxidative stress is a possible cause and hallmark of AD that is apparent decades before the disease manifestation. State-of-the-art metabolomics studies have proved that arginine and branched-chain amino acids metabolism disturbances accompany AD and contribute to its pathogenesis. Repetitive failures to find an efficient anti-amyloid or anti-Tau treatment, which would face the challenges of the complex AD pathology, led to the hypothesis that hyperphosphorylated Tau and deposited

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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A β proteins are hallmarks, not the ultimate causes of AD. Accordingly, the modern scientific vision of AD etiology and pathogenesis must reach beyond the hallmarks and look for alternative strategies and areas of research.

Keywords: Alzheimer's disease; arginase; arginine; branched-chain amino acids; oxidative stress; urea cycle

INTRODUCTION

Alzheimer's disease (AD) is a severe chronic neurodegenerative disorder and the leading cause of dementia (1). The gradual progression of cognitive decline is associated with characteristic brain atrophy, amyloid plaques deposition, and neurofibrillary tangles (NFT) formation (2). More than 100 years ago, AD has been described as an extremely rare pathology and, in fact, it was uncommon before the baby-boomers began to reach retirement age. Nowadays, it looks like one of the most significant medical, social, and economic challenges that faces the 21st century. Growing life-expectancy, high sugar and fat diet, and sedentary life-style have led to an epidemic-like and exponential dissemination of the disease within various social and national strata. Today, more than 50 million individuals suffer from the stage of AD that we refer to as dementia worldwide, and this number is expected to triple by 2050 (3).

Despite a century-long rigorous investigation, there is no complete scientific consensus regarding the causes of AD. The prevailing current view among scientists centers upon the amyloid cascade hypothesis (4, 5). However, growing clinical and empirical evidence points to extremely complex systemic pathophysiology accompanying AD-associated cognitive impairment and even contributing to its development decades prior to the clinical manifestation (6, 7).

The recent introduction of novel biomarkers for early detection and clinical management of AD has improved the diagnostic precision and qualification of neuropathology. The new techniques provide practical tools for more objective assessment of the treatment outcomes and early therapeutic strategy correction, with emphasis on the molecular mechanisms of the disease. Moreover, this systems-level approach identifies sex and age-specific differences and further advances the development of personalized medicine.

AD is an incredibly complex illness, which constitutes a combination of numerous interrelated pathological events that include neurovascular, inflammatory, bioenergetic, and systemic metabolic processes. In addition to the classic, distinctive hallmarks, the disease is characterized by systemic abnormalities and brain metabolic aberrations, which are evident at molecular and biochemical levels. Accordingly, the typical contemporary description of AD-related pathology includes neuroinflammation, activation of apoptosis, mitochondrial dysfunction, metabolic impairment, and chronic oxidative stress.

Notably, oxidative damage is considered to be the earliest event in AD pathology. Reliable data demonstrate an inverse correlation between levels of oxidative damage and both beta-amyloid (A β) deposition and duration of dementia (8). Moreover, the formation of intraneuronal NFT is associated

with reduced oxidative damage as well, which further supports the view that the onset of oxidative damage is an early event in AD pathogenesis.

Causes of brain oxidative stress include brain hypoperfusion due to advanced atherosclerosis or endothelial dysfunction, traumatic brain injury (TBI), infections, autoimmune disorders, insulin resistance (IR), and other diseases leading to neuroinflammation. Of note, the very first AD patient autopsy disclosed substantial brain atrophy and apparent arteriosclerosis (9). Recent converging evidence suggests that chronic cerebral hypoperfusion follows progressive aging due to cerebral atherosclerosis and endothelial dysfunction (10). These two interrelated pathological processes lead to brain energy crisis and trigger the characteristic neurodegeneration (11) (Figure 1).

Initial studies with focal ischemic insults and chronic cerebral hypoperfusion in rats have shown increased amyloid precursor protein (APP) translation levels followed by local $A\beta$ deposition in the brain parenchyma (12). Furthermore, chronic vascular insufficiency induces cleavage of the APP into $A\beta$ -sized fragments in a rodent model (13). The used model of chronic blood-vessel occlusion demonstrated progressive accumulation of $A\beta$ peptide in the aged rats. Of note,

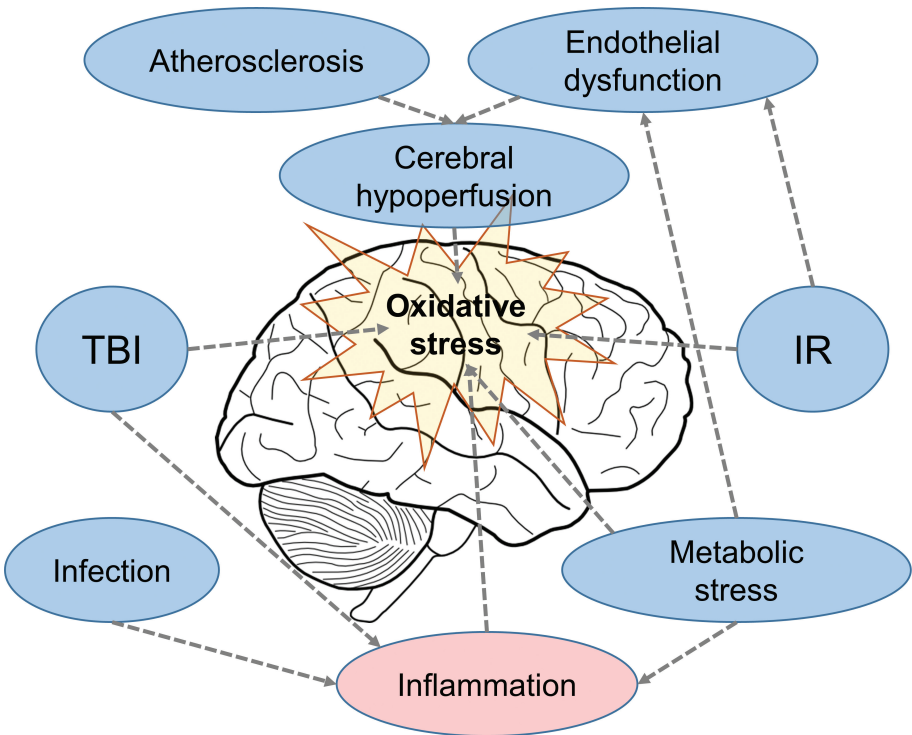


Figure 1 Main pathogenic factors of AD development. Cerebral hypoperfusion, metabolic stress, traumatic brain injury (TBI), and insulin resistance (IR) are the main causes of AD development.

A β deposition pattern displayed a gradual shift from neurons to the extracellular matrix, mimicking the characteristics of sporadic AD. The described hypoxia-induced response is attributed to a significant increase in the activities of APP amyloidogenic proteases (β - and γ -secretases), although nonamyloidogenic α -secretase activity declines (14). Additionally, proinflammatory cytokines, and in particular tumor necrosis factor (TNF), prompt transcription of the *APP* gene via direct regulation of its promoter, which leads to overproduction and deposition of A β (15).

Brain tissue deprivation of arginine has been suggested as a possible pathogenic mechanism leading to oxidative damage (16). Arginine deprivation leads to endothelial nitric oxide synthase (NOS3) substrate deficiency and enzymatic “uncoupling” due to induced arginase activation (16, 17). Uncoupling changes NOS3 enzymatic profile radically. As an alternative to oxidizing arginine to citrulline and NO, uncoupled enzyme reduces molecular oxygen to superoxide anion, which leads to neuronal oxidative stress (18).

Additionally, recent metabolomics studies have indicated characteristic branched-chain amino acids (BCAAs) deficiency as a metabolic signature of AD (19). BCAAs play an important role in glutamine/glutamate brain metabolism and provide nitrogen for at least one-third of the cerebral glutamate (20). Therefore, perturbations of BCAAs levels have a substantial impact on brain function and tip the scale between excitation and inhibition. Of note, BCAAs supplementation has been intensively investigated preclinically, demonstrating a therapeutic potential in different animal models of atherosclerosis (21), obesity (22), metabolic syndrome (23), and AD (24).

According to our model (Figure 2), AD is a spectrum of disorders, which has a mutual downstream pathway and pattern of manifestation with deviant biological reactions that eventually culminate in clinical dementia. We comprehend brain amyloidogenesis as a natural evolutionary conserved reaction to oxidative and metabolic stresses, which can be induced by numerous factors including nutrient imbalances. This view corresponds with the notion of A β antioxidant functions in the aging and AD brain (27) and an influential concept, which deals with intraneuronal accumulation of A β , is a protective cellular mechanism to cope with oxidative insults (28). Moreover, amyloid aggregation and formation of extracellular amyloid plaques, where amyloid is in an insoluble form, are also an adaptive mechanism of the brain (29). This bioprocess reduces the concentration of the soluble toxic oligomeric and fibrillar species, which impair synaptic function and induce an inflammatory response. For that reason, there is a gradual reduction of A β concentration in the cerebrospinal fluid (CSF) of AD patients (30), the index that is inversely correlated with the cognitive decline (31).

EARLY- AND LATE-ONSET AD ARE TWO DIFFERENT ENTITIES

Advanced age is the main risk factor of AD (32). Nevertheless, its early onset is relatively common, representing about 5% of all cases (33). The very first case described by Alois Alzheimer was a woman who died at just 55 years from the disease. In fact, this case should be classified as an early-onset AD (EOAD) incident. This form is defined in the literature by clinical symptoms appearing

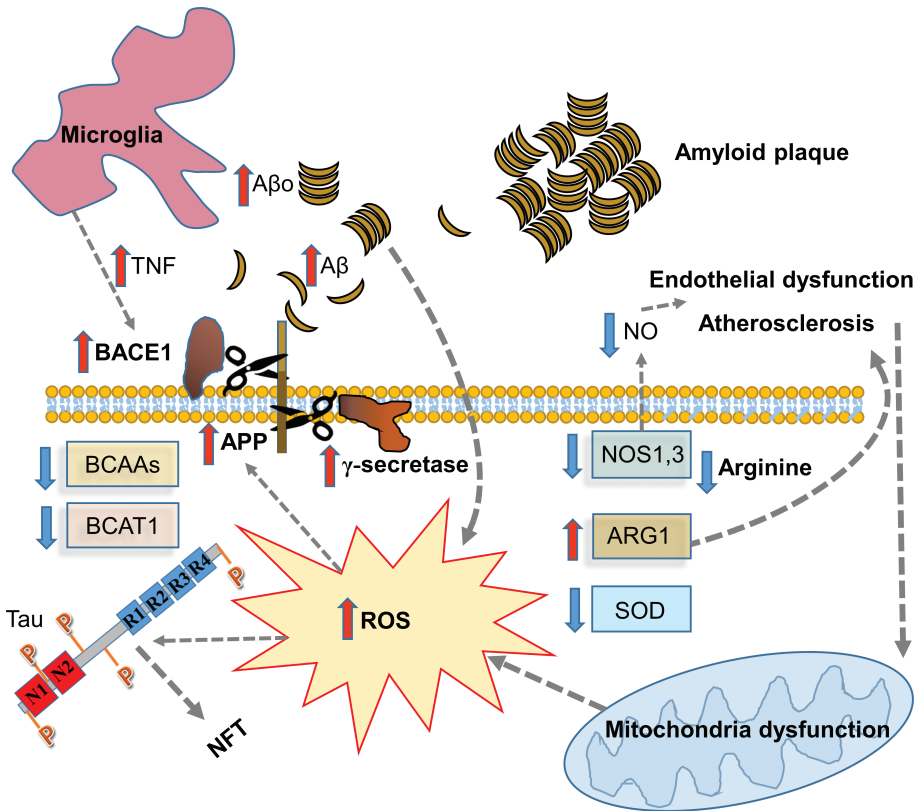


Figure 2 Proposed model of AD pathogenesis. The diagram presents oxidative stress induced by mitochondrial dysfunction, inflammation, or metabolic stress as the principal pathogenic AD event. Oxidative stress leads to an elevation in ROS levels and accumulation of oxidation products in neurons, which results in overexpression and increased processing of *APP* gene and eventually plaque formation (25), hyperphosphorylation of Tau and NFT pathology, which in turn produces more ROS and results in neurodegeneration and cellular death (26). $A\beta$ directly induces the production of ROS and further exacerbates oxidative stress and impairs endogenous antioxidant system including the activity of SODs.

before the age of 61 years (34). Generally, EOAD is inherited following dominant Mendelian fashion, although it represents a genetically heterogeneous group (35). Epidemiological data suggest that autosomal dominant familial AD (FAD) with *PSEN1*, *PSEN2*, and *APP* mutations accounts for about 0.5% of all AD cases (36); yet, the share of familial form in the group of EOAD rises to 13% (34). Late-onset AD (LOAD) demonstrates a high heritability, with much more genes implicated in its development; however, the progression of LOAD is believed to be driven by a combination of genetic and environmental factors (37), and thus it remains to be principally idiopathic.

EOAD frequently manifests with distinguishable cognitive profile from LOAD. No evident amnesia characterizes the disease course, sometimes presenting just with language discrepancies, apraxia, and other uncommon functional

deficits (38). Moreover, a specific memory impairment itself presents distinct patterns in EOAD and LOAD cases, with significantly more impaired semantic memory in LOAD than in EOAD patients (39). Recent objective data have demonstrated that EOAD CSF and fludeoxyglucose F 18 (^{18}F -FDG) positron emission tomography (PET) features substantially contrast with LOAD. CSF t-Tau shows significantly higher levels in EOAD patients (40). Moreover, ^{18}F -FDG PET scans of EOAD patients present the asymmetric patterns of hypometabolism with a localization that prominently differs from LOAD. Likewise, dementia severity in relatively young patients strongly correlates with amyloid plaques burden, but this direct relation progressively weakens with age and even disappears in the ninth decade of life (41). Of note, the term “dementia” itself is an umbrella term for cognitive impairment that interferes with one’s ability to conduct routine daily affairs, and therefore extremely varies between different social groups.

Remarkably, at a molecular level, the A β oligomeric subtypes show a distinct pattern in each of AD forms. Amyloid pentameric species in the insoluble fraction are more abundant in EOAD than in LOAD (42). Additionally, elevated inflammatory markers, together with impaired renal function, distinguish LOAD, which points to substantial differences in pathogenesis and development between the two clinical forms of the disease (43).

These observations indicate that EOAD afflicting presenile populations represents a categorically separate pathological entity, which is characterized by distinctive pathophysiological mechanisms accountable for its unambiguous genetic background and uncommon clinical manifestation. In our opinion, only this form presents classic AD or presenile dementia of Alzheimer type.

In opposition to presenile form, the etiology of LOAD disease is much more heterogeneous, with a combined contribution of numerous genetic, age-related, and environmental factors. Unlike EOAD, LOAD often presents in comorbidity with diabetes and hypertension (44). Of note, no two patients have the same combination of the disease-related factors; therefore, the clinical appearance and the treatment strategies for this form have to be accurately personalized. Moreover, despite the apparent differences between presenile and senile forms of AD, taxonomically they are still the same illness. In our opinion, LOAD is a syndrome, but not a stand-alone disease. It is a concurrence of correlated with each other convergent symptoms, and concurrence literally means syndrome (45). Thus, we suggest that the presence of the same confluent hallmarks, which characterize the EOAD and LOAD, does not reflect their mutual etiology and pathogenesis; therefore, attempts to link these two forms of AD to a single common causative agent are futile. For that reason, this chapter deals only with more common LOAD, which has a distinct metabolic signature.

LOAD AS A SYSTEMIC METABOLIC DISORDER

Converging evidence points to severe metabolic dysfunction as a leading cause and hallmark of AD (46). State-of-the-art metabolomics and imaging studies dealing with the immense complexity of the AD phenotype have disclosed this aspect of the disease. Gradual decline in cerebral metabolic rate is one of the earliest indicators that distinguish patients with mild cognitive impairment (MCI) and

poses the clinical suspicion of prodromal AD (47), which suggests a key role of metabolic dysfunction in initial mechanisms of AD development. Likewise, advanced analyses of the brain tissue could detect explicit metabolic perturbations associated with AD, both in humans (48) and mice (49).

A recent human postmortem unbiased lipidomics and metabolomics study has disclosed 34 metabolites, which distinguish frontal cortices' composition of AD patients from healthy controls (50). The authors identified six biochemical pathways, which are significantly altered in AD brains. The list of the pathways by their significance rate includes alanine, aspartate, and glutamate metabolism; arginine and proline metabolism; cysteine and methionine metabolism; glycine, serine, and threonine metabolism; purine metabolism; and pantothenate and CoA biosynthesis (50).

Metabolomics profiling of human plasma, which combines high-resolution mass spectrometry and advanced chemometrics and pathway enrichment analysis, indicates differentially affected polyamine and arginine metabolism in MCI subjects converting to AD (51).

Animal studies support and advance these findings. Multivariate statistical analysis of metabolite profiles of the brain, liver, and kidney tissues from APP/PS1 and wild-type (WT) mice indicates systemic nature of AD-associated pathophysiology (52). Liver and kidney samples from 6-month-old mice were fingerprinted using a high-throughput multi-platform metabolomics approach based on gas chromatography/mass spectrometry and reversed-phase liquid chromatography. Several observations pointed to the systemic character of the disorder with severely impaired glucose metabolism, mitochondrial dysfunction, and abnormal metabolism of BCAAs (52). Another longitudinal research performed in APP/PS1 transgenic and wild-type mice (6, 8, 10, 12, and 18 months of age) with deep profiling of the brain and plasma metabolome proved severely disturbed polyamines and BCAAs metabolism (53).

Growing clinical evidence points to a widespread AD-related systemic disorder characterized by severely affected peripheral parenchymal organs and blood in similar magnitude as the brain (54). Remarkably, the scope and features of AD-associated metabolic abnormalities resemble advanced pathology observed in obese and diabetic patients (55). These common aberrations led to the hypothesis that AD represents a unique form of diabetes. A novel term "type 3 diabetes" has been coined and accepted in the scientific literature (56). This term reflects a substantial overlap at molecular and biochemical levels between AD and diabetes mellitus type 2 (57). Diabetic elderly patients were shown to develop extensive vascular abnormalities, which are associated with classic AD pathology (58). Likewise, recent data evidently and causatively relate obesity and AD (59).

Remarkably, several common treatment strategies for the abovementioned metabolic diseases are extremely effective, which proves mutual pathophysiology. Various preclinical and clinical studies have verified that a long list of drugs that are conventional in the treatment of diabetes, atherosclerosis, and other metabolic disorders improves the overall status, behavioral and cellular functions of AD patients. For instance, insulin-based therapy has emerged as a promising approach to halt AD-associated cognitive decline (60). Wang et al. evidenced a substantial effect of metformin upon neurogenesis and spatial memory acquisition in mice (61). A significant neuroprotective effect of metformin was demonstrated in rodents on a high-fat diet (HFD) (62). A recent meta-analysis study has proved

that metformin use is associated with reduced risk of dementia in patients with diabetes (63). In order to evaluate the potentials of the drug as a disease-modifying medicine in AD, a randomized 2-month-long placebo-controlled crossover study was performed, verifying the metformin-associated improvement in executive functioning (64).

Additionally, animal and human studies with thiazolidinediones have shown the potential to treat AD and diabetes. The treatment improves memory via facilitation of synaptic transmission and reduction of neurodegeneration (65, 66). Likewise, a broad variety of antioxidants are shown to be promising in atherosclerosis, AD (67), and diabetes mellitus (68). It is worth mentioning that chronic curcumin treatment improves the function of insulin-producing β -cells, reduces A β -associated cytotoxicity, mitigates Tau protein hyperphosphorylation, and alleviates neurodegeneration (69, 70).

Curiously, despite the lack of consensus about the AD etiology and pathogenesis, and absence of disease-modifying therapy, the disease prevalence in the western world has declined gradually over the last two decades (71). Several population-based studies have suggested that despite the growing absolute number of elderly people with dementia, age-specific risk of dementia is declining (72). In the USA alone, the proportion of elderly people with dementia has decreased by about 24% between 2000 and 2012 (73). A similar trend was observed in England between 1991 and 2011 (74).

One possible explanation for the phenomenon might be recent considerable achievements in treatments of cardiovascular diseases and diabetes. The innovative widespread prevention and treatment strategies for these disorders include intensive medication with novel effective medicines. Therefore, the progress in the control of main dementia risk factors substantially assisted in reducing the prevalence of dementia among the target age groups.

Recent evidence suggests that AD-associated cognitive impairment is the outcome of extremely complex pathophysiology. In the light of new findings, more thorough consideration of the complexity of AD as a syndrome is required. Moreover, strategies targeting β -amyloid or Tau protein are not adequate to cure the disease; therefore, attempts to treat single hallmarks of AD, such as plaques and tangles, are futile.

A CONTRIBUTION OF THE UREA CYCLE AND POLYAMINE METABOLIC PATHWAY IN THE DEVELOPMENT OF AD

The human brain weighs just 2% of the entire body weight but consumes about a fifth of the total glucose-derived energy, and consequently is highly vulnerable to oxidative stress (75). Neurons particularly are strongly dependent upon oxidative phosphorylation as an energy source, compared to other cells. As a general rule, oxidative stress increases with aging (76), which is followed by escalation of protein oxidation and extensive lipid peroxidation in susceptible organs and, particularly, in the brain. In the course of the progression of age-related or AD-related neurodegeneration, neurons gradually lose their capacity of maintaining an appropriate redox balance. This imbalance leads to progressive accumulation of reactive oxygen species (ROS), mitochondrial dysfunction, and,

eventually, to neuronal injury (77). Moreover, A β deposits are directly associated with the free-radical generation, forming a vicious circle of AD pathogenesis (78, 79) (Figure 2).

Antioxidants are capable of transferring electrons to and from oxidizing agents, inhibiting free radicals production and reducing potential cell damages (80). Generally, antioxidants are classified into enzymatic agents (superoxide dismutase [SOD], catalase, glutathione peroxidase, glutathione reductase, etc.) and non-enzymatic agents (coenzyme Q10, carotenoids, vitamins E and C, and arginine) (81).

Arginine is a potent free radical scavenger (82) and protects neurons against oxidative stress through its antioxidant potentials (83). Its cationic nature contributes to the unique protonative properties and ability to react directly with the superoxide anion radical (84). Thus, arginine and its derivatives regulate membrane peroxidation processes (85). Although the human cells are capable of synthesizing arginine, its external supplementation is necessary for infants and the elderly, making arginine conditionally essential (86). Moreover, some clinical conditions lead to depletion of endogenous arginine resources, which escalates the demand for it. Among these conditions are severe infections, burns, wounds, intensive physical activity, and sterility (87).

Several recent studies have explored the association between age-related cognitive function decline and aberrations in brain arginine metabolism. An animal study has disclosed altered arginine metabolic profile even prior to any memory deficit (88), which proves the parallel development of brain arginine metabolism aberrations and behavioral deficits in AD mice. Moreover, behavioral deficits and brain profile alternations follow the changes in plasma arginine metabolic profile, which advocates the use of arginine-centric antemortem biomarkers for the early diagnosis of AD (88). More recent data from the same laboratory have demonstrated a significantly altered brain arginine metabolism in a mouse model of tauopathy (89). Noticeable changes were observed in ornithine, polyamines, and glutamate concentrations, which further suggest a shift of arginine metabolism to the direction of arginase–polyamine pathway in AD rodent models brain.

Additional evidence indicates severe arginine metabolism disturbances in various brain areas and points to significantly escalated arginase activity in the hippocampi of AD patients (90). Another study has reported decreased levels of arginine in the cortices of AD patients (91). Moreover, innovative capillary electrophoresis–mass spectrometry metabolomics investigations of AD patients' CSF detect a decline in arginine levels (92, 93). Remarkably, urine levels of arginine in amnesic MCI patients are also significantly lower than in normal controls (94). Additionally, these patients demonstrate a reduced global arginine bioavailability ratio, the index, which is positively correlated with the Mini-Mental Status Examination score, making urinary arginine levels a potential diagnostic biomarker for MCI. Of note, numerous animal studies have further implicated altered arginine metabolism in the pathogenesis of AD (95, 96).

Arginine was shown to mitigate hydrogen peroxide-induced apoptosis and protect against A β ₍₂₅₋₃₅₎-induced toxicity in cultured PC-12 cells (97). The amino acid supplementation improves cognitive function in demented elderly (98). Additionally, its administration within 30 min of a stroke significantly decreases the frequency and severity of symptoms (99).

Arginine overcomes biological barriers via ubiquitously expressed high-affinity permeases or cationic amino acid transporters (CATs), which are involved in the transport of the cationic amino acids (arginine, lysine, histidine, etc.) (100). Arginine is generally transported from the circulating blood into the brain via CAT1, which is excessively expressed at the blood–brain barrier (BBB) (101, 102). The amino acid influx transport in the rat model has been proven to be saturable with a Michaelis–Menten constant (K_m) value of 56 μM . Of note, the physiological serum concentration of arginine is about 170 μM in rodents and about 100 μM in men (103). Consequently, the capacity of its transport system is substantially limited (104) that makes traditional arginine supplement insufficient to demonstrate all of its possible effects. Therefore, the pharmacological targeting of enzymes that metabolize arginine in order to improve its availability is a likely beneficial method to treat neurological conditions (17).

Arginase cleaves arginine to produce urea and ornithine at the last step of the urea cycle, which generally protects the cells against ammonia toxicity, while ornithine and its downstream derivatives participate in collagen formation, induce cell proliferation, and influence other vital physiological processes (Figure 3). A substantial increase in arginase activity contributes to vascular dysfunction in the atherosclerotic (apolipoprotein E deficient) mice by interfering in the function of the neurovascular unit, which leads to BBB leakage and neuroinflammation (105).

Arginine is the immediate precursor of NO and other bioactive molecules (Figure 3). Nitric oxide synthases (NOSs) utilize arginine as a substrate to produce NO and citrulline (106). Consequently, the bioavailability of arginine is a regulating factor for NO synthesis (107). Arginine-derived NO serves as a potent antioxidant agent protecting cells from damage caused by ROS (108). It causes vasodilation and improves blood supply to neurons, which reduce their susceptibility to oxidative stress (109). Likewise, NO moderates Ca^{2+} influx into the neurons, protecting them from excitotoxicity (110). Remarkably, under physiological conditions, the molecule represents a key endothelium protective factor (111) but becomes detrimental under oxidative stress. Substrate deficiency leads to NOS3 uncoupling and deviation from NO synthesis, converting it to a superoxide-producing enzyme (112). A significant reduction of NOS activity in AD brains, with a decrease in the levels of NOS1 and NOS3 proteins, has been reported (90). Moreover, AD-associated arginase overactivation substantially limits mutual substrate availability, and is followed by a decrease in NO production (113). This mechanism is particularly important in the statuses with limited extracellular resources of arginine, like advanced age, for example.

The arginase expression is induced by various stimuli, including cytokines, catecholamines, lipopolysaccharide, TNF, oxidized low-density lipoprotein, and hypoxia (114, 115). In the brains of the AD model mice, arginase 1 (Arg1) was shown to be not only localized in the cells but also distributed in the extracellular space. In the hippocampus, it displays a spatial correlation with A β deposition, and Iba1 expression (16). In addition, activation of arginase 2 (Arg2) is associated with translocation from the mitochondria to the cytosol (116, 117) (Figure 3).

Recent evidence points to escalated *Arg2* gene expression in AD brains (118). Moreover, *Arg2* deficiency reduces the rate of hyperoxia-mediated retinal neurodegeneration (119), suggesting the contribution of arginase in the neuronal

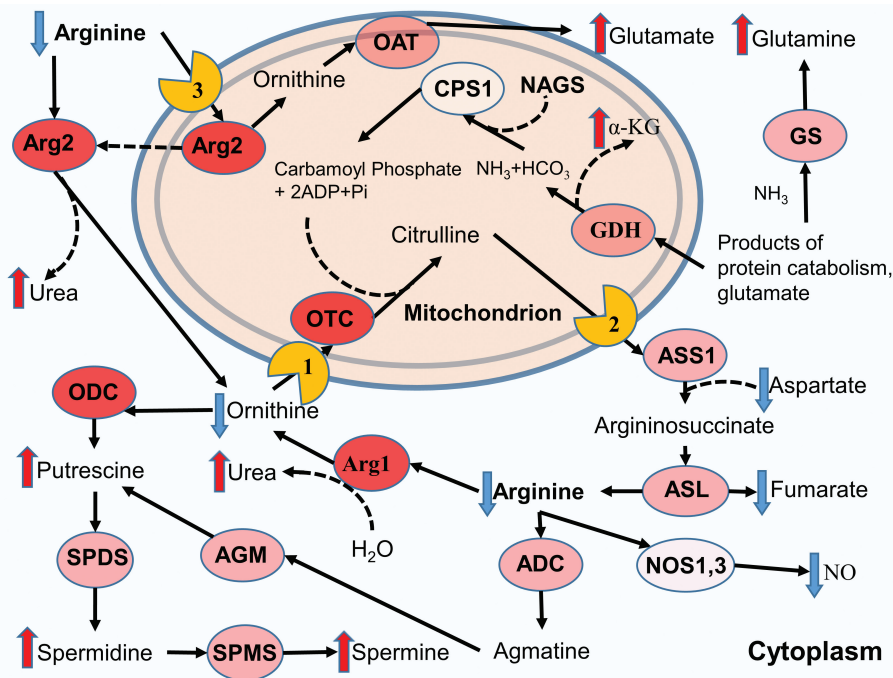


Figure 3 Arginine metabolic pathways and their deviations in AD brain. Arginine is primary substrate metabolized by nitric oxide synthases (NOS1 and NOS3 under physiological conditions), arginase 1 (Arg1) and arginine decarboxylase (ADC). Arginase 2 (Arg2) plays a role in extra-urea cycle arginine metabolism. Arginine is cleaved by arginase to form urea and ornithine at the final step of the urea cycle. The urea cycle consists of N-acetylglutamate synthase (NAGS), which is an allosteric cofactor for catalytic enzyme carbamoyl phosphate synthase (CPS1), and other four catalytic enzymes: ornithine transcarbamylase (OTC), argininosuccinate synthetase (ASS1), argininosuccinate lyase (ASL), and arginase 1 (Arg1). NAGS, CPS1 and OTC are localized in the mitochondria, while ASS1, ASL, and ARG1 are in the cytosol. Two enzymes: OTC and CPS1 are present in very low concentrations in the human brain. As a result, the brain urea cycle is not efficient and to remove ammonia and relies on alternative glutamine synthesis by glutamine synthetase (GS). Glutamine concentration rises in AD brain. Glutamate dehydrogenase (GDH) catalyzes the deamination of glutamate to α -ketoglutarate (α -KG), which concentrations also increase in AD brain, and ammonia (NH_3). The mitochondrial ornithine transporter (1), citrin (2), and the mitochondrial cationic amino acid transporter type 1 (3). Red arrows indicate elevated levels; blue arrows designate reduced ones. The intensity of the circles' color reflects the level of activation (arbitrary scale). Argininosuccinate lyase (ASL), argininosuccinate synthetase (ASS), nitric oxide (NO), ornithine decarboxylase (ODC), spermidine synthase (SPDS), spermine synthase (SPMS), agmatinase (AGM), ornithine aminotransferase (OAT).

degeneration via overactivation of the N-methyl-D-aspartate receptors (120). Accordingly, targeting Arg2 has been proposed as a means of decelerating age-related diseases treatment (121).

Inhibition of ornithine decarboxylase (ODC) with α -difluoromethylornithine has been proved to be neuroprotective in a rodent model of AD (16). The authors speculated that arginine deprivation is a critical AD pathogenic factor, which eventually leads to neuronal death and cognitive deficits. We have hypothesized

that upregulation of arginase activity and consequent arginine and NO deficiency, in the brain areas characterized by excessive amyloid deposition, contribute to the clinical manifestation of AD (17). Accordingly, we targeted arginase, but not ODC, with its uncompetitive inhibitor, norvaline, to ameliorate the symptoms of the disease (117).

Norvaline has been proven to be a potent inhibitor of urea synthesis in isolated rat liver cells (122). It also inhibits arginase *in vivo* via negative feedback inhibition mechanism due to its structural similarity with ornithine (123). Moreover, the inhibition process is enantiomer dependent because its stereoisomer, D-norvaline, does not affect NO production (113). The potency of norvaline to amplify the rate of NO production has been evidenced *in vitro* (113). In addition, the substance was effectively used in a rat model of artificial metabolic syndrome (23).

Remarkably, norvaline also effectively inhibits ornithine transcarbamylase (OTC) activity, the mitochondrial enzyme converting ornithine to citrulline (124) (Figure 3). OTC is extensively expressed in AD brains, but not in controls, which is followed by about ninefold increase in OTC activity in the CSF (125). Epidemiological studies have revealed that single nucleotide polymorphism of the *OTC* gene promoter is associated with AD morbidity, suggesting that the *OTC* gene is a minor genetic AD determinant (126). *OTC* activation leads to apparent ornithine deficiency (90) and, in turn, arginase activation via product inhibition insufficiency. Thus, the vicious circle of metabolic changes acts in the AD brain (Figure 3). Accordingly, norvaline is capable of correcting the AD-related arginine metabolism aberrations by inhibiting two central enzymes of the urea cycle.

A PUTATIVE ROLE OF BCCAS IN THE DEVELOPMENT OF AD

BCAAs are the amino acids possessing branched aliphatic side-chains. There are three proteinogenic BCAAs—valine, leucine, and isoleucine, which are essential amino acids—and several non-proteinogenic BCAAs, including 2-aminoisobutyric acid and 2-aminopentanoic acid (norvaline) (127). It is worth mentioning that the vast majority of essential amino acids are metabolized in the liver; however, BCAAs escape the first-pass hepatic catabolism and are mainly oxidized in skeletal muscles, adipose tissue, and the brain (128).

BCAAs catabolism initiates with a transamination reaction catalyzed by the branched-chain aminotransferases (BCATs). The family of BCATs consists of two isoforms: mitochondrial BCAT2 and cytosolic BCAT1. BCATs are mutual to all three BCAAs, and transamination by BCATs is the exclusive reaction for BCAAs only. The products of the reaction are glutamate and three different branched-chain α -ketoacids (BCKAs). Of note, other non-proteinogenic BCAAs (for instance, norvaline) are competent to be substrates for BCAT in rodents and humans (129).

There are indications that BCAAs play a different role in the brain compared to other tissues. BCAT1 and BCAT2 are expressed prominently in the brain cells, where the enzymes maintain the continuous supply of the principal excitatory neurotransmitter glutamate. Remarkably, BCAT1 is present predominantly in neurons, while the appearance of BCAT2 is limited to astrocytes (130, 131).

In the mammalian brain, BCAAs are involved in several vital processes. Among them are key neurotransmitters' metabolism, protein synthesis, and energy production (132). Glutamate is the principal excitatory neurotransmitter of the mammalian brain (133), and its concentrations are substantially higher in brain than in plasma (134). Glutamate does not cross the BBB in considerable quantities, except in regions with fenestrated capillaries (135); therefore, neuronal glutamate has to be continually synthesized from constantly accessible and reliable precursors. Its synthesis requires an efficient amino group donor, which is transported rapidly into the brain and is readily transaminated. BCAAs meet these needs optimally. Their unique properties and availability allow them to play a central role in glutamate metabolism. It was estimated that at least one-third of the cerebral glutamate contains nitrogen derived from the BCAAs (20). Consequently, perturbations in the levels of BCAAs meaningfully influence the whole function of the central nervous system, and the balance of excitation and inhibition, in particular.

González-Domínguez et al. utilized gas chromatography coupled with mass spectrometry to profile low-molecular-weight metabolites in serum of newly diagnosed sporadic AD patients who had not received any medication yet (136). Alterations of 23 metabolites were detected, including significantly decreased valine levels. In a more recent study including hundreds of participants conducted by Toledo et al., lower plasma valine levels were shown to correlate with the rate of cognitive decline. Likewise, the coefficient for valine was negatively associated with actual ventricular volume changes. Accordingly, an increase in valine concentration was associated with a significantly decreased risk of AD (137). Another study by Tynkkynen et al. utilized innovative profiling of blood metabolites via nuclear magnetic resonance and mass spectrometry (19). Remarkably, lower levels of all three BCAAs were strongly associated with an increased risk of dementia and AD in a combined meta-analysis with a replication sample.

In our original studies in a rodent model of AD, we provided the mice with arginase inhibitor non-proteinogenic BCAA norvaline, which is an isoform of valine (117). The animals treated with norvaline demonstrated significantly improved spatial memory acquisition, associated with an increase in hippocampal spine density, and reduced neuroinflammation. Moreover, the rate of the brain amyloidosis was significantly diminished due to a reduction in the expression levels of the APP, which was followed by a significant increase in [Cu-Zn] superoxide dismutase levels, suggesting improvement of the internal antioxidant mechanisms (24). Further investigations will shed light on the potential of BCAAs to halt AD progression.

CONCLUSION

Scientific society has already sought a potent AD-modifying medication for more than a century. Unfortunately, its best efforts have been to no avail. A cornucopia of agents has been trialed, hoping to preclude the impending calamity, but with no conclusive results. The primary cause of the continual failures is the misleading and highly controversial hypothesis, which besets the development of adequate AD therapy.

The chronic absence of an AD-modifying drug, despite multibillion dollar research and development investment, puzzles the best scientific minds and enigmatizes the entire field of knowledge. Continual failure to rise to the challenges of the multifaceted AD pathology and offer an efficient disease-modifying therapy predicated upon the dominant during the last 30 years amyloid cascade hypothesis, with aggressive anti-amyloid or anti-Tau treatments, led to the suggestion that hyperphosphorylated Tau and deposited A β proteins are just hallmarks and not the ultimate causes of AD (139, 140). Accordingly, treatment strategies targeting beta-amyloid or Tau protein are not competent to cure the disease (140). As a result, a novel trend in academic research and preclinical drug development is directed toward the discovery of therapeutic agents targeting altered brain metabolism and energetics (141). Recently proposed novel strategies based on a universal approach to the problem of AD and a progressive vision of the disease etiology and pathogenesis reaching beyond the conventional hallmarks provide a hope to halt the looming epidemic.

Current metabolomics techniques are based on a comprehensive understanding of AD pathophysiology, which is predicated upon the detailed knowledge of its peculiarities, the disease onset coincidences, and the precise order of the pathology development. In this context, an emerging metabolic hypothesis of AD, which is strongly supported by empirical evidence, and treats the classic hallmarks of the disease as the epiphenomena of the major complex pathology, has promising potential to offer a competent therapeutic solution.

Moreover, this new concept proposes a novel approach to the clinical classification and the treatment strategy for two distinct forms of AD. There is a consensus about the considerable differences between EOAD and LOAD. These two forms of AD have dissimilar courses, different genetic backgrounds and clinical manifestations, and are followed by unrelated metabolic impairments. Therefore, they have to be treated as separate entities.

In categorizing LOAD as a brain expression of a systemic complex metabolic disorder, which shares similarities and pathogenic pathways with diabetes mellitus, obesity, and atherosclerosis, we suggest common treatment and preventive strategies for all these pathologies. Therefore, regular physical and mental activity, diet, blood glucose, cholesterol levels monitoring and regulation, and antioxidants supplementation have particular importance in AD prevention and treatment. Moreover, novel emerging potent medicines, which have been successfully trialed in patients with various systemic metabolic diseases, might be extremely effective in AD patients as well.

We suggest that inclusive AD treatment strategies, targeting both brain and systemic abnormalities, are more effective than strategies that target CNS abnormalities alone. Such approaches should include an auxiliary intervention into the metabolic pathways and personalized correction of imbalances. Likewise, the systemic management of AD comorbidities and mutual risk factors is a central part of preventive AD therapy.

In addition, we argue that, in the case of LOAD, early prevention is the best healthcare salutary strategy. Consequently, the most critical current objectives are the empowerment of people with the ability to change their lifestyle, and the arming of doctors with the appropriate tools and medicines to halt the AD development.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Gene Ontology: A Resource for Analysis and Interpretation of Alzheimer's Disease Data

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch2>

Abstract: Gene Ontology (GO) is a universal resource for analyses and interpretation of high-throughput biological datasets. GO is developed and curated by several different groups, based at scientific institutions around the world, working together under the auspices of the GO Consortium. GO annotations capture biological functional knowledge by associating gene products with GO terms. GO term and gene product records all have computer-readable accession numbers; therefore, these annotations can be easily used for analyses of large datasets while retaining human-readable labels. The UCL Functional Gene Annotation group focuses on GO annotation of human gene products. Our group has led initiatives to systematically annotate proteins and microRNAs across specific biomedical fields, and our current biocuration effort, funded by the Alzheimer's Research UK foundation, is focused on dementia and Alzheimer's disease. Our group has also contributed to the development and revision of the ontology describing neurological domains of biology. Here we present an overview of GO and explain how our work, as well as the work of other members of the GO Consortium, is improving the neurological domains of the GO resource. These biocuration efforts will benefit the dementia and Alzheimer's research community by rendering GO more suitable for analyses of neurological datasets.

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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Keywords: annotation; biocuration; Gene Ontology; high-throughput analysis; neurobiology

INTRODUCTION

Several genes associated with monogenic Alzheimer's disease (AD) have been identified (1); however, the disease can also be caused by polygenic and environmental risk factors (1, 2). To understand the cellular processes and risk factors associated with AD, numerous transcriptomic, proteomic, and genome-wide association (GWA) studies have been conducted (3–5). Researchers are now turning to pathway-based GWA analysis and Next Generation Sequencing (NGS) to identify the genes contributing to the “missing heritability” (6, 7).

The process of finding gene variants that are causative, or modifiers, of disease is often time-consuming. Bioinformatics-based analyses can aid the identification of AD risk variants, based on the variant's association with a gene product implicated in neurobiological processes and pathways impaired in dementia. Such approaches are reliant on bioinformatics resources, including Gene Ontology (GO) (8, 9), KEGG (10), Reactome (11), and molecular interaction databases (12, 13). These resources provide connections between gene products and biological pathways or networks, which are relevant to AD. The end result of these analyses is the identification of both the risk variant and the candidate gene associated with the risk (14, 15). In addition, considerable research is now focused on the selection of biomarkers for AD (16), and the creation of biomarker panels is likely to be more successful if it is known what biological pathways the candidate biomarkers have in common.

GENE ONTOLOGY

The majority of analyses of high-throughput approaches rely on high-quality annotation data (4, 5) because these bridge the gap between data collation and data analysis (4, 17). Gene annotation datasets provide functional knowledge about gene products, such as proteins or microRNAs, in a computationally accessible format, thus these data can be exploited by systems biology investigators. The main resources used to identify significantly enriched pathways in “omics” studies are those provided by GO (8, 9), KEGG (10), Reactome (11), and protein interaction databases (12, 13). GO annotation data are frequently used because it can describe a gene product's role in a process or its location in a cell, even when the basic molecular activity of this gene product is still under investigation (Figure 1) (18). In contrast, Reactome and KEGG provide very specific information about the molecular function of a gene product within a pathway, with the “reaction” catalyzed or facilitated by each gene product clearly identified within a pathway diagram. Consequently, gene products whose role has not been fully elucidated cannot be included in these resources. Furthermore, although the human and mammalian phenotype ontologies (HPO, MP) (19) are being used to interpret NGS data, understanding how multiple genes contribute to a single





































Gene Product	Symbol	GO Term	Evidence	Annotation Extension
UniProtKB:Q95782	AP2A1	GO:0050750    low-density lipoprotein particle receptor binding	ECO:0000353  IPI	activated_by (CHEBI:64646) more...
UniProtKB:P30533	LRPAP1	GO:0150093    amyloid-beta clearance by transcytosis	ECO:0000315  IMP	has_input (UniProtKB:P05067:PRO_0000000093) more...
UniProtKB:Q00610	CLTC	GO:0072583    clathrin-dependent endocytosis	ECO:0000315  IMP	has_input (UniProtKB:Q07954) more...
UniProtKB:Q00610	CLTC	GO:0050750    low-density lipoprotein particle receptor binding	ECO:0000353  IPI	activated_by (CHEBI:64646) more...
UniProtKB:Q00610	CLTC	GO:0150093    amyloid-beta clearance by transcytosis	ECO:0000315  IMP	has_input (UniProtKB:P05067:PRO_0000000093) more...
UniProtKB:Q07954	LRP1	GO:0006898    receptor-mediated endocytosis	ECO:0000315  IMP	has_input (UniProtKB:P05067:PRO_0000000093) more...
UniProtKB:Q13492	PICALM	GO:0072583    clathrin-dependent endocytosis	ECO:0000315  IMP	has_input (UniProtKB:Q07954) more...
UniProtKB:Q13492	PICALM	GO:0050750    low-density lipoprotein particle receptor binding	ECO:0000353  IPI	activated_by (CHEBI:64646) more...
UniProtKB:Q15109	AGER	GO:0016324    apical plasma membrane	ECO:0000314  IDA	part_of (CL:0002144) more...

Figure 1 A selection of Gene Ontology annotations. This list of Gene Ontology annotations was downloaded from the QuickGO browser (37). All of these annotations, based on the experimental data presented by Zhao et al. (20), were created by the UCL Functional Gene Annotation group. The annotations were filtered by 'PMID:26005850'. The columns, in order from left to right, are as follows: Symbol, HGNC-approved gene symbol; GO term, GO term identifier and name; Evidence, one of the many Evidence and Conclusion Ontology (ECO) codes (38) associated with each GO annotation to indicate the type of experiments that support the annotation (IDA, Inferred from Direct Assay; IMP, Inferred from Mutant Phenotype; IPI, Inferred from Physical Interaction); Annotation Extension, additional information about the annotations, for example, the location of the function (occurs_in CL:0002144, capillary endothelial cell), or the entity that activates the function (activated_by CHEBI:64646, amyloid-beta polypeptide 40).

disease or phenotype will require resources, such as GO, that describe the cellular roles of these genes.

The GO resource (8, 9) is maintained, curated, and made available through the concerted efforts of the GO Consortium, whose aim is to provide both an ontology of terms and gene product annotations. Consequently, the GO Consortium includes skilled biocuration scientists, ontology editors, and software engineers. The ontology enables the description of attributes of gene products, including proteins, macromolecular complexes, and noncoding RNAs, in three key domains: *molecular function*, *biological process*, and *cellular component*. Fully defined computer-readable GO terms are used by the GO Consortium annotation groups, including our Functional Gene Annotation group at UCL, to create links (annotations) between GO terms and gene products across many species, based on published scientific findings, providing a computable and traceable summary of individual experiments. GO terms are used to describe gene products by their molecular functions (e.g., *scavenger receptor activity*), the biological processes they contribute toward (e.g., *microtubule cytoskeleton organization*), and their subcellular locations (e.g., *extracellular region*). For instance, GO curators have contributed 46 GO annotations based on experimental evidence presented by Zhao et al. (20), of which a selection is presented in Figure 1.

The gene product annotations contributed by GO biocurators are regularly submitted to the GO knowledgebase, where the most current and complete collection of GO terms and annotations is publicly available to all users (9).

Providers of bioinformatics tools, such as g:Profiler (21), Cytoscape (22), or DAVID (23), import GO data into their tools for use in enrichment analyses of large datasets. Therefore, the association of GO terms with gene product records (to create annotations) and the use of GO annotation data in analysis tools together enable groups of similarly annotated gene products, within an “omics” dataset, to be identified as significantly enriched (18, 24, 25). Thus, dysregulated pathways, functions, and macromolecular complexes can be identified within high-throughput datasets. However, GO annotation is a continuously ongoing initiative with certain biological aspects annotated more thoroughly than others. Insufficient annotation of key biological processes and pathways relevant to dementia can hinder the interpretation of outcomes from GWA studies, microarray, and proteomic approaches to dissect AD and other AD-relevant diseases (26). Consequently, these analyses may identify partial protein networks or only general GO terms as enriched in the dataset, for example *mitochondrion* (27) and *calcium-mediated signaling* (4). Having recognized this deficit, the Functional Gene Annotation group at UCL have, for the last 5 years, focused on the annotation of gene products relevant to Parkinson’s and Alzheimer’s diseases (26, 28, 29). This has led to substantial improvements in the representation of processes such as mitophagy, amyloid precursor protein processing, oxidative stress, and tau-associated processes.

Improving the GO to represent dementia-relevant processes

The GO is structured as directed graphs, with each GO term having a unique term name, for example, *phosphatidylcholine-sterol O-acyltransferase activity*, *proteasomal protein catabolic process*, or *high-density lipoprotein particle*, and a definition (Figure 2) as well as a computer-readable numerical identifier. In addition, the ontology is a dynamic resource, with the ontology itself continually being expanded and refined to capture current knowledge. Although GO terms exist which describe most gene products’ processes, functions, and locations, many of these terms are very general and are not specific enough to fully describe the role of AD-associated gene products. The UCL Functional Gene Annotation group has begun to address this issue through the development of the ontology to provide more specific and descriptive GO terms, by improving the existing term definitions and by revising the existing ontology structure (26, 28, 29). The association of these more specific GO terms prevents the loss of valuable descriptions of gene products, based on experimental information, that would have been unavailable if the more general GO term had been applied. For example, we have improved the ontology domains describing the unfolded protein response (UPR) (28), autophagy (29), and neuron projection development (26). These improvements have led to an expansion of the number of GO terms describing these processes, as well as revision of relationships between terms within the ontology. All of these biological processes have relevance to AD as well as Parkinson’s disease and other neurological conditions.

Although GO terms are categorized into three key domains, as introduced above, revisions in one domain are often done in conjunction with another domain describing the same biological niche. For instance, our work on *neuron projection development* (26), a biological process GO term, resulted, first, in

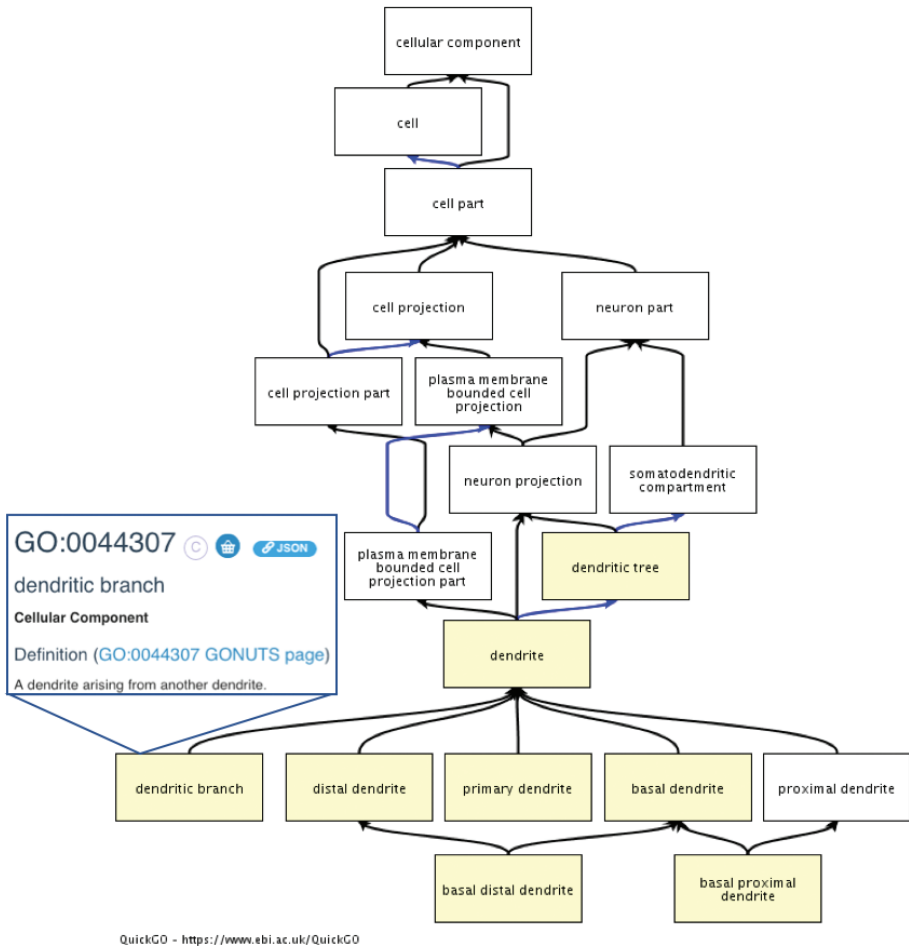


Figure 2 A selection of the dendrite Gene Ontology graph. This figure was generated by the QuickGO browser (37) and shows the *is_a* (black arrows) and *part_of* (blue arrows) hierarchy of just a small number of terms within the *dendrite* branch of the ontology; currently, the dendritic GO domain has 36 terms. The general term *dendrite* is used to group different types of dendrites, for example, *primary dendrite* and *distal dendrite* are both more descriptive child terms of *dendrite*. The definition (as displayed in QuickGO) of one of the GO terms, *dendritic branch*, is also included. The yellow highlighted terms were contributed by the UCL Functional Gene Annotation group.

contribution of new, more descriptive, GO terms, such as *neuron projection arborization*, *dendrite morphogenesis*, or *dendrite arborization*. Yet, simultaneously, we also improved the *dendrite* branch of the cellular component GO aspect, as shown in Figure 2. Similarly, curation of the autophagy (29) processes led to not only generation of highly specific *biological process* GO terms, but also resulted in revisions of related *cellular component* terms, such as *autophagosome*, *amphisome*, or *late endosome*. Thus, enhancing one ontology branch within a specific domain

of GO is often done in conjunction with improvements in other branches and domains, consequently enriching the ontology resource more broadly.

The neuroscience research community will also have benefited from curation work of the SYSCILIA research Consortium, which involved revisions and improvements to cilia-related biology in GO, resulting in contribution of 50 new GO terms (30). Among others, ciliary dysfunction has been shown to affect Sonic hedgehog signaling in the brain, a pathway with demonstrated implications in Alzheimer's (31), Parkinson's (32), and Huntington's (33) diseases. Consequently, revisions and new contributions to the ciliary niche will have improved the representation of cilia biology in GO and, therefore, resulted in more informative analyses of neurological datasets with changes in ciliary proteins.

Another ongoing biocuration initiative with direct relevance to elucidation of Alzheimer's data is the SynGO project and the associated synaptic GO portal (34). SynGO is a collaboration between the Stanley Center for Psychiatric Research at the Broad Institute (Cambridge, MA, USA), the Center for Neurogenomics and Cognitive Research at the Vrije Universiteit (Amsterdam, The Netherlands), and the GO Consortium, thus combining the efforts of experts in synapse biology and GO biocurators to generate the best possible representation of synapse biology in GO.

The UniProt Knowledgebase (EMBL-EBI, Cambridge, UK) has also been improving the representation of Alzheimer's data in their resource, an initiative which includes GO annotation as well as IntAct (13) curation of protein–protein interaction and/or curation of disease variants, as a part of a project funded by the National Institutes of Health (USA). The ultimate goal of this project is to create an online AD portal with thoroughly annotated and easily searchable information on the disease and biological pathways impaired in dementia (35). Importantly, all biocuration scientists, aiming to improve the representation of dementia-relevant biology in GO, work together under the auspices of the GO Consortium, thus ensuring GO annotation consistency and quality.

The creation of GO annotations

There are two major approaches that rely on concerted efforts of skilled biologists and software engineers (36), which result in high-quality GO annotations: manual techniques that depend on the knowledge and expertise of biocuration scientists and computational methods that generate annotations, for instance, based on sequence similarity algorithms. Every annotation is attributed to an identified reference, often a publication identifier, such as PMID, and each annotation must indicate what kind of evidence supports the association between the gene product and the GO term (Figure 1).

The computational annotation approach is a high-throughput and efficient method of associating high-level terms to a large number of gene products across all genomes. These annotations are often assigned, based on specific protein domains with known functions or cellular locations, or based on orthology to a manually curated gene product. However, to provide more specific annotations, GO biocurators read the published scientific literature and use the published data to manually associate highly descriptive GO terms to gene products. Consequently, complete, highly detailed annotation of the processes and networks

that a single gene product is involved in may take a considerable time. Depending on the number of published papers describing the gene product, a curator will annotate an average of 1–3 experimental papers per day.

Furthermore, as there is no limit to the number of GO annotations that can be assigned to a gene product record, it is possible to describe the many different roles that the gene product may have, depending on the cell type it is expressed in, the developmental stage of the organism, and the environmental stimuli the cell is responding to. The UCL Functional Gene Annotation group takes an unusual approach to annotation, in that we usually focus on annotation of a specific process involving a number of gene products, such as amyloid precursor protein processing, rather than working through an unrelated set of gene products. This enables us to develop a better understanding of the biology and apply a consistent annotation approach to all gene products involved in the process, thus providing depth to the annotations. In addition, at UCL we annotate full papers, whereas some groups will curate only the information in a paper that is relevant to a specific prioritized gene. This approach enables us to provide annotations to a large number of relevant gene products, involved in a specific process, which may not be included in the list of annotation priorities. For example, after completing the annotation of 84 proteins and protein complexes, prioritized for annotation as part of the amyloid-beta or tau projects, we had, in total, annotated 526 proteins and complexes (26).

Furthermore, in response to the research community's needs (39), at UCL our annotation procedure involves inclusion of annotation extensions (40) to capture information about the cell and tissue types in which a particular gene product is active, as well as the specific target of a protein or a microRNA. These detailed annotations provide critical knowledge for biomarkers, diagnostics, and drug discovery and will be of considerable value to the research community and allow users of GO to query a variety of data. For example, a GO user could investigate all targets of a particular protein ubiquitin ligase, or, more specifically, search for all proteins involved in catabolic pathways in microglial cells. Unfortunately, although biocurators have been contributing the annotation extension data for over 6 years, there are no tools that are using this data, and only a few browsers display it (9, 41). In the near future, the annotation extension information will be ported to Gene Ontology Causal Activity Modeling (GO-CAM) (42).

Gene products annotated using GO

Historically, GO was used specifically for annotation of proteins. Recently, the GO Consortium has extended the range of gene products that are annotated; rather than only annotating proteins some members of the GO Consortium are now annotating protein complexes (43) and microRNAs (26, 44, 45). To curate these entities, it has been necessary to create new identifiers (43, 46) and develop strict guidelines to ensure that a consistent annotation approach is applied. For example, there are many papers describing the coregulation of a microRNA or a set of microRNAs with the transcription of a panel of mRNAs and implying that these microRNAs therefore regulate the coregulated mRNAs. Such data do not comply with quality standards implemented by the GO Consortium and are not being captured as GO annotations (44). Instead microRNA GO annotations are

contributed based on more precise low-throughput functional experiments, involving microRNA mimics or knockdown, followed by an assessment of the expression of a panel of specific mRNAs. In addition, reporter assay data, confirming a direct interaction between a microRNA and an mRNA, are being captured using specific GO terms (e.g., *mRNA binding involved in posttranscriptional gene silencing*). Furthermore, in these cases the annotation extension will be used to capture the identifier of the targeted mRNA. The resulting interaction data are not only available in the GO annotation files, but also within the EBI-GOA-miRNA dataset from the PSICQUIC web server (45).

The impact of improving the GO resource on data interpretation

By creating an open access dataset of high-quality annotations, which describe the cellular role of those proteins and microRNAs that contribute to pathways dysregulated in AD, the GO provides an invaluable resource for researchers. GO annotations are incorporated into over 50 functional analysis tools, the majority of which are freely available, such as g:Profiler (21), PANTHER (47), Cytoscape (22), and DAVID (23), but others are subscription based, such as Ingenuity Pathway Analysis (QIAGEN Bioinformatics) (48) and MetaCore (Clarivate Analytics) (49). These tools, and many other functional analysis tools, are used by researchers to analyze a variety of high-throughput data, including transcriptomic (4, 50–53), proteomic (5, 54, 55), and GWA (6, 14, 56) data. In addition, existing pipelines ensure that the GO annotations are included in widely used public resources such as UniProt (57), NCBI Gene (58), Ensembl (59), RNAcentral (46), and even Wikipedia. GO annotations associated with individual protein, RNA, or macromolecular complex records are used by researchers to extract a synopsis of the cellular role of a gene product. These gene summaries have many uses in research, for example, they can help guide researchers to the most likely candidate gene associated with a risk locus (14, 18). However, it is the use of GO for the interpretation of data from high-throughput analyses where this resource can be exploited to the full.

The quality of the GO annotations used in the analysis of large biological datasets will determine how informative the outcomes of this analysis will be. Without highly descriptive annotations the analysis can only identify GO functions, processes, or location that are not very specific, such as *site of polarized growth*, *wound healing*, and *cell migration* (54). The identification of more informative enriched terms is dependent not only on the presence of highly descriptive GO terms describing biological knowledge, but also on the association of these terms with a sufficient number of gene products to enable the term to be detected as significantly enriched. A recent meta-analysis of late-onset AD, that included over 94,000 individuals, identified over 100 new risk loci, associated with amyloid-beta and tau processes, as well as immune response pathways and lipid processing (14). This meta-analysis took a wide range of approaches to identify new risk loci, one of which was the use of the pathway analysis software, MAGMA (60), and GO annotation files (36). The GO terms *plasma lipoprotein particle assembly*, *reverse cholesterol transport*, *regulation of amyloid precursor catabolic process*, and *activation of immune response* were identified as processes with relevance to AD. The first three of these GO terms provide a good description of the processes involved, whereas the last term *activation of immune*

response is too general to really give an indication of the mechanism involved. This is likely to reflect the considerable investment in annotation of cardiovascular (18, 61, 62) and nervous system genes (26, 28), and the lack of focused annotation of the immune system. In addition, papers describing the immune system are often highly detailed and more challenging for biocurators without a background in immunology to fully annotate (63). Thus, the annotation of immune-associated pathways does not reflect the volume of literature and knowledge in this domain.

Another study aimed to elucidate protein expression in different brain regions in Alzheimer's cases relative to controls to provide a broader understanding of molecular pathways impaired in dementia (64). In this study, GO analysis was used to identify the *biological processes* that had the largest numbers of differentially expressed proteins associated with them. A wide variety of processes were identified, in this way, including *regulation of apoptosis* associated with the hippocampus and *protein transport* associated with the cerebellum and cingulate gyrus, therefore allowing researchers to identify new routes for potential therapeutic interventions.

GO term enrichment analysis has also been implemented in pilot studies aiming to identify biomarkers associated with dementia, which can be detected using noninvasive methods in easily accessible bodily fluids, such as blood (65) and urine (66). For instance, Chouliaras et al. (65) used GO enrichment together with KEGG pathway analysis to demonstrate the relationships between the identified blood biomarkers with neurological processes and neuronal components. Significantly enriched GO terms included *regulation of amyloid-beta formation* and *amyloid-beta binding*, *main axon*, and *ion channel complex*, whereas KEGG pathways included *glutamatergic synapse* and *Alzheimer's disease*, thus confirming their relevance to cognitive impairments.

Similarly, Watanabe et al. (66) used GO term enrichment and KEGG pathway analyses to delineate the roles of proteins differentially expressed in urine of Alzheimer's patients relative to healthy controls to identify a urine biomarker signature, which could be used for noninvasive diagnostic purposes. *Lipoprotein metabolism*, *heat shock protein 90 signaling pathway*, and *matrix metalloproteinase signaling pathway* as well as *redox regulation by thioredoxin* were among the molecular pathways with the highest enrichment scores, providing evidence for impairment of vascular processes key to the development of dementia (66). In addition, Watanabe et al. (66) also supplemented their functional GO and KEGG analyses with an *interrelation* network analysis to determine, which of the proteins differentially expressed in the Alzheimer's urine samples interact with each other (either directly or via an intermediate). This network analysis of molecular relationships enabled these researchers to further elucidate which GO biological processes and KEGG pathways should be prioritized in future studies and whether they correlate with and confirm other findings. An alternative approach to using GO annotations is to visualize them on an interaction network. This provides the researcher with an overview of the contribution that a network, or part of the network, makes to a particular process or the cellular location of the interacting entities, as shown in the example in Figure 3. Thus, the use of multiple, interoperable, annotation resources provides the opportunity to fully exploit and interrogate individual datasets.

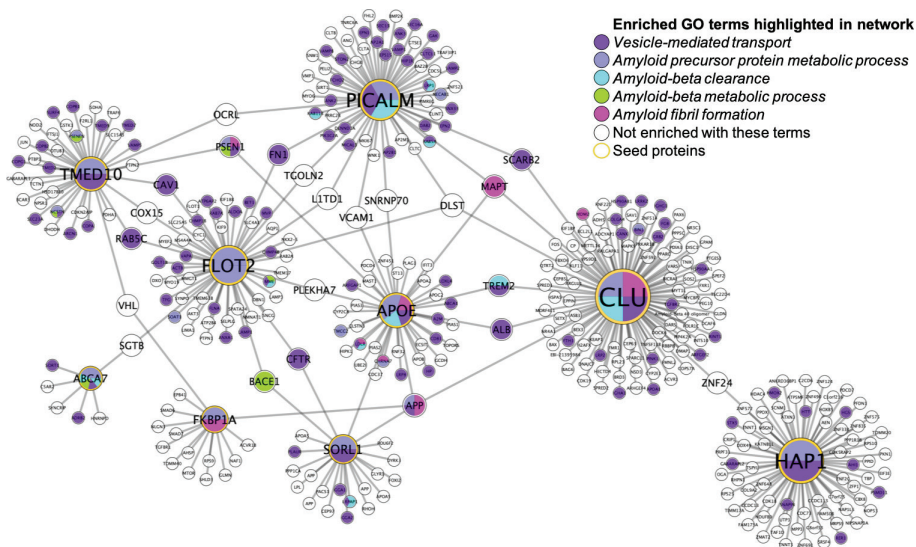


Figure 3 Network of proteins identified in Alzheimer's disease meta-analysis. Nine proteins identified in an Alzheimer's disease meta-analysis (14) due to their association with the GO term "regulation of amyloid precursor protein catabolic process" were used to seed an interaction network using Cytoscape (22) and five files available on the PSICQUIC web server (67) (IntAct, BHF-UCL, UniProt, MINT, and EBI-GOA-non-IntAct). The seed proteins are outlined in yellow. The network was analyzed using Golorize (68), BiNGO (69), and GO ontology and annotation files (36), as described in Denny et al. (29) (downloaded March 29, 2019). The proteins associated with a selection of the enriched GO terms (or one of their child terms, including regulation child terms) are shown in the network.

The above examples demonstrate how continuous, systematic, and consistent improvements to the GO resource, including contribution of new descriptive GO terms, and their association with gene products in the form of GO annotations, impact more informative outcomes of analyses of high-throughput datasets. The functional analyses relying on GO allow researchers to, first, plan and design further studies leading to a better understanding of the molecular mechanisms underlying dementia, and, second, to develop noninvasive diagnostic methods, which collectively will help to improve the management and treatment of AD.

CONCLUSION

The GO resource (8, 9, 70) adds value to published experimental data by creating computer-readable annotations that describe specific functions of a gene product, such as protein, complex, or noncoding RNA, and the biological processes and pathways it contributes to. This benefits all biological areas, including the AD field, on which the UCL Functional Gene Annotation team has recently been focusing their biocuration efforts. Gene annotations using GO terms enable groups of gene products, with similar cellular roles or locations in the cell, to be

easily identified within a dataset, such as a list of differentially expressed genes from AD cases. Thus, dysregulated pathways, functions, and macromolecular complexes can be identified within high-throughput datasets using GO annotation data and functional enrichment tools. GO annotation data are therefore needed for pathway construction, enrichment analyses and interpretation of large-scale datasets (3–5) and to inform biomarker selection decisions (27), and can also be used to identify novel drug targets or novel repurposing of drugs. Furthermore, the AD-focused and comprehensive efforts of the UCL Functional Gene Annotation team have improved and continue to improve the GO resource, enhancing its applicability to this neurobiological research domain and facilitating analyses and interpretation of AD *big data*.

Acknowledgments: The UCL Functional Gene Annotation group has been supported by Alzheimer's Research UK grants ARUK-NSG2016-13, ARUK-NAS2017A-1, and ARUK-NSG2018-003 and the National Institute for Health Research University College London Hospitals Biomedical Research Centre. We thank the many biocurators, editors, and other members of the GO Consortium who have contributed to the annotation of dementia-relevant gene products and the development of the Gene Ontology, especially Dr Rachael P. Huntley. The GO Consortium is supported by a grant from the National Human Genome Research Institute (grant no. U41 HG002273 to P.D. Thomas, P.W. Sternberg, C.J. Mungall, J.M. Cherry, and J.A. Blake).

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Using Proteomics to Understand Alzheimer's Disease Pathogenesis

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch3>

Abstract: Our current understanding of the molecular changes that drive Alzheimer's disease (AD) pathogenesis is incomplete. Unbiased, mass-spectrometry-based proteomic studies provide an efficient and comprehensive way to quantitatively examine thousands of proteins at once using microscopic amounts of human brain tissue. Recently, the number of proteomic studies that examine protein changes in AD brain tissue has been increasing. This chapter reviews the different proteomic approaches currently being used to identify pathological protein changes in AD brain tissue including bulk tissue studies that examine protein changes throughout the progression of AD, studies of the insoluble proteome in AD, studies using proteomics to examine selective vulnerability in AD, studies of the amyloid plaque and neurofibrillary tangle proteome, studies of the synaptic proteome, and studies of the interactome of beta amyloid and tau. Combined, these complementary proteomic approaches provide increased understanding about the protein changes that occur in the AD brain. Results from these proteomic studies provide an excellent resource for future hypothesis-driven targeted studies and will help identify new biomarkers of disease and new drug targets for AD.

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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Keywords: Alzheimer's disease; interactome; mass spectrometry; neuropathology; proteomics

INTRODUCTION

Alzheimer's disease (AD) is a complex, multifactorial disease. Various genetic, environmental, and lifestyle risk factors have been associated with the development of AD; however, none of these have been shown to definitively cause late onset AD (1). AD is diagnosed at autopsy by the presence of characteristic neuropathology: amyloid plaques and neurofibrillary tangles (NFTs), which primarily consist of aggregated beta amyloid ($A\beta$) and hyperphosphorylated tau, respectively (2). The development of these neuropathological lesions is associated with increased neuroinflammation, synaptic loss, neurodegeneration, and ultimately the development of cognitive impairment that clinically characterizes AD. Imaging and biomarker studies suggest that AD begins ~20 years before the development of dementia, resulting in a long preclinical stage of disease before clinical symptoms are apparent (3).

There are still significant gaps in our understanding about the molecular mechanisms that underlie the pathogenesis of AD. For example, we do not know what causes AD, what factors drive the development of neuropathology, what factors cause the development of cognitive impairment, or what factors are responsible for the considerable heterogeneity in the rate of progression in people with AD. A greater understanding of all of these factors is essential for the development of effective therapeutics and discovery of new biomarkers for AD. New therapeutics are particularly needed for AD as the previous record for AD clinical trials has been very poor: 99.6% of AD clinical trials have failed, and currently, no disease-modifying treatment is available. This high failure rate has been attributed to various factors including starting treatment too late in the disease process, having the wrong drug targets, or relying too heavily on results from preclinical studies that use animal models of AD that poorly reflect human disease (4–6).

THE BENEFITS OF USING PROTEOMICS TO STUDY PROTEIN CHANGES IN AD BRAIN TISSUE

Traditionally, studies examining the molecular mechanisms that drive AD pathogenesis have used a targeted, hypothesis-driven approach that focuses on select proteins of interest. This approach has uncovered many of the major players involved in AD pathogenesis, most notably identifying beta amyloid ($A\beta$) as the major protein present in amyloid plaques (7, 8), identifying tau as the major protein present in NFTs (9), and identifying apolipoprotein E (apoE) as the most significant genetic risk factor for late onset AD (10, 11). However, using a targeted approach precludes the discovery of novel disease-associated proteins and limits the ability to understand these protein changes in the broad context of AD.

Unbiased, hypothesis-free “omics” studies such as genomic, transcriptomic, epigenetic and proteomic studies offer a comprehensive, highly efficient way to identify genes or proteins that are involved in the pathogenesis of AD. The high-throughput nature of “omics” studies means that they can be performed using microscopic amounts of human tissue samples, which are essential to study when examining diseases that are unique to humans, such as AD (12). Genomic and epigenetic studies have successfully identified new genetic risk factors for late-onset AD and have provided the basis for new hypothesis-driven studies examining how these genetic variants and epigenetic changes are involved in AD (13–16). Unbiased, mass-spectrometry-based proteomic studies of human AD brain tissue are essential to complement these genomic studies, particularly given that proteins are the druggable targets in AD. Furthermore, there is a poor correlation between RNA expression and protein levels in AD brain tissue; therefore, transcriptomic or genomic studies do not provide a complete picture of the pathogenic changes in the AD brain (17). Using mass-spectrometry-based proteomics to study the pathogenesis of AD has many advantages including the following: thousands of protein differences can be quantified simultaneously using microscopic amounts of brain tissue, the unbiased nature of these studies permits the discovery of novel proteins involved in AD pathogenesis, and proteomics can detect post-translational modifications on proteins (e.g. phosphorylation, oxidation, and ubiquitination) that are known to have an important pathological role in AD. The large amount of data generated in proteomic studies provides a comprehensive, bird's eye view of all protein differences that occur in AD, which can provide insight into the molecular mechanisms that cause AD at a network/systems level, which is particularly useful when studying complex diseases like AD (18, 19). Mass-spectrometry-based proteomic studies have been limited in the past by technical and financial constraints; however, these factors have recently become less restrictive, and consequently, the number of proteomics studies using AD brain tissue has increased.

AD PROTEOMIC STUDIES USING BULK TISSUE HOMOGENATES

The majority of proteomic studies examining AD brain tissue have defined the proteomic changes between AD and age-matched, cognitively normal controls using bulk tissue samples. In these studies, proteomics is used to compare protein expression between AD and controls in brain homogenate, usually limited to one vulnerable brain region. Early liquid chromatography-mass spectrometry (LC-MS) studies generated preliminary findings about protein differences between AD and control brains, but were typically restricted by small sample sizes and therefore struggled to detect protein differences after correcting for multiple comparisons (20–26). More recent studies have included a larger number of samples, which are consequently sufficiently powered to detect hundreds of protein differences in AD brains (17, 27–34). Encouragingly, meta-analysis of these recent studies shows that many of the significantly altered proteins in AD brains are consistent, leading to increased confidence that these altered proteins are relevant to the pathogenesis of AD.

The most comprehensive studies have been conducted by researchers at Emory University, USA (17, 30, 31). Their studies primarily examined protein differences in the frontal cortex throughout the progression of AD, specifically comparing protein levels in advanced AD, asymptomatic AD (also referred to as preclinical AD), and age-matched cognitively normal subjects. Combined, these studies identified hundreds of protein differences present at different stages of AD. They found that the number of protein differences steadily increased with disease progression, suggesting that the number of protein differences is reflective of increased dysfunction involving more pathways as AD progresses. Their analysis allowed the identification of subsets of proteins that were exclusively altered in the symptomatic phase of AD and those that were altered prior to the onset of clinical symptoms. For example, they showed that proteins involved in synaptic function and synaptogenesis progressively decreased throughout AD, starting before clinical symptoms were present. They also showed that altered RNA metabolism and increased inflammation were present in AD brains in the earliest stages of disease prior to cognitive impairment. In contrast, astrocyte and microglia proteins increased in late stage AD and showed a strong correlation with the number of NFTs present. A consequent study by the same group specifically focused on the protein differences present in AD cases stratified by ApoE genotype (33). ApoE is the major genetic risk factor for late onset AD (35, 36). The three alleles of ApoE (apoE2, apoE3, and apoE4) confer different risk for AD: apoE4 increases risk for AD and apoE2 decreases risk for AD. Their proteomic results suggested that apoE may confer risk in AD through a combination of effects on inflammation, metabolism, and cerebral vasculature, and using their proteomic approach, they were able to pinpoint the specific proteins involved (33).

One important factor to be mindful of when interpreting and comparing proteomic studies is the type of tissue lysis method used prior to mass spectrometry. Different lysis methods enrich for different populations of proteins or even different pools of the same protein. For example, soluble and insoluble forms of the same protein may require different lysis methods for detection. Therefore, the use of various lysis methods can complicate meta-analysis of multiple proteomic studies as the same proteins are not always detected by each lysis method. However, one advantage of using varied lysis methods is that combined analysis of proteomic studies that use various lysis methods provides a richer view of molecular changes in the AD brain. For example, some studies have specifically examined differences in the insoluble proteome in AD (21, 25, 30, 37), which enriches for proteins that are associated with the insoluble plaques or NFTs in AD, as well as other proteins that are independently prone to insolubility in the AD brain. Of these studies, Hales et al. provide the most comprehensive analysis of insoluble protein changes in AD (30). Interestingly, they showed that the number of differentially expressed proteins in the insoluble fraction increased with disease severity and that many of these insoluble proteins were involved in mitochondrial function, which is known to be decreased in AD (30). Other recent studies have used proteomics to answer specific questions about which proteins are primarily affected by post-translational modifications in AD. Two recent studies have used enrichment strategies to identify all proteins that are phosphorylated and ubiquitinated in AD (38, 39). These studies showed that the number of ubiquitinated proteins was much higher in AD brains than in control brains, which is consistent

with the accumulation of insoluble and misfolded proteins during AD and reflects the proteolytic stress present in AD (38). Examination of phosphorylated proteins confirmed that tau was the most highly phosphorylated protein in AD in comparison to controls and also identified an additional 142 proteins that were phosphorylated to a greater extent in AD brains (39).

THE USE OF PROTEOMICS TO UNDERSTAND SELECTIVE VULNERABILITY IN AD

One of the most striking features of AD is that specific brain regions are particularly vulnerable to the development of amyloid plaques, NFTs, and neurodegeneration, while other regions are comparatively resistant to pathology. Why this occurs is still unknown. However, various factors have been proposed to contribute to vulnerability including: gene expression, long axonal projections or large neuronal size, being an excitatory neuron, containing low levels of calcium buffering proteins, or containing high levels of metastable subproteome proteins that are prone to aggregate in times of stress (40–42). Defining a particular brain region as vulnerable or resistant in AD can be complex, as it depends on the neuropathological factor you use to define vulnerability. This is important because some brain regions are preferentially vulnerable to developing amyloid plaques, while others are preferentially vulnerable to developing NFTs or neurodegeneration, and the presence of these different types of neuropathology does not always correlate. In general, regions that are particularly vulnerable to the development of AD include the hippocampus, entorhinal cortex, basal forebrain, and locus coeruleus. Comparatively resistant regions include the cerebellum and occipital cortex.

Transcriptomics studies suggest that there is likely a distinct protein signature of vulnerable neurons in AD (43); however, this has not yet been comprehensively examined at the protein level. Proteomic studies of selective vulnerability in AD are complex as additional variables need to be considered in their experimental design. For example, basal protein differences between different brain regions have to be accounted for when interpreting protein differences that appear to be associated with increased vulnerability to AD. This is particularly important when comparing brain regions that are morphologically different such as the cerebellum and the hippocampus. Disparate basal protein expression between brain regions complicates interpretation of results as protein differences could be due to either basal brain region differences or AD associated differences. Accounting for these variables is possible, but ultimately results in large, complex studies that require a large number of samples to perform all analyses with sufficient power.

The majority of bulk tissue proteomic studies have only analyzed one or two brain regions, usually focusing only on vulnerable brain regions, meaning that they cannot be used to examine the protein changes associated with selective vulnerability in AD. Two recent studies have aimed to fill this knowledge gap. Xu et al. (44) performed the most extensive analysis of proteomic changes in the AD brain that are associated with selective vulnerability. They compared protein expression in three highly affected regions (hippocampus, entorhinal cortex, and

cingulate gyrus), two lightly affected regions (sensory cortex and motor cortex), and one comparatively unaffected region (cerebellum). As expected, the majority of protein differences between AD and control brains were observed in the highly affected regions, and these protein changes were reflective of increased innate and adaptive immune responses in the brain and increased apoptosis. The fewer protein differences in the lightly affected regions appeared to be reflective of early stage pathology, suggesting that the same molecular changes that drive pathogenesis of AD eventually spread to these lightly affected regions. Intriguingly, the cerebellum actually showed a large number of protein differences between AD and controls, even more so than the lightly affected regions. However, these protein differences appeared to be reflective of potentially protective molecular changes such as increased expression of proteins associated with growth factors, increased oxidative defense proteins, and decreased transfer RNA synthetases. Mendonca et al. (45) also performed a comprehensive study looking at the proteomic differences in brain regions preferentially vulnerable to tau pathology in AD. They compared the proteome in AD and controls in two brain regions that are highly vulnerable to the development of NFTs (parahippocampal cortex and entorhinal cortex) and two brain regions that are moderately vulnerable to the development of NFTs (temporal cortex and frontal cortex). In doing so, they generated a complex dataset that will be useful for future data mining studies examining the protein changes associated with tau pathology in AD. In the future, expanding these studies to include comparisons between multiple brain regions at multiple stages of AD will be useful for defining the protein differences that underlie selective vulnerability in AD and to definitively determine whether mildly affected regions show molecular changes that are similar to those in early stage AD.

PROTEOMICS OF NEUROPATHOLOGICAL FEATURES PRESENT IN AD

Other groups, including my own, have recognized the importance of performing localized proteomic studies that specifically focus on disease-associated neuropathological features or specific cell populations. Using a localized approach that focuses specifically on areas highly affected by disease has the potential to reveal protein differences between AD and controls that are particularly relevant to pathogenesis. We have focused our efforts on using a localized proteomics approach to determine the proteome of amyloid plaques, NFTs, and vulnerable neurons. In this approach, neuropathological features or vulnerable neuron populations are microdissected from sections of human brain tissue, and their protein composition is analyzed using mass spectrometry (46–48). A key advantage of our approach is that it can be performed using formalin-fixed paraffin-embedded (FFPE) tissue. This is important because the majority of human tissue specimens available for research are FFPE blocks of tissue that are collected and used during autopsy. Therefore, developing a method that is compatible with FFPE tissue greatly increases the feasibility of human tissue studies, particularly those using rare or unique cases. A second key advantage of our method is that it can be performed using microscopic amounts of tissue. We have successfully performed

proteomics using as little as 1.5 mm² of tissue, which is the equivalent of approximately 550 amyloid plaques or 4000 NFTs. This number of plaques and tangles can typically be collected using <4 tissue sections, showing just how little tissue is required for these studies. But the most important aspect of our approach is that we can quantify over a 1000 proteins at once using these microscopic tissue samples, which therefore provide a comprehensive analysis of the proteins that are associated with neuropathological features in the AD brain and proteins that are associated with selective vulnerability of specific neuronal populations. For example, we showed that amyloid plaques consistently contained hundreds of proteins in addition to A β and that many of these were novel proteins that had not previously been associated with AD (49, 50). Importantly, we also showed that the protein composition of amyloid plaques was significantly different in people with rapidly progressive AD in comparison to typical sporadic AD, suggesting that different molecular mechanisms may underlie plaque development in different subtypes of disease. We also recently examined the proteome of NFTs and identified over 500 proteins in NFTs in addition to tau, many of which were novel (51). These examples show the power of an unbiased localized proteomics approach to efficiently identify hundreds of proteins that are associated with amyloid plaques or NFTs. These findings can be used as the basis for future targeted studies that aim to determine the mechanistic involvement of these proteins in AD.

One example protein that we discovered using proteomics and have since followed up on in a targeted study is secernin-1. Very little is known about the function of secernin-1, and no study has previously associated secernin-1 with AD. We identified secernin-1 as a novel amyloid plaque protein in our previous proteomic study of amyloid plaques (49). We have since performed a comprehensive neuropathological study of secernin-1 accumulation in early and late stage AD (52). Surprisingly, we found that secernin-1 abundantly and specifically accumulated in NFTs in AD and that its presence in amyloid plaques was limited to accumulation in the dystrophic neurites present in neuritic plaques. Co-immunoprecipitation showed that secernin-1 directly interacted with phosphorylated tau in AD brains, suggesting that it could have an important role in mediating the toxic actions of tau in AD. Intriguingly, secernin-1 colocalized with phosphorylated tau aggregates only in AD and not in other neurodegenerative diseases that also show the presence of aggregated phosphorylated tau including Pick's disease, progressive supranuclear palsy, and corticobasal degeneration. This suggests that secernin-1 could be a new potential biomarker that discriminates between AD and other tauopathies. These results show that localized proteomics studies are capable of identifying new biomarkers of disease and new potential drug targets. Secernin-1 is just one example protein from a list of many new potential candidates that we have identified in our proteomics studies that can be examined in future mechanistic studies.

A small number of other groups have also used a similar localized proteomics approach to study the proteome of neuropathological features or vulnerable cell populations/brain regions in AD. Two small studies have examined the proteome of human amyloid plaques (53, 54), and two small studies have examined the proteome of human NFTs (55, 56). Three other studies have examined the proteome of cerebral amyloid angiopathy (CAA), which is present when A β pathologically accumulates in blood vessels (57–59). Combined, all of these studies provide preliminary data that have hinted at new proteins that are associated

with these neuropathological features; however, the small number of cases included in these initial studies means that further studies are needed to provide a comprehensive understanding of the proteome of amyloid plaques, NFTs, and CAA. Future studies examining larger numbers of cases that are stratified by AD subtype will be very informative in helping to identify proteins that have a particular interaction with neuropathological features and to determine whether proteins associated with these neuropathological features are different between subtypes of AD.

PROTEOMICS OF SYNAPTIC FRACTIONS IN AD

Synapse loss is an early feature of AD that closely correlates with cognitive impairment (60–63). Understanding the synaptic protein changes in AD could help us understand what is driving this process. Multiple studies have been completed that have analyzed the proteome of synaptosomes and post-synaptic density in control human brains, which have been nicely combined in a recent meta-analysis (64). However, a comprehensive analysis of the synaptic proteome in AD has not yet been performed. Preliminary results have been generated that analyzed the proteome of synaptosomes (65, 66) or post-synaptic density fractions (67). However, the small sample sizes used in these studies (between $n = 2$ and $n = 6$) mean that their findings are not yet definitive. Other studies have used their bulk tissue homogenate results to look specifically at synaptic protein changes (34, 68); however, these results could potentially miss differences in low abundance synaptic proteins. To date, all studies examining synaptic protein differences in AD have compared advanced AD and controls. Given that synaptic loss is an early feature of AD, it would be particularly useful to determine the protein changes that contribute to synapse loss in either mild cognitive impairment or preclinical AD. Larger studies examining differences in the synaptic proteome in early AD are currently ongoing in the field, and these will likely provide a greater overview of the specific protein changes that contribute to synaptic loss in AD. Future results detailing the synaptic protein differences in AD will be very interesting given that it has been recently suggested that synaptic proteins in the cerebrospinal fluid may also be excellent new biomarkers for early AD (64, 69).

ANALYSIS OF THE A β OR TAU INTERACTOME IN AD

Another useful proteomics approach to study AD pathogenesis is using affinity purification-mass spectrometry to identify the proteins that interact with toxic A β or tau species in AD. In this approach, particular species of A β or tau are isolated from human brain samples using antibodies. Proteins that interact with A β or tau are isolated at the same time, and mass spectrometry is used to identify these interacting proteins. This is a powerful approach because it allows the efficient and comprehensive examination of all proteins that interact with A β or tau in an unbiased manner. It can also determine which proteins interact with particular species A β or tau, which is important as some species are more toxic than others.

Results from these studies have the potential to increase our understanding about how A β and tau are involved in the pathogenesis of AD and could lead to the discovery of new drug targets.

Despite A β being the predominant focus of AD research for decades, there is a surprisingly limited number of studies that have used affinity purification mass spectrometry to examine the A β interactome. One possible reason for this is that it is difficult to find an appropriate antibody that specifically recognizes A β and not its longer precursor protein (amyloid precursor protein; APP). Accordingly, a number of studies have instead examined the interactome of APP in mouse brain tissue (70, 71) and in cells expressing human APP (72, 73). However, despite this limitation, there have been two recent studies that have developed alternative ways to examine the A β interactome. The first study isolated aggregated A β complexes from human brain samples using a non-specific A β antibody (that also recognizes APP), but limited their downstream proteomic analysis to only those proteins present in the insoluble fraction, with the assumption that the resulting interacting proteins were limited to those present in insoluble A β -containing aggregates rather than APP (37). The second study used a more traditional approach of binding recombinant monomeric A β 42 or oligomeric A β 42 to beads that were then used to pull down interacting proteins from human brain samples (74). Combined, these studies identified over 100 proteins that interact with A β , including some proteins that preferentially interacted with oligomeric A β in comparison to monomeric A β . However, more studies are needed in the future that compare the interactome of different A β species (such as A β 40, A β 42, and pyroglutamate modified A β) and that determine the endogenous pathological interactions present in AD brain tissue, as these may be different than those present in artificial *in vitro* experiments.

To date, all studies examining the tau interactome have used total tau antibodies that identify proteins that interact with all tau species. Two studies have examined using human brain tissue (37, 75), while others have examined tau interactors in mouse brains (76–79) and in cells expressing human tau (80). These studies found that different isoforms or domains of tau regulate different protein interactions, identified the major protein families that tau preferentially binds to, and identified new potential drug targets for preventing tau toxicity. However, one limitation of these studies is that using a total tau antibody results in the identification of all proteins that interact with both physiological and pathological tau in the brain, therefore making it difficult to determine which interactions are specific to the pathological phosphorylated tau species present in AD brains. Therefore, we have recently completed the first study of the phosphorylated tau interactome in human AD brain samples (51). Our results showed that phosphorylated tau in AD brains preferentially interacted with neuronal proteins, which is consistent with the intraneuronal location of phosphorylated tau in AD. We found that phosphorylated tau particularly interacted with proteins associated with two of the main protein degradation systems in the cell: the ubiquitin–proteasome system and the phagosome–lysosome system. The specific proteins involved suggested that phosphorylated tau may be potentially interfering with degradation of proteins by the proteasome and may contribute to lysosomal dysfunction in AD via interference with vacuolar ATPase proton pumps that are responsible

for acidification of lysosomes. Impairment of both of these processes has been previously associated with AD (81–83); however, this is the first study to show that tau may be involved in this process. This is an example of the informative nature of interactome studies, showing that they can provide a complete and unbiased overview of the pathogenic brain changes that occur in AD that are directly linked to a specific toxic protein species.

Going forward, performing these studies in a systematic manner that directly compares the interactome of multiple A β or tau species will help determine which protein interactions are particularly important for disease progression. Determining these key interactions that drive toxicity and that drive the formation of plaques or NFTs will help identify new potential drug targets for AD.

CONCLUSION

In conclusion, proteomics studies using human tissue are very useful for increasing our understanding about the pathogenesis of AD. The combined proteomic results from studies described above provide a powerful resource for generating new hypotheses about the cause of AD. Unbiased, proteomic studies using AD brain tissue have been previously limited by concerns about cost, technical limitations, and the assumption that very large sample sizes are required to counteract the large inter-patient variability in AD. However, recent studies have shown that hundreds of significant protein differences can be detected using sample sizes as low as 5 when comparing AD and controls. Larger sample sizes appear to be required when comparing different stages of AD (e.g., preclinical AD vs. advanced AD) or different subtypes of disease (e.g., rapidly progressive AD vs. sporadic AD); however, even in these studies, 20 samples/group are sufficient to identify hundreds of protein differences between groups. These results show that discovery proteomic studies using AD brain tissue are feasible. Importantly, meta-analysis of proteomics studies using AD brain tissue shows that many altered proteins in AD brain tissues are consistent between studies, therefore also validating these findings.

Going forward, it will be useful to expand the scope of these previous studies. Focusing on localized proteomics changes, either in neuropathological features, vulnerable neuron populations, or synaptic fractions, has the potential to greatly increase our understanding about what protein changes drive the development of neuropathology or neurodegeneration in these particularly affected regions. Systematic examination of the proteins that interact with specific species of A β or tau will help identify how these two proteins cause toxicity in AD. Results from localized or interactome studies have the potential to identify new drug targets or biomarkers of disease that are directly associated with AD neuropathology. Determining the protein changes that occur throughout the progression of AD is also particularly important to examine in future studies: the ideal drug targets for AD are pathological changes that occur in the earliest stages of disease; therefore proteomic studies that characterize protein changes in preclinical AD or mild cognitive impairment should be a priority.

Combined, proteomic studies are capable of providing a roadmap of protein changes that are associated with AD. These studies pinpoint the protein networks

that are most involved in disease as well as the specific proteins that are involved. Overall, these studies provide an excellent resource for future hypothesis-driven targeted studies that will hopefully help identify new biomarkers of disease and will help in the development of new drugs for AD.

Acknowledgments: This work was supported by funding from Bluesand Foundation, Australia and Dementia Australia, Australia.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Common Proteomic and Genomic Contribution to Ischemic Brain Damage and Alzheimer's Disease

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch4>

Abstract: Ischemic brain damage is associated with the deposition of folding proteins, such as all fragments of the amyloid protein precursor and tau protein, in the intra- and extracellular spaces of neurons. In this chapter, we summarize the protein changes associated with Alzheimer's disease and their gene expression (amyloid protein precursor and tau protein) after cerebral ischemia and their role in the ischemic etiology of Alzheimer's disease. Recent advances in understanding the ischemic etiology of Alzheimer's disease have revealed dysregulation of *amyloid protein precursors*, *β-secretase*, *presenilin 1 and 2*, *autophagy*, *mitophagy*, *apoptosis*, and *tau protein* genes after ischemic brain injury. However, reduced expression of mRNA of the *α-secretase* in cerebral ischemia causes neurons to be less resistant to injury. In this chapter, we present the latest evidence that Alzheimer's disease-related proteins and their genes play a key role in brain damage with ischemia-reperfusion and that ischemic episode is an essential and leading provider of Alzheimer's disease development. Understanding the underlying processes of linking Alzheimer's disease-related proteins and their genes in brain ischemia

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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injury with the risk of developing Alzheimer's disease will provide the most significant goals for therapeutic development to date.

Keywords: Alzheimer's disease; amyloid; brain ischemia; secretases; tau protein

INTRODUCTION

Newer studies show that brain ischemia with reperfusion can be associated with a fully developed Alzheimer's disease (1, 2). It is generally suggested that cerebral ischemia triggers Alzheimer's disease, and an ischemic change in the permeability of the blood–brain barrier additionally causes amyloid transportation from the blood to the brain, and this is the last element that causes the full-bloom sporadic Alzheimer's disease (3, 4). Ischemic human stroke and experimental ischemia-reperfusion brain injury are serious, life-threatening neuropathological episodes with severe complications such as post-ischemic cognitive impairment and physical disability (5–12). The evidence to date suggests that there is a potential compatibility among neuropathogenesis of brain ischemia and Alzheimer's disease. First, clinical observations have shown that Alzheimer's disease is a contributing factor to the development of ischemic brain damage and vice versa (13). Second, ischemic brain injury and Alzheimer's disease have the same risk factors like hypertension, hyperlipidemia, diabetes, and age. Third, experimental ischemia-reperfusion brain injury produces a stereotypical pattern of selective death/loss of neurons in the hippocampus with severe brain atrophy, which is similar to the neuropathology observed in Alzheimer's disease, indicating active, slowly progressive neuropathological processes (14–18). Fourth, inflammatory changes appear to play a key role in the progression of brain ischemia and Alzheimer's disease (19). Fifth, the data indicate that ischemic brain damage can cause the pathology of proteins typical for Alzheimer's disease by inducing the generation and deposition of the β -amyloid peptide and other fragments of amyloid protein precursor (16, 20–22). Finally, studies show that tau protein dysfunction also plays a key role in regulating brain ischemia-reperfusion episodes (23–33). Together, these results point to common proteomic and genomic factors in ischemic brain injury and Alzheimer's disease in the neuropathological processes.

In this chapter, we present the current knowledge about the dysregulation of genes involved in the amyloidogenic processing of the amyloid protein precursor, which is associated with the generation of the β -amyloid peptide in the brain after ischemia. In addition, we pay attention to whether the signal pathway of the amyloid protein precursor is involved in the induced ischemic death of neurons in the CA1 area of the hippocampus and medial temporal cortex. Also, we take into account the importance of ischemic gene expression associated with Alzheimer's disease, such as autophagy, mitophagy, and apoptosis during clinical onset, progression and maturation of brain injury after ischemia in the etiology of Alzheimer's disease. With regard to the latest exciting discoveries after brain ischemia injury, we combine data from the proteomic and genomic point of view. In recent years, several researchers have documented that brain ischemia-reperfusion episode is an important element in the development of Alzheimer's disease and plays a key role in proteomic and genomic (e.g., amyloid protein precursor, amyloid

processing secretases, autophagy, mitophagy, caspase 3, and tau protein) changes of this disorder (1, 2, 31). Below we summarize the latest evidence that Alzheimer's disease-related proteins and their genes play an essential role in brain ischemia-reperfusion injury, and ischemic episode is a necessary and most important supplier for the start and progress of the full development of sporadic Alzheimer's disease.

AMYLOID STAINING AND BLOOD LEVEL AFTER BRAIN ISCHEMIA

Although a significant progress has been made in research on the pathogenicity of amyloid in Alzheimer's disease, the underlying molecular amyloid machinery affecting neurodegeneration after ischemic brain injury is unclear. Herein we present the existing facts regarding amyloidogenic processing of the amyloid protein precursor into amyloid during brain injury due to ischemia and reperfusion, which is associated with the production and accumulation of the N- and C-terminal of amyloid protein precursor and amyloid in the brain. The appearance of an elevated level of β -amyloid peptide in the blood and its staining in the brain after ischemic injury sheds new light on a better understanding of the role of amyloid in the development of neurological deficits following an ischemic episode.

In animals

Different fragments of the amyloid protein precursor staining were observed in the extra- and intracellular spaces after experimental ischemic brain injury (15, 20, 34–37). In animals that survived up to 6 months after brain ischemia with recirculation in the extracellular space of the hippocampus, brain cortex, white matter, and around the lateral ventricles, the N- and C-terminal deposits of the amyloid protein precursor and the β -amyloid peptide were observed (16, 20). The accumulation of different parts of the amyloid protein precursor in various cells, such as the neuronal, glial, microglia, oligodendrocyte, endothelial, pericyte, and ependymal cells, has also been found (15, 20, 38–42). Especially astrocytes around microvessels showed intense staining of many very long, thin processes that adhered to or embraced capillaries. More than 6 months of survival after cerebral ischemia, only the C-terminal staining of the amyloid protein precursor and the β -amyloid peptide was observed (16). Accumulation of β -amyloid peptide in response to transient focal ischemic brain injury does not appear to be a temporary phenomenon, as diffuse β -amyloid peptide deposits turn into plaque about 9 months after ischemic episode (43). After ischemia-reperfusion brain injury, the β -amyloid peptide arises as a result of neuronal ischemic damage (34), and it is likely that this peptide with its own neurotoxic activity further affects ischemic neurons.

In humans

Examination of human ischemic brains has shown that ischemia is associated with the accumulation of β -amyloid peptide in brain tissue (44–46). Studies have

shown both diffuse and senile β -amyloid peptide plaques in areas of the brain prone to ischemia, at arterial border zones and cortex after focal and global cerebral ischemia (44–46). The middle layers of the cerebral cortex, which are very susceptible to ischemic injury, were most commonly affected by amyloid (44–46). The number of amyloid plaques in brain tissue correlated positively with age (44–46). In brains after global cerebral ischemia with a survival of up to 1 month, strong staining of the β -amyloid peptide in neurons and perivascular areas was found (45). The staining of neurons depended on the area of the brain. Neurons from the cerebral cortex and hippocampus were the most intensely stained. The ependymal and epithelial cells were also stained on the β -amyloid peptide. Not all brains had senile amyloid plaques in the cerebral cortex. The cerebral white and gray matter vessels were surrounded by β -amyloid peptide deposits. Deposits in the perivascular space looked like cuffs. In some brains, the walls of the meningeal and cortical vessels were stained for the β -amyloid peptide. Accumulation of amyloid in the perivascular blood vessel space of the blood–brain barrier suggested that the β -amyloid peptide was derived from blood. Some evidence to support this hypothesis comes from clinical studies showing that the β -amyloid peptide in the blood has been elevated in patients after ischemic brain injury (22, 47). According to another study, β -amyloid peptides 1–40 and 1–42 staining were found in the human hippocampus after ischemia (21). This intense staining of various β -amyloid peptides may contribute to the progression of ischemic hippocampus neurodegeneration.

In the brains of patients after global cerebral ischemia caused by cardiac arrest, the immunostaining of the receptor for advanced glycation end products was located both in the cells of the choroid plexus epithelium and in the ependymal cells bordering the brain ventricles (48). These cells form both the cerebrospinal fluid–brain barrier and the blood–cerebrospinal fluid barrier. The β -amyloid peptide was noted by staining in the blood vessels of the choroid plexus and in the basal membrane of the choroid plexus epithelium (48). The data showed that the choroid plexus epithelium and the lining cells, equipped with a receptor for advanced glycation end products, play not only a significant role in the accumulation of the β -amyloid peptide in the brain parenchyma but also are a place where amyloid can be removable.

After ischemic brain injury in humans due to cardiac arrest, approximately 70-fold increase in beta-amyloid peptide 1–42 in the serum was found (22). The level of amyloid growth correlated negatively with the complete clinical outcome after ischemic brain injury, which in turn probably reflects the severity of ischemic damage (22). The data confirm that brain ischemia may play a key role in the amyloidogenic processing of the amyloid protein precursor.

TAU PROTEIN STAINING, PHOSPHORYLATION, AND BLOOD LEVEL AFTER BRAIN ISCHEMIA

Although there has been significant progress recently in research on the pathogenicity of the tau protein in Alzheimer's disease, the basic molecular processes associated with the tau protein that affect neurodegeneration after ischemic brain trauma have not been finally clarified. In this analysis, we show that both

ischemia–reperfusion brain damage and the permeability of the blood–brain barrier after ischemia induce tau protein dysfunction. As a result, we suggest that modifications of the tau protein by phosphorylation are dangerous for microtubule activity, especially in neurons, and are involved in the development of irreversible neuropathology in the ischemic brain with Alzheimer's disease dementia.

In animals

Early experimental studies documented tau protein staining in neuronal and glial cells in the hippocampus, thalamus, and cortex after permanent and focal brain ischemia (36, 49–53). The modified tau protein was also observed in microglial cells both in ischemic penumbra and in brain tissue, respectively, after focal and global cerebral ischemia (29, 54). The above data showed that some neuronal and glial cells had changes in the tau protein after ischemic brain damage (52), which may be the main pathological stage of ischemic processes in these cells (53). Another study revealed that tau protein alone can block the transport of amyloid protein precursor in neurons, which leads to the accumulation of the amyloid protein precursor in the body of neuronal cells (55).

Studies have also shown that the phosphorylation patterns of tau protein differed in different models of cerebral ischemia (32). The tau protein was dephosphorylated after total and focal cerebral ischemia (51, 52, 56). During total brain ischemia, the tau protein was dephosphorylated, and during recirculation, it was re-phosphorylated and accumulated in the brain tissue (56). Transient local ischemic brain injury in rats with 24-h recirculation induces site-specific hyperphosphorylation of tau protein (57). An experimental combination of reversible total brain ischemia with hyperhomocysteinemia resulted in an approximate 700-fold increase in the number of hyperphosphorylated positive tau protein neurons in the cerebral cortex compared to control conditions (31). Recent studies indicate that following brain ischemia, hyperphosphorylated tau protein in cortical neurons is integrated with apoptosis (24, 27, 29, 30, 54, 57, 58). Khan et al. (30) showed an increase in the production of paired helical filaments of tau protein after forebrain ischemia in mice. Wen et al. (24, 57, 58) provided evidence that brain ischemia with recirculation is involved in neurofibrillary tangle-like development after local ischemic cerebral injury. Finally, tau protein dysfunction, a typical hallmark of Alzheimer's disease, worsens experimental ischemic brain damage *via* tau protein-mediated iron export (59) and excitotoxicity depending on the tau protein (28, 60).

In humans

Early studies have shown that tau protein staining in neurons and glia is present in the hippocampus, thalamus, and cerebral cortex in the human brain after ischemia (61–63). The modified tau protein was also observed in microglial cells (63). It was noted that microglial cells' tau protein passes independent of phosphorylation modification following cerebral ischemia with recirculation in humans (63). Finally, in one of the studies, many neurofibrillary tangle-bearing neurons were observed in the nucleus basalis of Meynert ipsilateral to a massive focal cerebral infarction (23).

Tau protein was detected in human plasma after complete ischemic brain injury with two peaks after 2 and 4 days, which probably indicates the degree of neuronal damage after ischemia–reperfusion episode (25). The observed bimodal changes in the tau protein in the blood are consistent with the 2 types of neuronal death: first, by necrosis, and second, by delayed neuronal death (26). The presented research suggests that the increase in blood tau protein can be used as a biomarker to assess neurological damage to the brain after ischemia (25, 26).

mRNAs ASSOCIATED WITH THE AMYLOID PROTEIN PRECURSOR AFTER BRAIN ISCHEMIA

Due to the fact that there are some new data in the literature in human and animal studies regarding changes in amyloid protein precursor following ischemia–reperfusion brain damage in this part of the review, we present the first steps in mRNA studies related to the metabolism of the amyloid protein precursor after various types of brain ischemia. This indicates that there is urgent need for data on the new causative pathological role of amyloid in cerebral ischemia, which molecule presumably has an irreversible effect on the post-ischemic outcome.

mRNA of the amyloid protein precursor

After experimental focal ischemic brain damage with reperfusion, the mRNA level of the amyloid protein precursor increased both in the core and in the penumbra, by 150 and 200%, respectively, in 1 week of recirculation (64, 65). In addition, after permanent local ischemic brain injury without recirculation, the mRNA domain of the Kunitz-type protease inhibitor domain-containing amyloid protein precursor in the cortex of the brain was induced for 3 weeks (66). Also after transient local cerebral ischemia, the amyloid protein precursors, 770 and 751 mRNAs, were induced within 1 week of recirculation (67). In addition, 1 h after local ischemic brain damage in ovariectomized rats, the increased mRNA level of the amyloid protein precursor was observed in ischemic brain structures (64). In contrast, estrogen treatment reduces the mRNA level of the amyloid protein precursor in the ischemic brain (64). These data suggest that estrogen therapy can be used to lower the mRNA of the amyloid protein precursor after the ischemic episode.

mRNA of enzymes metabolizing the amyloid protein precursor

The amyloid protein precursor is metabolized by α -secretase, and this process is a non-amyloidogenic process. After experimental ischemic brain injury, the level of α -secretase mRNA decreases (68, 69). The second process is called amyloidogenic process, and the amyloid protein precursor is metabolized by β -secretase and γ -secretase to produce the β -amyloid peptide (70). Some studies have demonstrated that ischemic episode of the brain activates the production and activity of β -secretase after ischemia (71–74). Another study showed changes in mRNA levels of three enzymes that metabolize the amyloid protein precursor: β -secretase,

cathepsin B, and glutaminyl cyclase, which increased in the cortex and hippocampus after ischemia (75).

Three days after ischemic brain injury, the highest level of presenilin 1 mRNA was observed in the neuronal cells of CA3 area of the hippocampus (76). This observation suggests that an elevated level of presenilin 1 mRNA probably is associated with the response of neuronal cells to ischemia. In another study, the increased level of presenilin 1 mRNA showed the maximum growth in the striatum, cortex, and hippocampus after focal ischemic brain damage (77). In the above study, the increased level of presenilin 1 mRNA was greater on the side opposite to local ischemic brain injury. This observation may reflect the disappearance of brain neurons on the ipsilateral side. The mRNA of presenilin 1, which increased after brain ischemia (76, 77), is involved in the production of the β -amyloid peptide by the γ -secretase complex (70, 78). The above data will help understand the progressive neuronal disappearance following the ischemia–reperfusion episode of the brain and the slow, prolonged accumulation of the β -amyloid peptide in ischemic brain tissue (16).

EXPRESSION OF GENES INVOLVED IN THE PRODUCTION OF AMYLOID AFTER BRAIN ISCHEMIA

The ischemic–reperfusion episode of the brain is undoubtedly one of the most common multifactorial forms of neurodegeneration, including many pathological processes occurring during ischemia and recirculation and gradually spreading to various areas of the brain. It seems that the ischemic event in humans and animals is associated with the development of Alzheimer's disease type of neurodegenerative pathology, such as the accumulation of all parts of the amyloid protein precursor after its processing in the amyloidogenic process and dysregulation of Alzheimer's disease-related genes involved in this process. Progress in understanding new proteomic and genomic processes caused by ischemic brain damage in various brain structures that have not yet been fully elucidated will result in new strategies for the treatment of neurodegeneration of the Alzheimer's disease type with full-blown dementia due to ischemia.

CA1 area of the hippocampus and medial temporal cortex

In the CA1 region of the hippocampus and temporal cortex, the expression of the *amyloid protein precursor* gene was below the control value within 2 days after ischemia (79, 80). In the above areas, 7 and 30 days after cerebral ischemia–reperfusion, the expression of the *amyloid protein precursor* gene was above the control value (79, 80). The expression of the β -secretase gene increased above the control value following brain ischemia injury in the CA1 area of the hippocampus 2 to 7 days after recirculation (79). But, 30 days after brain ischemia, the expression of the β -secretase gene was below the control value (79). The expression of the β -secretase gene was above the control value in the temporal cortex after 2 days from ischemic episode (80). The expression of the β -secretase gene was reduced in the temporal cortex 7 and 30 days after

ischemia (80). In the CA1 region, the expression of the *presenilin 1* and *2* gene was increased 2 and 7 days after ischemia (79). But, 30 days post-ischemic injury, the gene expression of *presenilin 1* and *2* was below the control value (79). In the temporal cortex, *presenilin 1* gene expression was lowered below the control value, but *presenilin 2* was above the control value 2 days after ischemia (81). Seven days after ischemia, the gene expression of *presenilin 1* was reduced, and *presenilin 2* was elevated (81). Thirty days post-ischemia, the expression of *presenilin 1* gene was above the control value, and *presenilin 2* was below the control value (81).

EXPRESSION OF THE *TAU* PROTEIN GENE IN THE CA1 AREA AFTER BRAIN ISCHEMIA

In the neurons of CA1 area of the hippocampus, the tau protein encoding gene expression increased above the control value on the 2nd day after brain ischemia (33). On the 7th day of reperfusion after ischemic episode, the gene expression oscillated in the range of control values (33). On the 30th day of recirculation after brain ischemia, the expression of the *tau protein* gene was below the control value (33). The statistical significance of changes in the expression of the *tau protein* gene after brain ischemia–reperfusion injury in rats was between 2 and 7, and 2 and 30 days of recirculation (33).

EXPRESSION OF GENES INVOLVED IN THE DIRECT DEATH OF NEURONS AFTER BRAIN ISCHEMIA

One of the risk factors of Alzheimer's disease is aging, and for that reason, a large number of scientists believe that the main cause of Alzheimer's disease is brain ischemia closely related to age. It seems that brain injury caused by ischemia and reperfusion facilitates the development of irreversible neurodegeneration similar to Alzheimer's disease as a result of neuronal death, synaptic dysfunction, inflammatory changes, white matter damage, and general brain atrophy, which changes are closely related to genes involved in neuronal death in Alzheimer's disease. Despite the years of expansion, the amyloid Alzheimer's disease theory has not solved the etiology of the disorder (82), and the current research suggests that brain ischemia leads to neurodegeneration of Alzheimer's disease through numerous terminal events, such as dysregulation of genes that cause cell death in various brain structures of varying intensity. Understanding the basic pathological pathways causing proteomic and genomic changes associated with Alzheimer's disease and induced by cerebral ischemia will help in the development of neurodegenerative dementia treatment after ischemia.

CA1 area of the hippocampus

Expression of the *autophagy* gene in the CA1 region of the hippocampus after brain ischemia with 2, 7, and 30 days of recirculation was within the control

limits (83). Two days after ischemic brain injury, the expression of the *mitophagy* gene in the CA1 region increased above the control value. Seven and 30 days after ischemia–reperfusion injury of the brain, the gene expression was within the control range. Overexpression of the *caspase 3* gene in the CA1 region was observed after 2 and 7 days of recirculation. However, 30 days after ischemic brain injury, the gene expression was below the control value.

Medial temporal cortex

Two days after ischemic brain injury, *autophagy* gene expression increased above the control value in the medial temporal cortex (84). However, 7 and 30 days after ischemia–reperfusion brain injury, *autophagy* gene expression decreased. Two days after cerebral ischemia, *mitophagy* gene expression decreased below the control value (84). Nevertheless, 7 and 30 days after ischemic brain injury, the expression of the *mitophagy* gene increased above the control value. Two days after cerebral ischemia, the expression of *caspase 3* gene decreased below the control value (84). However, 7 and 30 days after brain injury due to ischemia and reperfusion, *caspase 3* gene expression increased above the control value.

THE RELATIONSHIP BETWEEN IRON DYSHOMEOSTASIS AND AMYLOIDOGENESIS

Both the amyloid protein precursor and iron play a key role in brain neurodegeneration due to Alzheimer's disease and cerebral ischemia (59, 85–88). Alzheimer's disease is primarily characterized by the deposition of amyloid plaques and the formation of neurofibrillary tangles which co-localize with iron (88). Under physiological conditions, the amyloid protein precursor is processed primarily on the non-amyloidogenic pathway by α -secretase, thereby producing the neuroprotective ectodomain of the soluble amyloid protein precursor α and the carboxy-terminal fragment α . Alternatively, a small pool of amyloid protein precursor is processed by the amyloidogenic pathway using β -secretase, thereby producing a soluble amyloid protein precursor β and carboxy-terminal fragment β . The carboxy-terminal fragment β is further cleaved by γ -secretase, resulting in β -amyloid peptides.

Iron is gradually deposited in selected areas of the brain during Alzheimer's disease, as well as in the course of ischemic neurodegeneration (59, 85–88). In the brain, iron is present in neurons, oligodendrocytes, astroglia, and microglia cells. Excess iron is associated with oxidative stress and neuronal damage because iron accumulation in neurons can cause free radical production and mitochondrial dysfunction and ultimately lead to neuronal death. In addition, iron can induce hyperphosphorylation and aggregation of tau protein. Deficiency of tau protein leads to iron accumulation, which is associated with impaired transport of the amyloid protein precursor to the cell membrane (59, 87). Therefore, iron accumulation in brain cells must be strictly regulated to maintain basic cellular function and avoid cytotoxicity. The evidence obtained confirms the role of the amyloid protein precursor in maintaining iron homeostasis

in brain tissue (86). It has been demonstrated that the amyloid protein precursor and soluble amyloid protein precursor α facilitate iron outflow by stabilizing the iron exporter ferroportin 1 on the cell membrane (86, 87). In contrast, ablation of the amyloid protein precursor in neurons causes iron retention (87), while the knockout of the amyloid protein precursor in mice causes iron accumulation in the brain (86). While the amyloid protein precursor affects iron export, the inverse is also true because iron modulates the metabolism of the amyloid protein precursor (86). Iron and interleukin 1 levels in cells regulate translation of the amyloid protein precursor by acting on an iron-responsive element found in the 5' untranslated region of the amyloid protein precursor mRNA (87, 89). Iron has also been shown to affect the processing of the amyloid protein precursor and the production of β -amyloid peptides. In addition, the activation of α -secretase and β -secretase is proteolytically modulated by furin; furin protein levels are reduced under conditions of excess iron, which promotes β -secretase activity, thereby promoting amyloidogenesis (87). Iron and inflammation promote amyloid toxicity (87). Recent experimental studies showed that: (i) iron overload increased retention in the neurons of the soluble amyloid protein precursor α , (ii) iron overload reduced the extracellular levels of the soluble amyloid protein precursor α and β -amyloid peptide, and (iii) the direct molecular target of iron is β -secretase (86).

Given the key physiological and pathological role of the amyloid protein precursor and its cleavage products in the brain, it is likely that iron overload may affect neuronal activity, interfering with the normal processing of the amyloid protein precursor. Although it is unclear what mechanism causes abnormal intracellular retention of the soluble amyloid protein precursor α , there is evidence that cell accumulation of the soluble amyloid protein precursor α may be due to intracellular cleavage of the amyloid protein precursor by α secretase or the internalization of the extracellular soluble amyloid protein precursor α by cell surface receptors (90, 91). Together, evidence of the beneficial role of the secreted soluble amyloid protein precursor α indicates that iron overload mediates the decrease in secreted soluble amyloid protein precursor α , which can lead to harmful consequences. This possibility is particularly important in neurological diseases, given that the secretion of the soluble amyloid protein precursor α affects many brain disorders, including Alzheimer's disease and cerebral ischemia (85–88). In addition, it has recently been suggested that the loss of β -amyloid peptide function, rather than its accumulation, plays a pathogenic role in Alzheimer's disease (92). In summary, iron overload affected non-amyloidogenic as well as amyloidogenic metabolism of the neuronal amyloid protein precursor. In addition, it was confirmed that the soluble amyloid protein precursor α is an endogenous inhibitor of β -secretase activity, potentially affecting the production of β -amyloid peptide (86). As iron directly inhibits β -secretase activity, it is likely that increased iron primarily inhibits β -secretase and the amyloidogenic pathway and promotes the non-amyloidogenic pathway and retention of the soluble amyloid protein precursor α . β -secretase activity is then inhibited by the growth of the soluble amyloid protein precursor α (86). These abnormal iron-induced changes form a *vicious circle* that leads to dysregulation of the processing of amyloid protein precursors in neurons.

CONCLUSION

Although there are reasonable doubts about the effects of cerebral ischemia on the development of Alzheimer's disease, the mounting evidence on the ischemic theory of Alzheimer's disease should not be ignored. Ignoring the numerous scientifically substantiated clinical and experimental data on the connection between brain ischemia and Alzheimer's disease will hamper not only the proper understanding of the disease mechanism but also the development of complementary and alternative strategies for the treatment and management of Alzheimer's disease. The conclusions drawn from the study of ischemia-induced Alzheimer's disease-associated proteins and their genes in the hippocampus and the medial temporal cortex, which contribute to the death of neurons, the production of the β -amyloid peptide, and neurofibrillary tangle-like formation, are important for the development of treatment goals in the therapy of Alzheimer's disease. As deposits of amyloid and tau protein may not be the cause in the pathogenesis of Alzheimer's disease, further research is needed in this field. Animal models of cerebral ischemia seem to be a useful experimental approach in determining the role of folding proteins and their genes in the neurodegenerative process of sporadic Alzheimer's disease.

Acknowledgments: The authors acknowledge the financial support from the following institutions: the Mossakowski Medical Research Centre, Polish Academy of Sciences, Warsaw, Poland (T3-RP) and the Medical University of Lublin, Lublin, Poland (DS 475/19-SJC).

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Contributing Factors of Neurodegeneration in Alzheimer's Disease

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch5>

Abstract: Alzheimer's Disease (AD) affects at least 5.7 million Americans, and it is the sixth leading cause of death in the United States. At the onset, patients experience minor memory problems. Next, impairments in speech and motor function manifest as a limitation to well-being and independence. Slowing this pandemic rise is critical, since AD also bears a huge socioeconomical burden. Unfortunately, there is limited prevention and no effective cure has been found, as all clinical trials for promising AD drugs have failed thus far. The pathological hallmarks of AD include amyloid- β plaques (A β), neurofibrillary tangles (NFT), and neuroinflammation. Other factors include *APOE4* and environmental stressors, such as metal dyshomeostasis, which contribute to AD pathogenesis. Herein, we review major contributing factors involved in AD pathophysiology. Deeper understanding of associated molecular mechanisms underlying AD pathogenesis is critical for developing novel AD theranostics.

Keywords: Amyloid- β ; amyloid precursor protein; metals; β -site of APP cleaving enzyme 1 (BACE1 or β -secretase); neurotoxicity; NF- κ B; presenilins

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

Alzheimer's disease (AD) is a progressive neurodegenerative disorder and is the most represented form of dementia. It is the 3rd most common disease affecting the population, inflicting at least 5.7 million Americans as the trend continues to rise at a pandemic rate. It is the leading cause of age-dependent disability on a global scale (1). AD reduces the quality of a patient's life, as irreversible cognitive decline becomes apparent due to pathological and morphological changes such as cortical atrophy, neuroinflammation, loss of synaptic connections, and cellular death (2) leaving the individual dependent on significant care, as their memories and motor function deteriorate.

Fortunately, technological advances have afforded researchers the ability to characterize neuronal loss in the hippocampus and cortices (3). Additional work has acknowledged perspectives on multifaceted complexities that have linked risk-associated genes and environmental factors to these differences (4). For example, increased exposure to air pollution, chemicals, and ionizing radiation is harmful (5, 6) and potentially contributes to dementia-related diseases. Unfortunately, AD has no efficacious treatments, and thus, the disease is a critical health concern and has incurred a colossal socioeconomic burden. Recently, the Alzheimer's Association reported the cost as \$236 billion and is projected to rise to \$1.1 trillion in 2050 (1). Therefore, identifying an accurate diagnosis and effective treatment is urgent.

The hallmarks of AD are evident, with neuroinflammation and aggregated A β plaques followed by neurofibrillary tangles (NFT). In fact, recent studies observed plaque deposits within cognitively normal individuals up to 20 years before the onset of cognitive decline (7). Why A β fibrils aggregate into plaques has yet to be elucidated; however, there is evidence that its exacerbated presence is toxic to neuronal cells. For example, A β inhibits respiratory function, reduces ATP levels (8), and leads to mitochondrial dysfunction (9). In vitro studies of PC12 cells observed depolarization of the mitochondrial membrane potential and decreased activity of mitochondrial electron transport chain complexes. As A β aggregates, it leads to signaling impairments causing the cells to undergo apoptosis. Anti-A β drugs tested in human clinical trial have failed to produce promising results. As such, the credibility of the amyloid hypothesis has been questioned, and the true role of A β is currently being investigated.

AMYLOID PRECURSOR PROTEIN

Amyloid plaques, or the insoluble A β peptides, in the brain form through the cleavage of amyloid precursor protein (APP) by the b-site of APP cleaving enzyme 1 (BACE1 or β -secretase) and γ -secretase (10, 11). APP is located on chromosome 21, and it is a type I transmembrane protein involved in secretory and endocytic processes (12). It contains a metal-binding domain, heparin, collagen, laminin, and a protease inhibitor domain (13). Although the function of APP is unclear, there is evidence to suggest that the ectodomain of APP may be involved in cell adhesion, trophic support, cell growth, and differentiation of neuronal stem cells (14). Conversely, the intracellular domain may modulate mitochondrial function (15).

APP can be processed through two pathways: the amyloidogenic pathway and the non-amyloidogenic pathway. In the amyloidogenic pathway, β -secretase cleaves APP at amino acid 671 releasing APP β (sAPP β). Next, the CTF99 embedded in the plasma membrane is cleaved by γ -secretase, made up of 4 subunits (16, 17), including the catalytic domains *Presenilin1* gene (*PS1*) and *Presenilin2* (*PS2*) (18). BACE1 is a rate-limiting step for A β production, and knockout studies result in complete inhibition of A β generation (19). In the non-amyloidogenic pathway, APP is cleaved by α -secretase at amino acid 687, releasing soluble APP α (sAPP α). The remaining protein, CTF83 is cleaved by γ -secretase releasing a soluble p3 fragment. α -secretase belongs to a family of single-pass transmembrane and secretes zinc-containing endopeptidases that are dominant in neurons (20). Aggregated A β function in normal physiology remains to be elucidated (19); however, A β disrupts postsynaptic trafficking in glutamate receptors such as α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA) receptors (21) and N-Methyl-D-Aspartate (NMDA) receptors (22). Their actions may be important for learning and memory, and synaptic plasticity (23–25). A β has also been shown to modulate the inhibitory neurotransmitter gamma-aminobutyric acid (GABA) through interaction with KCC2 (26). A study by Senechal et al. investigated APP knockout mice and discovered dysregulated long-term potentiation (LTP) and learning deficits (27, 28). Moreover, theta–gamma oscillation phase–amplitude coupling was also diminished in regions of the parietal cortex and hippocampus compared to the wild type (27). As such, the function of APP is complex, and data so far have linked the role of the protein in neurite growth (29–31), axon guidance (32), and neuronal cell adhesion (33).

β -SITE OF APP CLEAVING ENZYME 1

β -site of APP cleaving enzyme 1 (BACE1) is a major drug target for therapy (34) because its expression correlates not only with the onset of AD but also with glucose intolerance. Importantly, this downstream effect is a risk factor for diabetes. Studies on mouse models which inhibit BACE1 expression resulted in improvements in glucose homeostasis, lowered leptin levels, and decreased hypothalamic inflammation (35, 36). However, depletion of BACE1 leads to other harmful effects as evidence suggests it important in regulating adult hippocampal neurons responsible for memory (37, 38) and other important neuronal processes. For example, mice models that possess faulty BACE1 expression result in deficits in synaptic transmission and plasticity in the hippocampal region (39). Furthermore, the cell adhesion molecule Neuregulin-1 (Nrg1), which must be cleaved by BACE1, mediates radial migration of glutamatergic and GABAergic neurons. It is also responsible for myelination and synaptic plasticity (40) and is required for the formation of new synapses while strengthening existing ones. Interestingly, BACE1 null mice result in a reduction of Nrg1 cleavage, resulting in characteristics of schizophrenia (41). Similarly, *Sez6* is a protein that is concentrated in areas associated with morphological plasticity. This includes areas within the hippocampus and cerebellum in postnatal brains. *Sez6* is also cleaved by BACE1 and mediates dendritic arborization of cortical neurons (42) which is critical for neuronal transfer of information. Thus, defective BACE1 leads

to poor motor coordination, weak balance, and cognitive deficits. Lastly, BACE1 deficiency also affects Jagged-1 (Jag1) that regulates astrogenesis/neurogenesis through Notch signaling pathway (43, 44) and contributes to memory formation. Therefore, suppression of this enzyme is a double-edged sword and more research is needed to help in AD patients.

GENETIC RISK FACTORS OF ALZHEIMER DISEASE PATHOLOGY

There are two forms of AD: sporadic and familial. The majority of the cases (approximately 95%) are classified as sporadic late-onset AD (LOAD), while about 5% are classified as familial early-onset AD (EOAD) with an autosomal dominant inheritance pattern. Sporadic AD is influenced by complex genetic variants combined with environmental factors (45). However, there is little evidence to define how this occurs. Early onset is caused by rare mutations in three genes located on chromosome 21 (46, 47) and chromosome 14 (48). The summary of genetic mutations implicated in LOAD is shown in Table 1 and EOAD is given in Table 2 (45).

TABLE 1
A summary of genetic mutations implicated in LOAD

Gene	Protein	Chromosome	Risk change %	Proposed molecular phenotype
<i>APOE</i>	Apolipoprotein E	19q13	~400–1500%	Clearance of A β Lipid metabolism
<i>ABCA7</i>	ATP-binding cassette subfamily A member 7	19p13.3	~20%	Lipid metabolism Cellular signaling
<i>BINI</i>	Bridgin integrator 1	2q14	~15%	Production of A β Clearance of A β Cellular signaling
<i>CRI</i>	Complement component (3b/4b) receptor 1	1q32	~15%	Clearance of A β Innate immunity
<i>PICALM</i>	Phosphatidylinositol-binding clathrin assembly molecule	11q14	~15%	Production of A β Clearance of A β Cellular signaling
<i>CD2AP</i>	CD2-associated protein	6p12.3	~10%	Cellular Signaling
<i>CD33</i>	CD33 (Siglec 3)	19q13.3	~10%	Innate immunity Degradation of
<i>CLU</i>	Clusterin	8p21.1	~10%	Clearance of A β Innate immunity
<i>EPHA1</i>	EPH receptor A1	7q34	~10%	Cellular signaling Innate immunity
<i>ATXN1</i>	Ataxin 1	6p22.3	NA	Production of A β

TABLE 2

A summary of genetic mutations implicated in EAOD

Gene	Protein	Chromosome	Molecular phenotype
<i>APP</i>	Amyloid β protein precursor	21q21	Increased $A\beta_{42}/A\beta_{40}$ ratio Increased $A\beta$ production Increased $A\beta$ aggregation
<i>PSEN1</i>	Presenilin 1	14q24	Increased $A\beta_{42}/A\beta_{40}$ ratio
<i>PSEN2</i>	Presenilin 2	1q31	Increased $A\beta_{42}/A\beta_{40}$ ratio

Mutations in *APP*, *Presenilin1* (*PS1*), and *Presenilin2* (*PS2*) genes have been integral in the development of AD as they cause a disruption in the ratio of $A\beta_{42}$ production (49). In normal physiology, presenilins, needed for the production of $A\beta$ peptides via both β - and γ -secretases-mediated cleavage (50, 51), are responsible for autosomal transmission and the promotion of amyloid plaque. *PS1* regulates calcium homeostasis and mediates neurotransmission (52, 53). The largest amount of mutations occurs for *PS1* at an estimate of 200 mutants, whereas *APP* and *PS2* have 10–25 mutants on the AD and frontotemporal dementia mutation database.

Meta-analysis revealed at least 15 potential loci where variations may predispose one to developing AD (46). However, a particular gene appears to be the most burdensome, the *ApoE* gene. It has four different isoforms: ApoEe1, ApoEe2, ApoEe3, and ApoEe4. Apolipoprotein E (ApoE) regulates synaptic function, promotes plasticity, increases the number of dendritic spines, and regulates protein trafficking across neurons (54). It is responsible for the regulation of triglyceride and cholesterol metabolism. Binding of lipidated ApoE facilitates $A\beta$ uptake in an isoform-dependent manner, and inhibited clearance contributes to $A\beta$ accumulation. One variant of *ApoE* gene has been identified as the largest risk factor for late-onset AD through computational analysis (55–57). It is important to note that possessing ApoEe4 over the e3 (common) or e2 (other variant) alleles is not enough to cause AD but it acts as a determinant which increases overtime as the patients ages (45). Analyses reveal that a heterozygous pair increases AD by threefold, whereas a homozygous pair increases the risk by 15-fold (58). It is thought to be the least effective in binding to, and facilitating the uptake of, $A\beta$. Additionally, its strong ties to neurovascular dysfunction further confirm its contribution in AD manifestation (56). The allele can be investigated for potential biomarkers and to unearth new targets for AD drug discovery due to significant clinical and neurobiological correlations. Among them, *ApoE e4* allele and low CSF level of $A\beta_{42}$ have been reported (59). Patients with the *e4* allele tend to present with early-onset memory impairment, decrease in global cognitive function, and weak episodic memory (60). Interestingly, the *ApoE e2* variant seems to reduce the risk of dementia compared to the common e3 allele, despite its association with an increased amyloid burden (56). Overall, monitoring *ApoE* gene can play an important role in understanding the AD pathophysiology and be used as an assessment tool for at-risk patients.

Other genes that have a strong association with late-onset AD include *SORL1*, which mediates protein trafficking (61), and *ACE*, which regulates blood pressure (62). Furthermore, testing a single nucleotide for any association with disease

pathology can be accomplished through GWAS technology. One avenue leads to the discovery of GRB2, which mediates tau phosphorylation and has a high affinity for APP and the presenilins (63, 64). Other findings identified ATXN1, which affects A β levels by modulating β -secretase levels and cleavage of APP (65), and BIN1 (66), which is highly expressed in the central nervous system and plays a role in receptor-mediated endocytosis (67). Furthermore, ADAM10 mutations have impaired enzyme activity and lead to the onset of AD in the elderly (67). Lastly, CD33 has been an interesting discovery because it helps strengthen that A β acts as an AMP (11, 68–70).

THE NEUROIMMUNE SYSTEM

There are many challenges in understanding the complexity of inflammation in relation to AD in order to develop appropriate therapeutics. Clinical analysis of AD patients exhibited chronic neuroinflammation, insufficient energy metabolism, and redox stress in postmortem brains (71). These observations have been replicated in both animal and cell culture models. Increased inflammatory cascade by microglia has been observed in areas of A β deposits and activation of NF- κ B (72, 73).

Due to their high affinity for A β deposits, understanding the role of microglia may help identify therapeutic targets. In brief, microglia are recognized as the brain macrophage and play an integral role in housekeeping. Upon signal detection, they act to remove debris, toxins, pathogens, and apoptotic neurons (74, 75) by releasing a cascade of inflammatory factors. As such, they release reactive oxygen species and Th1 cytokines including interleukin 1-beta (IL-1 β), IL-6, tumor necrosis factor alpha (TNF- α), and interferon-gamma (76) to ramp up the immune system. Furthermore, they are integral in upregulating MCHII complexes, leading to an inflammatory cascade in innate immune response in many disorders such as Parkinson's disease, HIV, and multiple sclerosis (77–80). In AD brain, microglia are constantly aggregated around A β plaques (81) to form a barrier between healthy tissue and areas of injured or infected tissue. Since there is no evidence to suggest microglia can degrade A β , they undergo a state of compromised phagocytosis, in which the semi-degraded A β are ultimately expelled from the microglial cell (82) causing a dysregulation of homeostasis. Extended exposure to A β leads to disrupted calcium homeostasis within astrocytic cells, which also leads to degeneration of neurons (83).

NF- κ B regulates the expression of more than 400 genes (72) and can be induced by ROS, interleukin IL-1 β , TNF- α , bacterial lipopolysaccharides (LPS), isoproterenol, and ionizing radiation (73, 84). Its activation is dependent on growth factors and the neurotransmitter, glutamate (85). Thus, NF- κ B plays an important role in DNA transcription and cellular survival. In general, high levels of NF- κ B expression are associated with normal aging and upregulate microglial activity (85–87). This overexpression increases the susceptibility for AD through upregulating *BACE1* and *APP* genes (88).

Furthermore, rodent models have demonstrated the outcomes of unregulated NF- κ B, resulting in a destructive feedback loop (89, 90). For example, mice that overexpressed NF- κ B had clinical signs of increased apoptosis in the hippocampal

region through triggering TNF- α and iNOS when exposed to neurotoxins (91, 92). Moreover, *drosophila* studies that overexpressed NF- κ B in the hypothalamus-like pars intercerebralis resulted in deficits in learning, inadequate memory consolidation, and increase in mortality rates compared to the controls (93). Upon clinical analysis, imaging studies resulted in severe neurodegeneration (94).

Studies regarding the relationship between AD and lifestyle choices concluded that an increased risk of AD was associated with diabetes, high blood pressure, and smoking (95–97). Type 2 diabetes mellitus (T2DM) increases a patient's risk of developing AD by over 50% (45), and it affects the increase of A β pathology by its ability to upregulate NF- κ B and the expression of BACE1 (98, 99). As researchers continue their efforts in drug therapeutic development, alternative approaches have been sought, including cognitive exercises that have improved the production of dopamine and vitamin C (100, 101). Rats that were subjected to pro-inflammatory diets, and adhered to aerobic exercise, resulted in attenuated NF- κ B expression in the liver and muscles. Similarly, regular exercise resulted in an increase of endurance, cognition, and performance (102–104). Unfortunately, standard models are not adequate in analyzing the effect of nutrition on the onset of AD, and no study to date can definitively state the relationship (101).

BLOOD–BRAIN BARRIER

The blood–brain barrier (BBB) plays a vital role in the longevity of an individual's health, and it is responsible for the clearance of A β ; thus, any insult that compromises the integrity of BBB can cause neuronal cells damage (105–107). New studies have observed the progression of AD along with compromised BBB (108). This negative effect is alarming as any damage to the neurovascular unit (NVU) results in toxic substance leaking into the CNS circulating in the blood. In fact, the mechanism of transporting A β out of brain is impaired in AD patients, which contributes substantially to its accumulation (107). One example is the dysfunction of P-glycoprotein (Pgp) (109) resulting in increased deposits and age-associated cognitive impairments. Furthermore, mediating glucose transport for neuronal functionality is integral for astrocytes and neurons, and expression of GLUTs is downregulated in patients. This decreases brain energy supply as confirmed by brain imaging studies (110). Other risks associated with an impaired BBB lead to insufficient nutrient supply and toxin removal, and altered protein expression, all impacting and upregulating the role of neurodegeneration (111, 112). Although it is not elucidated how the mechanism works, therapeutic interventions in alleviating the disease progression are necessary. Recent findings conclude that AD risk factors can be modulated with lifestyle changes in regard to increase in educational levels, exercise, and healthy dietary choices (113–115).

METALS

Strong evidence suggests that biometals in the brains of AD patients are insufficiently maintained, thereby promoting cognitive loss. Due to their structure and function, the proteins that play a role in AD pathophysiology have capabilities

of interacting with metals, especially zinc and copper. Other transitional metals include lead, aluminum, and iron, which may negatively impact human health if the homeostasis is not maintained (116, 117). Neuronal damage can occur due to dysregulation of integral metals needed to maintain brain function. The accumulation of Cu ions has been identified around plaques in postmortem AD brains (118), suggesting the impact of Cu on AD progression. As such, excessive dietary Cu on high-cholesterol diet in rabbits and AD mouse model induces hallmark pathologies. Research has found that chronic exposure to Cu contributes to an increased risk of AD by facilitating A β accumulation (118).

Additionally, zinc regulates many proteins such as SNAP25, PSD95, AMPA receptors, and NMDA receptors. ZnT3, a zinc transporter, allows for the release of zinc from neurons into synapses and is involved in cognition and memory. The disruption in mechanism results in cognitive decline (120). Likewise, AD mouse brains have irregular protein levels of CamKII, spinophilin, NMDA receptors, and BDNF (119, 121). Interestingly, AD transgenic mice studies indicated A β amyloid aggregated in areas of high Fe, Cu, and Zn levels, indicating accumulation of metals within the brain promotes the aggregation of the A β peptides (122, 123). Recent studies have found that APP can regulate iron levels in the brain by removing it from cells, similar to ceruloplasmin. In AD, this activity is decreased by 70% in cortical tissue (122, 123). Tau knockout mice lacked the ability to clear out iron and developed age-dependent neurodegeneration. Rescue studies provided clues that quinoline activity may be a possible therapeutic for AD (124).

PBT2, currently in clinical trials, is a disease modifying drug that does not act like a chelator but as an ionophore (119, 121). Administration of PBT2 for 12 weeks improved mild forms of AD cases through executive function and composite cognitive z-scores and reduced the levels of A β in cerebrospinal fluid (125, 126). Other studies also showed increased neurite outgrowth in vitro and decreased tau phosphorylation (121, 127).

Iron is critical for maintaining neuronal tissue and is involved in the synthesis of myelin and neurotransmitters. Conversely, excessive accumulation can enhance A β production and tau dysfunction leading to neuronal cell death. Parallel to how iron increases expression of ferritin and ferroportin, iron also increases the processing of APP (128, 129). This causes formation of senile plaques and leads to oxidative stress, resulting in oligomerization and more A β generation (130). Iron dysregulation increases NFT (131) creating an iron-rich population within oxidatively stressed environments (132). Quantitative mapping that displays an increase in iron loading shows a strong predictor for cognitive decline. The disruption of iron levels affects neuronal populations within the hippocampus through Fenton and Haber–Weiss reactions (133), producing oxidative lipids that further increase the neurotoxicity and AD pathogenesis (134). As stated, NFT is the integral for trafficking APP to neuronal membrane to facilitate iron efflux from neurons (122, 135), and thus, the loss of tau expression increases the risk for cognitive loss and cortical atrophy in mice (124).

The effects of aluminum on neurodegeneration have attracted attention since it can cause mitochondrial dysfunction and ATP depletion at the cellular level, and decline in memory and cognitive performance on a psychiatric level (136, 137). It can also cause apoptosis in neurons (138). Biopsy studies have confirmed elevated levels of aluminum in LOAD brains, possible source being drinking water (139).

CONCLUSION

AD significantly reduces patients' quality of life. Therefore, there is an urgent need to develop early detection diagnostics and preventive measures to slow the progress of the onset until the discovery of a cure. Serial failures of clinical trials for AD experimental drugs have led us to reevaluate the pathology of this devastating disease and to embark on further understanding of the underlying AD pathophysiology and associated contributing factors. Agents against targets such as BACE1 and APP amyloidosis have proved to be ineffective against AD progression so far. Therefore, further studies in AD pathogenic mechanisms and future utility of artificial intelligence (AI)-based drug discovery tools may aid in developing novel theranostic agents for AD (140, 141).

Acknowledgments: This work was partially supported by a grant from NIH National Institute on Aging (R01AG056614 to XH).

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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The Role of Trace Metals in Alzheimer's Disease

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch6>

Abstract: The extracellular aggregation of insoluble protein deposits of amyloid- β (A β) into plaques and the hyperphosphorylation of the intracellular protein tau leading to neurofibrillary tangles are the main pathological hallmarks of Alzheimer's disease (AD). Both A β and tau are metal-binding proteins. Essential trace metals such as zinc, copper, and iron play important roles in healthy brain function but altered homeostasis and distribution have been linked to neurodegenerative diseases and aging. In addition, the presence of non-essential trace metals such as aluminum has been associated with AD. Trace metals and abnormal metal metabolism can influence protein aggregation, synaptic signaling pathways, mitochondrial function, oxidative stress levels, and inflammation, ultimately resulting in synapse dysfunction and neuronal loss in the AD brain. Herein we provide an overview of metals and metal-binding proteins and their pathophysiological role in AD.

Keywords: Amyloid beta; copper; iron; metal-binding; zinc

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

Essential trace metals and those with biological functions (biometals) play a vital role in many physiological processes in the human body. As free ion, some of them can participate in cellular signaling pathways, while bound to proteins they may have a structural or regulatory role in protein folding and function. The fact that about 10% of the genes in the human genome encode for proteins with zinc (Zn)-binding motif points to the evident dependency of biological processes on this trace metal. This number of Zn-binding proteins is not even accounting for Zn coordinated between two proteins in protein–protein interactions (1). In addition to Zn, several proteins and processes depend on other essential trace metals, the most important of which are iron (Fe), manganese (Mn), copper (Cu), and selenium (Se) (a metalloid). The average human body contains about 4.2 g Fe, 2.3 g Zn, 0.072 g Cu, 0.015 g Se, and 0.012 g Mn (2). However, the distribution of trace metals can vary depending on the organ considered. In the human brain, Fe is the most prevalent trace metal, which can be found both as heme (bound to hemoglobin in blood) and non-heme Fe. Heme-bound Fe may be a major contributor to the overall concentration. Therefore, Zn, the second most prevalent metal, may play an even more prominent role in the brain, which is underlined by its function as neurotransmitter/neuromodulator (3). Additionally, within the brain, some trace metals are enriched in particular brain regions (Figure 1). For example, the hippocampus is a brain region that is high in Zn, while the nucleus caudatus has higher levels of Fe than several other brain regions (4, 5). This unequal concentration of trace elements in different tissues demands a tightly regulated distribution. Given that charged molecules such as metal ions cannot freely pass the cellular membrane, a plethora of transport proteins evolved, with very specific regional and also developmentally and environmentally dependent expression. Especially, the regulation of metal concentrations in the brain faces a tight control at the level of the blood–brain barrier (BBB), a barrier composed of endothelial cells of the brain capillaries, pericytes, astrocytes, and the basement membrane (6). Together, they form a functional unit, mediating the exchange of trace metals between neurons, capillaries, and glia, while protecting against neurotoxicity of non-essential trace metals or excessive levels of essential trace elements. A specific set of transporters allows the crossing of trace metals into the brain. For example, only for Zn, 24 different transport proteins are known in humans (7), which allow the establishment of zinc homeostasis in tissues.

The maintenance of a balance between biometals is complicated by the influence different metals have on each other. Their concentration is regulated by complex interactions between trace metal ions and their ligands. For example, due to their physicochemical nature, Zn and Cu are known to compete for the binding sites of some transporters and metal-binding proteins, resulting in an antagonistic relationship, where low levels of Zn increase Cu levels and vice versa (8). Due to these interactions, the loss of, or increase in, one trace metal can lead to the establishment of a completely new biometal profile affecting many other trace metals of a system (9).

Metal homeostasis can be challenged in many ways. In fact, our body is not only exposed to essential trace metals. Through the environment (e.g., air, food,

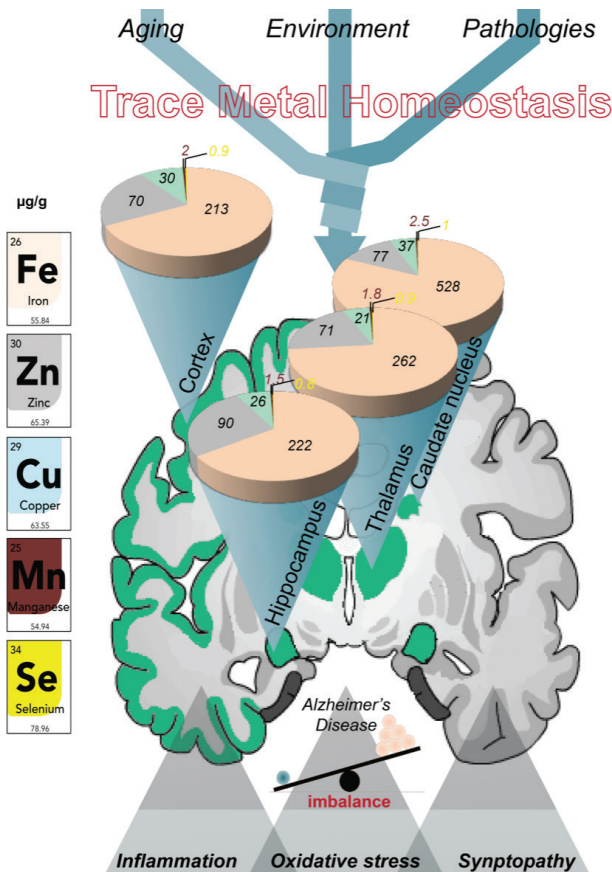


Figure 1 Trace metal concentration in different brain regions. Within the brain, trace metals are unequally concentrated in different brain regions. The figure shows the concentrations in µg/g brain tissue in the human cortex, hippocampus, thalamus, and caudate nucleus for Fe, Zn, Cu, Mn, and Se. This metal homeostasis can be challenged by environmental factors, the presence of pathologies such as aggregators of metal-binding proteins, and aging.

medical devices, and cosmetic products), other nonessential trace elements such as lead (Pb), mercury (Hg), and aluminum (Al) may enter our system. Indeed, these metals are present in all humans at low levels (e.g., 0.060 g Al, 0.012 g Pb, and 0.006 g Hg). Some of these metals are currently reported to have no or little effect on the body [e.g., titanium (Ti)], while others can produce adverse effects even at concentrations slightly above the normal background levels [e.g., Pb, Hg, and cadmium (Cd)]. These toxic effects are usually due to a chemical nature similar to that of an essential metal that allows binding to metal-binding sites of metal transporters and other proteins, leading to competition with essential trace metals. However, toxic metals are often not able to produce the biological effect of essential metals, and therefore, they act antagonistically. Recent evidences put synaptic signaling, synapse formation and

plasticity, oxidative stress, inflammation, and protein aggregation at the forefront of disease-relevant processes caused by abnormal trace metal homeostasis (Figure 1).

The enrichment of biometals in a tissue may occur through several mechanisms, such as mutations in metal import and export proteins, proteins buffering metals through transient binding (e.g. metallothioneins) (10), and also the abnormal accumulation of metal-binding proteins that occurs in several neurodegenerative diseases such as Parkinson's disease (alpha-synuclein protein) (11) and Alzheimer's disease (AD).

In AD, a contribution of abnormal trace metal homeostasis and signaling has been extensively reported (9). However, changes in trace metals' levels in AD are complex and can rarely be directly associated with systemic alterations that can be measured in easily accessible biosamples such as serum. The most likely reason for this is the ability of senile plaques to sequester specific metal ions that in turn become mislocalized instead of decreasing or increasing systemically. Cu, Zn, and, to a lesser extent, Fe are known to associate with senile plaques made of beta-amyloid (A β) protein (see below). It is hypothesized that this association causes several biological effects. For example, sequestration of Cu and Zn into plaques leads to an abnormal distribution of these metals, initially resulting in a deficiency of Cu and Zn in the vicinity of plaques (12, 13) and not throughout the whole brain.

Therefore, findings concerning alterations in metal ions in AD are highly dependent on the tissue and resolution used for analysis. Regarding essential metals, although results vary in some studies, Mn, Cu, Fe, and Zn seem to show an inverse correlation with senile plaque load and thus a decrease in the cerebrospinal fluid (CSF) (14) of AD patients.

The accumulation of trace elements, including Al, Pb, Hg, Cu, and Fe, has been implicated in AD through an increase in oxidative stress (15). In particular, a disruption in the homeostasis of Cu and Fe, two redox-active metals, may increase lipid peroxidation, and the oxidative damage to neurofibrillary tangles (NFTs), senile plaques, and nucleic acids (16). Oxidative stress is induced by an imbalance in the redox state, involving the generation of excessive reactive oxygen species (ROS) or the dysfunction of the antioxidant system (17). Cu is a potent mediator of the highly reactive hydroxyl radical (OH \bullet) and is highly concentrated in senile plaques. Consequently, Cu contributes to the increase of oxidative stress in AD. In addition, increased levels of Fe, transferrin, and ferritin may contribute to NFT formation, possibly due to the binding of Fe to the tau protein. In the brain, oxidative stress may cause serious damage via several mechanisms, including the release of excitatory amino acids and neurotoxicity (18). Although Zn is redox-inert, Zn signaling plays a role in the regulation of proteins (e.g., enzymes kinases and phosphatases) controlling redox-signaling pathways. Therefore, while not acting as an electron donor, Zn plays a role in redox biology, where zinc, in general, is considered as an antioxidant. However, these indirect antioxidant-like effects are present only in certain conditions and both a lack and excess of Zn can result in pro-oxidant effects (19).

In addition to changes in trace metal homeostasis resulting from AD, it is likely that alterations may also facilitate and trigger the development of AD pathology. For example, it has been shown that the levels of Zn decrease during

aging as a result of more restricted food choice (20, 21), which may facilitate inflammatory processes (22), increase oxidative stress (19), and decrease memory as seen in several animal models for Zn deficiency (23). More importantly, key proteins involved in the etiology of AD, and especially early-onset AD (familial AD), such as amyloid precursor protein (APP), presenilin 1 (PS1), and presenilin 2 (PS2), have been shown to bind to or regulate metals. For example, PS are important for cellular Cu and Zn turnover (24). Further, metals have been shown to interact with the two major disease-related proteins of AD, namely A β and tau.

METAL INTERACTIONS WITH APP

The APP is expressed in various tissues of the human body, in particular in the brain. Its general function within the brain has been linked to neurite outgrowth and neuronal cell migration (25). However, it becomes increasingly evident that APP can be considered to act as a metalloprotein, which is involved in the regulation of Cu, Fe, and ferroxidase homeostasis (26). Recent studies indicate furthermore that metals are involved in the proteolytic processing of APP.

APP displays two putative metal-binding sites, which are located within the E1 (124–189, APP770 numbering) and E2 (376–554) domains (27, 28). Cu binds to APP between residues 142 and 166 (29). It has been demonstrated that the two Cu-binding residues 149 and 151 are involved in the metabolism, folding and stability, and homodimerization of APP (30). Besides, Cu ions have been shown to promote cell surface localization of APP (31). Furthermore, it has been shown that cellular Cu levels can influence the expression of APP in vitro at both gene and protein levels (32).

APP also displays an evolutionary conserved Zn-binding site between amino acid positions 170 and 188 (33, 34). The binding of Zn to APP has been reported to play a similar role as Cu-binding in the homodimerization of APP (35) (Figure 2A).

Fe is involved in the direct regulation of APP translation. The APP mRNA displays an Fe response element (IRE) in its 5'-untranslated region (5'-UTR) sequence (36), and APP levels increase after a rise in cytosolic free Fe levels (37). Additionally, APP has been suggested to be involved in Fe export in the brain through the stabilization of ferroportin (Fpn). Deletion of APP in vitro in primary neurons impairs Fe export, which can be fully restored by the addition of APP (38).

A β is derived from APP by the sequential proteolysis by β - and γ -secretases. Metals have also been shown to indirectly influence A β generation by modifying the proteolytic processing of APP (28). Interestingly, all three secretases (α , β , and γ) involved in the enzymatic cleavage of APP interact with metal ions. The enzymatic activity of the α -secretase TACE is regulated by a "cysteine switch" motif, which is based on an intramolecular bond between cysteine (Cys) and a Zn atom in its catalytic site (39). Furthermore, the major β -secretase involved in APP processing displays a Cu-binding site in its C-terminal domain (40). Further, Zn has been shown to enhance the synthesis of PS1, the active subunit of the γ -secretase (41).

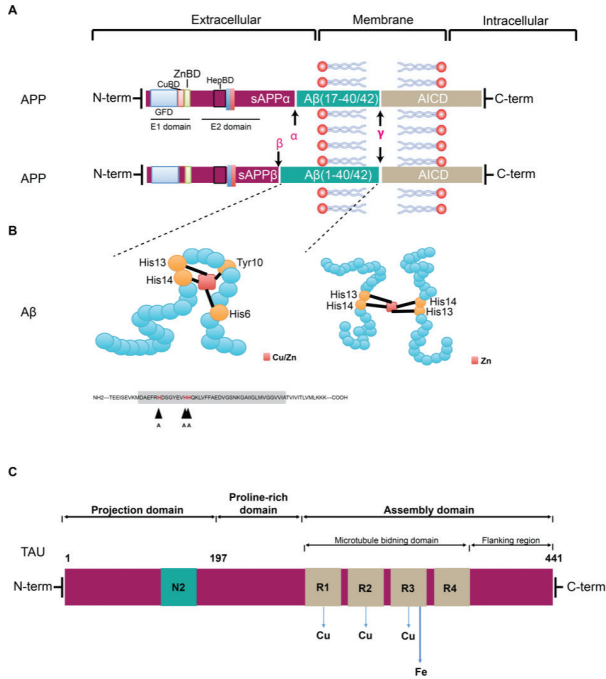


Figure 2 APP cleavage and APP and tau metal-binding sites. **A**) Cleavage of APP by α - and γ -secretases creates the sAPP α and A β _{17-40/42} fragments (upper panel). Cleavage by β - and γ -secretases creates the sAPP β and A β _{1-40/42} fragments (lower panel). The N-terminal part of APP contains a CuBD, copper-binding domain; ZnBD, zinc-binding domain; HepBD, heparin-binding domain; GFD, growth factor-like domain. **B**) Two of several possibilities of metal interaction with A β . Below: Sequence of A β , 3 His in the A β peptide domain of human wild type (wt) A β are important for metal coordination. **C**) Representation of the three main domains studied in tau protein. The picture shows the binding sites of Cu and Fe, respectively, through R1, R2, and R3 regions in the MTB ensuring the binding to the microtubules.

METAL INTERACTIONS WITH AMYLOID-BETA (A β)

The A β domain of APP is another region that can directly bind Zn and Cu ions; however until now, there is no evidence that this region interacts with metal ions prior to the enzymatic cleavage mediated by α -, β -, and γ -secretases (42) (Figure 2B).

Aggregation of A β into insoluble fibrils is a key pathological event in AD and is mediated by the interactions of A β with metals, in particular, Zn, Cu, and Fe. Early studies have shown that in particular, the histidine (His) residues in A β are responsible for the metal-mediated aggregation of A β (43). Interestingly, in mice and rats, the same His residues are not present, which might explain why these animals are more resistant to the amyloid pathology compared to other mammals (44).

The strong chelation properties of A β of Zn, Cu, and Fe explain the enrichment of these ions in amyloid plaques and suggest that one potential pathological influence of A β might be to sequester metal ions (45) and, through increasing concentrations of redox-active Cu and Fe ions in amyloid plaques, to promote oxidative stress.

Zinc and Amyloid-Beta

Zn is a factor contributing to the neurotoxicity of A β through the stabilization of amyloid fibrils (46). Various coordination sites have been proposed for the binding of zinc to A β with particular importance of His13 and His6. In vitro studies demonstrated that Zn induces the rapid and extensive aggregation of synthetic A β (34, 47), which might act as a seeding factor in the formation of amyloid plaques. In support of these studies, high levels of Zn have been found in the senile plaques of postmortem tissue of AD patients (45) and plaques of genetic AD mouse models. Interestingly, A β deposits fail to develop into mature plaques in the cerebellum where vesicular Zn is absent. Scavenging of Zn ions through A β may itself be a pathomechanism of AD. A locally decreasing Zn level in the vicinity of plaques contributes to synapse loss (13).

Copper and Amyloid-Beta

Homeostasis is fundamental for all metal ions, but for Cu it is critical because this metal is redox-active and can catalyze and activate O₂, generating reactive oxygen species (ROS) involved in oxidative damage. The soluble monomeric A β displays three high-affinity His Cu-binding sites (His6, His13, and His14), which along with the N-terminal amino group and aspartate form a tetragonal complex with Cu ions (48, 49). Cu(II) has been demonstrated to play a crucial role in the formation of β -sheet structures, which are thought to be a preliminary step of the toxic aggregates of the fibrillar form of A β . Thus, Cu binding to A β has been proposed to play a major role in the neurotoxicity of A β . In line with this, a series of studies have reported that Cu chelators rapidly induce the inhibition of A β accumulation in transgenic AD mouse models (50, 51).

Other essential trace metals and Amyloid-Beta

Because of Fe³⁺ hydroxide species precipitation, the binding of Fe³⁺ to A β seems implausible. Instead, Asp1, Glu3, and the three His residues (His6, His13, and His14) are involved in binding of Fe²⁺. However, iron mineral deposits in the cortical tissue may occur in vivo and contain magnetite (Fe₃O₄). They have been found in tissue extracted from human AD brain and brain from APP/PS1 transgenic mice (52). The aggregation state of A β appears to affect iron redox cycle and consequently may lead to the release of free radicals via Fenton chemistry. Interestingly, the degree of altered iron accumulations in AD is correlated with the amount of A β plaque pathology. However, these changes appear to occur after the development of the AD pathological hallmarks (53). Increased aggregation of

A β has been observed through the down-regulation of the enzymes that regulate the degradation of extracellular A β deposits induced by high Mn levels (54).

Toxic trace metals and Amyloid-Beta

Several studies have suggested that Al interacts with A β . Al has been detected in both the A β plaques and NFTs. Treatment of neuronal cultures with Al resulted in a marked accumulation of A β aggregates in vitro. However, the relevance of this for AD pathology in vivo is currently not well understood (48). Similarly, Hg exposure has been shown to promote the accumulation of A β deposits in vitro. Cd, like Mn, has been reported to reduce the expression of A β -degrading enzymes, resulting in an increased A β accumulation(48).

METAL INTERACTIONS WITH TAU

In AD, Tau aggregates due to hyperphosphorylation, abnormal splicing, or mutation in the tau encoding gene (55, 56). AD is the most common tauopathy among degenerative brain diseases. The tauprotein, with a molecular weight between 50 and 68 kDa, is encoded by a single gene (*MAPT*) located on chromosome 17q21 in humans. Tau is mainly localized in neuronal axons, but also dendrites (57), in the central nervous system (CNS). Tau is a microtubule-associated protein (MAP) implicated in the stabilization and integrity of microtubules (MT) in neurons, and its activity is regulated through a phosphorylation-dependent mechanism (58). In physiological conditions, tau is phosphorylated (facilitating the disassociation of the protein from the MT) and dephosphorylated (promoting the binding with MT) through the activity of tau kinases and phosphatases (59). In the human brain, under developmental control, six different isoforms of tau exist with a variation in size from 352 to 441 amino acids. The isoforms differ in the inclusion or exclusion of N repeats (0N or 1N or 2N) at the amino-terminal region and for the presence of three (3R) or four (4R) MT-binding domain (MTB) repeats (R) in the carboxyl-terminal part of the molecule (60).

The major domains identified in the tau protein are the *projection domain*, situated in the acidic N-terminal part, and the *assembly domain*, localized in the basic C-terminal domain. The two domains with the opposite charge are separated from one another by the *proline (Pro)-rich region*, situated in the middle part of the protein. Here, tau interacts with proteins containing an SH3 domain. Further, the Pro-rich region is the target of different Pro-directed kinases and also FYN-tyrosine kinases (61). The assembly domain, through R1–R4 repeat regions and flanking domain, binds microtubules and supports their assembly. This domain is the key in the regulation of the phosphorylation state of the tau protein (62). On the contrary, the projection part does not interact with microtubules but projects away from their surface interacting with other cytoskeletal elements, mitochondria or the neuronal plasma membrane (63, 64).

Phosphorylation of tau plays a crucial role in the pathogenesis of AD (65, 66) introducing negative charge(s) that promote an electrostatic interaction with metal ions (67) (Figure 2C). Tau abnormal phosphorylation leads to an abnormal structure, that is, polymerized into paired helical filaments (PHFs) which may further

aggregate to form NFTs, assuming the shape of a toxic protein deprived of the biological functions typical of the MAP family. It was reported that in AD brains, NFTs include metals, confirming an association between endogenous redox-active transition metals and metal-binding sites in tau (68). Binding of a series of metal ions including the essential biometals, Zn, Cu, Fe, Mg, and Mn, and non-essential trace metals, Pb, Cd, Hg, and Al, may promote tau hyperphosphorylation and induce tau aggregation. In contrast, Fe and lithium (Li) reduce the abnormal phosphorylation of tau (48). For this reason, biometal homeostasis is essential, and the disruption of this balance may play a key role in the pathogenesis of AD.

Zinc and Tau

A disruption in the Zn homeostasis leads to a series of pathogenic conditions in the AD brain, including the formation of NFTs composed of hyperphosphorylated tau. Recent studies show that Zn is involved in the mechanism of tau hyperphosphorylation via two different interactions: *in vitro*, Zn can directly affect tau at serine (Ser) and Pro sites, at threonine (Thr) and Pro sites or via two Cys residues: C291 and C322 (69). At the same time, Zn can indirectly hyperphosphorylate tau protein, by activating kinase and phosphatase pathways, for example activating Raf/mitogen protein kinase and inhibiting phosphatases such as PP2A (70, 71).

These two independent ways of action have different effects on tau toxicity. It has been demonstrated that the direct interaction between tau and Zn plays an important role in tau toxicity: after removing the Zn-binding site, tau toxicity is completely abolished, assuming that the toxic effect of tau necessitates both the presence of hyperphosphorylation and Zn bond. Tau hyperphosphorylation pathways appear to be less toxic, compared to tau toxicity that occurs from the direct binding between tau and Zn (72). Recently, it has been discovered that Zn could be considered a catalyst, accelerating the aggregation of tau-R3 complexes and, at the same time, promoting the formation of tau oligomers (73, 74). Thus, correct Zn homeostasis in AD is fundamental because abnormally high concentrations of this mineral induce the development of granular tau aggregates, while abnormally low concentrations of Zn lead to amyloid fibril formation (75).

Copper and Tau

A high concentration of Cu (0.4 mM) was reported in amyloid plaques and NFTs. Thereby, NFT may be linked to high levels of redox-active Cu (68). Besides, Cu is involved in tau hyperphosphorylation by activating the cyclin-dependent kinase (CDK)5/p25 complex. Tau hyperphosphorylation resulting from the activation of GSK-3 β kinase by Cu is controversial: some studies suggest that GSK-3 β kinase is activated by Cu (76, 77), while other studies propose that GSK-3 β kinase may not necessarily be involved in the abnormal phosphorylation of the protein (78). The binding between tau and Cu is highly selective. Studies revealed that the full-length Human Tau40 isoform (K32) can bind one Cu for each monomer (1:1 binding stoichiometry) with a dissociation constant (K_d) close to 1 μ M via two Cys residues. The sequences mediating the binding of Cu are ²⁸⁷VQSKCGS²⁹³ and ³¹⁰YKPVDSLKVTSKCGS³²⁴. An analysis conducted by circular dichroism and nuclear magnetic resonance (NMR) spectroscopy showed only limited formation

of aggregates after binding Cu because the addition of Cu to K32 does not affect the secondary structure, and thus, tau remains mostly disordered (79). In vitro, it has been demonstrated that Cu can bind different tau fragments containing diverse MTBR such as R1 and R2, showing alterations in the secondary structure (80, 81). Furthermore, the interactions between tau R2 and Cu lead to the production of H_2O_2 (82). The repeat R3 can be associated with more than one Cu ion via two His residues (83).

The role of Cu-binding to tau remains controversial, although some studies suggest that the binding between Cu and tau inhibits the formation of abnormal aggregates in vitro (78, 81). For example, increasing intracellular Cu levels by the addition of Cu–bis (thiosemicarbazone) complexes, inhibits tau hyperphosphorylation (76).

Iron and Tau

Fe dysregulation is linked to oxidative stress in tauopathies. Fe, as Zn and Cu, interacts with some of the isoforms of the tau protein, causing irreversible structural changes. The result of this interaction is protein aggregation and/or oxidative stress, through the Fenton reaction, perpetuating a condition of cellular damage. Analysis of postmortem AD brains shows increased Fe levels in several brain regions (84).

In the human body, Fe is available in two oxidation states: Fe^{3+} (redox-inert state) that is stored in ferritin and Fe^{2+} (redox-active). The iron status associated with NFTs in AD is Fe^{3+} , which can induce the aggregation of hyperphosphorylated tau. Fe-binding sites using His residues have been identified in tau (85). The hyperphosphorylated status of tau may not involve Fe^{3+} interacting with the protein, but Thr phosphorylation can regulate the interaction between tau and Fe^{2+} (86). Thus, the phosphorylation level of tau causes conformational changes of tau to mediate tau–Fe interactions (87). In addition to a direct interaction, Fe induces tau hyperphosphorylation, both in vitro and in vivo, by activating the CDK5/p25 complex and GSK-3 β and MAP kinases (88). This evidence suggests a possible role of iron involved as a co-factor for tau aggregation.

Other essential trace metals and Tau

In AD patients, Mg levels appear lower (540–625 $\mu\text{g/g}$) compared to the physiologic range (620–680 $\mu\text{g/g}$) (89). In vivo, data obtained from an AD transgenic mouse model show that Mg increases the phosphorylation of the GSK-3 β kinase at Ser9, which in turn reduces the hyperphosphorylation of tau protein (90). Additionally, in postmortem brains of patients affected by AD, the level of Mn appears to be higher (91). An increase of Mn levels is related to abnormal tau aggregation and its hyperphosphorylation, mediated by GSK-3 β kinase (92).

Toxic trace metals and Tau

Al is the most widely exogenous metal ion distributed in the environment. As Fe^{3+} , Al^{3+} is a trivalent cation that influences protein phosphorylation of tau (93, 94). Recent data show that Al can promote the formation of sodium dodecyl

sulfate (SDS)-resistant tau oligomers after tau phosphorylation (95). The role of Al in AD has been intensively investigated since NFT-like deposits were discovered in mammalian brains after intracerebral Al injection (96). Al has been shown promoting tau aggregation through the down-regulation of PP2A activity and an increase of CDK5 and GSK-3 β kinase levels (97). Thus, Al, although not directly binding to tau, may have a role as co-factor in AD (98).

Further, heavy metals such as Cd, Pb, and Hg have been implicated in AD pathology (99). Data show that Cd is involved in the formation of NFTs (100, 101). Both in cell models and in *in vivo* studies, Cd increases the activation of GSK-3 β kinase, causing the hyperphosphorylation of tau (102). Similarly, Pb has been reported to modulate tau aggregation by increasing the activity of CDK5/p25 complex and GSK-3 β kinase (103). Hg was demonstrated to inhibit tubulin that has a very high-affinity binding-site for Hg (104). Once Hg binds tubulin, the structural integrity of the protein is impaired. The final result of this interaction between Hg and tubulin is the formation of NFTs (105). Also, Hg is involved in tau hyperphosphorylation; the mechanism starts with the oxidative stress induced by Hg, ultimately affecting tau phosphorylation status (106).

OTHER METAL-BINDING PROTEINS AND THEIR ROLE IN AD

Several of the effects of an altered trace metal status in AD such as increased oxidative stress, neuroinflammation, and effects on synapses are mediated by excess or lack of trace metals for binding to proteins other than A β and tau. Together with several other factors in AD, oxidative stress leads to an activation of the immune system. The immune system is highly dependent on trace metal biology. Especially, Zn signaling seems to be a key mediator of inflammatory responses. For example, the activity of NF- κ B (nuclear factor kappa-light-chain-enhancer of activated B cells), a major regulator of pro-inflammatory cytokines such as interleukins (IL) (107), is regulated, among others, by Zn through Zn binding of the IKK (I κ B kinase) complex member IKK β (108). Further, the formation of senile plaques made of A β aggregates stimulates inflammasomes, such as the NLRP3 (nucleotide-binding domain and leucine-rich repeat-containing family, pyrin domain-containing-3) inflammasome that detects the inflammatory A β aggregates and responds by forming active IL-1 β through secreting caspase-1 (Casp-1) (109). IL-1 β acts as an inflammatory cytokine (110), which leads to the creation of an inflammatory environment around the plaque. This ultimately decreases plaque degradation and destruction by microglia cells. Zn deficiency and/or high Cu levels facilitate NLRP3 inflammasome activation (111) and thereby the production of IL-1 β in macrophages (112).

Initially, Pro-IL-1 β is expressed in response to damage-associated molecular patterns (DAMPs) that bind to pattern recognition receptors (PRRs) on the macrophage to upregulate pro-inflammatory gene expression. Inflammation, protein misfolding, and aggregation, as well as neurodegeneration, lead to increased levels of so-called alarmins or DAMPs that include several cytokines including those from the S100 family. The S100 proteins are engaged in classical calcium-activated signaling but recent work has shown their involvement in new biochemical mechanisms in the brain related to the prevention of protein aggregation (113) and

sensing of neuronal Ca and Zn levels (114). Therefore, S100 alarmins are implicated in the maintenance of protein homeostasis (proteostasis) and metal ion homeostasis (metallostasis) in the brain. Upon activation and at high (μM) concentrations, S100 proteins act as extracellular cytokines via RAGE (receptor for advanced glycation end-products) mediated signaling. RAGE persistent engagement increases S100 extracellular levels via NF- κB activation resulting in a positive feedback cycle (115). Glial S100B and S100A9 proteins show increased expression in response to several risk factors for AD, including aging (116). Interestingly, S100B undergoes metal-binding-induced conformational changes and thereby delays the onset of A β aggregation by interacting with A β_{1-42} monomers inhibiting primary nucleation (113). However, high levels of S100B can elicit alterations in intracellular Zn concentrations (114).

The increase in S100B proteins and accumulation of A β as a factor for trace metal imbalances also has direct effects on Zn signaling at excitatory glutamatergic synapses. It has been shown that the dynamics of major postsynaptic scaffold proteins of these synapses (SHANK2 and SHANK3) are dependent on Zn availability (117). Studies have shown that SHANK platform disassembly is linked to the molecular pathology of AD (118, 119), and recent research confirmed that the progressive accumulation of A β results in decreased Zn concentrations at the synapse, which in turn leads to disruption of SHANK3 scaffold formation, and ultimately, loss of synapses (13). Thus, Zn sequestration by protein aggregates in AD may be a contributor to the cognitive impairments caused by the loss of synapses through trapping synaptic Zn rather than through neurodegeneration in general (120). In addition, NMDA receptors at synapses are Zn-binding proteins (121). Increased trapping of Zn lowers the inhibitory activity of Zn on the NMDAR. Excessive stimulation of receptors at the excitatory synapse has been linked to neuronal death through excitotoxicity leading to chronic neurodegeneration in AD (122). Together, these metal-imbalance-driven signaling pathways create a vicious cycle leading to increased inflammation, oxidative stress, and neuronal damage (Figure 3).

METAL DETECTION FOR AD DIAGNOSIS

Several metal bioimaging strategies have been developed not only to examine the distribution of metals in human clinical AD brain tissue and AD mouse models but also to diagnose and monitor the progression of AD (123). In the clinical setting, the most common imaging tool is magnetic resonance imaging (MRI). This technique focuses on Fe due to its magnetic properties and its abundance in the brain. The latest MRI technology provides sufficient resolution to detect regional differences and has the major advantage that it can be applied to living patients rather than being a tool for postmortem analysis only (124). The presence of localized Fe can be detected by MRI (T2). However, although detecting general metal dyshomeostasis, MRI has limitations in visualizing metal-loaded plaques directly with high resolution. Further development of metal-based compounds or compounds visualizing metal homeostasis, such as a Cu-64-labelled-bis (thiosemicarbazonato) complex for clinical application in positron emission tomography (PET), and improvement of imaging devices may lead to more precise

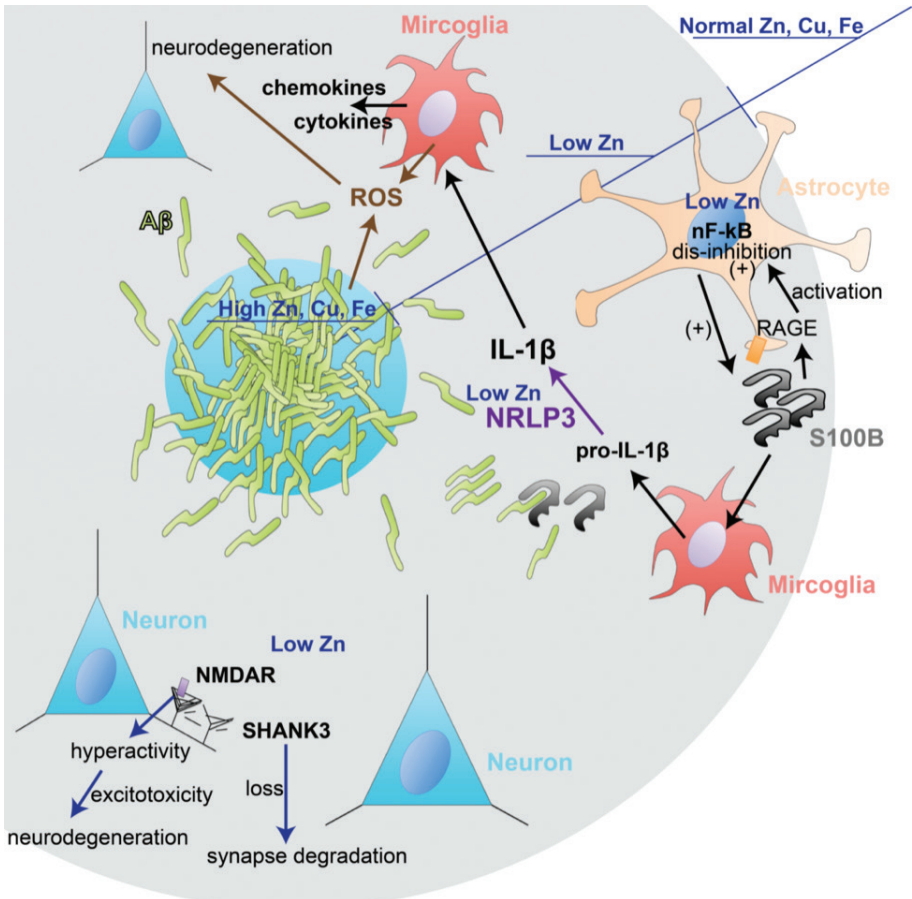


Figure 3 Interaction between A β plaques, glial cells and trace metals. Senile plaques sequester large amounts of Zn, Cu, and Fe, creating a zone of metal depletion, especially Zn depletion, in their vicinity. While high levels of Cu and Fe at the center of plaques may contribute to the generation of ROS and damage neurons through oxidative stress, Zn deficiency in a zone surrounding plaques will lead to further effects: Accumulation of A β aggregates leads to the release of S100B from astrocytes. S100B as DAMP can initially prevent A β aggregation. However, S100B signals back to astrocytes via RAGE receptor activation that will, in turn, activate NF- κ B. Active NF- κ B is dis-inhibited by low levels of Zn and thus results in further production of S100B, which enters a positive feedback cycle. High levels of S100B further deplete Zn through Zn binding. In response to high DAMP levels (S100B), microglia cells will produce pro-IL-1 β . This will be cleaved by Casp-1-dependent processes through the NLRP3 inflammasome. NLRP3 activity is further increased by low Zn levels. Production of IL-1 β leads to further generation of ROS and release of cytokines and chemokines from microglia cells that facilitate NFT formation and neurodegeneration. Further, low Zn levels facilitate excitotoxicity through dis-inhibition of NMDAR signaling, and low levels of Zn destabilize the postsynaptic Shank3 scaffold resulting in synapse loss.

diagnosis and monitoring of progression and therapeutic effects based on the role of trace metals in AD in the future (124).

METALS HOMEOSTASIS AS A THERAPEUTIC STRATEGY FOR AD

Based on the interactions of metals with several key proteins of the AD pathology, different therapeutic approaches aimed at restoring or manipulating metal homeostasis and, thereby, regulating oxidative stress, tau phosphorylation, A β aggregation, and inflammation have been developed in the last decade.

For example, metallothionein 3 (MT-3), a key regulator of metal homeostasis in neural tissue, has been found down-regulated by up to 30% in AD brains. Given that MT-3 contributes, among others, to detoxification and storage of heavy metals, regulation of Cu and Zn metabolism, and modulation of A β endocytosis of astrocytes (125), increasing MT-3 levels in AD has been explored as therapeutic strategy. In vivo studies demonstrated that effects of Zn-loaded MT-3 treatment in a mouse model for AD (Tg2576 mice) are inconsistent if MT-3 is injected subcutaneously. However, MT-3 injected intracerebroventricularly is able to ameliorate behavioral deficits and hippocampal impairments in APP/PS1 mice. In these mice, MT-3 treatment was also able to restore metal homeostasis, inhibit A β aggregation, and reduce oxidative stress and neurodegeneration (125).

Another interesting treatment strategy is based on metal protein attenuating compounds (MPACs): Clioquinol (CQ) represents the prototypic MPAC. It is a small hydrophobic molecule that can cross the BBB and that has moderate affinity for metal ions. When administered to Tg2576 mice, a 49% decrease of A β in the brain of AD model mice compared to control mice was shown (126). In humans, oral CQ treatment for 36 weeks of severely affected AD patients was able to significantly prevent cognitive deterioration. Subsequent clinical studies of this compound were not pursued. However, PBT2, a highly soluble derivate of CQ (a second-generation MPAC), has been used first in APP/PS1 mice and then in human clinical trials (phase I and II). The results showed improved cognitive performance and reduced A β load in the mouse model. A 12-week-long treatment of 78 patients with early AD showed that PBT2 is safe (127). Although the effects of PBT2 were inconsistent, executive dysfunction was significantly reduced in the patients. Several other metal chelators were engineered over the last years, and most of them are currently investigated for use in AD. Some of them have been shown to be effective at inhibiting A β -metal interactions both in vitro and in vivo. For example, it has been demonstrated that the normally insoluble A β deposits of postmortem brain tissue from AD patients can be solubilized in aqueous media in the presence of specific Cu chelators (128).

Another promising approach is the delivery of metals directly to the brain using nanotechnological approaches. Polymeric g7-poly-lactide-co-glycolide (PLGA) nanoparticles (NPs) are able to cross the BBB and release metals within the brain. This system has been considered as a Trojan horse strategy to effectively deliver Zn to the brain with a low-toxicity profile (129). Three hours after ip injection of NPs, an increase of Zn levels in the brain and the increase of zinc-sensitive

genes such as MT and Zn transporters were seen (130). The same pharmacological approach applied to APP23 mice, an animal model of AD, showed promising effects such as A β dis-aggregation, a reduction of inflammation, and synapse stabilization (129). Thus, both redistribution of metals bound to A β through MPACs and increase in metal levels that has dropped through trapping of metals in A β deposits have beneficial effects. However, additional research is necessary to re-define time point of application, duration, and concentration of NP-based metal delivery.

CONCLUSIONS AND FUTURE PERSPECTIVES

In general, impaired biometal homeostasis and/or the accumulation of non-essential trace metals have significant effects, most prominently on proteotoxic stress, synapse function, oxidative stress, and inflammatory processes. Building on the metal-binding abilities of key proteins in AD, brain imaging-based methods for the diagnosis of AD in humans have been, and are, currently developed. However, despite improving techniques for the detection of trace metals in the brain, re-establishing metal balances remains a difficult task. Initial studies using Zn ionophores have been promising and showed that targeting metal homeostasis in AD may be one of the most auspicious therapeutic strategies. However, new targeted and improved approaches are needed in the future.

Acknowledgments: The authors acknowledge the networking support by the COST Action TD1304 (Zinc-Net).

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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N-Terminally Truncated A β Peptide Variants in Alzheimer's Disease

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch7>

Abstract: The accumulation and aggregation of amyloid- β (A β) peptides in the brain is believed to be the initial trigger in the molecular pathology of Alzheimer's disease (AD). In addition to the widely studied full-length A β peptides (mainly A β ₁₋₄₀ and A β ₁₋₄₂), a variety of amino-terminally truncated (N-truncated) peptides, such as A β _{PE3-x} and A β _{4-x}, have been detected in high abundance in autopsy samples from sporadic and familial AD patients. N-truncated A β species adopt specific physicochemical properties resulting in a higher aggregation propensity and increased peptide stability, which likely account for their neurotoxic potential. The presence of N-truncated A β peptides in transgenic mouse models of AD and the selective overexpression of specific N-truncated variants in the murine brain have facilitated their investigation in relevant *in vivo* settings. In this chapter, we address the pathological relevance of N-truncated A β peptide species and summarize the current knowledge about the enzymatic activities that might be involved in their generation.

Keywords: ADAMTS4; Alzheimer's disease; amyloid; N-truncation; protease

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

The deposition of extracellular plaques consisting of amyloid- β ($A\beta$) peptides in the brain parenchyma is one of the neuropathological hallmarks of Alzheimer's disease (AD). Although these deposits have also been found in non-demented control individuals, they are believed to play an important role in the disease process, and their presence and abundance is an obligatory criterion for a diagnosis of AD. Full-length $A\beta$ peptides composed of 40 ($A\beta_{1-40}$) or 42 ($A\beta_{1-42}$) amino acids constitute the main components of extracellular amyloid plaques, together with other proteins such as ubiquitin and different proteoglycans. These peptides are generated by sequential proteolytic cleavage of the amyloid precursor protein (APP), a large type-I transmembrane protein that in rare families was found to carry mutations causative of inherited cases of AD. After an initial cleavage by either α - or β -secretase, which facilitates shedding of the APP ectodomain, the remaining membrane-bound β - or α -C-terminal fragments (CTFs) are cleaved by γ -secretase within their transmembrane domains. In the latter case, a small peptide fragment named p3 is released, while the cleavage of β -CTFs results in the generation of $A\beta$ peptides (1) (Figure 1).

The analysis of brain samples from non-demented control cases, pathological aging (which is being regarded as a prodromal phase of AD), and AD revealed that, apart from full-length $A\beta_{1-40}$ and $A\beta_{1-42}$, N-truncated $A\beta_{x-42}$ species were the most abundant in AD with considerable overlap in pathological aging samples (2). This is interesting from a pathological point of view as full-length $A\beta$ peptides are normal metabolites generated under physiological conditions. The exact physiological function of these peptides remains unresolved; however, it has been hypothesized that modulation of endogenous $A\beta$ production might play an important role in the regulation of neuronal activity via a feedback loop mechanism (3). Other possible physiological functions include promoting recovery from traumatic brain injury, sealing leaks in the blood-brain barrier, or antimicrobial activities (4). While full-length $A\beta$ peptides starting with an aspartic acid (Asp) residue at position 1 of the $A\beta$ sequence are generated by an enzymatic activity called β -site APP cleaving enzyme 1 (BACE1) (5, 6), much less is known about the proteases responsible for the production of N-truncated $A\beta$ peptides.

$A\beta$ peptides with varying N-termini were described more than 30 years ago. In 1984, the identification of full-length $A\beta$ peptides starting with an Asp residue in position 1 purified from cerebrovascular amyloid deposits was reported (7). The following year, N-terminal sequencing of $A\beta$ peptides purified from amyloid plaque cores from AD cases demonstrated the presence of peptides starting with phenylalanine (Phe) in position four ($A\beta_{4-x}$), as well as with serine (Ser) or glycine (Gly) in position eight ($A\beta_{8-x}$) or nine ($A\beta_{9-x}$) (8, 9). By means of immunohistochemistry, N-truncated $A\beta$ species with post-translational modifications such as pyroglutamylation at position 3 ($A\beta_{pE3-x}$) and 11 ($A\beta_{pE11-x}$) were subsequently described in human AD brains (10, 11). The loss of charged amino acids at the N-terminus changes the biophysical properties of the $A\beta$ peptides, thus influencing their aggregation propensity and toxicity. As a consequence, efforts to understand the relevance of N-truncated $A\beta$ species in the pathogenesis of AD, as well as the mechanisms responsible for their generation, have recently increased.

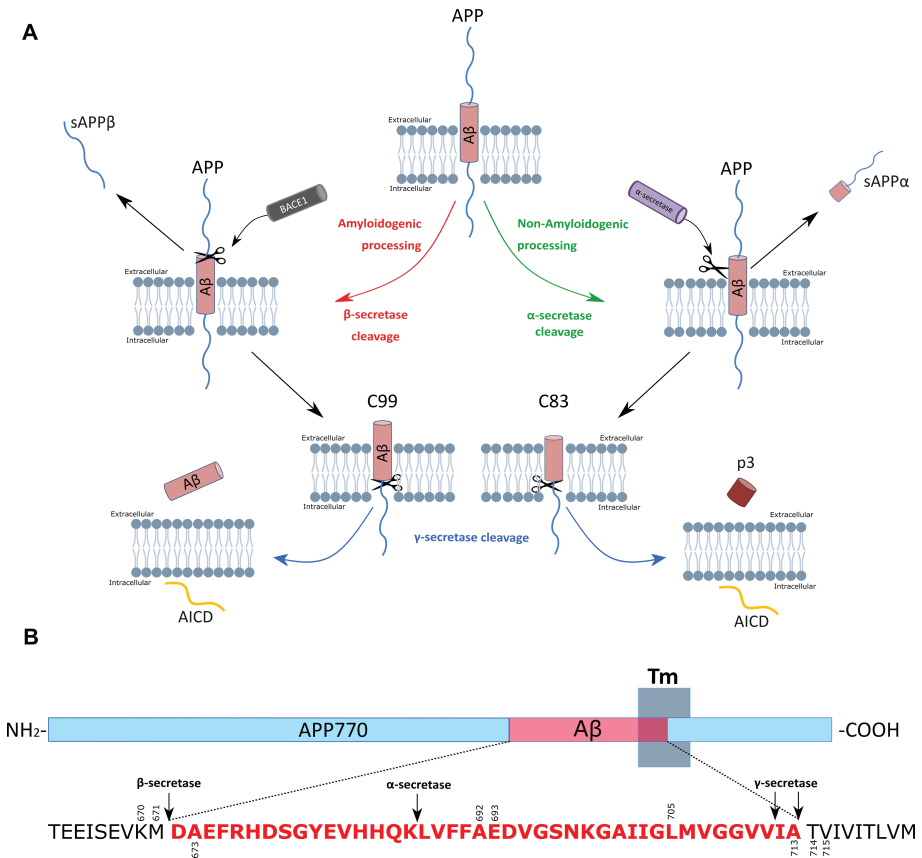


Figure 1 APP processing pathways. **A**) The non-amyloidogenic processing pathway (depicted on the right) is initiated through cleavage by α -secretase, which cleaves within the A β domain and generates the soluble ectodomain sAPP α . Subsequent cleavage of the membrane-bound C-terminal APP fragment C83 by the γ -secretase complex releases the soluble fragments p3 and the APP intracellular domain (AICD). Amyloidogenic APP processing (left panel) is initiated by β -secretase cleavage with the liberation of the soluble sAPP β fragment. The remaining C-terminal fragment C99 is then cleaved by γ -secretase generating A β peptides as well as AICD. **B**) APP is a large transmembrane protein containing up to 770 amino acids. The A β peptide sequence (in red) starts within the ectodomain and ends within the transmembrane (TM) domain.

HETEROGENEITY OF N-TRUNCATED A β SPECIES IN AD BRAIN

Several studies employing mass spectrometry (MS) that intended to analyze the full spectrum of A β peptides in postmortem brain samples of AD patients have been published. In the earliest of these studies, purified amyloid core and cerebrovascular amyloid peptides were sequenced using matrix-assisted laser-desorption-time-of-flight (MALDI-TOF) mass spectrometry. While the amino acid composition of cerebrovascular A β peptides consisted mainly of species

starting with residues 1 or 2, the preparations from amyloid cores were more heterogeneous, corresponding to peptides beginning with every residue between Asp-1 and Glu-11 (Figure 2), with major signals for peptides starting with Phe-4, Ser-8, and Glu-11 (12). In good agreement, using surface-enhanced laser desorption/ionization time-of-flight (SELDI-TOF) mass spectrometry, $A\beta_{4-42}$ was also identified as the major N-truncated species in postmortem brain samples from aged controls, patients with vascular dementia, and AD patients (13). This suggested that N-truncated species account for a substantial proportion of total $A\beta$ in the aged human brain, a finding that was corroborated in subsequent studies. The entire spectrum of $A\beta$ peptides ranging from $A\beta_{1-x}$ to $A\beta_{pE11-x}$ was detected in frontal cortex samples of a sporadic AD case and of an individual affected by the FAD-associated presenilin (*PSEN1*) V261I mutation. This mutation is associated with the deposition of the so-called cotton wool plaques, which are lesions lacking a central amyloid core (14). By investigating non-demented individuals with incipient amyloid pathology as well as AD patients, it was further demonstrated that initial insoluble $A\beta$ aggregates are largely composed of N-truncated $A\beta_{42}$ variants such as peptides starting at positions 4-, 5-, 8-, or 9-42 (15). Portelius et al. also studied the $A\beta$ isoform pattern in the hippocampus, cortex, and cerebellum of non-demented controls, sporadic AD cases, and patients suffering from familial AD (FAD). In all groups, $A\beta_{1-42}$, $A\beta_{1-40}$, $A\beta_{pE3-42}$, and $A\beta_{4-42}$ were identified as the dominant isoforms (16), which is in good agreement with the most recent studies from other investigators (2, 17, 18).

N-TERMINALLY TRUNCATED $A\beta$ SPECIES IN TRANSGENIC MOUSE MODELS OF AD

Transgenic mouse models overexpressing mutant forms of human APP, either alone or in combination with mutant forms of *PSEN1* or *PSEN2*, are valuable and

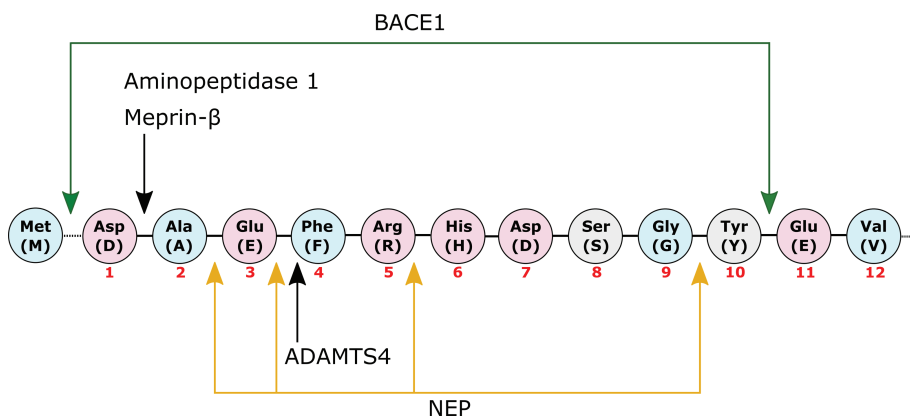


Figure 2 Sequence of the $A\beta$ N-terminus with indicated cleavage sites and enzymes involved in the generation of N-truncated $A\beta$ species. Amino acids (AA) are color-coded according to their properties (red: charged AA; grey: uncharged AA; blue: nonpolar hydrophobic AA).

widely used model systems to study AD-associated pathological alterations such as extracellular amyloid deposition, inflammatory responses, and cognitive deficits (19–21). The analysis of A β peptide species in brain samples using mass spectrometry revealed that most transgenic AD mouse models only partially reflect the A β spectrum in human sporadic AD. While the overall heterogeneity of N-terminal truncated A β species could be reproduced in mouse models such as APP/PS1KI (22) or 5XFAD (23, 24), the ratio of full-length A β peptides to N-truncated variants is much different in human brain samples. While N-truncated variants such as A β_{pE3-x} or A β_{4-x} might be present in comparable quantities compared to full-length A β_{1-40} or A β_{1-42} species in human samples (16), full-length peptides comprise by far the majority of all A β peptides in transgenic AD models (23, 25, 26). This is likely explained by the fact that most of these models (e.g., Tg2576 (27), APP23 (28), APP/PS1KI (22), 5XFAD (29), or APP^{swe}/PSEN1^{dE9} (30)) utilize the Swedish APP mutation. Cell lines transfected with the Swedish APP670/671 mutation have been shown to release three to six times more A β peptides than wild-type cells (31, 32). Due to the location of the double mutation in the immediate vicinity of the β -secretase cleavage site (Figure 1), the Swedish mutation increases the affinity of the substrate APP for BACE1, thus favoring the generation of full-length A β peptides starting with Asp in position 1 (33).

Using two-dimensional gel electrophoresis with subsequent mass spectrometry analysis, a variety of N-truncated A β species have been detected in APP/PS1KI mice. While full-length A β_{1-42} peptides were already detectable in young mice at 2.5 months of age, other A β variants such as A $\beta_{2/3-42}$, A β_{pE3-42} , and A $\beta_{4/5-42}$ became apparent only at later time points (22). Mass spectrometry analyses have also supported that N-truncated species represent only a small percentage of the total A β peptide amount in mouse models such as 5XFAD or APP23, although variable ionization efficiencies for the different A β species might contribute to a distorted image of the A β peptide composition in both mouse and human brains (23, 34). In conclusion, N-truncated A β species are substantially underrepresented in transgenic mouse models compared to human AD brain samples (34, 35).

MAJOR N-TERMINAL TRUNCATED A β SPECIES DETECTED IN HUMAN BRAIN

As pointed out above, a huge variety of different N-terminal truncated A β species has been identified by either MS or immunohistochemical staining methods in brain samples from human AD patients. In this section, we discuss the current knowledge on the most important variants in more detail.

A β_{2-x}

In AD patients, a consistent elevation of A β peptides lacking the N-terminal Asp residue have been observed in the detergent-soluble pool of brain extracts, as well as in cerebrospinal fluid (CSF) samples (36). Using SELDI-MS, several A β peptides including those starting with Ala-2 were found in extractions from senile plaques (13). Immunohistochemical analysis of postmortem brain samples using

an $A\beta_{2-x}$ -specific polyclonal antibody confirmed the presence of $A\beta_{2-x}$ peptides in both parenchymal and vascular deposits of sporadic AD cases as well as transgenic mouse models such as APP/PS1KI or 5XFAD (37). As the sequence of full-length $A\beta$ starts with an Asp residue in position 1, it has been suggested that proteolysis of $A\beta_{1-x}$ peptides by the exopeptidase aminopeptidase A, which releases Glu and Asp residues from the N-termini of proteins, could result in the generation of $A\beta_{2-x}$ species (38). However, the evidence in this study was limited to showing that Western blot immunoreactivity with an $A\beta_{1-x}$ -specific antibody was reduced after the co-incubation of purified aminopeptidase A with recombinant full-length $A\beta_{1-40}$ peptides (Table 1). The identity of specific degradation products and, in particular, the generation of $A\beta_{2-x}$ species, was not confirmed by mass spectrometry or other methodology (38). In contrast, it has been convincingly demonstrated in cell-free and cell-based assays that cleavage of APP or $A\beta$ by the metalloprotease meprin- β can result in the generation of $A\beta_{2-x}$ species (39, 40). In both HEK293T and CHO cells, co-expression of human APP and meprin- β facilitated the secretion of $A\beta_{2-40}$ peptides, whose identity was confirmed by mass spectrometry, and this was blocked by treatment with a γ -secretase but not a β -secretase inhibitor, indicating that $A\beta_{2-40}$ peptides were produced through a BACE1-independent mechanism. Later, these results were partially confirmed by another group (41). Still missing is in vivo proof that meprin- β is responsible for the brain production of $A\beta_{2-x}$ peptides in AD mouse models. However, this experiment is complicated by the fact that meprin- β does not generate $A\beta_{2-x}$ peptides with Swedish mutant APP as a substrate, which excludes most of the commonly used APP-transgenic strains as in vivo model systems (40).

$A\beta_{pE3-x}$

Pyroglutamate-modified $A\beta_{pE3-x}$ represents a major $A\beta$ species identified in human AD brains (16, 50). In 1995, Saido et al. reported the identification of these

TABLE 1
List of proteases involved in the generation of N-truncated $A\beta$ species

Protease	Levels/activity in human AD brain versus control	Cleavage site	Potential $A\beta$ peptides	References
BACE1	Increased (42)	Met(-1) ↓ Asp(1) Tyr(10) ↓ Glu(11)	$A\beta_{1-x}$ $A\beta_{11-x}$, $A\beta_{pE11-x}$	(6)
Aminopeptidase A	Reduced (43)	Asp(1) ↓ Ala(2)	$A\beta_{2-x}$	(38)
Meprin- β	Unknown	Asp(1) ↓ Ala(2)	$A\beta_{2-x}$	(39, 40)
Nephrilysin (NEP)	Increased (44) Reduced activity (45)	Asp(2) ↓ Ala(3) Ala(3) ↓ Phe(4) Arg(5) ↓ His(6) Gly(9) ↓ Tyr(10)	$A\beta_{3-x}$, $A\beta_{pE3-x}$ $A\beta_{4-x}$ $A\beta_{6-x}$ $A\beta_{10-x}$	(46, 47) (48, 49)
ADAMTS4	Unknown	Ala(3) ↓ Phe(4)	$A\beta_{4-x}$	(24)

post-translationally modified peptides in which the glutamate at position three becomes converted to pyroglutamate through intramolecular dehydration (51). This cyclization alters the physicochemical properties of A β and results in increased hydrophobicity due to the loss of a negative charge, faster aggregation kinetics compared to full-length A β peptides in *in vitro* assays (52–54), and increased insolubility and stability (55). Importantly, higher abundance of these peptides in AD as compared to age-matched non-demented control patients has been demonstrated (56–58). With regard to their toxic properties, increased neurotoxicity compared to full-length A β peptides (59) has been reported; however, some studies found full-length and A $\beta_{\text{pE3-x}}$ peptides to be equally toxic (60, 61), while others suggested that A β /A β_{pE} hetero-oligomers constitute the main neurotoxic A β fraction (62). Interestingly, related properties have also been reported for pyroglutamylated ABri and ADan peptides, representing the major peptide species accumulating in the neurodegenerative disorders familial British dementia and familial Danish dementia (63, 64).

The formation of A $\beta_{\text{pE3-x}}$ peptides appears to be at least a two-step process, with removal of the first two amino acid residues from full-length A β followed by cyclization. Recently, it has been suggested that meprin- β might not only generate A β_{2-x} but also A β_{3-x} peptides as substrates for cyclization (41). However, A β_{3-x} peptides were not detected in an earlier study by mass spectrometry (39), and whether genetic deletion of meprin- β would reduce A $\beta_{\text{pE3-x}}$ peptide formation *in vivo* is unknown. In contrast, solid evidence supports that glutaminyl cyclase (QC) is at least one of the enzymes capable of catalyzing the second step of A $\beta_{\text{pE3-x}}$ formation (65). Treatment using an orally available QC inhibitor resulted in a reduction of the A $\beta_{\text{pE3-42}}$ burden in transgenic mouse models of AD (66). The same was also seen in 5XFAD mice on a QC knock-out background and was accompanied by a rescue of behavioral deficits (67). The observation of a significant age-dependent increase of the A $\beta_{\text{pE3-x}}$ parenchymal plaque burden at the expense of A β_{1-x} full-length peptides suggested that A $\beta_{\text{pE3-x}}$ formation might occur late in the process of amyloidosis and could involve the remodeling of existing extracellular amyloid deposits (68). On the other hand, the presence of A $\beta_{\text{pE3-x}}$ peptides has been also described within neurons both in mouse models (22, 69) and human AD samples (53, 70), raising the question of whether the localization is important for toxicity. In order to address such questions, transgenic mouse models have been developed with constructs that only encode the A β_{3-x} peptide, with a glutamate to glutamine substitution at the initial position to facilitate cyclization (71–73). This construct is expressed under the control of the murine neuron-specific Thy1-promotor and contains the thyrotropin-releasing hormone (TRH) signal peptide sequence to ensure liberation of the peptide preferentially in the secretory pathway (74). In contrast to other models, these mice do not express human full-length APP or any FAD-associated mutations, but impress with a rapid onset of behavioral deficits, neuron loss, and microgliosis (71, 72).

A β_{4-x}

A β_{4-42} was one of the first A β peptide species that was detected in the amyloid plaque cores of human AD brains (9). More recently, novel A β_{4-x} specific antibodies have been described, and the localization of A β_{4-x} to amyloid plaque cores has been confirmed in immunohistochemical studies in both human AD and

transgenic AD mouse models (75, 76). In addition, $A\beta_{4-x}$ peptides were also found within blood vessels in the majority of the analyzed AD cases (76). Similar to $A\beta_{pE3-x}$ peptides, $A\beta_{4-42}$ peptides lacking another charged amino acid residue have also been described to quickly aggregate into soluble oligomers and fibrillar, high-molecular weight aggregates (61, 75, 76). Quantitatively, $A\beta_{4-42}$ peptides seem to be among the most abundant $A\beta$ species in human AD brain with equal or even higher amounts compared to $A\beta_{1-42}$. It should be noted again, however, that in studies using mass spectrometry to assess $A\beta$ peptide patterns, the ratios between the respective peptide variants cannot be regarded as a direct reflection of their abundance (16, 77). With regard to their neurotoxicity, $A\beta_{4-42}$ and $A\beta_{4-40}$ demonstrated equal toxicity as $A\beta_{1-42}$ or $A\beta_{pE3-42}$ using in vitro assays with primary neuronal cultures. This was also observed in an in vivo setting in which freshly prepared $A\beta$ peptides were applied by intraventricular injection followed by an analysis of working memory using a Y-maze task after 5 days (61).

The metalloprotease neprilysin (NEP) has been proposed as a candidate enzyme responsible for the generation of $A\beta_{4-x}$ peptides by cleaving between Glu-3 and Phe-4 among other sites, with full-length $A\beta_{1-x}$ peptides acting as the immediate substrate. This has been shown by high-performance liquid chromatography analysis yielding several product peaks after incubation of $A\beta_{1-40}$ with either recombinant soluble NEP produced in Sf9 cells or NEP purified from rabbit kidney cortex (46). More recent studies using synthetic $A\beta$ peptides and recombinant human NEP confirmed the generation of $A\beta$ peptide fragments starting with Phe-4 (such as $A\beta_{4-9}$ or $A\beta_{4-16}$ but also the existence of several other cleavage sites, at least under the given in vitro conditions (48, 49). Therefore, it is currently unclear whether NEP might contribute to the generation of longer $A\beta$ peptides such as $A\beta_{4-40}$ and $A\beta_{4-42}$. However, we regard this possibility as unlikely as in vivo studies have demonstrated that the rate-limiting step in the proteolysis of $A\beta$ by NEP is cleavage of the Gly-9–Tyr-10 bond, which would rule out the generation of full-length $A\beta_{4-40}$ and $A\beta_{4-42}$ peptides (78).

Most recently, it was shown that APP contains a cleavage site for the metalloprotease ADAMTS4 (a disintegrin-like and metalloprotease with thrombospondin type 1 motif) between Glu-3 and Phe-4 of the $A\beta$ peptide sequence (24). ADAMTS proteases constitute a family of secreted Zn^{2+} -metalloproteases that degrade or modify major components of the extracellular matrix (79). ADAMTS4 participates in the proteolytic degradation of proteoglycans like aggrecan, brevican, and versican (80). Aggrecan is a hyaluronan-binding proteoglycan, which is present in large amounts in the articular cartilage. In an important pathological process leading to osteoarthritis and rheumatoid arthritis, aggrecan is degraded by ADAMTS4 and the homologous family member ADAMTS5, leading to the exposure and subsequent degradation of collagen fibrils by collagenases (81). Co-expression of ADAMTS4 and APP in HEK293 cells resulted in the secretion of $A\beta_{4-40}$ peptides as measured by mass spectrometry and ELISA, while several species of $A\beta_{1-x}$ peptides were not affected (24). $A\beta_{4-40}$ secretion was not blocked by treatment of the cells with a potent β -secretase inhibitor indicating that $A\beta_{4-x}$ peptides were generated in a BACE1-independent fashion. IHC analysis of ADAMTS4 reporter mice showed that ADAMTS4 was exclusively expressed in oligodendrocytes in the adult murine brain. Consistently, the culture of murine oligodendrocytes demonstrated that these primary cells secrete $A\beta_{4-40}$ peptides among a spectrum of other $A\beta$ species very similar to established cell lines. However, $A\beta_{4-40}$ peptides were

undetectable in primary oligodendrocytes derived from ADAMTS4 knockout (KO) mice, providing genetic proof that ADAMTS4 is responsible for A β_{4-40} peptide generation in this cell type. In vivo, the crossing of 5XFAD mice to ADAMTS4 knockout mice reduced A β_{4-40} levels by 50%, but the overall amyloid plaque load and the distribution of A β_{4-x} peptides in amyloid plaque cores appeared to be unchanged, clearly suggesting that other mechanisms for A β_{4-x} generation beside ADAMTS4 must exist. Compellingly, abundant A β_{4-x} immunoreactivity was observed in white matter structures of 5XFAD mice, and this signal was entirely abolished in the ADAMTS4 knockout background (24). This could be of pathological relevance as numerous neuropathological, biochemical, and imaging studies have reported white matter abnormalities and oligodendrocyte dysfunction in AD patients (82, 83). However, further studies are required to define a potential detrimental role of A β_{4-x} peptides in white matter structures. In any case, the recent link of ADAMTS4 to AD risk as well as single-cell transcriptomic data supporting that many oligodendroglia-specific and myelination-associated genes are dysregulated in human AD brains should provide new urgency to consider the role of oligodendrocytes in AD (84, 85).

As a tool to investigate the in vivo role of A β_{4-x} peptides, a transgenic mouse model has been generated that only expresses A β_{4-42} peptides under the control of the murine Thy1-promotor. These mice develop age-dependent behavioral deficits with spatial or working memory impairments, which are detectable in paradigms such as Morris water maze or novel object recognition task, as well as motor deficits. These mice do not develop amyloid plaque pathology but show a robust hippocampal CA1 neuron loss correlating with the transgene expression pattern in a gene-dose dependent manner (61, 86). Interestingly, altered basal excitatory synaptic transmission with A β_{4-42} -dependent neuronal hyperexcitability is already obvious in young Tg4-42 mice preceding neuron loss and behavioral deficits (87).

A β_{5-x}

A β peptides starting with an Arg residue at position 5 have been detected in brains of transgenic mice such as APP/PS1KI (22) or 5XFAD (23), as well as in human AD brains (15–17) by mass spectrometry. Conditions of BACE1 inhibition resulted in strongly increased levels of A β_{5-x} species in cellular models (88–90). This clearly suggests that A β_{5-x} peptides are produced through a BACE1-independent pathway, with some evidence supporting α -secretase-like proteases (e.g., ADAM family proteases such as TACE or ADAM10) as potential candidate enzymes (88).

In vivo studies with several BACE1 inhibitors in beagle dogs confirmed the absolute signal reduction of all A β isoforms in the CSF except for A β_{5-40} peptides, and an analysis of relative levels demonstrated a clear increase of A β_{5-40} (90). This was further corroborated in a placebo-controlled study in healthy human subjects in which dose-dependent increases in A β_{5-x} levels were measured in the CSF upon treatment with the BACE1 inhibitor LY2811376 (91). Immunohistochemical analyses using A β_{5-x} selective antibodies confirmed the presence of A β_{5-x} peptides in brain tissues samples from sporadic AD patients showing immunoreactivity primarily in vascular deposits (88, 92). In cases from individuals harboring FAD-associated *APP* or *PSEN1* mutations, both vascular

and parenchymal deposits were detected, while in mouse models such as 5XFAD, APP/PS1KI, or 3xTg A β_{5-x} , immunoreactivity was confined to extracellular plaques (92).

A β_{11-x} /A β_{pE11-x}

In addition to the cleavage site between methionine and aspartate in position 1 (Asp-1) generating β -CTFs, BACE1 has also been shown to cleave APP between tyrosine and glutamate in position 11 (Glu-11) of the A β sequence resulting in N-truncated A β_{11-x} species (β' -cleavage) (6). There is evidence that the BACE1 cleavage preference depends on the intracellular localization, with β' -cleavage being favored in the trans-Golgi network (93). A β_{11-x} peptides have been detected in brains from AD and Down's syndrome patients (94) and have been shown to accumulate within neurons in cellular models upon BACE1 overexpression (95). Similar to Glu-3, the free Glu residue in position 11 can also undergo cyclization and modification to an N-terminal pyroglutamate (A β_{pE11-x}). In contrast to A β_{pE3-42} , which is mainly confined to mature plaque cores in AD patients, unmodified A β_{11-40} and A $\beta_{pE11-40}$ peptides have been detected in the vasculature using selective antibodies (95). Within amyloid plaques cores, A β_{pE11-x} has been found to co-localize with full-length A β peptides but also with A β_{pE3-x} (96).

CONCLUSION

There is substantial evidence that N-truncated A β species, in addition to the extensively studied full-length A β peptides, might play an important role in the molecular pathology of AD. In recent years, new candidate proteases and nonneuronal cell types have been linked to the generation of N-truncated A β species. Novel antibodies specific for some N-truncated A β peptides have been developed, and this should allow the development of quantitative detection assays to better define their abundance in relation to full-length A β peptides. To advance the functional analysis of N-truncated A β peptides, novel animal models might be needed as N-truncated A β species are underrepresented in the available AD models. These efforts should improve our understanding of the pathological role of N-truncated A β peptides. They could provide novel insights into currently unexplained aspects of AD pathology, and they might be crucial to develop novel therapeutic approaches.

Acknowledgments: This work has been supported by the Alzheimer Forschung Initiative (grant #16103 to OW), Gerhard Hunsmann Stiftung and Alzheimer Stiftung Göttingen (to OW).

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Insulin Resistance and Oligodendrocyte/Microvascular Endothelial Cell Dysfunction as Mediators of White Matter Degeneration in Alzheimer's Disease

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch8>

Abstract: In Alzheimer's disease (AD), white matter (WM) degeneration begins early, increases with disease progression, and contributes to cognitive impairment, yet the mechanisms are poorly understood. This article reviews the roles of myelin loss, oligodendrocyte dysfunction, and microvasculopathy in relation to AD WM degeneration. Myelin loss impairs axonal function and its breakdown promotes oxidative stress, inflammation, and lipid peroxidation, further compromising the structure and function of axons. Oligodendrocyte dysfunction impairs homeostatic mechanisms needed to maintain myelin. Microvascular disease with endothelial cell pathology leads to thrombin activation and pro-inflammatory cytokine release, oxidative stress, and increased vascular permeability. Progressive fibrotic

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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replacement of smooth muscle cells reduces vaso-responsiveness to metabolic demands. Fibrotic thickening of vessel walls narrows the lumens, rendering them more susceptible to occlusion, endothelial cell injury, and thrombin activation. Since normal physiological functions of oligodendrocytes and microvascular endothelial cells rely on intact insulin/insulin-like growth factor (IGF) signaling through cell survival, metabolic and anti-inflammatory pathways, conceivably, WM degeneration in AD is mediated by insulin and IGF resistance with attendant pathogenic targeting of oligodendroglia and endothelial cells. The apolipoprotein E- ϵ 4 genotype may serve as a co-factor in AD-associated glial-vascular WM degeneration due to its role as a mediator of insulin resistance.

Keywords: Alzheimer's disease; Insulin resistance; oligodendrocytes; thrombin; white matter

INTRODUCTION

Alzheimer's disease (AD) is the 6th leading cause of death and the most prevalent aging-associated dementia, afflicting over 5 million people in the United States. Despite intense and comprehensive research efforts over the past 4–5 decades, we still lack effective disease-modifying therapies, and thus, the annual economic burden of over \$170 billion continues to grow (1). Perhaps one of the main obstacles to success has been the failure to appreciate the full spectrum of disease which extends well beyond cerebral accumulations of amyloid-beta ($A\beta$) and neuronal structural pathologies caused by abnormally phosphorylated tau. AD is mechanistically linked to: (i) insulin resistance; (ii) neuroinflammation; (iii) white matter (WM) atrophy with myelin loss and axonal degeneration; (iv) vasculopathy; (v) leukoaraiosis; (vi) blood–brain barrier disruption; (vii) oxidative stress; (viii) mitochondrial dysfunction; (ix) loss of neuronal plasticity; and (x) synaptic disconnection. Furthermore, consideration should be given to the concept that different mediators of neurodegeneration may emerge at various time points and could be inter-dependent. These points are not addressed by the present-day diagnostic and therapeutic approaches.

In light of the varied and complex nature of AD-associated pathologies, it is not surprising that mono-therapeutic strategies have failed to remediate this disease. The development of a more rational and effective therapeutic design requires that we attain a greater understanding of how various pathogenic processes contribute to the onset and progression of AD. Furthermore, additional information about systemic and central nervous system (CNS) forces that drive the cascade of neurodegeneration could lead to preventive strategies. For example, a better understanding of how co-factors such as vascular disease, head trauma, and lifestyle exposures modify risk and the phenotypic features of AD could ultimately help refine and personalize diagnostics and therapeutics. In this regard, the role of vascular disease in AD has been strongly suggested by the finding that at least 40% of people with clinically diagnosed AD have significant cerebrovascular disease yet neither disease process would be regarded as sufficient to cause dementia (2). Correspondingly, the relatively recent incident decline in AD severity in the United States has been attributed to improved vascular protective care (3).

Now it is time for investigators to re-focus their efforts by capturing a better understanding of the protean pathogenic factors that drive progressive neurodegeneration. Evidence- and mechanism-based approaches are needed to develop multi-pronged therapeutics, utilizing strategies that already have been successful for cancers and other chronic diseases.

AD-ASSOCIATED WM PATHOLOGY

White matter degeneration is a major and consistent but vastly under-studied abnormality in AD (Figure 1). Its occurrence was initially characterized in 1986 by Brun and Englund (4, 5) and subsequently shown to be an early pre-clinical abnormality (6). WM atrophy in AD is most pronounced in the parietal and temporal lobes, followed by the frontal lobes, whereas the occipital lobes tend to be spared (6). Consequently, the severities of WM atrophy correspond with the distribution and degree of cerebral cortical pathology. WM degeneration in AD is associated with loss of myelin and myelinated axons, together with dysfunction or loss of oligodendrocytes, increased activation of astrocytes, that is gliosis, and microvascular disease (7–9). Leukoaraiosis, an extreme form of WM degeneration in which the loss of myelinated axons is extensive and associated with WM hyperintensities by magnetic resonance imaging (MRI) (7–9), is most prominently distributed in periventricular and central compared with subcortical WM (5, 6, 10–15).

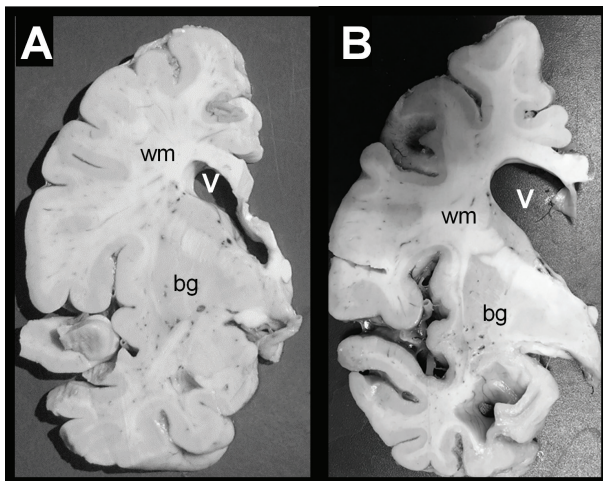


Figure 1 White matter atrophy in AD. Postmortem coronal slices of the left cerebral hemisphere from patients with (A) normal aging or (B) advanced AD. Panels A and B show approximately the same coronal slice levels depicting the cingulate gyrus, corpus callosum, basal ganglia (bg), central and periventricular posterior frontal white matter (wm) and lateral ventricle. Note the markedly atrophic white matter and associated ex vacuo enlargement of ventricles (V) in (B) AD relative to (A) control.

The histopathologic correlates of myelin degeneration in AD have been characterized by assessing relative reductions in Luxol fast blue (LFB) staining intensity and uniformity. LFB reacts with phospholipids and lipoproteins and is suitable for detecting myelin pathology in formalin-fixed, paraffin-embedded tissue. However, additional approaches are required to evaluate axonal degeneration and attrition. Traditional histochemical stains, such as Bielschowsky, utilize silver impregnation to label cytoskeletal proteins in axons, dendrites, and degenerated or dystrophic fibers. Current, more specific approaches employ immunohistochemical staining with antibodies to phosphorylated neuronal cytoskeletal proteins such as neurofilament and tau. In AD, myelin loss and axonal degeneration, respectively, marked by pallor of LFB staining and fragmentation, irregular swelling, and rarefaction of fibers, tend to be more pronounced in central and periventricular compared with subcortical WM, and they increase with severity of AD.

ASTROCYTES, MICROGLIA, AND OLIGODENDROCYTES

Astrocyte activation or gliosis is a conspicuous feature of AD. Gliosis marks responses to cellular and tissue degeneration. One potential outcome of gliosis is tissue repair, but an alternative outcome is the elaboration of pro-inflammatory cytokines that promote oxidative stress and tissue injury, thereby worsening neurodegeneration. WM gliosis is marked by increased glial fibrillary acidic protein (GFAP) immunoreactivity in enlarged (hypertrophic) astrocytes and fibrillary deposits within the extracellular matrix (Figure 2). Dense fibrillary gliosis, which reflects severe degeneration, is most prominently distributed in periventricular and subcortical U-fiber regions. In contrast, central WM gliosis is generally less pronounced and associated with increased reactive hypertrophic astrocytes and variable densities of GFAP-positive fibrillary deposits.

WM gliosis, particularly in the early and intermediate stages of AD, is accompanied by microglial activation. Microglia have rod-shaped, curved, or twisted nuclei and can be detected by immunohistochemical staining with antibodies to common leukocyte antigen (CD45) or ionized calcium-binding adaptor protein-1 (IBA-1) (16). In AD, activated microglia together with reactive astrocytes promote neuroinflammation via increased elaboration of pro-inflammatory cytokines and chemokines and suppression of anti-inflammatory molecules (17). Neuroinflammation causes injury and degeneration of myelin and axons. Although the underlying causes of WM neuroinflammation have yet to be determined, plausible etiologies include insulin/insulin-like growth factor (IGF) resistance and microvascular ischemic injury since both have been demonstrated in AD and are well-documented mediators of inflammation, oxidative stress, and metabolic dysfunction.

Oligodendrocytes synthesize and maintain myelin sheaths needed to support axonal integrity and function. Oligodendrocytes, like neurons, are highly vulnerable to both insulin and IGF-1 resistance and ischemic injury. Loss or dysfunction of oligodendrocytes impairs myelin maintenance, axonal function, and ultimately axonal structure. To better understand the mechanisms of WM degeneration

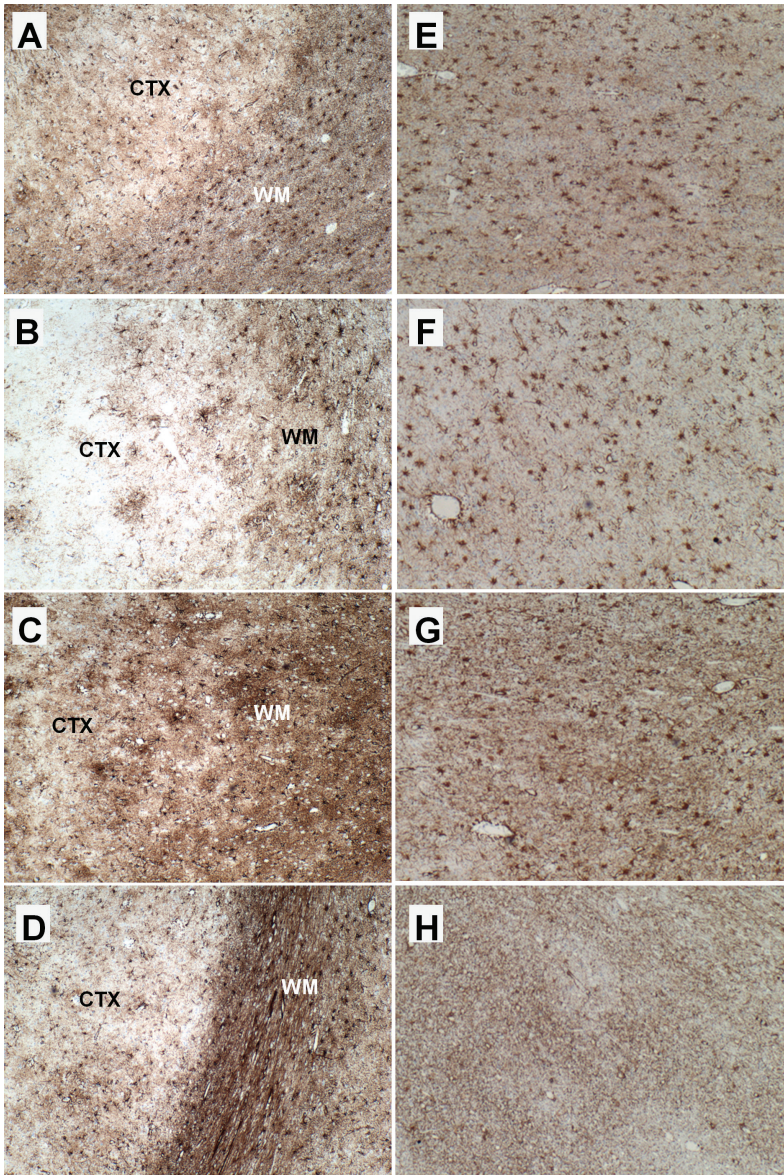


Figure 2 WM gliosis exhibits regional variation in AD. Immunohistochemical staining was used to detect glial fibrillary acidic protein (GFAP) in the (A, E) anterior frontal, (B, F) posterior frontal, (C, G) parietal, and (D, H) occipital cortex (CTX) and underlying white matter (WM) in formalin-fixed paraffin-embedded human postmortem brain tissue. Immunoreactivity was detected with biotinylated secondary antibodies, horseradish peroxidase-conjugated avidin-biotin complexes, and diaminobenzidine (brown precipitant). Panels A–D (100x original magnification) show intense GFAP immunoreactivity in white matter (wm) and variable labeling of the cortex (ctx). Panels E–G (200x original magnification) show abundant GFAP-positive hypertrophic reactive astrocytes (dot-like structures) in a background of diffuse fibrillar labeling, whereas Panel H shows predominantly fibrillar labeling of central occipital WM.

in AD, more information is needed about the biochemical and molecular nature of oligodendrocyte injury and dysfunction leading to myelin and axonal loss. However, recent advances in adult brain WM cell isolation techniques (18), lipidomics mass spectrometry (19, 20), and targeted gene array analysis now provide practical methodologic approaches for characterizing WM oligodendrocyte and myelin lipid pathologies.

BIOCHEMICAL AND CELLULAR BASIS OF WM PATHOLOGY IN AD

White matter is largely composed of myelinated axons. Traditionally, the integrities of myelin and axons are studied by histochemical or immunohistochemical staining. However, overlapping responses to various types of injury and degeneration limit the utility of these approaches for characterizing disease-specific pathologies and responses to treatment. To better understand the nature of AD-associated myelin pathology, biochemical approaches that assess reproducible alterations in lipid composition are needed.

CNS myelin, a specialized membrane synthesized by oligodendrocytes, has a much higher dry mass of lipids (70–85%) compared with proteins (15–30%) and plays a major role in insulating axons to support conductivity. Myelin lipids primarily include cholesterol, glycosphingolipids, sulfatides, gangliosides, phospholipids, and sphingomyelin (21). Many diseases that impair the structural and functional integrity of WM are associated with abnormalities in the expression and metabolism of phospholipids and sulfatides (20, 22–28). Membrane phospholipids have important roles in regulating lipid rafts and receptor functions. Sulfatides, located on extracellular leaflets of plasma membranes (29) and generated via sulfonation of galactocerebroside, regulate neuronal plasticity, memory, myelin maintenance, protein trafficking, adhesion, glial-axonal signaling, insulin secretion, and oligodendrocyte survival (30). Degradation of sulfatide via galactosylceramidase and sulfatidase yields ceramide (29, 31), which promotes neuroinflammation, apoptosis, and production of reactive oxygen species (ROS), and impairs signaling through survival and metabolic pathways (32). Furthermore, deficiencies in membrane sulfatide disrupt myelin's structure, function, and capacity to support neuronal conductivity (32). Thus, imbalances in sphingolipid composition that reduce sulfatide and increase ceramide are potentially important mediators of WM degeneration and attendant cognitive impairment.

Potential role of oligodendrocyte dysfunction as a mediator of WM degeneration

Oligodendrocytes generate and maintain CNS myelin by controlling the expression and activity of enzymes that modulate its biosynthesis, turnover, and degradation (33–36). Loss or damage to myelin impairs neuronal conductivity and

compromises axonal integrity, releasing neurofilament and myelin sulfatides (37). Increases in lipid peroxidation after myelin breakdown exacerbate oxidative damage, neuroinflammation, and astrocyte activation (gliosis). Therefore, the presence of WM atrophy and degeneration early in the course of AD, including in its pre-clinical stages (6), could be due to pathogenic processes that impair function and survival of mature oligodendrocytes and promote secondary reactive injury via increased oxidative stress, inflammation, and lipid peroxidative. In light of the known importance of insulin and IGF signaling for maintaining a broad array of homeostatic functions in both neurons and oligodendrocytes (38–40), and strong evidence for brain insulin and IGF deficiencies and resistances beginning early in the course of AD (41, 42), it is plausible to hypothesize that impaired signaling through the insulin and IGF receptors also mediates oligodendrocyte dysfunction in AD.

Many critical functions of oligodendrocytes, including cell survival, myelin synthesis, and myelin maintenance, are supported by insulin and IGF-1 signaling (43–46). Consequently, disruption of related networks decreases oligodendrocyte viability, increases oxidative stress, and impairs myelin maintenance and maturation. Likewise, experimental models of chronically impaired brain insulin and IGF signaling exhibit WM atrophy and degeneration (47, 48) together with oligodendrocyte dysfunction (49), all of which can be partly reversed or prevented by early treatment with insulin sensitizers (47, 49). Another consequence of impaired insulin/IGF signaling is dysregulated sphingolipid metabolism resulting in decreased sulfatide and increased ceramide levels (23, 26–28, 50–52). Increases in ceramide can cause WM degeneration via several mechanisms, including inhibition of insulin/IGF signaling through pathways needed for oligodendrocyte survival and metabolic functions, and stimulation of pro-inflammatory and oxidative stress responses (28).

Besides lipids, oligodendrocytes synthesize integral membrane proteins whose expressions are differentially modulated at each stage of myelin maturation as well as in response to injury. As immature oligodendrocyte precursor cells (OPC) pass through phases of differentiation to eventually become mature myelin-producing oligodendrocytes, the proteins needed to support the structure and function of myelin also change. Mature oligodendrocytes express myelin basic protein (MBP), myelin-associated glycoprotein (MAG), myelin oligodendrocyte glycoprotein (MOG), proteolipid protein (PLP) (53), and adenoma polyposis coli (APC) (54), as well as O4 sulfatide (54). PLP is the most abundant protein in CNS myelin (55, 56). Olig 1–3 transcription factors are expressed at various stages of oligodendroglial maturation (54). Injury and degeneration of myelin cause the populations of intact mature functional oligodendrocytes to decline. That effect can lead to the proliferation of immature oligodendrocytes that express different myelin glycoproteins, transcription factors, and myelin glyco- and phospholipids which may not support optimum conductivity and CNS function. The conspicuous abnormalities in oligodendrocyte myelin-associated gene and lipid expression observed in human brains with AD and relevant experimental models including those linked to brain insulin and IGF resistance (19, 22–24, 57), lend strong support the hypothesis that oligodendrocytes are targets of WM atrophy and neurodegeneration in AD.

VASCULOPATHY, VASCULAR DEGENERATION, AND ISCHEMIC INJURY IN AD

Small vessel disease is a recognized component of WM degeneration in AD, but its pathogenesis and contributions to neurodegeneration are poorly understood. The nature of vasculopathy and its progression to vascular degeneration and attendant ischemic injury require mechanistic understanding to guide preventive and therapeutic measures. Important initial steps include drawing distinctions between amyloid and non-amyloid associated vasculopathy and degeneration and characterizing the mediators and consequences of non-amyloid microvasculopathy, which is a feature of WM degeneration in AD.

The well-established AD-associated progressive declines in cerebral blood flow, glucose metabolism, and oxygen utilization suggest that impairments in brain perfusion are important components of AD (58, 59). However, the extent to which vascular disease causes AD or represents an integral component of neurodegeneration remains controversial. Postmortem studies demonstrated cerebral vascular pathology in over 80% of brains with AD (60). In a separate postmortem study, substantial overlap was observed between AD and vascular-mediated injury, but very few cases of dementia could be attributed to vascular disease alone (2). The Gothenburg study reported that mental slowness and deficits in executive function were linked to WM vascular dysfunction and pathology but not cortical vasculopathy (37). Together, these studies suggest that although CNS vasculopathy contributes to AD, it is seldom sufficient to cause dementia on its own (37).

In AD, there are two major types of microvascular pathology: amyloid angiopathy and non-amyloid vasculopathy (Figure 3). Amyloid angiopathy affects vessels in the cerebral cortex and leptomeninges, but not WM (61–63). In AD, non-amyloid vascular degeneration occurs in microvessels, including capillaries, arterioles, and venules in the cerebral cortex, WM, and subcortical nuclei. Non-amyloid microvascular disease is characterized by fibrotic thickening of vessel walls (sclerosis), loss of endothelial cells, thickening of basement membranes, attrition of perivascular tissue (64), reduced vascular density (micro-vasculopenia), and increased vessel coiling (65). Mural sclerosis leads to extreme narrowing of the lumens and reduced vaso-responsiveness, restricting perfusion, particularly in times of increased metabolic demand (66). Chronic hypoperfusion of WM causes ischemic injury ranging from myelin loss to fiber attrition, and in extreme cases, leukoaraiosis and micro-infarcts (5, 13). Another consequence of microvascular pathology is weakening and increased permeability of vessel walls as that occurs in diabetic nephropathy (67). Leakiness of microvessels enables toxins and inflammatory mediators from the peripheral circulation to enter the brain and cause perivascular tissue injury and attrition (58, 68–74).

Potential role of nitric oxide in cerebral microvascular dysfunction and pathology

Nitric oxide (NO) is an important physiological modulator of vascular smooth muscle function and blood flow. However, NO in high concentrations can be cytotoxic due to the activation of stress and inflammatory responses.

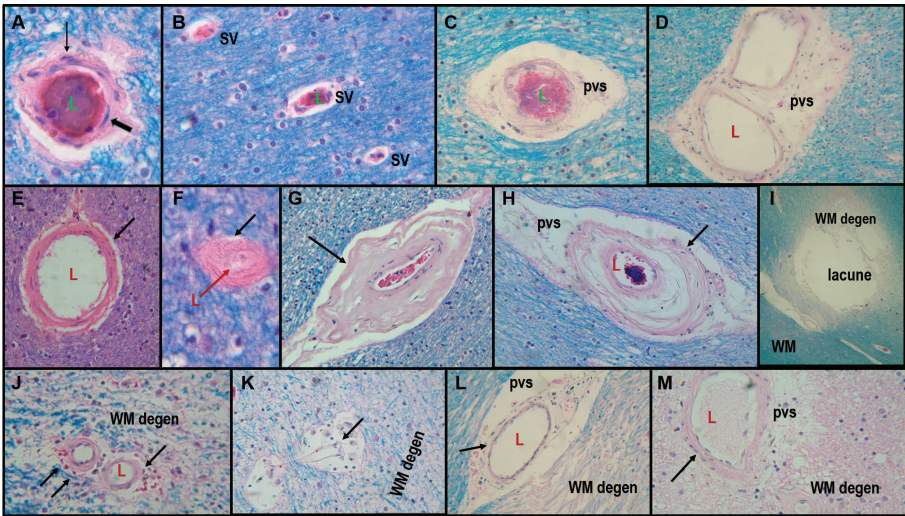


Figure 3 White matter (WM) vascular pathology in AD. Human postmortem parietal lobe samples were fixed in formalin, embedded in paraffin, and stained with Luxol fast blue (LFB), hematoxylin and eosin (LHE). (A, B) Control white matter (A) medium size and (B) small vessels (sv). Fine arrow in A shows normal smooth muscle cells and the broad arrow shows a normal endothelial cell. L = lumen. Panels C–M depict vascular pathology in AD WM. (C) Medium size vessel with reduced smooth muscle and a widened perivascular space (pvs) reflecting to perivascular tissue attrition. (D) Vascular fibrosis with enlarged pvs containing lipid-laden macrophages and hemosiderin deposits. (E) Vascular fibrosis (arrow) and myelin loss (markedly reduced LFB staining compared with A–D, and F–I). (F) Severe microvascular disease with fibrotic thickening (black arrow) and an extremely narrow lumen (red arrow; L). (G, H) Severe arteriosclerosis with degeneration and splitting of vessel walls, narrowing of lumens and in (H), widened pvs. (I) WM lacune (micro-infarct) associated with severe vascular degeneration and circumscribed area of WM degeneration. (J–M) Progressive WM degeneration associated with vasculopathy. WM degeneration is associated with loss of myelin staining, perivascular tissue attrition, and fiber loss. (M) Absent LFB staining and cystic degeneration of WM.

Microvascular degeneration is ultimately mediated by oxidative stress and inflammation. The potential role of NO as a mediator of vascular degeneration in AD was suggested by the findings that high levels of nitric oxide synthase (NOS) activity were co-localized with nuclear p53 in cerebral vessels (75) and cells with increased expression of pro-inflammatory and immune signaling genes (76). A later independent study of postmortem human brains demonstrated increased endothelial NOS (NOS3) immunoreactivity co-localized with nuclear p53 in AD microvascular smooth muscle and endothelial cells, confirming a role for aberrant NOS expression in cerebrovascular cells with increased proneness to apoptosis (77). Together, these findings suggest that non-amyloid vascular degeneration in AD is mediated by increased NO production and activation of inflammatory mechanisms.

However, the simultaneous detection of many sclerotic vessels with increased nuclear p53 but no detectable NOS3 immunoreactivity in either smooth muscle or endothelial cells, that is NOS3 expression was aberrantly down-regulated, suggests additional mechanisms mediate vascular dysfunction in AD (77).

For example, degenerative vascular sclerosis compromises vaso-responsiveness and flow, resulting in chronic ischemic injury that can be exacerbated by repeated and multifocal thrombotic microvascular occlusions. Furthermore, fibrotic degeneration disrupts vessel wall integrity, rendering them more permeable to toxic-inflammatory factors from the peripheral circulation. This phenomenon could account for the perivascular tissue attrition that accompanies microvascular degeneration in AD (Figure 3).

Thrombin activation, inflammation, microvascular occlusion, and ischemic injury in AD

In AD, the cerebral microcirculation is pathophysiologically activated due to endothelial cell overexpression of bioactive, neurotoxic, and inflammatory proteases including thrombin. Endothelial-derived thrombin is a multifunctional protease which in AD, besides promoting vascular occlusion, functions as a stress-activated neurotoxin (78, 79). Mechanistically, thrombin initiates neuronal apoptosis via activation of glial and microglial cells, leading to increased oxidative stress and neuroinflammation (80). Thrombin also stimulates A β precursor protein production and cleavage, mediates proteolytic processing of tau, and causes tau hyperphosphorylation and aggregation (80, 81). In essence, vessel-derived thrombin could represent a critical modulator of AD pathology via its regulation of inflammatory and bioactive protein expression. In this regard, thrombin activation of endothelial cells enhances expression and release of many pro-inflammatory proteins including monocyte chemoattractant protein-1 (MCP-1), intercellular adhesion molecule-1 (ICAM-1), IL-1, IL-6, and IL-8 (80, 81). Thus, microvascular disease could initiate and propagate neuroinflammation in AD.

Pro-inflammatory cytokine activation in endothelial cells leads to oxidative stress and thrombin release, with attendant thrombotic luminal occlusion or vessel wall injury causing increased permeability (82). However, the same responses can be mediated by up-regulation of the thrombin receptor protease-activated receptor 1 (PAR-1) or down-regulation of the brain thrombin inhibitor, protease nexin-1 near blood vessels (80). Since brain endothelial cells produce thrombin and also express functionally active PAR-1 and PAR-3 (79, 83), thrombin may initiate autocrine stimulation of a noxious feed-forward cycle. In addition, the intimate proximity of microvascular endothelial cells to microglia, astrocytes, and oligodendrocytes enables secretory products, including thrombin to influence cellular responses via a paracrine-type stimulation. For example, treatment of human microglia with thrombin induces TNF- α /TNR-dependent up-regulation of NF- κ B (84). In astrocytes, thrombin activation of PAR-1 leads to increased MMP-9 expression through the regulation of several signaling pathways including PKC, JNK, and MAPK (85).

Microvascular endothelial cells elaborate trophic factors that positively impact oligodendroglia, but under conditions of stress, injury, or inflammation, endothelial cell dysfunction can adversely affect oligodendrocytes. An important role for endothelial-derived factors in oligodendroglial health was suggested by studies showing that endothelial cell-conditioned media enhances survival of OPCs (86, 87). On the other hand, in an experimental animal model of cerebral small vessel disease, early development of endothelial cell dysfunction was found to promote

secretion of heat shock protein 90alpha and subsequently block oligodendroglial differentiation and production of mature myelin (88). Mechanistically, oxidative stress impairs the capacity of endothelial cells to generate trophic factors (89) needed to support critical functions of mature oligodendrocytes, including myelin maintenance.

In AD, WM degeneration could stem from both endothelial and oligodendrocyte dysfunction. Endothelial cell dysfunction leading to excess thrombin release could cause micro-ischemic injury due to thrombosis or perivascular toxic injury mediated by increased vessel wall degeneration and permeability. At the same time, increased thrombin release would compromise the functional integrity of oligodendroglia, impairing survival and maintenance of mature myelin (79, 90–92). The concept that increased thrombin release could impair oligodendrocyte function is supported by the findings that the PAR1 thrombin receptor is a critical extracellular switch that controls myelination and that PAR1 deletion increases myelination (93), survival, maturation, and myelin maintenance. Altogether, the findings suggest that increased thrombin signaling by any one of several mechanisms can lead to micro-vessel-related WM injury in AD. However, the missing link is that we still do not understand the underlying causes of brain microvascular degeneration and endothelial cell dysfunction that lead to thrombin activation. One potential etiopathic candidate is insulin resistance since type 2 diabetes mellitus and other insulin resistance diseases are typically associated with microvascular disease and increased thrombin activation, accompanied by oxidative stress, platelet aggregation, vascular occlusions, and ischemic injury (94, 95). Correspondingly, insulin inhibits thrombin-induced endothelial dysfunction and mitigates microvascular permeability by decreasing thrombin-mediated vascular endothelial-cadherin translocation to the cytoskeleton/nuclear compartment (96).

INSULIN AND INSULIN-IGF SIGNALING IMPAIRMENTS AS MEDIATORS OF WM GLIAL-VASCULAR DEGENERATION IN AD

Considerable research had already demonstrated roles for impaired insulin and IGF-1 signaling in AD cortical and subcortical gray matter structures. However, little information is available regarding alterations of these same signaling pathways in AD WM degeneration, despite evidence that oligodendrocyte survival and function are dependent upon intact insulin and IGF networks. Therefore, additional research on the nature, mechanisms, and effects of impaired insulin and IGF signaling in relation to brain WM degeneration could generate a solid foundation for enhancing a broader understanding of the spectrum of brain pathology in AD.

In AD, deficits in brain energy metabolism, particularly concerning glucose utilization have been recognized for years (97–100). Positron emission tomography (PET) imaging with (18) F-fluoro-deoxyglucose (FDG) is a standard approach for detecting early impairments in brain glucose uptake and utilization (101–103). Insulin and IGF are major regulators of energy metabolism in the

brain, and they have critical roles in maintaining broad neuronal and oligodendrocyte functions (38, 40). Impairments in brain insulin/IGF signaling due to insulin/IGF deficiencies or receptor resistances cause deficits in learning and memory (104).

Postmortem human studies demonstrated that AD is associated with significantly reduced expression of brain insulin and IGF polypeptides and receptors, insulin and IGF receptor tyrosine phosphorylation and receptor binding, activation of downstream pathways that promote cell survival, metabolism, neuronal plasticity, and myelin maintenance, and inhibition of signaling mechanisms that promote oxidative stress, neuroinflammation, cell death, and lipid peroxidation (42, 105, 106). Insulin/IGF deficiencies and resistances increase with Braak stage severity of AD (41, 105) and therefore correlate with accumulations of A β and pTau pathologies. The finding that cerebrospinal fluid (CSF) insulin levels decline in the early or intermediate stages of AD (107), and overlap with progressive accumulations of A β and advanced glycation end-products (AGEs) (Figure 4A) (52, 107, 108) which cause oxidative stress and neuroinflammation, suggests that insulin deficiency contributes to progressive neurodegeneration in AD.

The human studies linking AD pathogenesis and progression to impairments in brain insulin/IGF signaling are supported by data from experimental models of sporadic AD produced by intracerebral (i.c.) administration of streptozotocin (STZ). STZ, a pro-diabetes toxin, injected into the cerebral hemispheres and ventricles, causes selective insulin deficiency and resistance in the brain with deficits in learning and memory, elevated levels of pTau, A β , and ubiquitin, loss of neurons, gliosis, oxidative stress, neuroinflammation, WM atrophy, and microvascular disease (47–49, 104, 109). Importantly, data from these models support the concept that sustained and progressive deficits in brain insulin/IGF signaling cause nearly all of the known structural, functional, biochemical, molecular, and neurobehavioral abnormalities identified in AD. Correspondingly, insulin administration improves working memory and cognition (110–113) and enhances A β clearance (114). Moreover, CNS-appropriate insulin sensitizer drugs have been shown to prevent or reduce AD-associated abnormalities in experimental animals (49, 109, 115).

Until now, the adverse effects of brain insulin/IGF deficiencies and resistances have been focused on neurodegeneration and the functional impairments in gray matter structures due to the interest in linking them to standard neuropathological processes. Additional research is needed to determine how insulin/IGF-1 metabolic dysfunction mediates other aspects of AD. In this regard, recent preliminary studies showed that with the increasing severity of AD, WM atrophy and degeneration are associated with corresponding impairments in the expression of Akt pathway proteins and phosphoproteins (de la Monte, S.M. and Tong, M, Unpublished). Compromised signaling along these pathways could lead to loss of structural and functional integrities of oligodendrocytes and myelin. Although the steps leading from brain insulin and IGF deficiencies and resistances to WM degeneration have not yet been delineated, clues may be harnessed from data generated via unrelated experiments. For example, several studies have shown that WM atrophy and degeneration in other models of brain insulin and IGF resistances were associated with significant oligodendrocyte dysfunction. For example, in a rat model of i.c. STZ, WM degeneration was associated with reduced expression of mature myelin-associated genes and increased expression of

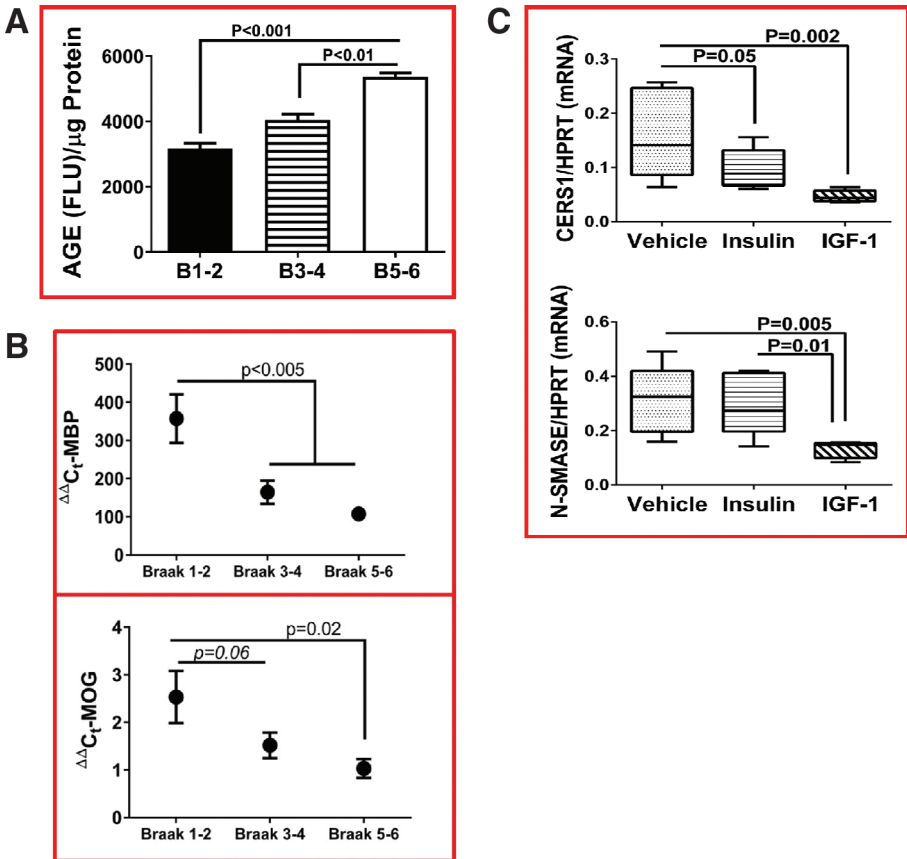


Figure 4 Cellular signaling abnormalities mediating WM degeneration. (A) Advanced glycation end-product (AGE) immunoreactivity was measured in postmortem frontal WM homogenates from humans with normal aging (Braak 0–2; B0–2), moderate AD (B3–4), or severe AD (B5–6) AD using a direct binding ELISA (107). Immunoreactivity was detected with horseradish peroxidase-conjugated secondary antibody and Amplex Red fluorophor. Fluorescence light units (FLU) were measured (Ex 579 nm/Em 595 nm) in a Spectromax M5, and results were normalized to protein content. (B) AD WM atrophy and degeneration are associated with reduced expression of mature MAGs. Quantitative RT-PCR was used to measure mRNA levels of MAG 1 and myelin oligodendroglial glycoprotein (MOG). PCR primer pairs were designed with Primer 3 (<http://primer3.sourceforge.net/>) software. PCR reactions were performed in a Roche Lightcycler 480 System (116). Gene expression was analyzed using the $\Delta\Delta C_t$ method with results normalized to hypoxanthine-guanine phosphoribosyl transferase, HPRT. (C) Insulin and IGF-1 suppress expression of genes encoding enzymes that produce ceramides or break down sphingomyelin. Frontal lobe WM slice cultures from an i.c. STZ adult Long Evans rat model of sporadic AD (109) were stimulated for 24 h with 10 nM insulin, 10 nM IGF-1, or vehicle (control). Graphs depict the mean \pm S.E.M. for each group. Intergroup comparisons were made by one-way ANOVA with the post hoc Tukey's test. Significant P-values and trends are indicated.

immature myelin-associated genes (116), corresponding with deficits in myelin maturation and striking alterations in WM structure (117). Similar observations have been made in human postmortem brains with different severities of AD and WM atrophy (Figure 4B).

An additional feature of experimental brain insulin resistance with WM atrophy is that oligodendrocyte dysfunction is associated with altered expression of sphingolipid metabolizing enzymes such that ceramide accumulation and sulfatide depletion would be favored (Figure 4C) (118, 119). In humans and experimental animals, reductions in brain sulfatide and increases in ceramide correlate with cognitive impairment, oxidative stress, lipid peroxidation, and neuroinflammation (22–24, 120). Ceramides inhibit insulin signaling through PI3K-Akt (25, 121) and increase oxidative stress, A β , pTau, and pro-apoptosis activation (122). Furthermore, preliminary studies suggest that insulin and IGF-1 stimulation suppress expression of enzymes that generate ceramides via degradation of sphingomyelin (Figure 4C). Therefore, it is likely that impairments in insulin/IGF-1 signaling in oligodendrocytes are important in the pathogenesis of WM atrophy and degeneration and mediate disease progression in AD.

Proposed role of APOE- ϵ 4

Apolipoprotein E is the major lipid transport protein in the CNS. This 34 kDa protein has three major isoforms (APOE- ϵ 2, APOE- ϵ 3, and APOE- ϵ 4) that differ by single amino acid substitutions at residues 112 and 158 (123). The ϵ 4 allele is the strongest genetic risk factor for late-onset sporadic AD (124–127) in that carriers account for over 50% of all AD cases (128); however, the APOE- ϵ 4 risk assessments vary across different countries and ethnicities (129). AD risk is increased by three- or fourfold among APOE- ϵ 4 carriers, and 15-fold in APOE- ϵ 4 homozygotes. APOE- ϵ 4 confers increased risk for AD by reducing brain glucose metabolism in the preclinical stages of disease (130), and ultimately impairing signal transduction through the insulin receptor, reducing A β clearance, and increasing A β aggregation (131). APOE- ϵ 4 may also have a role in mediating AD-associated WM degeneration via insulin resistance (131) and attendant microvascular endothelial cell and oligodendrocyte dysfunction.

Insulin/IGF signaling impairments and glial-vascular WM pathologies in AD

Our overarching hypothesis is that in AD, WM degeneration is mediated by impairments in insulin and IGF signaling that cast a wide net of pathophysiological responses including oxidative stress, inflammation, and dysregulated glucose and lipid metabolism (Figure 5). In WM, the targets of degeneration are oligodendrocytes and microvessels. Reduced signaling through insulin/IGF receptors, IRS and downstream Akt pathways compromises oligodendrocyte survival, myelin maintenance and integrity, and sphingolipid homeostasis, favoring sulfatide depletion and ceramide accumulation. Ceramide-mediated neurotoxicity, inflammation, oxidative stress, lipid peroxidation, and further impairment of insulin signaling reinforce the cascade of WM degeneration.

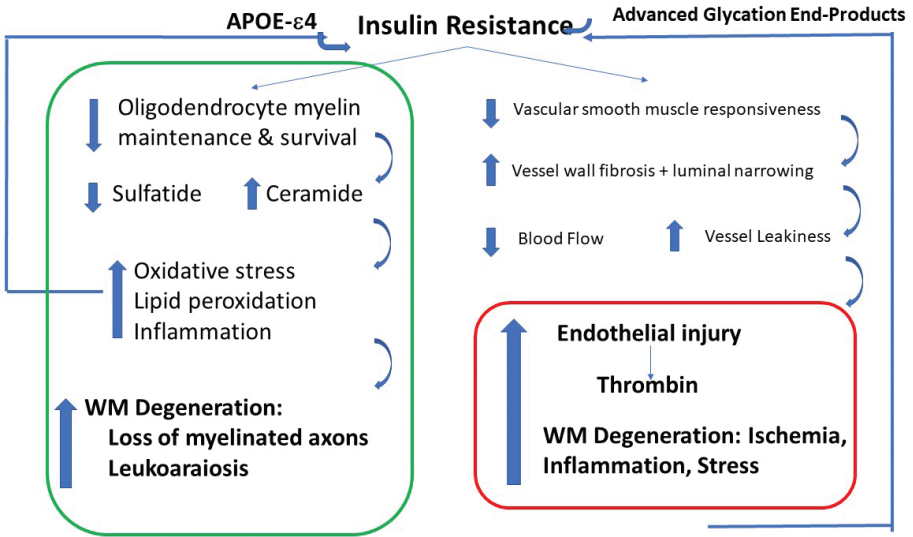


Figure 5 Hypothesis: White matter degeneration in AD is mediated by insulin and IGF resistances that target oligodendrocytes and microvessels. Reduced myelin and vascular integrity promote neuroinflammation, stress, and ischemic injury. APOE- ϵ 4 genotype, obesogenic diets, and poor lifestyle choices have cofactor roles in mediating WM degeneration due to exacerbation of insulin resistance.

Microvascular disease is also driven by insulin deficient and resistant states such as in types 1 and 2 diabetes mellitus. Initially, microvascular disease is mediated by combined effects of hyperglycemia, increased levels of AGE (Figure 4A), up-regulation of receptors for AGE (RAGE), and reduced responsiveness to NOS/NO (67, 132). Therefore, insulin and IGF resistances negatively impact microvascular structural integrity, vaso-responsiveness, and endothelial function. In later stages, microvascular disease is associated with the replacement of smooth muscle by collagen (sclerosis) leading to degenerative mural fibrosis and luminal narrowing, restricted blood flow, reduced vessel wall integrity marked by increased leakiness, and endothelial damage with attendant up-regulation and release of thrombin. Thrombin activation drives inflammation (cytokines), oxidative stress, microvascular occlusions. Microvascular occlusions cause ischemia which can injure oligodendrocytes, myelin, axons, and vessels. Also, vessel wall leakiness exposes perivascular tissue to toxins from the peripheral circulation. Late and probably permanent microvascular-associated WM pathologies in AD include leukoaraiosis with loss of myelin and degeneration of axons, micro-infarcts, perivascular tissue attrition, and vasculopenia (vessels can be destroyed by ischemic necrosis). Finally, microvascular disease can drive WM degeneration by worsening insulin resistance, oxidative stress, and inflammation.

Inflammation and oxidative stress are recognized mediators of neurodegeneration in AD (26, 39, 133). Potential sources of stress and inflammation include increased levels of AGE and RAGE expression (107, 108, 132, 134–137), impaired insulin/IGF signaling through Akt pathways, lipid peroxidation linked to myelin

breakdown, and ceramide accumulation. Neuroinflammation in AD is associated with increased pro-inflammatory cytokine expression in astrocytes and microglia (133, 138, 139). Although TNF- α , IFN- γ and IL-1 β are key players, preliminary data suggest that neuroinflammatory responses are broader and include activation of pro-inflammatory and inhibition of neuroprotective cytokines/chemokines (17, 140).

CONCLUSION

Combined effects of oligodendrocyte and microvascular dysfunction interact to cause WM degeneration, including leukoaraiosis in AD. Insulin resistance exacerbation by APOE- $\epsilon 4$ may accelerate AD-associated WM molecular, biochemical, and structural pathologies linked to impaired function of oligodendrocytes and microvascular endothelial cells. Therefore, WM degeneration and cognitive impairment may be preventable or reversible by lifestyle measures that restore insulin responsiveness in the CNS.

Acknowledgments: This research was supported by grants AA11431, AA024092, and HD057100 from the National Institutes of Health.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Relationship between Alzheimer's Disease and the Human Microbiome

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch9>

Abstract: Alzheimer's disease (AD) is a neurodegenerative disease characterized by memory and language disorders, and the accumulation of amyloid- β and tau protein in the brain has been considered a feature of AD. The accumulation of amyloid- β has been reported to be observed 15 to 20 years before the onset by image analysis-based diagnostic methods. In addition, it has been reported that AD is associated with various diseases such as type 2 diabetes, periodontal disease, and obesity. It is conceivable that these diseases trigger the onset of AD. The human gut and brain form a network called "brain-gut-microbiota axis," and it is suggested that the gut microbiota is involved in brain diseases. Recently, the microbiota has also been reported to be involved in diseases such as depression and Parkinson's disease, and so attention is being paid to the relationship between AD and gut microbiota. This chapter outlines the relationship between AD and the human microbiome.

Keywords: amyloid- β ; behavior; brain-gut-microbiota axis; gut microbiota; metabolome

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

The cause of Alzheimer's disease (AD) is presently unknown, but its onset has been shown to involve mainly genetic and environmental factors. About 700 risk genes (as of April 2019) are registered in Alzforum (<https://www.alzforum.org/>) as the genetic factors of AD. Other factors found to be involved include lifestyle habits such as sleep, exercise, diet, and educational history. Recently, it has been reported that sleep is related to the accumulation of amyloid- β , which is a characteristic of AD. In healthy middle-aged men, sleep reduced amyloid- β 42 in cerebrospinal fluid by 6%, while lack of sleep abolished that reduction (1). In a study investigating the relationship between the Mediterranean diet and dementia, it was noted that the traditional Mediterranean diet that consists of a large amount of fruits, vegetables, and cereals reduces the risk of developing dementia and AD (2). In addition, Ozawa, upon following more than 1000 subjects over 17 years, has reported that the incidence of AD decreased significantly with increased intake of milk and dairy products (3). Lifestyle plays an important role in the prevention of AD, and dysregulation of lifestyle leads not only to AD but also to various other diseases. This chapter first outlines the relationship between lifestyle diseases and AD, and then the relationship between gut microbiota and AD.

AD AND DIABETES

Association of AD to diabetes led to the classification of a new category of diabetes called type 3 diabetes (4). Ott et al. (5) examined the association between diabetes and dementia in 6330 people aged 55–99 years, and the results suggest an association between diabetes mellitus and dementia. In addition, in a prospective population-based cohort study among 6370 elderly subjects, diabetes mellitus reportedly doubled the risk of dementia and AD. The study also reported that patients treated with insulin had four times higher the risk of dementia. A cohort study of 2574 men reported that patients with type 2 diabetes are associated with dementia, AD, and vascular dementia (6). The same study concluded that these associations are stronger in patients carrying the APOE ϵ 4 allele (7). Furthermore, borderline diabetes is also associated with the increased risk of dementia and AD (8). Conversely, Michal et al. (9) reported that in the hippocampus of AD patients, diabetics had significantly lower plaque ratings than the non-diabetics. In addition, inflammation in the brain by the intake of a high-fat diet promotes accumulation of amyloid in diabetes model mice, regardless of the decrease in insulin (10). Thus, prior studies suggest that the factors like eating habits, mild glucose intolerance, and onset of type 2 diabetes are involved in the onset of AD. On the other hand, amyloidosis is a key pathological feature of both AD and type 2 diabetes (11). Bacterial endotoxin lipopolysaccharide and bacterial cell wall peptidoglycan are involved in amyloidosis, suggesting that chronic bacterial inflammation may link the two diseases. In addition, recent advances in gene analysis technology have revealed the relationship between intestinal bacteria and diabetes. Adachi et al. (12) have reported the relationship between type 2 diabetes and short-chain fatty acids (SCFAs), the metabolites of the microbiota, in the

Japanese population. From these studies, it can be considered that changes in the microbiota affect the production of SCFAs, thereby promoting the onset of type 2 diabetes as well as AD.

AD AND PERIODONTAL DISEASE

Periodontitis is considered as a risk factor for dementia and AD. Periodontal disease is a chronic disease caused by gram-negative bacteria such as *Porphyromonas gingivalis*, *Treponema denticola*, and *Tannerella forsythia*. It has been clarified that this chronic inflammation is related to the accumulation of amyloid- β and cognitive impairment that are characteristic of AD (13). In addition, tumor necrosis factor- α and antibodies against periodontitis in plasma have been reported to be biomarkers of AD (14, 15), and periodontal disease has been suggested to be a probable trigger for AD. Recently, gingipain, a protease produced by *P. gingivalis*, has been detected in the brains of patients with AD (16). The concentration of gingipain is high in the brain of patients with AD, and the accumulation of tau protein is promoted, whereas the accumulation of amyloid- β is suppressed by the gingipain inhibitor. Furthermore, oral administration of *P. gingivalis* to mice promotes the accumulation of amyloid- β (17). Gingipain reportedly activates microglia and causes inflammation in the brain (18). These activated microglia cause accumulation of amyloid- β and cognitive decline (19). However, Noble et al. (20) have reported that, in a cohort study of 219 subjects (consisting of 110 patients with AD and 109 healthy volunteers), subjects with high serum IgG against *Actinomyces naeslundii* (which is associated with periodontal disease) were at a high risk of developing AD. Thus, the periodontitis bacteria have been linked to AD through the microbial toxins, inflammatory substances, and serum antibodies. Chronic inflammation developed by these bacteria is a predisposing factor for AD.

AD AND OBESITY

Obesity is considered as one of the risk factors associated with AD. Recently, the relationship between obesity and AD has been studied extensively. Animal studies have shown that mice fed with high-fat diet significantly increases the accumulation of amyloid- β in the hippocampus and are involved in cognitive decline (21–23). Another clinical study characterized by magnetic resonance imaging (MRI) scan of the brains of 700 patients having mild cognitive impairment (MCI) inferred that higher body mass index (BMI) is associated with brain volume deficits (24). Gustafson reported the relationship between BMI and risk of dementia as investigated in an 18-year follow-up of 392 Swedish adults (aged 70–88 years) without dementia. Higher body weight was observed in women who developed AD compared to women without dementia (70, 75, and 79 years). In particular, at the age of 70 years, every 1.0 increase in BMI showed a 36% increase in AD risk (25). In addition, Luchsinger's study has shown that the waist to hip ratio is related to a higher risk of AD (26). In the

Swedish, 8534 twin individuals over the age of 65 were assessed to detect cases of dementia. Overweight (BMI 25–30) and obesity (BMI over 30) at midlife were related to dementia with odds ratios of 1.71 and 3.88, respectively (27). However, the risk for dementia associated with obesity gradually reduced with increasing age (28). Obesity has been implicated as a risk factor for AD in middle age, whereas its associated risk decreases with increasing age. Conversely, weight loss and low BMI have been found to be associated with increased risk of AD in older adults (29).

MICROBIOTA AND AMYLOID ACCUMULATION

The relationship between microbiota and amyloid- β accumulation has been studied by Harach et al. (30). APPPS1, an AD mouse model, presents accumulation of amyloid- β in the brain in an age-dependent manner. The generation of germ-free APPPS1 mice was inhibited by the accumulation of amyloid- β . In addition, the microbiota of this mouse model is different from that of the wild type, and it has been reported that accumulation of amyloid- β increases in mice transplanted with the microbiota of an AD mouse model. Furthermore, Ho et al. (31) found that valeric acid and butyric acid, SCFAs produced by the microbiota, strongly inhibit the aggregation of amyloid- β in an in vitro test. Furthermore, bacterial endotoxin may be involved in the inflammations associated with amyloidosis and AD (32). Although some bacteria such as *Escherichia coli* produce amyloids (33), the relationship between the amyloid that is caused by neurodegenerative diseases such as AD and bacterial amyloids has not been clarified (34). However, bacterial amyloid has been shown to activate signaling pathways that play a role in the pathogenesis of neurodegenerative diseases and AD, and microbiota is a noted key player that enhances inflammation associated with the accumulation of amyloid- β (35). Furthermore, the lipopolysaccharide of gram-negative bacteria promotes accumulation of amyloid- β in mouse brain and induces cognitive dysfunction (36, 37). Hence, it has been suggested that microbiota is involved in the accumulation of amyloids, which is known to be a pathological feature of AD, via metabolites such as extracellular components and SCFAs. In addition, bacteria that produce amyloids are also present in the enteric bacterial groups, but it is thought that further research is necessary to clarify whether amyloids derived from the bacteria are involved in AD progression.

EFFECTS OF DAIRY PRODUCTS AND PROBIOTICS IN AD

Acute and chronic inflammation is associated with neurodegenerative diseases such as AD and Parkinson's disease (38–41). Probiotics such as lactic acid bacteria and *Bifidobacterium* have attracted attention as tools to suppress this inflammation. In the Bonfili study, administration of the probiotic cocktail SLAB 51 (*Streptococcus thermophilus*, *Bifidobacterium longum*, *B. breve*, *B. infantis*, *Lactobacillus acidophilus*, *L. plantarum*, *L. paracasei*, and *L. delbrueckii* subsp. *bulgaricus*, *L. brevis*) in AD model mice (3xTg-ADmouse) affected changes in the microbiota, thus

affecting the content of metabolites of enteric bacteria such as SCFAs and cognitive function (42). Kobayashi et al. (31) also reported that oral administration of *B. breve* A1 led to behavior impairment to the same level as donepezil, a centrally acting cholinesterase inhibitor, in AD model mice injected with amyloid- β into the ventricles. Acetic acid, which is a metabolite of *Bifidobacterium*, is known to play an important role in the improvement of AD. However, there have been cases where improvement in memory due to probiotics was not observed. Benton et al. (43) confirmed the cognitive function by following 3 weeks of probiotic milk drink or placebo control consumption in 124 healthy volunteers (mean age 61.8 years), and the cognitive function was higher in the placebo consuming group than the probiotic drinking group upon 20 days of consumption. Furthermore, recent research has shown that consumption of not only these probiotics but also yogurt and cheese has been linked to AD and dementia. David et al. (44) reviewed that bioactive peptides in dairy products improve cognitive function. Ano et al. (45, 46) have also shown that in vivo experiments the peptides present in Camembert cheese improve the decline in memory and cognitive function. On the contrary, Rahman et al. (47), in an epidemiological study of 1056 subjects, reported that dietary intake of cheese is associated with a lower prevalence of cognitive impairment. Also, a study conducted on a total of 1006 community-dwelling Japanese subjects without dementia, aged 60–79 years (followed up for a median of 15 years), reported that high intake of milk and milk products reduced the risk of dementia (48). Although many model animals for AD and dementia are produced and their application to this field is advanced, further studies are needed to establish the influence of probiotics and dairy products on brain function.

AD AND GUT MICROBIOTA

Recently, the development of next-generation sequencing technology has made it possible to estimate the gut microbiota rapidly at a low cost, and the relationship between various diseases and the gut microbiota has been studied extensively. The Vogt study compared the microbiota in 50 subjects (Healthy control HC: $n = 25$ and AD: $n = 25$) and noted decreased microbial diversity in the AD subjects. It also reported a decrease in *Firmicutes* and increase in *Bacteroidetes* percentage abundance (49). Saji et al. (50) compared the microbiota of non-demented patients ($n = 49$) with demented patients ($n = 34$) among 128 Japanese subjects and found that *Bacteroides* decreased in demented patients compared to non-demented patients (Figure 1). Furthermore, Nguyen et al. (51) reported that butyrate-producing bacteria involved in cognitive function have been isolated from the microbiota of patients with AD. Liu et al. (52) reported that in a study of 97 subjects (AD: $n = 33$, MCI: $n = 32$, and HC: $n = 32$), the fecal microbial diversity was decreased in AD patients compared with MCI patients and healthy volunteers. In addition, it also reported a decrease in *Firmicutes* and increase in *Proteobacteria* abundance. There are similar reports on the relationship between gut microbiota and AD as the studies stated above. Therefore, further research is needed to clarify the difference. With the growing research in this field, future boom in AD cure research might as well be directed toward microbiome research.

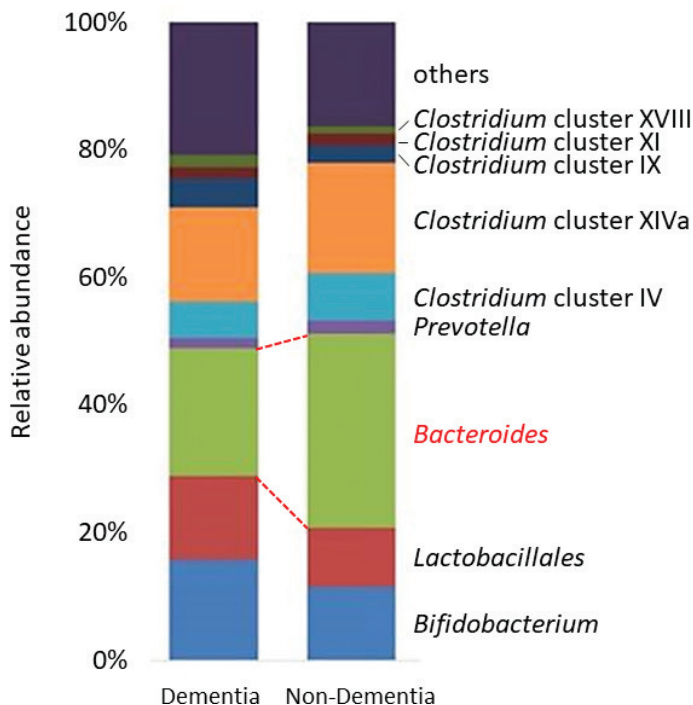


Figure 1 Relative bacterial abundance in the gut microbiota of dementia and non-dementia patients. It was suggested that a lower prevalence of *Bacteroides* is seen in the gut of dementia patients than non-dementia patients (50).

GUT MICROBIOTA AND BEHAVIOR

Human intestine and brain form a network called the “brain–gut–microbiota axis” through physiologically active substances. The gut microbiota has been shown to play an important role in this network. Researchers have transplanted mice with different microbiota and compared their response to stress with adrenocorticotropic hormone and corticosterone as indicators (53). Specifically, as compared with specific pathogen-free mice, adrenocorticotropic hormone and corticosterone levels have been reported to significantly increase in germ-free mice due to restraint stress. In addition, the effect is also seen in mice transplanted with *B. infantis*, suggesting that the effect differs depending on the microbe transplanted and that the microbiota also affects neurotransmitters in the brain (54, 55). Kim et al. (56) reported that pregnant mice colonized with the human commensal bacteria (a mix of 20 human bacterial strains), which induce intestinal Th17 cells due to poly (I:C)-induced inflammation, produced offspring that were found to have increased anxiety behaviors such as increased ultrasonic vocalization, enhanced repetitive behavior with marble burying test, and shortened time in the center of the open-field arena. In contrast, these anxiety behaviors were not observed if the mothers were pre-treated with interleukin-17a blocking antibody, since interleukin-17 production of intestinal Th17 cells induced by human

commensal bacteria contributes to the development of anxiety behaviors in mouse offspring. Thus, it was revealed that the gut microbiota of the mother mouse is involved in the behavior of the offspring mouse. In addition, the authors previously reported cognitive behavior decline in germ-free mice transplanted with the microbiota of AD patients (57). Cognitive behavior was assessed by Object Location Test (OLT) and Novel Object Recognition Test (ORT). A significant deterioration of cognitive function was observed through both OLT (70 and 75 weeks of age vs. 10 weeks of age; 55, 70, and 75 weeks of age vs. 15 weeks of age) and ORT (70 weeks of age vs. 10 weeks of age; 35, 55, 65, 70, and 75 weeks of age vs. 15 weeks of age) in mice transplanted with microbiota from affected patients. Moreover, significant reduction of cognitive function of these mice was confirmed by both OLT (55 and 70 weeks of age) and ORT (55, 60, 65, and 70 weeks of age) in comparison with cognitive function of mice transplanted with microbiota of healthy volunteers (Figure 2). In this article, these data were re-analyzed by linear regression analysis (Figure 3). A significant decrease in cognitive function was confirmed in mice transplanted with microbiota from affected donors in relation

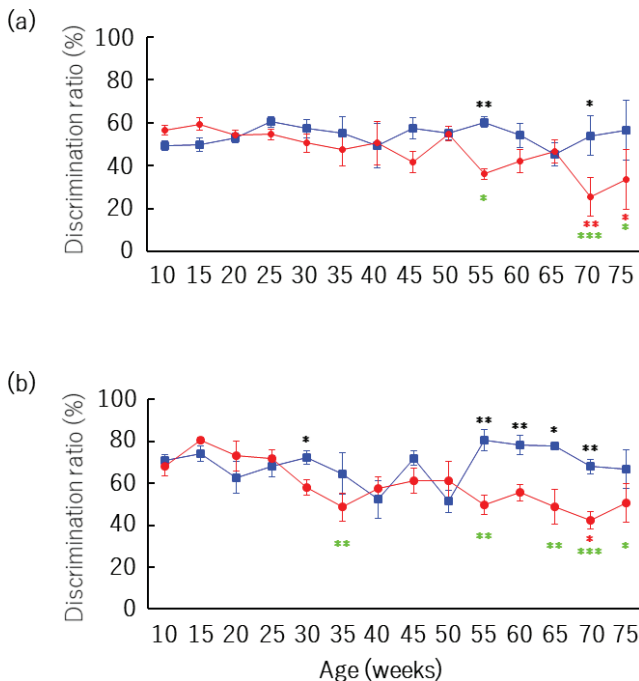


Figure 2 Novel object recognition test in mice transplanted with microbiota. (A) Ratio of time spent exploring a familiar object in a new location to time spent exploring a familiar object in an old location. (B) Ratio of time spent exploring a novel object to time spent exploring a familiar object. Blue and red lines indicate the ratio of time spent by mice transplanted with microbiota from a healthy donor and a patient with Alzheimer's disease, respectively. Black, * and ** indicate comparison between groups; red, * and ** indicate mice transplanted with microbiota from a patient with Alzheimer's disease had significantly altered cognitive function at respectively weeks of age compared with that at 10 weeks of age; green, *, **, and *** indicate mice transplanted with microbiota from a patient with Alzheimer's disease had significantly altered cognitive function at respectively weeks of age compared with that at 15 weeks of age. Data are mean \pm SEM. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$ (57).

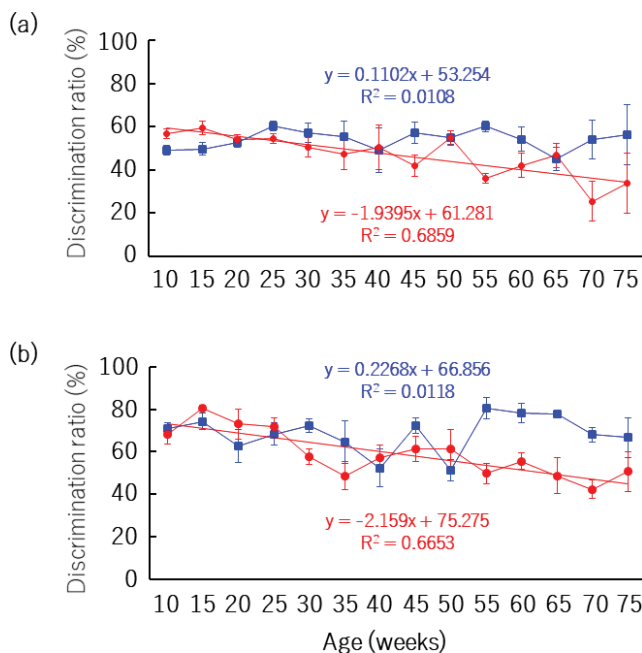


Figure 3 Regression analysis of two behavior tests. (A) Ratio of exploring novel objects in the 5 min of OLT. Blue square and red circle indicate healthy control (HC) group and Alzheimer's disease (AD) group, respectively. (B) Ratio of exploring for novel objects in the 5 min of object recognition test. In both panels means \pm SEM are shown (57).

with age. The regression analysis results showed association between cognitive decline and age in mice transplanted with microbiota from affected patients, but not in mice transplanted with microbiota of healthy volunteers. Therefore, it was clear that mice transplanted with microbiota from affected patients had reduced cognitive function. This was further investigated by fecal metabolome analysis. The principal component analysis of the metabolites from individual mice exhibits separate clusters representing each of the mice categories (Figure 4). And the different metabolites from affected donors to mice transplanted with microbiota included gamma-aminobutyric acid, taurine, and valine, all of which are involved in central nervous system function. In addition, a difference in the concentration of other amino acids such as tryptophan, tyrosine, propionic acid, and SCFAs was also reported. Thus, it was suggested that the microbiota influences host behavior through its metabolites.

CONCLUSION

AD is known to cause deposition of amyloid- β , which is the main component of senile plaques in the brain. This deposition of amyloid- β is caused by the accumulation of amyloid generated from the amyloid precursor protein (APP) by the action of two enzymes β -secretase and γ -secretase in the cerebral cortex of the brain.

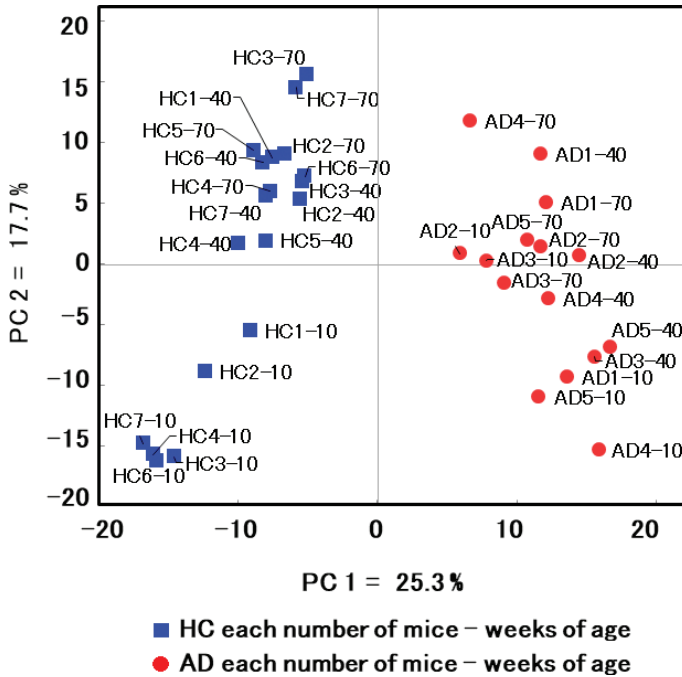


Figure 4 Comparison of metabolites in HC and AD mice feces. Principal component analysis of fecal metabolites in mice transplanted with microbiotas from a healthy volunteer (blue) and a patient with Alzheimer's disease (red) (57).

It has been clarified that this accumulation of amyloid- β starts 15–20 years before the onset of AD. At the same time, after a decrease in cognitive function is observed, there is not much change in the accumulation of amyloid- β , and no effect is seen in a drug targeting amyloid- β . Hence, some investigators have questioned the involvement of amyloid- β in AD. However, further studies are needed to investigate whether AD caused changes in the gut microbiota or vice versa.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Ocular Exploration in the Diagnosis and Follow-Up of the Alzheimer's Dementia

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch10>

Abstract: The retina is part of the central nervous system (CNS), and therefore, in Alzheimer's disease (AD), retinal and optic nerve degeneration could take place. This degeneration leads to neurofunctional changes that can be detected early and followed up throughout the evolution of the disease. As opposed to other CNS structures, the eye is easily accessible for in vivo observation. Retinal organization allows for the identification of its different neurons, and in consequence, detection of minimal changes taking place during neurodegeneration is possible. Functional vision studies performed on AD patients in recent years have shown how visual acuity, contrast sensitivity, color vision, and visual integration vary with the progression of neurodegeneration. The development of optical coherence tomography in ophthalmology has meant a breakthrough in retinal exploratory techniques, allowing the obtention of high-resolution images using light. This technique enables retinal analysis in the earliest stages of AD, being considered as a biomarker of neuronal damage. Given AD's high prevalence and its expected increase, it is important to

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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perform easy tests that cause minimal discomfort to the patients at a low cost while offering abundant information on the stage of the disease.

Keywords: Alzheimer's disease; biomarker; neurodegeneration; retina; visual system

INTRODUCTION

Alzheimer's disease (AD) is recognized by the World Health Organization as a global public health priority. AD is the single principal cause of dementia, between 50 and 75%, and is primarily a condition of aging, roughly doubling in prevalence every 5 years after age 65 (1). The incidence of AD increases with age, and the prevalence is growing as a result of the aging of the population (2); however, there are no disease-modifying therapies currently available, and none have been successful in late-stage clinical trials (3).

Late-onset AD is likely to be driven by a complex interplay between genetic and environmental factors, implicating inflammatory, cholesterol metabolism and endosomal-vesicle recycling pathway (4) and the presence of the APOE+4 allele (5). In addition, AD is frequently associated with vascular dysfunctions and inflammation (6). In particular, it is now recognized to play a key role in AD pathogenesis the microglial activation in response to amyloid deposition (7).

The basis of AD has not been fully elucidated. However, the progressive accumulation of β -amyloid ($A\beta$) plaques and abnormal forms of phosphorylated tau (tau tangles) within and outside of neurons and neuroinflammation, both of which could lead to neuronal loss and synaptic dysfunction (8), are considered to be the neuropathological hallmarks (9–11).

The "amyloid cascade hypothesis" (12) is based on the progressive deposition of fibrillar $A\beta$ as diffuse plaques, which activates an inflammatory response, altered ion homeostasis, oxidative stress, and altered kinase/phosphatase activity, leading to the formation of NFTs and widespread synaptic dysfunction and neuronal death (13). Recently, it has been demonstrated that an $A\beta$ plaque environment can accelerate the templated spread of tau pathology (14, 15).

Hyperphosphorylation of tau has numerous pathogenic effects. It reduces tau's affinity for microtubules and increases its possibility to aggregate and fibrillize (16). This impact leads to weakening of microtubules with consequent axonal transport failure and neurodegeneration (15).

In the past decade, remarkable advances have been made in disease-specific biomarkers based on the detection of amyloid or neurodegeneration. With the knowledge that the pathological changes occur years previous to symptoms, the arrival of biomarkers of $A\beta$ and tau pathology, and nuclear imaging measures of atrophy, diagnostic criteria have evolved to allow for the diagnosis to be made both earlier and with increased molecular specificity.

These biomarkers not only enable the diagnosis of AD in the stage of dementia but also beforehand, in the prodromal stages of AD. However, these biomarkers are not applicable as population-wide screening tools because they are invasive, not easily applicable and expensive.

EYE AND BRAIN: SYMBIOTIC RELATIONSHIP

Over the last few decades, in neurodegenerative diseases of the central nervous system (CNS), the importance of ophthalmic examination has reportedly increased. It is not surprising that the retina, as an extension of the CNS, is impaired in patients with CNS degeneration (17). The eye has unique physical structures and is host to specialized immune responses similar to those in the brain and spinal cord (18–20). In fact, abnormal results were found in AD patients in test exploring visual processing/visual pathways and also in those examining the retina (17).

The neuroinflammatory changes could be detected using a routinely diagnostic technique used in ophthalmology, the optical coherence tomography (OCT). OCT allows to see the anatomic detail of pathological changes in the retina and optic nerve. Changes in OCT measurements have been used to study the course of neurodegenerative diseases such AD (21–25), suggesting that the data compiled may be useful as a biomarker in diagnosing and treating neurodegenerative disease.

The retina is made up of specialized neuron layers that are interconnected via synapses (photoreceptors, bipolar cells, horizontal cells, amacrine cells, interplexiform cells and ganglion cells) (18, 26). In the eye, the light that enters is captured by the photoreceptor cells in the outer retina, initiating a cascade of neural signals that finally reach the retinal ganglion cells (RGCs), whose axons form the optic nerve. These axons project to the lateral geniculate nucleus in the thalamus and to the superior colliculus in the midbrain, whose information is then transmitted to specialized visual processing centers in the brain that provide a perception of the world.

The first study, showing postmortem anomalies in the optic nerve of patients with AD, demonstrated not only widespread axonal degeneration but also a reduction in the number of RGC and the thickness of nerve fiber layer (NFL), with a 25% decrease of ganglion cell layer (GCL) (27–29). More recent OCT studies also found a decrease in the thickness of inner retinal layers (NFL and GCL) (30–41).

The presence of A β plaques in GCL could explain the RGC degeneration in the AD course (19, 27, 42). In fact, it has been demonstrated that most of the A β plaques deposited in the retina are located in the GCL (43, 44). Deposits of A β trigger a neurotoxic effect in the RGC, inducing apoptosis (45). This apoptosis is dose- and time-dependent (45). Some pieces of evidence showed that A β expression is greater in the central retina than in the periphery of the eye of an AD mouse model (46). As in the brain, A β deposits in the retina have the classical plaque structure, forming clusters along the blood vessels (47). A β accumulations were located inside and around melanopsin retinal ganglion cells (mRGC) and more evident in the superior quadrant of the retina (47).

In the last few years, it was found that mRGCs also showed a significant loss in postmortem AD retinas (47). These cells represent the 1–2% subpopulation of RGC that are intrinsically photosensitive (47, 48). The mRGC send ambient light information to the hypothalamus nucleus via the retinohypothalamic tract (48), regulating circadian rhythms, pupil size, sleep alertness, and pineal melatonin synthesis (49–51). This mRGC loss could contribute to circadian dysfunction in AD (47). Indeed, its presence in the early stages of AD of circadian dysfunction was postulated as the worst prognostic value in AD (47).

All these retinal changes could be responsible, in part, for the visual deficit that occurs in AD patients. The acetylcholine decrease is also characteristic of this disease, and therefore contributes to the visual deficit that occurs in AD patients because acetylcholine is essential for the correct visual process of healthy retinas (52).

VISUAL FUNCTIONAL TESTS IN THE EXPLORATION OF AD

Aging affects visual function because light transmission diminishes inside the eye, whereas the scattering of light increases. With age, there is not only a decrease in the density of photoreceptors in the retina, but there is also less efficiency in phototransduction and photopigment regeneration (53). In addition to aging, visual processing is affected in AD patients. The brain's visual areas are involved in AD pathology (in the dorsal and ventral regions), worsening the perception of movement; angular and color discrimination; and form and face identification (54–60). There are several tests such as the visual acuity test, and the contrast sensitivity and color vision test to explore this visual processing in the ophthalmology practice.

Visual acuity

Visual acuity (VA) is a measure of the spatial resolution of the visual system to detect and discriminate an object. In patients with AD, it is very important to choose the correct VA test. It was demonstrated that VA tests present better values if the letters are isolated (61).

Contrast sensitivity and color vision

The contrast sensitivity (CS) test assesses the capacity of the visual system to distinguish an object from the background in which it is placed. The CS test allows us to ascertain the integration of the information of the ganglion cells receptor field and their cortical processes. CS is measured by a threshold curve in which the spatial frequencies examined are depicted. Color vision is an illusion created by the interactions of the neurons in our brain. It is intimately linked to the perception of form where color facilitates detecting borders of objects (62). Parvo- and magnocellular ganglion cells are located in the GCL and lead to two different visual pathways that identify color and contrast (63). Parvocellular ganglion cells are smaller and more numerous than other retina ganglion cells, with smaller receptor fields located in the macular retinal area. They give rise to the parvocellular visual pathway, specialized in pattern identification and color; and it is most sensitive to high spatial frequency (51). The magnocellular pathway originates in magnocellular retina ganglion cells, which are larger and more numerous, and have larger receptor fields that are more sensitive to low spatial frequencies (63). There is a third type of ganglion cell that is called koniocellular, which receives information from short wave cones. Koniocellular cells are also sensitive to blue–yellow tones (64, 65). CS is a really important visual function. Even several studies showed that a CS loss is the best predictor of the ability of elders to perform daily life activities (66, 67).

Visual fields

The visual field (VF) refers to the total space in which objects can be seen in the side (peripheral) vision as your eyes are focused on a central point. The fovea, where the cone photoreceptor density is at its highest, is the area of greatest sensitivity. The visual sensitivity comes down further from the fovea. Traditional perimetry is carried out under photopic conditions, and therefore, rod photoreceptors do not contribute to the visual field (68). The normal visual field extends to approximately 60° nasally, 90° temporally, 60° superiorly and 70° inferiorly. In the area of the optic nerve head, temporal part of the VF, exists a blind spot that indicates an area with no photoreceptors (69).

Visual integration

Identifying a visual stimulus requires not only physical input analysis but also the contact between the neuronal representations of the stimulus and the memories that the perceivers have accumulated through their life experiences with the objects. Object identification arises from the dynamic interaction between a sensorial/physical process (upstream processing) and a cognitive process (downstream processing). Spatial frequency is an important physical property of the image. The extraction of visual sensory characteristics follows a course to a fine processing scheme where the low spatial frequency represents the overall information about the shape and orientation of the stimulus, while the high spatial frequency corresponds to the configuration information and fine details (70–75).

OPHTHALMOLOGICAL METHODS FOR RETINAL ANALYSIS

Over the past decade OCT has evolved as one of the most important tests in ophthalmic practice. It is a non-invasive imaging technique that provides high-resolution, cross-sectional images of the retina.

Optical coherence tomography

OCT was first demonstrated for cross-sectional retinal imaging in 1991 by a Massachusetts Institute of Technology (MIT) team (76). OCT synthesizes cross-sectional images from a series of laterally adjacent depth-scans giving a non-invasive clinical tool to evaluate the structural anatomy and the evaluation of the integrity of the retina.

Optical coherence tomography angiography

Optical coherence tomography angiography (OCTA) is a promising new method for visualizing the retinal vasculature and choroidal vascular layers. A key advantage of OCTA over traditional fluorescein angiography is that it provides depth-resolved information without contrast. The basis of OCTA is to repeatedly scan a region and then examine the resultant images for changes. Stationary tissue

structures will show little change, whereas moving structures, such as blood flowing through vessels, can show changes between images. Contrast is generated based on the difference between moving cells in the vasculature and the static surrounding tissue. This imaging technique can be performed in patients for whom fluorescein angiography or indocyanine green angiography may not be indicated (77). OCTA is clinically used as an *en face* imaging modality, which is generated by summarizing the flow information within the depth range encompassed by the current scheme. This scheme subdivides the retinal circulation into two plexuses and choroidal circulation into two slabs. Angiograms, which are similar to fluorescein angiography or indocyanine green angiography, are also produced (78).

FUNCTIONAL CHANGES IN AD

Nowadays, it is known that, in AD, in addition to altering brain structures, the involvement of the different regions of the visual system also occurs, with a manifestation of distinct symptoms and signs that can be detected by clinical history and ophthalmological studies.

VA has proven to be a controversial test in AD. Studies have not found an alteration in AD patients (79–86), and others have found VA loss and linked them to visual hallucinations (87, 88) (Table 1). Moreover, these alterations of VA are

TABLE 1

Eye changes in AD patients

	References
Visual alterations	
Visual acuity	87, 88
Contrast sensitivity	82, 84, 85, 90–102, 103, 104
Visual field	105–109
Color vision	58, 84, 93, 110, 113–116
Visual integration	93, 117
Structural alterations	
Retinal A β deposition	19, 27, 42–47
Optic nerve	27–29
Macular thickness	
Inner retinal layers	30–41, 138, 140–145
Outer retinal layers	135
Peripapillary thickness	21, 24, 30–38, 120–127
Retinal vascularization	148–150
Choroid thickness	125, 148, 151–153

AD: Alzheimer's disease; A β : beta-amyloid

related to difficulties in writing and reading (89). On the other hand, recent studies have found that CS testing is a more sensitive tool than VA testing to identify the subclinical impairment of visual function (90, 91). CS precedes the development of dementia at 10 years of the longitudinal follow-up in a well-phenotyped, prospective, community-based cohort (90, 91). It has been shown that the CS function is affected in AD patients. The impairment ranges from a reduction in all spatial frequencies (85, 92–99) to a greater decline in high (92, 93, 98, 100) or low spatial frequencies (82, 84, 101, 102). Such discrepancies in the affected frequencies could be due to differences among the CS test used as well as the patients included in the studies (17, 66). Recent works show that CS is the main manifestation during the initial disease stage. There is a progressive impairment throughout the disease course (93, 103, 104) (Table 1). CS impairment in AD has consequences for cognitive abilities and daily functions, given that the most affected spatial frequencies are the higher frequencies corresponding to macular function (17). The presence of reduced CS years before the clinical onset of dementia suggests that this association is not simply a consequence of later stage dementia. Furthermore, reduced CS can precede the clinical onset of cortical or subcortical dementia neurodegeneration (90).

Visual field test requires significant cooperation from the patient. Therefore, the reports of VF and AD are scarce, and most are case reports (17, 68). However, it has been observed that decreased VF sensitivity correlated with cognitive impairment. A large prospective study of threshold VF perimetry in patients with probable AD demonstrated that the most common VF abnormality was bilateral inferior constriction of the VF in an arcuate-like pattern (105, 106). AD patients underwent a diffuse sensitivity loss and defects that involved the central field. In 39% of AD patients, the density of plaques and tangles was greater in the cuneal compared with lingual gyri, supporting the theory that cortical disease is responsible for the VF loss (105). Recent findings show that the side of the homonymous defect is predicted by lateralized occipital atrophy (107–109) (Table 1).

Another manifestation of AD is the fluctuations in color perception, which are mainly errors in color recognition due to the involvement of the parvocellular pathway (110).

In the color perception, some studies using the Farnsworth test and Ishihara test found no differences between AD patients and control group (96, 111, 112). On the other hand, some tritan-axis defects were found, showing a correlation with the cognitive decline (58, 84, 93, 113, 114). The discrepancy in the results of both studies may be due to the fact that each study used a different color vision method. A recent investigation showed that the Ishihara color vision test could discriminate between AD and vascular dementia (115). The Ishihara test may involve dorsal cortical pathways that extend from the occipital to the parietal lobes. In the Ishihara test, the patients have to identify a number occluded in a pattern made up of small color forms with different tones. AD patients usually present simultagnosia caused by an occipitoparietal dysfunction, and therefore, they cannot recognize the pattern that is presented in the Ishihara test. The problem does not lie in the color sense, but in the inability to reconstruct the pattern (115). Using the Farnsworth-Munsell 100 hue test, a significantly decreased color discrimination was found in AD. In addition, the number of color discrimination errors was inversely related to Mini-Mental State Examination scores (MMSE) (110). Some studies using the Farnsworth color testing methods, not influenced

by dorsal stream dysfunction, suggest that AD patients tend to have tritan color defects (58, 93) while others have found a protanomaly (116) (Table 1).

The perception digital test (PDT) is a sensitive method in mild AD patients developed for evaluating their visual-perception disorders (117). The test is designed to assess the visual recognition of familiar situations. PDT has a significant correlation with the cognitive decline of the AD patient, indicating that patients with mild AD have significantly more failures in PDT than controls (93, 117) (Table 1).

STRUCTURAL CHANGES IN AD

The retinal nerve fiber layer (RNFL), RGC and inner retinal layers are considered indirect biomarkers of the CNS, allowing the prediction of brain pathology in patients suffering from different neurological diseases (118, 119). Many studies focus on the thickness of segmented peripapillary RNFL (superior, inferior, nasal, and temporal) in patients with AD comparing them with controls. Some works showed a decrease in the peripapillary RNFL thickness in all areas (30, 31, 34, 36–38). However, others authors found that the peripapillary RNFL thinning occurred in the inferior and superior regions (35, 39, 40), while other works demonstrated that peripapillary RNFL thinning appeared only in the superior region (120–124). Some studies reported thinning in the RNFL associated with a progressive cognitive decline (21, 24, 123, 125, 126) (Table 1). The variance in peripapillary RNFL thickness reported in AD might be due to differences in disease progression among patients studied since patients with greater peripapillary region alteration were those with a more advanced stage of AD. In any case, thinner peripapillary RNFL indicates fewer RGCs in AD, which confirmed the differences in OCT measurements in AD patients (127). The loss of RGCs is matched with the pathologic cascade hypothesis in AD, which affects both the cerebral neuron and the RGCs in the retina (36). This whole peripapillary RNFL controversy is the result of studies based on small size samples and important methodological heterogeneity (37, 128–130). In line with this hypothesis, pattern electroretinography showed a decrease in their wave response, suggesting that RGCs are directly involved in AD (38, 92, 131–133).

Some authors did not show any statistical significance with respect to the macular outer retinal thickness analysis between the neurodegenerative disease and control groups (134). However, other studies in the context of early AD observed a loss in the outer nuclear layer that could suggest retrograde transsynaptic degeneration (135). In AD, most of the studies have been done with OCT, and they have focused on the inner retinal layers, whereas less attention has been devoted to the outer retinal layers. The discrepancy in results could be due to technical variability, examination time and OCT interpretation (129, 136, 137). By using human *postmortem* tissue in the eyes of severe AD patients with confirmed neuropathology, different patterns of thinning in the superior-nasal and superior-temporal regions of the retina relative to the optic nerve have been found. Also, they found a gradient of thickness reduction whereby thinning was greatest for the inner layers of the retina, followed by the outer layers of the retina (138). This thickness profile matches the distribution of the retinal A β deposits in the mid- and

far-periphery of the superior quadrants of these tissues as previously demonstrated (19, 28, 29, 47, 139).

In the last few years, some studies focusing on the analysis of patients with mild cognitive impairment (MCI) found a thinning in the macular inner layers (140). By contrast, a macular volume increase was found in MCI compared with controls in others works (141). This finding could be explained as a possible inflammation and gliosis prior to neurodegeneration.

CHANGES IN THE EARLY AD AND THEIR PROGNOSTIC VALUE IN THE DETECTION AND FOLLOW-UP

In the most incipient AD stages, the macular RNFL thickness and total macular volume measured by OCT have better prognostic values in mild AD patients than in healthy subjects. The thickness of the inner superior macula seems to have the highest diagnostic value in early AD neurodegeneration. Possibly, the macular area is the first affected area of the retina, which may be due to the large number of ganglion cells in this retinal area (21, 24). Other studies have primarily assessed retinal thickness changes in the macula to explain the visual symptoms experienced by AD patients (138). The earliest detectable structural retinal change associated with AD is suggested to be a decrease in macular RNFL volume, and it is related to neocortical $A\beta$ accumulation in the very early AD (135). In healthy eyes, the macular region of the retina is physiologically very active, and this hyperexcitation might be diminishing in the preclinical stage of AD (28). In support of this theory, *postmortem* histological studies have found pathological alteration of RGC in the macular region in AD patients (28, 47). In a meta-analysis of 17 studies comparing AD patients with healthy controls and in five studies comparing individuals with MCI with controls, there were significant decreases in the thickness of the macular region in all four quadrants compared to controls, thus suggesting that the degenerative process affects the entire macular region (130). Another work, using a multivariate regression model show the existence of specific areas of thickening, interspersed with areas of thinning in the macula of AD and MCI patients. This finding supports the idea that inner retinal layers may be suffering dynamic changes during the course of AD progression (142). The retinal thickening in MCI was attributed to gliosis preceding neuronal loss and atrophy of the axonal projections in the RNFL (143). This theory has been supported by histopathology work, suggesting that gliosis precedes human AD pathology in the brain (144, 145). However, other studies in OCT suggested that the outer retinal thickness did not show any statistical significance between the neurodegenerative disease groups and controls (134). Other authors consider that many other findings have been described such as a reduction in macular volume, RGC layer thickness, choroid thickness and some vascular alteration. These results might be promising biomarkers for dementia staging and AD progression (146, 147).

In recent years, thanks to the development of the OCTA, several studies analyzed the retinal vascularization and the choroid. Most of the studies, published in moderate AD, have found a loss of the retinal vascular density in the macular area with slower blood flow and an increase in the foveal avascular

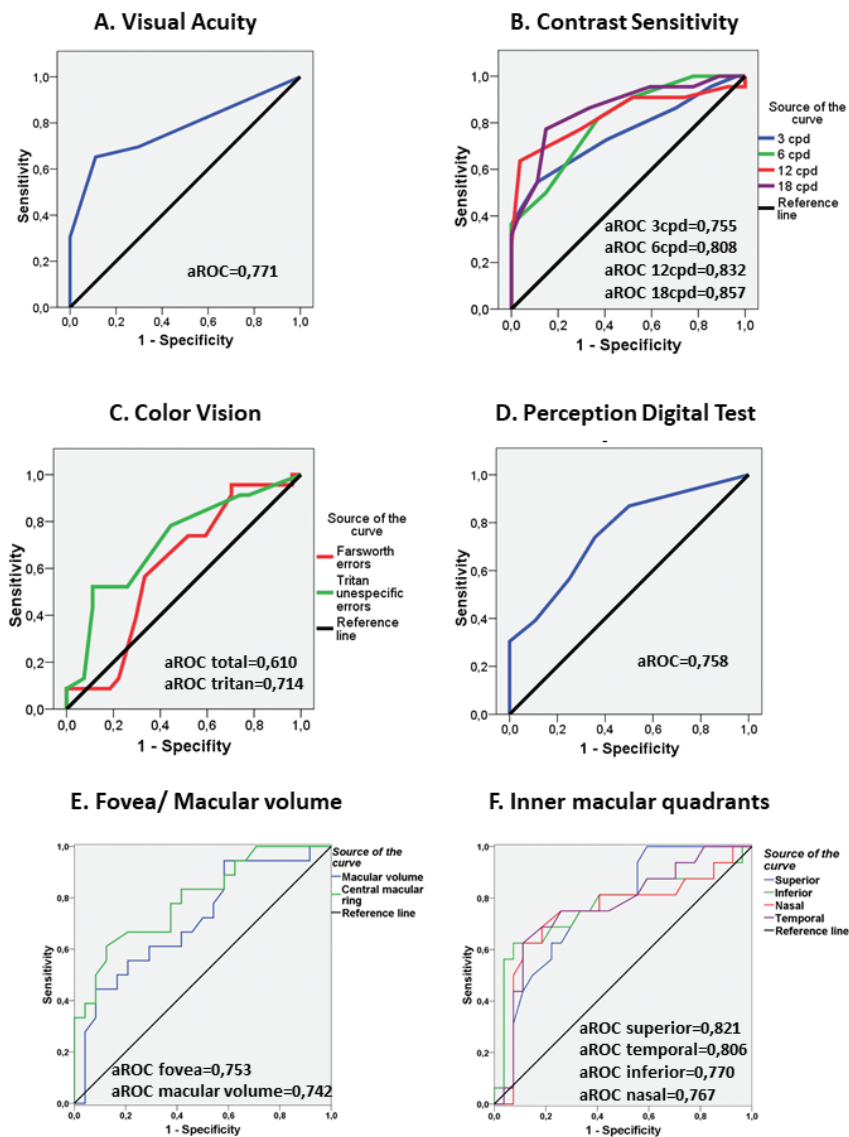


Figure 1 Areas under the ROC curves of the psychophysical tests (A–D) and macular OCT (E–F) in discriminating between mild AD patients and control subjects. (A) Visual acuity (dec), (B) contrast sensitivity, (C) Rue 28-hue color test, (D) perception digital test, (E) fovea and macular volume, and (F) inner macular quadrants. Modified from (A–D) Salobar-Garcia et al., 2015 (93) and (E–F) Garcia-Martin et al., 2014 (21).

zone (148–150). All these parameters presented a correlation with the disease stage (148). In the same way, a thinning of the choroid, measured by OCT, was also found (125, 148, 151–153) (Table 1).

All these changes could be explained as a consequence of the amyloid angiopathy, which occurs in AD, in which amyloid deposits formed in the walls of the blood vessels. This process resulted in an ocular vascular occlusion and the diminishing of blood flow (120, 148, 149, 154).

It is possible that retinal AD biomarkers can only be obtained after having integrated various of the already cited biomarkers, which include both neuroretinal (such as RFNL, GCL, macular thickness) and retinovascular parameters (vessel morphology among others), in a composite biomarker (128).

The analysis of the ophthalmological tests prognostic value of AD showed that VA, CS, color perception, and visual integration (93) have a significant predictive value in early AD disease (Figure 1). The CS is the best predictive test in the diagnosis of the AD with an aROC between 0.857 and 0.755 (93), while the aROC curves of the OCT showed the best prognostic value is found in the macular area with values of $r = 0.821$ (21) (Figure 1). The focus must be centered on these tests to see the visual changes in the AD disease.

CONCLUSION

In conclusion, several alterations have been shown in the visual perception and the retinal structure in the eyes of AD patients, even in the earliest stages. The VA, CS, color perception, and visual integration tests, as well as macular OCT, have been altered in the early stages. When the disease progresses in the eyes of moderate AD patients, retina alteration reaches the peripapillary area, showing the progression of neurodegeneration in the eye.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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The Deterioration of Semantic Networks in Alzheimer's Disease

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Abstract: Language impairments in Alzheimer's disease may appear at the prodromal stage. The most significant impairment is found at the lexical-semantic process level, which is explained either by a degradation of the areas that store the semantic network or by a failure at retrieving the information from that network. Regardless of the retrieval failure happening, there is evidence of the degradation of the semantic network at some levels. Several studies support the bottom-up breakdown, according to which the loss starts at the specific concept attribute level, along with the link with its coordinates, while superordinates are preserved. Some characteristics can affect this loss such as familiarity, age of acquisition, frequency, or affective features. While classic studies have focused on concrete neutral nouns, recent research is exploring the role of emotion. Since emotional processes strengthen the semantic relationship between concepts, it could be a relevant dimension for the preservation of the semantic network.

Keywords: conceptual knowledge; concreteness; emotion; language impairments; lexical-semantic access; semantic memory; semantic network

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

Language impairments appear in most Alzheimer's disease (AD) patients early in the course of the disease, and by the end of it, language becomes completely absent. Although memory impairment is thought to be the first and more evident symptom, an increasing interest in the progression of the deterioration of language throughout the disease shows that language impairments are also present since its prodromal stage (1). An important aspect of language impaired in AD is the ability to access meaning, the representation of knowledge that allows us to understand the world.

Language is strongly based on semantic memory, a storage of concepts linked to linguistic labels. These linkages allow speakers to process the meaning of a linguistic input and to elaborate an appropriate output in response. Language as a cognitive function is sustained by semantic networks, that is, a framework of concepts linked through verbal associations. This network system would be compromised in AD, as the most remarkable impairments in the early stages of AD are related to the lexical-semantic processes. Such difficulties are most commonly thought to be caused either by a progressive deterioration of the associative structures of a patient's semantic memory, or by a degradation of their content itself (2). In either way, this would cause a loss of concept representation or a severe disorganization of semantic knowledge, which would lead the patients to present with difficulties to find some words and to access to their meaning or attributes, along with a rising number of comprehension errors, and a reduction of the production of semantic features (3). In contrast to that theory, some researches state that the semantic network is preserved, and the difficulties may be due to an impairment in executive processes that causes a failure to retrieve information (4). Consequently, the failure to modulate semantic memory would cause errors and slowness in the search of words.

This chapter intends to summarize the course and characteristics of the semantic deterioration due to Alzheimer's disease and to shed light on the ongoing debate about the underlying impairments. It will start with a brief overview of language impairments, continuing with the course and characteristics of the semantic impairment.

LANGUAGE IMPAIRMENTS IN ALZHEIMER'S DISEASE

Language suffers several changes throughout the course of AD. First impairment to become evident is anomia and, as a consequence, a deficit in verbal fluency tasks (5). In the mild stages, patients show comprehension as well as production problems, their anomia worsens and their language is characterized by paraphasias, circumlocutions, and lack of content. Verbal production becomes unintelligible when other symptoms such as dysarthria, echolalia, palilalia, and lack of coherence appear in the later stages of the disease. Lastly, the final stage is characterized by mutism and a severe comprehension deficit, thus impeding any kind of social interaction (6).

Lexical-semantic access appears to be first impaired. This process involves searching for a concept in the mind, activating potential phonological candidates and selecting the appropriate one. Thus, the impairments on this regard are

evidenced by longer response time in lexical decision tasks, and patients face word-finding difficulties along with damage in the semantic processing (7). For this reason, verbal fluency and naming tasks are widely used for cognitive assessment in AD. In verbal fluency tasks, patients must produce as many words as possible in a given time; semantic categories - semantic fluency - or letters - phonemic fluency - may be used as cues. These tasks demand a significant involvement of executive processes, as they require the subject to search for and organize proper responses, monitor their previous ones, and inhibit inappropriate responses. Semantic (SF) and phonemic fluency (PF) differ in the processes involved, and they show divergent declines: while PF relies on lexical representations, SF does so on meaning associations with a superordinate. Moreover, SF tasks in patients with AD are more impaired than PF ones (8), which is explained by the distinct involvement of semantic memory. Other tasks affected by the semantic memory breakdown in AD are naming tests, in which the patients produce semantic paraphasias and, as the disease progresses, an increase in the number of non-response errors, reflecting a pure anomia (9).

In a linguistic level, language production is impaired at early stages, in both written and spoken. Using a description task, Croisile et al. (10) provided evidence of deterioration on both modalities. Overall, written performance was worse than oral, and this effect was found on healthy subjects as well. Regarding the speech of AD patients, they produced shorter responses with fewer information units than healthy older people. Written responses tended to be shorter than oral ones, but they were equally informative. Additionally, it was observed a significant reduction of word categories and an increase of semantic errors in both tasks in AD. Syntax is relatively preserved in the early stages (11), but it worsens through the course of the disease (12). In the beginning, syntax is correct and coherent, but not long afterwards patients start to produce syntactically simplified statements, using fewer subordinate clauses. When maintaining a conversation, AD patients may encounter difficulties responding to open questions and providing new information (13). Most of them are caused by their impairments in comprehension and lexical-semantic access, although damaged verbal pragmatics seems to be also affecting.

In recent years, new techniques of voice and speech analysis have allowed researchers to explore oral production in AD patients. These studies aim to explore if the changes in language processes have behavioral consequences in the vocal execution. In this regard, speech in AD is characterized by changes in different temporal and acoustic voice parameters, such as a greater number of voice breaks and hesitations, more pauses when speaking, lower rate of expressive articulation, longer phonation time, and higher mean of the fundamental frequency. All these changes that can be used for early diagnosis of AD (14, 15) are not only due to difficulties in finding the proper word but also caused by some impairments in the processes involved in planning language and how the words relate to each other semantically and syntactically.

SEMANTIC IMPAIRMENTS: PRECLINICAL CHANGES

Iris Murdoch was a renowned British writer and philosopher. After a prolific career with over 40 published works that had been applauded, critics found her

last novel, *Jackson's Dilemma*, to be disappointing. A couple of years later, Murdoch was diagnosed with Alzheimer's disease. Presumably, she had written her last work while the cognitive impairment was already present, in the years leading to the diagnosis. This finding led Garrard et al. (16) to analyze *Jackson's Dilemma* and two of her other works, written in different periods of her life, in search of early impaired language parameters as a consequence of AD. Among other subtle differences, they noted that content words (nouns, words, and descriptors) had an overall higher mean word frequency in *Jackson's Dilemma* than in her previous works.

Although it may seem anecdotal, the story of Iris Murdoch is supported by other studies that look for preclinical language markers of the disease by comparing AD, mild cognitive impairment (MCI) and healthy control patients, MCI involves a cognitive decline that it is not explained by normal aging and does not interfere with everyday life. It is expected that about 18% of the people with MCI will develop AD (17) and that is the reason why MCI is often considered a pre-clinical stage of the disease. In a study from Mueller et al. (18), early MCI patients had their speech recorded while describing the "Cookie Theft" picture from the Boston Diagnostic Aphasia Examination. The results showed that there was no decline in syntax and lexical processes; however, an interaction between age and cognitive status was found in semantic and fluency processes, showing a faster decline for patients in a preclinical phase of dementia. Therefore, semantics were affected, producing proportionally less nouns and more pronouns and verbs, which adds evidence to the notion that language may become semantically impoverished early on the continuum of cognitive decline. Another study used this same method to explore potential changes in healthy carriers of the E280A autosomal dominant mutation in the *presenilin-1* gene in chromosome 14, which is related to early onset Alzheimer's disease. These participants did not present clinical symptoms or cognitive problems at the time of the evaluation. Nevertheless, it was found that carriers produced a lower number of semantic units, used simpler sentences, and expressed less semantic information than their non-carriers counterparts, although the number of words employed was similar in both cases. Thus, it can be concluded that a deterioration of the conceptual system is present since the preclinical phase of AD (19). This has been confirmed through classical neuropsychological measures such as the Isaacs test, a semantic verbal fluency task, in which participants show a low performance up to 9 years prior to diagnosis of AD (20, 21).

Given the high rate of progression to AD, it is a current challenge to differentiate those subjects with MCI who will develop AD from those who will not. There is evidence that semantic verbal fluency tasks could be used for that purpose. A study comparing AD, MCI, and healthy control patients on several language measures found that, while the AD group showed widespread impairments on traditional semantic memory measures of naming, the MCI group did not differ significantly from controls, except on semantic fluency (22). In longitudinal studies, it has been observed that MCI subjects that will eventually develop AD present with a different pattern in verbal fluency tasks, showing a faster decline in semantic compared to phonemic verbal fluency tasks (23–25). However, these results are not such a promising tool to predict MCI conversion into AD, as MCI patients' patterns are still very similar to those of healthy controls (26, 27).

CHARACTERISTICS OF THE DETERIORATION OF THE SEMANTIC NETWORK IN AD

Semantic impairments in AD patients have been well documented through several cognitive tasks. Confrontation naming tasks consist on presenting images of items, animals, or famous person in order for them to provide the target name. As mentioned before, AD patients progress from subtle difficulties to find words to pure anomia. The pattern of errors produced by AD patients in confrontation naming tasks is characterized by a tendency to produce semantic or visuo-perceptive errors. Semantic errors usually result from producing the name of the correspondent category instead of that of the target, from mentioning another word from the same category as the target, or from committing circumlocutory errors by giving correct information about the target but not its proper name. As the disease progresses, first type of error become more prevalent, while the opposite occurs to circumlocutory errors. This suggest that less and more inaccurate information is available (28). Overall, this pattern seems to suggest the existence of a disruption in semantic knowledge. However, this might not be the case. Several studies suggest that the pattern is similar for healthy, MCI, and AD groups and that they only differ quantitatively in the number of errors and non-response errors, but not qualitatively. This, added to the fact that AD patients can improve their performance by using phonological clues, suggests that the semantic network might be preserved longer than thought as the information can still be accessed, and the disruption only occurs at later stages, when the non-response errors are more common (29, 30).

Another impaired task that gives clues about the state of the semantic associative network is verbal fluency, in which the participant must produce as many words as possible when given a cue. These tasks are widely used for assessing dementia of the Alzheimer's type due to the consistency of the impairment results found (31, 32). AD patients produce fewer exemplars per category than healthy controls and tend to produce more general category labels. Although the most common measure is the number of words produced, some other data from this task can be useful to explore the semantic network in AD. For instance, clustering (producing words within subcategories) and switching (shifting between subcategories) are two components that predict performance on verbal fluency tasks. Clustering would be related to the state of the semantic storage with an implication of the temporal lobe, while switching would be related to control, laying on the frontal lobe. According to Troyer et al. (33), AD patients produce smaller clusters than healthy controls, for both semantic and phonemic fluency tasks, but only in the semantic task they show significantly less number of switchings. Therefore, they conclude that the impairment found in fluency tasks is due to an impoverished semantic memory.

The organization of semantic knowledge seems to be compromised as well. In a series of studies using multidimensional scales and pathfinder analysis, Salmon et al. (34) checked the semantic network of AD patients. These techniques can be used to elaborate cognitive maps representing the distant and relationships between concepts by using different semantic tasks measures. In this kind of map, individuals who have never developed a degree of knowledge on an item or who have lost it get a chaotic representation with many unnecessary nodes and that is the case for AD patients.

For instance, these studies showed how healthy participants tended to produce clearly differentiated clusters of wild and domestic animals, while AD participants tended to mix them. Assuming that verbal fluency represents the activation spreading through the semantic network, this would mean that for AD, that differentiation is not clear and the network is disorganized (35).

Concepts are the basic units of semantic memory. They are constituted by attributes or characteristics and they appear to be structured in a hierarchical way on multiple levels based upon their relationships: super ordinates, coordinates, and subordinates. In AD, these levels of semantic associative relationships show a distinct deterioration. The bottom-up theory states that attributes and coordinates are earlier impaired while the higher level of super ordinates connections remain longer intact. As knowledge of attributes allow individuals to perceive and distinguish an object, the loss of this knowledge would affect different processes such as naming, comprehension, and encoding (36). Semantic priming tasks provide evidence of this theory. When pairing concepts with their attributes, AD patients show a significant slower response time. However, this degradation is not homogeneous as the more salient and significant the attributes are, the longer they are preserved. AD patients are still able to identify the core attributes, that is, those with a higher relative importance for the meaning of the concept (37, 38).

On the other hand, semantic priming tasks with pairs of words with a coordinate relationship show the opposite effect. A significant facilitatory effect for coordinate concepts appears in AD patients (39, 40). Semantically close concepts are defined by the number of attributes that they share and by those distinctive features that belong to only one of them. For example, both tiger and lion have fur, but only the tiger has stripes. According to this, the semantic priming effect should be related to the overlap of features between the prime and the target. In fact, it has been found that when a pair of words share many attributes and have few distinctive features, the priming effect is larger (41). These results of hyperpriming support the idea that semantic memory is suffering a progressive deterioration that starts with the loss of specific attribute information, and as a consequence, AD patients are no longer capable of distinguishing between two coordinate concepts. Lasney et al. (42) conducted an experiment based on the semantic priming paradigm in which words were paired either by a category coordinate or by an attribute relationship. In addition, they distinguished between close or distant relationships for coordinates, and between shared or distinctive attributes. They found the hyperpriming effect in both close and distant coordinates. On the attributes condition, an impaired priming effect was observed for the distinctive attributes at the beginning of the disease. Only at later stages, shared attributes were affected and showed a weak prime effect. Therefore, as mentioned earlier in the chapter, features shared by many concepts are more resilient to the damage caused by AD, while the distinctive features are more vulnerable. In this sense, the confusion between close concepts that causes the hyperpriming effect would be explained by a loss of distinctive attributes.

DEGRADED NETWORK OR FAILURE TO RETRIEVE?

Up to this point, we have described the characteristic deterioration of the semantic associative network of AD patients. Now, the challenge is to explain why

this happens. There are two possible explanations for the impairments described. The first theory states that the impairment is linked to a breakdown in the organization and structure of the semantic network. The degradation of the neocortical association areas, that are assumed to store the representation of concepts and their attributes, would cause an actual loss of this knowledge. Contrarily, the other theory defends that the cause is a failure to retrieve information from a preserved semantic network, due to impairments in the executive processes involved in accessing such representations (43). While many researchers think that the consistency of semantic impairments through different tasks proves the deterioration of the network, others argue that the fact that AD patients still can do most of the tasks—although slower than healthy controls—or that they can benefit from phonological cues supports the idea of troubled retrieval mechanisms.

Such controversy has been explored through tasks that imply different cognitive demands. AD patients' distinct performance on phonemic and semantic fluency tasks supports the notion that they may be experiencing a loss or a breakdown in the organization of the semantic memory rather than suffering from difficulties in the retrieval of semantic knowledge. Both phonemic and semantic modalities imply similar executive control demands, and therefore, the main difference is the implication of the semantic memory. This would suggest a degradation of the semantic store (31, 44). Rohrer et al. (45) conducted a study asking AD patients to produce words within small categories subsets, and it was found that they produced items faster than controls. This finding could be explained therefore by a loss of associations between concepts within the semantic memory. The degradation of the network would cause a reduction on the potential items that could be activated. Hence, as less items would be available, less time would be needed to reach to them.

The studies by Chan et al. (46) about the organization of semantic network also seem to support the hypothesis of a degraded storage. By analyzing the clusters in verbal fluency tasks, they concluded that AD patients tend to rely more on the size or other perceptual dimensions rather than on abstract features such as wilderness, compared to healthy controls. The distinct difficulties in accessing words through perceptual or through abstract features seem quite laborious to be explained by the retrieval deficit theory. However, this kind of breakdown can be explained by a disorganized network, the loss of associative relationships and the establishment of new atypical ones.

Errors in naming tasks and their relationship with the integrity of the semantic network has also been explored. There is a relationship between the ability of an AD patient to name an object and their knowledge of that same object. When they are asked to define an object whose name they cannot access, their descriptions are impoverished, providing less attributes, and even losing core features (8, 47).

On the other hand, it has been argued that the impairment found in explicit semantic memory tasks would be caused by the implication of attentional and executive control systems. Therefore, tasks that allow researchers to assess the integrity of the semantic memory while minimizing the influence of those systems can shed light on the matter. That is the case of implicit semantic priming paradigm, which is based on the idea that spreading activation throughout the semantic network requires intact connections within the system. If the network disappears, it should not be possible to prime the target at all. The evidence provided by this task, therefore, strongly supports the retrieval mechanisms

impairment, since different studies using it consistently found an intact semantic priming in AD patients (48–50). Nevertheless, it seems that this intact network is limited to superordinates, as AD patients show a decline in priming for coordinates and attributes. In this sense, there would be at least a partial disruption in the semantic storage (43).

As can be seen, there is evidence that support both perspectives and therefore there is not a clear conclusion for the debate. One way to address the question would be to demonstrate the complete loss of a concept, which would imply that the person cannot access to the word consistently in different tasks and times, they cannot benefit from semantic cueing and they lose knowledge about the item. Hodges et al. (2) made an attempt to explore that, in which they assessed the semantic memory of AD patients through several tests. They found that when patients were not able to use an item in one task, it was likely to be absent in other task using that same item as a target, thus evidencing a storage degradation. Nonetheless, the aforementioned evidence of an intact semantic network cannot be ignored. Therefore, it seems likely that both impairments occur and have consequences on the performance of AD patients. Neuroimaging seems to support this notion, as an abnormal functioning in the semantic control network and its connections with several areas involved in the semantic processing has been found (51). A conciliatory approach that has been proposed states that, at early stages, the retrieval deficit could be causing the difficulties to which later the degradation is added (52) causing, in the end, a total breakdown.

THE ORGANIZATION OF THE SEMANTIC NETWORK

There is an intense debate about the existence of amodal or modality-specific domains in the representation of semantic knowledge, with certain deficits providing evidence for both of them. Although it is not the objective of this chapter to discuss the principles by which semantic network is organized, it is noteworthy the amount of research questioning whether it exists category specific deficits or other features that determine that organization. Neurological pathologies with a localized lesion strongly support the notion that separated neural systems process different semantic domains, but the fact that in AD the deterioration affects many cortical regions and patients still seem to show specific domain impairments has created controversy.

It has been commonly reported a differential deficit for living and non-living things in which living things show a better performance (53–55). This difference is usually explained by a sensory-functional view, according to which the semantic representations of living things are identified by sensory properties while non-living things are so by functional properties. On the other hand, some authors have not found such effect or, having done it, they have attributed it to methodological issues (56–58). Moreover, they argued that the diffuse pattern of deterioration affecting many cortical regions would not justify a differential loss. Furthermore, the fact that some studies find an advantage of non-living things, or no difference at all, may be explained by the election of the tasks or the heterogeneity of the impairments of people with AD.

There are several factors that could be influencing the categorical deficits, such as word frequency, familiarity, imageability or age of acquisition (59, 60). All those variables are related to performance in several language tasks like naming, reading, or priming. Age of acquisition has been studied as a relevant variable due to the possible similarity to the impairment observed in autobiographical memory. That is, the same way that episodic memory for recent events deteriorates faster than for distant memories, concepts acquired later in life could be more easily affected by neural degeneration while early learned words would be more resilient (61, 62). In this regard, the patterns of deterioration would mirror the acquisition of semantic associative networks in life-span development.

The role of emotion in the processing of concepts is a fairly unexplored factor. Most studies have been conducted with neutral words. However, some recent studies have focused on the affective information of concepts. Although controversial, the idea of the emotional connotation of words having a role on semantic processes is interesting due to its implications. As emotional processes are relatively preserved in the early stages of AD compared with other domains, the affective value of concepts could support the preservation of semantic information and, therefore, it could be useful for communication with the patient. In AD patients, the affective information of concepts is longer preserved than other features (63), which would allow AD patients to retain links between close emotional concepts.

Concreteness is another ignored factor. The previous idea leads to the study of concreteness of concepts because there is an interaction between emotional and abstract ones, as the latter usually refer to internal states of the body. In healthy participants, the concreteness effect refers to a faster and more accurate processing of concrete concepts than abstract ones. In AD, as well as in other neurodegenerative diseases, this effect has been noted to suffer a reversal. Giffard et al. (64) conducted a study in which they compared the processing of different concrete and abstract words that could either have a positive, neutral or negative emotional valence. Their result supports the concreteness effect for neutral concepts, while there is no effect for emotional concepts. This suggests that the emotional component of words is the most relevant feature that binds abstract concepts and influences the reversal of the concreteness effect.

CONCLUSION

Further research on the impairments found in the semantic network of people with AD is required, as most questions concerning the mechanisms that store and retrieve meaning still have to be solved. For instance, the debate about the underlying processes that cause such impairments remains still open. It seems to be a growing agreement that both deterioration of the network and difficulties in retrieval have a role to some extent. It is noteworthy that in recent years, the discussion has moved from the reason why the semantic network becomes disrupted to how it does it. This is the result of an increasing interest in the way the brain processes meaning and stores semantic information. In this regard, Alzheimer's disease can teach us a lot about the pathological and, by extension, normal functioning of the brain, and contribute to increase the understanding of

cognitive processes. At the same time, the priority is to help those who suffer from AD or other neurodegenerative diseases by finding ways to support their abilities and preserve their communication.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Alzheimer's Disease: Memory Interference and the Role of Exercise

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch12>

Abstract: Alzheimer's disease is an irreversible, progressive brain disorder that damages memory, behavioral, and cognitive skills. This condition causes brain cells to degenerate and die leading to many cognitive issues. Although the exact cause is unknown, it is thought to be due to a combination of genetic, lifestyle, and environmental factors. Due to its progressive nature, symptoms can vary from mild memory loss to complete lack of ability to respond to one's surroundings. The memory impairments brought on by this disease can lead to specific problems with memory interference, which may be caused by dysfunction in working and semantic memory. When conducting experiments on Alzheimer's patients, there is also the added difficulty of the individual having trouble remembering the instructions and needing external cues to complete memory tasks. This chapter outlines the disease, its symptoms, risk factors, how it affects memory, and how exercise may be a prevention and treatment option.

Keywords: Alzheimer's disease; memory; memory interference; proactive interference; retroactive interference

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

Alzheimer's disease is an irreversible, progressive brain disorder which damages memory, behavioral, and cognitive skills (1–4). This condition causes brain cells to degenerate and die, leading to many cognitive issues (4). It is the most common cause of dementia, accounting for 60 to 80% of dementia cases (2). Although the exact cause is unknown, it is thought to be due to a combination of genetic, lifestyle, and environmental factors (2). Due to its progressiveness, there are different signs and symptoms throughout the stages (1, 5). Typically, Alzheimer's disease progresses through stages, including mild (early stage), moderate (middle stage), and severe (late stage) (6). Since the condition affects people in different ways, individuals may have a unique experience to each stage. In the early stage, an individual may experience mild memory loss or difficulty remembering newly learned information, whereas in the late stage, individuals may lose the ability to function independently or respond to their surroundings (2, 5). Early-stage signs include forgetting names, appointments, recent events, trouble following instructions, keeping track of responsibilities (e.g., remembering to pay the bills), or difficulty using familiar items in their home (e.g., how to operate the thermostat) (1, 2, 4–7). The middle stage is usually the longest stage in the disease progression and involves more serious signs of the first stage (6). An individual may have greater difficulty performing certain tasks and be more likely to become frustrated or withdrawn due to memory impairments (6). Signs of middle stage Alzheimer's disease include repeating statements or questions, routinely misplacing objects, getting lost in familiar places, losing track of the passing of time (e.g., forgetting which season it is), decreased or poor judgment, withdrawal from work or social activities, or changes in mood and personality (1, 2, 4–6). Personality and behavior changes often include depression, apathy, social withdrawal, mood swings, distrust, irritability, aggression, wandering, or delusions (4). Late stage is the final stage of Alzheimer's disease. The dementia symptoms are severe and individuals lose the ability to function independently or to react appropriately to their environment (6). During this stage, individuals may also lose their ability to control their motor movement and they will likely experience severe personality changes (6). At this stage, it is likely that the individual will need a full-time caregiver (6). Late-stage patients also become vulnerable to infections and other conditions due to memory impairment (e.g., dehydration, malnourishment) (6). Alzheimer's disease is the sixth leading cause of death in the United States, and on average, individuals live for 4 to 8 years after diagnosis (1). It is possible for people with Alzheimer's disease to live as long as 20 years post-diagnosis, but it is less common since it mostly occurs in individuals who are already 65 years or older (1).

RISK FACTORS

The greatest known risk factors for developing Alzheimer's disease is increasing age, as most individuals with Alzheimer's disease are 65 years or older (2). Another risk factor is family history (8). Individuals that have parents or siblings that have developed Alzheimer's disease are more likely to develop the disease (4, 8).

The risk increases as members of the family with a diagnosis increase. Genetics also play a role in developing Alzheimer's themselves (4, 8). Genes for developing Alzheimer's disease have been found to be both deterministic and risk genes, meaning that they both cause the disease and increase the risk of developing the disease (4, 8). The deterministic gene, which almost guarantees the individual will develop the disease, only occurs in less than 1% of the Alzheimer's cases (4). Experiencing a head injury is also a possible risk factor for Alzheimer's disease (8). The most effective ways to prevent head injury are wearing seatbelt in any motor vehicle, wearing helmets, and "fall-proofing" homes for the elderly (8). An example of fall-proofing is placing non-slip mats in strategic areas of the home, especially in the bathroom and in the shower.

Sex, a common risk factor for many diseases (e.g., breast cancer), is not a risk factor for Alzheimer's disease (8). More women than men are diagnosed with Alzheimer's disease mainly due to the fact that women live longer than men – making them more likely to develop Alzheimer's disease (8). Race may also play a role. Latinos and African Americans are more likely than Whites to develop Alzheimer's disease. This is not well understood, but it may be due to their increased rates of vascular disease (4, 8). Heart health and brain health are directly related, as dementia is associated with conditions that damage the heart and blood vessels (e.g., heart disease, stroke, high blood pressure, and high cholesterol) (4, 8). There is also evidence that plaques and tangles (physical evidence of Alzheimer's disease in the brain) are more likely to cause symptoms of dementia if damage to the brain's blood vessels is also apparent (4, 8).

Other lifestyle risk factors include lack of exercise, obesity, smoking, and poorly controlled type 2 diabetes (4, 8). All of these conditions are related to poor heart and brain health and can be modified by living a healthy active lifestyle that focuses on a whole food plant based diet (8). The Physician's Committee for Responsible Medicine recommends exercising regularly, limiting saturated and trans fats, eating plant based foods, eating foods rich in vitamin E, and taking a B12 supplement daily to prevent Alzheimer's disease (9). There is an increased risk for developing Alzheimer's disease in individuals with Down syndrome, which is most likely due to having three copies of chromosome 21, which also includes having three copies of the gene that is associated with Alzheimer's disease (8). Symptoms of Alzheimer's disease usually appear 10 to 20 years earlier in people with Down syndrome compared to individuals without it (8).

EARLY-ONSET ALZHEIMER'S DISEASE

When the condition occurs in individuals younger than 65, it is referred to as early-onset Alzheimer's disease (2). Early-onset Alzheimer's disease is less common, making up less than 5% of the population with Alzheimer's disease (around 200,000 people in the United States), and primarily affects people in their 40s and 50s (3). Since memory complications are less common in those under 65, it can be difficult to diagnosis early-onset Alzheimer's disease. The cause of early-onset is unclear, but there have been a few rare inherited genes that may play a factor in symptoms developing as early as 30 years old, referred to as "familial Alzheimer's disease" (3).

TREATMENT

There is no cure for Alzheimer's disease, but treatments for symptoms are available as research into the condition continues (2). These drug or non-drug treatments may relieve some symptoms or slow the rate of mental decline. Their goal is to increase quality of life for the individuals and their caregivers (10).

Drug treatment

Drug options to help with memory loss include cholinesterase inhibitors and memantine, which treat cognitive symptoms (memory loss, confusion, etc.) (10). These medications may not prevent the degradation of neuronal cells, but they can slow the speed at which they degenerate (10). They are usually well tolerated by patients, and side effects may include nausea, vomiting, and loss of appetite (10). The stage of disease will determine the dosage and type of medication prescribed (10).

Behavioral treatment

Behavioral treatment addresses behavior problems that may arise, such as irritability, anxiety, and depression (7). These symptoms may lead to difficulties caring for an individual with Alzheimer's disease, especially for the caregiver (7). Avoiding drastic changes is an imperative factor of behavioral treatment (7). Change can be stressful and increase the individual's fear and frustration as they are trying to make sense of the situation with their impaired cognitive function (7). Situations that may trigger frustration include moving to a new residence, admission to hospitals, or being asked to alter appearance (7). Sometimes, medications can increase these symptoms of fear and anxiety (7). As a caregiver, behavioral treatment can include avoiding confrontation with the individual, redirecting their attention, creating a calm environment, and allowing the individual adequate rest (7). These behaviors can not only prevent triggering episodes but also make the individual feel more at home. There are also medications that can assist with behavior modification if behavioral treatment is ineffective, including antidepressants for low mood, antipsychotics for delusions and aggression, and anxiolytics for anxiety or restlessness (7). The use of antipsychotics for Alzheimer's disease is a very hazardous option, as it has been associated with an increased risk of stroke and death in older adults with dementia (7).

MEMORY

Our memories define our character and have a completely unique perspective than everyone else's experiences. Creating a memory involves three stages. The first, encoding, occurs when a stimulus results in the formation of a new memory (11–13). This new formation is often referred to as an engram, which is thought to be a physical memory trace in the brain (14). This trace is very susceptible to decay until the next stage occurs, consolidation (14). Consolidation is the process in which a memory becomes stable and is assimilated into previously acquired knowledge (14). The final stage, retrieval, occurs when the memory is recollected (14).

Sometimes when we create a memory, it only lasts for a short period of time, when other memories last a lifetime (15, 16). Memories are temporally defined as long term or short term depending on the length of time the memory lasts. Short-term memories last less than 2 min, whereas long term memories can last 2 min to a lifetime (15, 16). Short-term memories usually are comprised of working memory (15, 16). Working memory typically involves small amounts of information that we only need to retain for a couple seconds, for example, the prices two items when comparing costs while shopping.

Types of memory

There are multiple types of memory and subdivisions within each type. The main two types are explicit (declarative) and implicit (nondeclarative) (15). When a memory is explicit, the individual is consciously aware of the memory, whereas with implicit memory, the individual is not (15). There are two subsets within explicit memory: episodic and semantic. Episodic, or autobiographical memories, include a what, where, and when aspect of the memory (16–18). Semantic memories are facts about the world around us (15). An example of semantic memory may be knowing that baseball is a sport, whereas an episodic memory may be remembering the first time you went to a baseball game. Implicit memories also have two subdivisions: procedural and priming (15). Procedural memories include motor skills and other actions we complete automatically without conscious thought (e.g., walking and writing) (15). Priming occurs when an individual is exposed to a stimulus that influences their response to a later stimulus (15). An example of priming may be seeing a flash of an image on a computer while taking a computer-based memory task.

Forgetting

Why are some memories retained yet others are lost? There are many reasons that we forget information we have learned or events we have experienced (19–21). The act of forgetting can occur actively or passively. Passive forgetting occurs through natural decay, or biological degradation, of neurons within a memory engram (19). Partial decay of an engram can make it challenging to activate the memory during retrieval (19). Active forgetting can occur through several mechanisms: interference, motivated forgetting, or retrieval-induced forgetting (19). Interference, which will be detailed later in this chapter, occurs when competing information makes it difficult to retrieve the correct memory (19). Motivated forgetting often occurs when an individual actively suppresses a memory due to some unpleasant quality (e.g., guilt, shame, and embarrassment) (19). Finally, retrieval-induced forgetting occurs when only parts of a memory are normally recalled, causing the other parts to degrade over time (19).

Memory Interference

As stated in the previous section, memory interference (MI) is a cause of forgetting. There are two types of MI, proactive and retroactive. Proactive interference (PI)

occurs when previously acquired information interrupts the recall of newly learned information (old \rightarrow new). For example, calling your new boyfriend by your old boyfriend's name. Retroactive interference (RI) occurs in the opposite direction, newly acquired information interrupts the recall of old information (old \leftarrow new). Following the previous example, this would be calling your old boyfriend by your new boyfriend's name. Interference can be benign to serious memory disruption depending on the situation. Interference is also linked to similarity of the content. If the competing material is similar, interference is more likely to occur.

In experiments, MI is measured using paired associate learning tasks. These tasks are typically comprised of lists of word pairs or figure pairs (e.g., "bread knife" or $\spadesuit \clubsuit$) that a participant is asked to memorize as a pair. Research participants memorize lists of the word or figure pairs and subsequently recall them (e.g., bread - ___ or \spadesuit - ___). There are multiple models of paired associate tasks, but ones commonly used include AB-CD, AB-AC, AB-ABr, and AB-DE AC-FG. For the models, the letter pairs (e.g., AB and CD) signify one list each (e.g., AB = List 1, CD = List 2), each letter in the name (e.g., AB-CD) stands for one word (A = bread B = knife), and the combined letters (e.g., AB) represent one word-pair (breadknife). Examples of measuring MI using various models are summarized in tables 1-4.

Alzheimer's disease and MI

Alzheimer's disease causes the decay of neurons which eventually leads to memory impairment (1, 4, 5, 9). Although there are a lot of research fields focusing on how Alzheimer's disease damages memory, there is less research focusing directly on MI effects on patients with Alzheimer's disease.

When investigating patients with Alzheimer's disease and those with mild cognitive impairments without Alzheimer's disease, Dewey et al. found that memory retention is much higher in these patients when there is minimal interference compared to a normal MI paradigm (22). Their findings align with previous literature

TABLE 1
AB-CD example

List 1 (AB)	List 2 (CD)
BABY HUNTER	SPIDER CANDLE
SUPPER SHERIFF	ARROW THEATER
WEDDING MOVIE	CHERRY MONEY
APPLE DIAMOND	TIGER HOTEL
MONKEY GARDEN	CANNON HAMMER
FOREST BATTLE	LADY BUTTER

In this model, AB signifies the first list and CD the second list. There are no repeating letters in the title of the model, meaning there are no repeating words within the lists. Each list consists of unique words with no overlap. Participants may be exposed to both lists (learn List 1 then List 2) and then asked to recall only one of them. To measure PI, the participants will learn List 1 (AB), List 2 (CD), then recall List 2. For RI, the participants will learn List 1 (AB), List 2 (CD), then recall List 1.

TABLE 2**AB–AC example**

List 1 (AB)	List 2 (AC)
BABY HUNTER	MOVIE WEDDING
SUPPER SHERIFF	APPLE CANNON
MONKEY GARDEN	BABY SALAD
FOREST BATTLE	MONKEY ENGINE
MOVIE CHERRY	FOREST CITY
APPLE TIGER	SUPPER JACKET

Similar to the previous model AB–CD, this model's first list (AB) has no repeating words, but as we can see "AC" has a repeating "A" word. This signifies that the "A" words from List 1 (AB) and List 2 (AC) will repeat, while the "B" and "C" words will not. When testing for PI, the participant will learn List 1, List 2, and then recall List 2. For RI, the participant will learn List 1, List 2, and then recall List 1.

TABLE 3**AB–ABr example**

List 1 (AB)	List 2 (ABr)
BABY HUNTER	SHERIFF CHERRY
SUPPER SHERIFF	DIAMOND BABY
WEDDING MOVIE	BATTLE SUPPER
SPIDER CANDLE	FOREST HUNTER
MONKEY GARDEN	MONEY MOVIE
FOREST BATTLE	SPIDER GARDEN
CHERRY MONEY	APPLE WEDDING
APPLE DIAMOND	CANDLE MONKEY

This model repeats all of the words from List 1 (AB) in the second list (ABr) except the words are rearranged into new word pairs. To reiterate, List 1 and List 2 comprised of the same words, but the way in which they are organized is different for List 2. This model can cause severe interference since the words are so similar. Participants learn List 1, List 2, then recall either List 1 or List 2 depending on the interference being measured.

demonstrating that memory dysfunction in patients with Alzheimer's disease is associated with an increased susceptibility to MI (22). The authors hypothesize that this may be due to a decline in the ability to consolidate new memories (22). The interference paradigm utilized in this experiment is strong at predicting which patients with mild cognitive impairments will or will not progress to Alzheimer's disease within 2 years, with 80% sensitivity and 100% specificity (22).

In term of semantic memory, or facts about the world (e.g., baseball is a sport), patients with Alzheimer's disease perform worse on these memory tasks, which may be due to a deficit in working memory and attention (23). As stated previously, working memory is short-term memory that lasts for a very short period of time with a concurrent interfering stimulus. Hartman describes how, in her experiment, there was no evidence that the patients with Alzheimer's disease utilized

TABLE 4

AB–DE AC–FG example

	Cued recall 1		Cued recall 2		MMFR
	A __, D __	List 2 (AC, FG)	A __, F __	D __	A __
List 1 (AB, DE)	A __, D __	List 2 (AC, FG)	A __, F __	F __	F __
BABY HUNTER	SPIDER _____	FOREST CITY	ARROW _____	BABY _____	
SUPPER SHERIFF	FOREST _____	ARROW THEATER	FOREST _____	CHERRY _____	
WEDDING MOVIE	BABY _____	BABY SALAD	TIGER _____	ARROW _____	
SPIDER CANDLE	CHERRY _____	TIGER HOTEL	SUPPER _____	SUPPER _____	
MONKEY GARDEN	MONKEY _____	MONKEY ENGINE	LADY _____	TIGER _____	
FOREST BATTLE	SUPPER _____	LADY BUTTER	CANNON _____	WEDDING _____	
CHERRY MONEY	APPLE _____	CANNON HAMMER	BABY _____	MONKEY _____	
APPLE DIAMOND	WEDDING _____	SUPPER JACKET	MONKEY _____	LADY _____	
				SPIDER _____	
				FOREST _____	
				APPLE _____	
				CANNON _____	

This paired associate task is more complex than the other designs because it includes control word pairs within each list, allowing for the measurement of proactive and RI within the same experiment. As before, List 1 (AB–DE) has repeating “A” words as List 2 (AC–FG). In this case, DE and FG are the control word pairs and AB and AC are the interfering word pairs. To use this model for an experiment, participants learn List 1, recall it, learn List 2, recall it, then recall the Modified Modified Free Recall (MMFR) list which is comprised of all of the word pairs from List 1 and List 2 in a pseudorandomized order.

semantic knowledge (relatedness) of word pairs during recall (23). When patients’ working memory is impaired, as is typical in Alzheimer’s disease, it is more difficult to retain relevant information about the relationships of words in paired associate tasks (23). Despite this experiment’s focus on working memory, its results shed light on MI impairments since semantically relating words is a typical strategy utilized when memorizing word pairs in paired associate tasks. When detailing the symptoms of Alzheimer’s disease, we noted that difficulty remembering and following instructions is common (23). This may also influence performance on memory tasks. Repeatedly needing external cues or verbal instructions may alter outcome scores, as mentioned elsewhere (23). Another study that focused specifically on proactive and RI compared mildly demented Alzheimer’s disease patients, patients with mild cognitive impairment without Alzheimer’s disease, and healthy elderly patients on interference tasks (24). When controlling for

overall memory impairment, mild Alzheimer's disease patients demonstrated higher rates of PI, but equal amounts of RI when compared to the cognitively impaired patients (24). As expected, the healthy elderly participants experienced the least amount of interference (24). Vulnerability to semantic interference may reflect early signs of the onset of Alzheimer's disease (24).

EXERCISE AND ALZHEIMER'S DISEASE

As stated previously, physical inactivity is a risk factor for developing Alzheimer's disease and is even considered the highest population attributable risk (25). In one systematic review, the majority of experiments demonstrated that physical activity was inversely associated with risk of developing Alzheimer's disease (26). Exercise has also been demonstrated to improve multiple types of memory, including long-term and short-term memory (27–33). Exercise may even prevent the onset of Alzheimer's disease by decreasing the risk of cardiovascular disease, increasing cerebral blood flow, increasing hippocampal volume, and improving neurogenesis (34). Higher levels of physical activity are associated with a reduced risk of developing the disease (34), with long-term prospective studies demonstrating that walking regularly is associated with a twofold reduced risk in cognitive impairment (25).

During exercise, many chemicals are released in the body, including brain-derived neurotrophic factor, which is directly associated with learning and memory (35). Research also demonstrates that regular physical activity prevents mental decline and improves thinking in populations with vascular cognitive impairment (34). It has been used clinically in the treatment of preclinical and late-stage Alzheimer's disease, as well as a prevention strategy (34). Recent prospective work, that compared sedentary individuals to those who were the most active, demonstrated a 38% reduction in incidence of Alzheimer's disease (36). In animal studies, mice with Alzheimer's disease that completed 16 weeks of treadmill exercise have been shown to elicit changes in therapeutic parameters at the cellular and molecular level, providing biological plausibility to exercise as a therapy (37).

In order to reduce the risk of developing Alzheimer's disease, to lessen the effects for those already suffering from memory loss, individuals should participate in regular physical activity. The American national guidelines suggest at least 150 min per week of moderate to vigorous physical activity (38). Meta-analyses have demonstrated mixed findings on which mode of exercise is best for improving specific types of memory; however, walking, cycling, and jogging are three of the most common exercises implemented, all of which have demonstrated beneficial effects (33, 39). Multicomponent exercise programs have also been effective in improving cognitive function in institutionalized older adults with mild to moderate Alzheimer's disease (40). One particular study found that incorporating a program that included supervised aerobic, muscular resistance, flexibility, and postural exercises for 45–55 min sessions twice per week for 6 months significantly improved patients' cognitive function when compared to a control group (40). These findings suggest that incorporating a variety of physical activities may be an effective non-pharmacological method for improving cognitive function, along with physical function, in those with Alzheimer's disease (40).

CONCLUSION

In summary, individuals with Alzheimer's disease may be more susceptible to MI, due to dysfunction of working memory and semantic memory. This can cause even more confusion, as patients already cope with a myriad of memory problems and other symptoms. The literature on Alzheimer's disease and MI is sparse, and therefore, it is imperative that the field continues to grow and search for methods to attenuate interference in this population – for example, through exercise, which has been demonstrated to increase memory performance. Experiencing MI, or difficulty recalling information because of competing memories, can be very frustrating and debilitating for anyone, but especially for patients with Alzheimer's disease. In experimental settings, paired associate tasks are often utilized to measure interference, but there are also other methods that are suitable. Due to the debilitating nature of Alzheimer's disease, it is important to focus on prevention and delaying the condition by keeping your mind and body active, eating a healthy diet, and wearing safety equipment to avoid head injury.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Sense of Self among Persons with Advanced Dementia

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch13>

Abstract: As humans, we have a sense of self, and at best, we are proud of our abilities and feel respected by other persons. Persons with dementia have been regarded losing their self. Quantitative research has shown that this is true, while qualitative research has shown that parts of self are severely affected while other parts remain even among persons with advanced dementia. These persons sometimes keep feeling “still the same” as before getting dementia. Their memory deficits help as does support from other persons. The theory of three aspects of self by the psychologists Rom Harré and Steven Sabat are presented, that is, the feeling that we are, who we are, and who we are together with other persons. Based on empirical research, suggestions will be given about how by promoting experiences of at-homeness, dignity, and being oneself related to others we can help persons with advanced dementia experience themselves as valuable persons.

Keywords: advanced dementia; anosognosia; confirmation; dignity; self

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

As human beings, we need to know that we are and who we are. We need to be proud of our abilities and feel respected by other persons. These experiences can often be hard to achieve for persons with dementia, partly due to symptoms of dementia and to a great extent due to other persons' reactions. There are reports that persons with dementia lose their self and also that it is at least partly preserved. A systematic review revealed that studies performed with quantitative methods generally described that among persons with dementia self was affected, while qualitative studies tended to find that self was at least partly preserved (1). These results are in line with Sabat (2) who argued that self should be investigated by sensitive methods.

The Latin root of the term dementia means to be out of one's mind (3), and dementia has been described as leading to affected persons losing their self and becoming non-persons (4). Thus, it seems reasonable that the term dementia has been subject to criticism, and the American Psychiatric Association has replaced it with the phrase "major neurocognitive disorder" in the Diagnostic and Statistical Manual (DSM-5) (5). Sabat (6) argues that we should not reduce persons to brains but see the persons behind the dysfunctional symptoms and remember our shared humanity. Those living with dementia are semiotic persons, that is, their behavior is driven by meaning, as they, for example, have the capacity to show shame and pride and to feel concern for other persons' well-being (7). They are also relational beings and their behavior is an effect of neuropathology, their reaction to these effects, others' ways of treating them and their reaction to that treatment (8). Healthy persons often use negative stereotyping of persons with dementia which may lead to these persons themselves using self-stereotyping (9).

There are several types of dementia diseases, with Alzheimer's disease as the most common type. The disease progresses from a mild stage, via a moderate stage, to an advanced stage in which affected persons are dependent on others in most situations (10). In the literature about care, the term "dementia" is sometimes used and sometimes the type of dementia is identified. Here, I use the term "dementia" when I refer to literature using the terms "Alzheimer's disease" or dementia without further specification.

SYMPTOMS OF DEMENTIA

The cognitive symptoms of dementia can be described as four A's, namely amnesia (impaired memory), apraxia (impaired ability to organize sequences of movements in space), agnosia (impaired perception), and aphasia (impaired language ability) (11). Amnesia affects first the short-term memory and later also the long-term memory. A decreasing autobiographic memory (incident memory about specific personal events including context and personal semantic memory such as names of friends) affects sense of self (12). In interviews, persons with moderate dementia can often provide short accounts of their experiences. They may narrate fragments of their life story: childhood, education, family life and professional life. Several persons describe specific events such as leaving home to go to school (13, 14) and narrate thoughts about their future life, that is, about possible selves (15). Apraxia causes

problems with performing everyday tasks like, dressing, eating, grooming, and walking. Agnosia causes difficulties in recognizing, for example, colors, persons, objects, odors, shapes, and sounds. Aphasia leads to difficulties with both speaking and comprehending speech (16). Persons with dementia use circumlocutions and paraphrases as they forget words, and they need prolonged time to understand the meaning of what has been said, and to formulate answers (17). They also often can compensate by using extralinguistic means such as gestures and tone (18).

SELFHOOD

There is no consensus about the meaning of the concepts of identity, person, personhood, self, and selfhood. The terms are often used interchangeably although there are many different conceptualizations (19–20). Studies on the sense of self in persons with dementia have used various concepts or failed to describe the concepts used. Here, I use the term “self” also when I refer to authors who use the terms “identity” or “personhood”. Thus, I use these terms as interchangeable.

The psychologists Sabat and Harré have together (21), separately (17, 22), and together with other researchers (23) published about a social constructionist theory of selfhood in persons with dementia.

The embodied, material human being they label “person,” and the linguistic expressions we use to refer to ourselves they label “self.” Selfhood is expressed both as speech and behavior in public discourse. Sabat and Harré describe self as tripartite: Self 1, Self 2 and Self 3. Self 1 (the self of personal identity) expresses our embodied experience of being singular continuous persons located in space, time and in a local moral order. We experience this aspect of selfhood in that each of us has one single point of view of the world, that is, our continuous experiences of events that form the narrative of our lives. Through the use of first-person singular pronouns, we take responsibility for our actions, feelings, and experiences as being our own and tell autobiographical stories. We manifest Self 1 when we speak in first-person indexicals (“I,” “me,” “mine,” “my,” “our”) or indicate Self 1 nonverbally for example by pointing to ourselves (21, 24). Self 1 is a necessary condition to be able to reflect on our personal attributes (Self 2) and exhibit them in appropriate social situations (Self 3).

Self 2 is comprised of how we perceive our physical and mental attributes such as eye pigmentation, height and weight, educational achievements, political and religious convictions, sense of humor, and vocational pursuits. We have beliefs about our attributes, such as that they are adequate or outdated and also emotions related to them such as pride or disdain. Some Self 2 attributes have long histories such as being a daughter, while some may be more recent such as being diagnosed with dementia. Self 2 can be restricted and unrestricted. The restricted Self 2 is about how we perceive ourselves to be in the moment, while the unrestricted Self 2 includes both how we are in the present, how we were in the past and may develop in the future, that is, our relatively constant, temporary or ever-changing attributes, such as traits, skills, and our beliefs regarding these attributes. We manifest multiple Selves 2 (22).

As persons with advanced dementia usually remember past attributes better than recent ones, they may feel proud of already lost attributes (25). For persons

with dementia, new Self 2 attributes include deficits connected to the neuropathology of the disease (24) and results of their attempts to adapt to the disease (26).

Self 3 (social personae) is a complex concept, in that it includes the perspectives of both the displayer and the perceiver. It is the display of Selves 1 and 2 to other persons. How we display Self 3, depends on the situation, on how other persons position us and how we position ourselves to them through actions or inner dialogues (23, 27–28). Persons with dementia may lose their sense of self-worth and feel depersonalized, depressed, and angry when healthy persons behave in manners that can be classified as “malignant positioning” (28–30). Previous research has described both the negative positioning of persons with dementia (27) and the understanding and support that they sometimes receive (13). It is obvious that support from other persons is important for preserving a sense of self (20, 30). If others focus on dysfunctional Self 2 attributes of persons with dementia, their Self 3 (social persona) is restricted to “the patient” (28). If other persons focus on remaining healthy Self 2 attributes, it is possible for the afflicted persons to construct worthy Self 3 that makes them experience pride and satisfaction. (24). We manifest multiple Selves 3 that are constantly reconstructed in the interplay among persons (22).

Studies based on the Harré–Sabat theory of selfhood have shown that among persons with mild to moderate dementia, Self 1 was not affected during the course of dementia, whereas Selves 2 and 3 were (13–15). A few studies using that theory concern persons with advanced dementia (e.g., 24, 31–33). Studies that do not use the Harré–Sabat theory have found that some aspects of sense of self were preserved while other aspects were reduced among persons with advanced dementia (e.g., 34–37). Kontos (38) argued that selfhood is an embodied dimension of human existence persists even with advanced dementia. These persons have several preserved abilities despite losses of cognitive functions, for example being able to assess their own internal state of being such as feeling cold (39) and experiencing pain (40). Here, I use the term “advanced dementia” to describe information in articles about persons with moderate to advanced dementia as well as with advanced dementia.

PERSONS WITH ADVANCED DEMENTIA

Having advanced dementia involves many strains. Neighboring persons, carers, and everyone who meets these persons need to provide them support.

Awareness and lucidity

Although persons with advanced dementia are often described as having lost their self (4), their sensory and perceptual awareness has been found retained (41). These persons show distinct individual reactions to particular kinds of stimuli, and they, for example, differentiate between pleasant and unpleasant experiences, or various pieces of music (42–44). If the self is lost, it is difficult to understand the meaning of *moments of lucidity* (cognitive fluctuations) that have been identified when persons with advanced dementia that seem “not there” suddenly show

that they understand, remember, and care (42, 45). It was evident that lucidity during conversations with a women with advanced dementia occurred when her communication partner supported her by showing that he shared her expressed view, repeating and reformulating her words, using positive words and statements, helping by suggesting words and starting, completing and ending sentences and not emphasizing errors in her speech (46).

Suffering

Living with advanced dementia includes several negative experiences. When writing about *suffering* among persons with advanced dementia, several researchers write about experiences of pain and bodily distress (47). Few writers have explicitly focused on the other various experiences of suffering in persons with advanced dementia although carers often feel that these persons indeed suffer.

Eriksson (48) described three categories of suffering: “suffering of life” (for example grief due to the death of a friend, or feeling abandoned when friends do not pay visits to the nursing home), “suffering of illness” (effects of having dementia such as not feeling at home, having problems communicating), and “suffering of caring” (distress caused by received care). An example of “suffering of illness” is that several persons with advanced dementia have neuropsychiatric symptoms such as apathy, depression, irritability, agitation, sometimes delusions, hallucinations, and sleeping disorders (49). Examples of “suffering of care” are reports that carers have been observed treating persons with advanced dementia as object (50) which reasonably cause them suffering. Living with advanced dementia can also be experienced as a relative well-being (29) mainly through carers’ compensating for problems related to the disease (51).

Anosognosia

Many persons with advanced dementia have been reported to suffer from explicit or implicit “mnemonic anosognosia” *anosognosia* that makes them seem unaware of deficits caused by neurodegeneration although they may demonstrate implicit awareness (52–54). Their memory deficits can make their sense of self become a “petrified self,” that is frozen in time and sometimes reflects the features that were accurate in early adulthood and perhaps even in childhood. Thus, memory impairments hinder the persons to update information about self. Sometimes, they may register impairment but they cannot integrate the information into a coherent picture of their situation. This may lead to stable but inaccurate evaluation of experiences and actions (54).

Moments of homecoming

Feeling at home is a fundamental aspect of human existence (55), and it is important for our sense of self (56). Thus, losing one’s home is losing one’s self. To feel at home through the life cycle has been described as feeling related to oneself, significant activities, significant others, significant places, significant things, and to feeling a sense of transcendence (57). Persons with advanced dementia often appear to feel homeless, they may walk around, asking where they are and

searching for their home. They have problems feeling at home both in their former homes and in their new places of residence (58). The understanding of how important the experience of at-homeness is for our sense of self and well-being has led to an endeavor to create care environments where persons with advanced dementia can feel at home. However, although carers try to furnish the rooms as homely as possible it is often hard to document positive effect on the persons' daily life (59). Observation of nursing home residents with advanced dementia showed that they alternated between expressing feeling at home (at-homeness) and not feeling at home (homelessness) both verbally and nonverbally. They showed often short lived moments of homecoming that were characterized by "being released from burdens and demands (e.g., not being required to make choices), being united with actions (e.g., being helped to use previously familiar routines when getting dressed), and being reached by language (e.g., being spoken to with familiar words)" (60). One woman seemed to live and feel at home in two worlds simultaneously, that is, she interpreted some things that happened at present as something that happened earlier in her life (61). In her "remembered-world," she took care of her small children and had coffee with her friends and expressed astonishment about the fact that some nice and friendly persons entered her room, made her bed and invited her to dinner. In her "care home-world," she could tell her carers about her grandchild having taken an exam.

Communication

Persons with advanced dementia may show some retained abilities to communicate, they for example sometimes are using politeness when communicating (62). Their *communication difficulties* are, however, more often acknowledged. They can show lack of interactional synchrony such as integrating verbal and nonverbal communicative cues to a whole and synchronize their actions with their communication partners by adequate turn-taking. First the carer talks, then the person answers, then the carer answers, then the person shifts theme etc. The lack of synchrony makes behavior chaotic and fragmented. The persons' sensitivity to representative meaning and less to affective meaning is reduced due to decreased arousal and attentiveness. They often send vague undifferentiated verbal and nonverbal cues that are difficult to interpret for the communication partner. They also show problems interpreting the communication partners' cues and they need prolonged time for responding to their partner. They may use short sentences but more often single words or even react with primitive reflexes (63). Communication partners sometimes have to impute or attribute meaning to the vague cues, that is, they make guesses that are based on their previous experiences with the person in question and with other similar persons or on empathy or intuition (50, 64). Sometimes, the communication can depend on the communication partners imitating each other (65). When I tried to help a person with advanced dementia to eat and the person did not seem to understand, I demonstrated what I meant by opening my own mouth, chewing and swallowing. I ate an air meal. Suddenly, the person seemed to understand and started eating (The author's experience). Both imputation of meaning to vague cues and imitation can help the persons feel like partners being answered, that is strengthening the Self 3.

At the end state, persons with advanced dementia may become mute (66). Hughes (67) argues that there are other means to understand persons with

dementia than understanding the words they use. It is about sharing a form of life, it is about understanding the context, and feeling what the persons express. This is like using affect attunement, that is, the carer tuning into the persons' affective state to be able to help them to reduce negative affect and increase positive affect (68, 69). In this way, communion between the partners is created. According to Stern (70), the sense of self starts with the parent and infant being in communion, that is, participating in and sharing emotions and vitality effects that, for example, are expressed through intensity and rhythm. Later, the sense of self gradually develops through interaction with others throughout one's history to also include cognitive dimensions. As their cognitive abilities decrease, persons with advanced dementia increasingly need to be in communion with carers to preserve their vulnerable self. Söderlund et al. (71) reported positive results from using the Feil's validation method during one-to-one conversations with persons with advanced dementia. The focus was not the facts about what was expressed but rather the feelings behind what the persons tried to talk about and the aim was to treat them as adults and increase their feelings of self-worth and well-being. Eggers et al. (72) described two somewhat different ways of interpreting the communicative cues of persons with advanced dementia, partly by establishing communion with them through affect attunement and partly by putting various fragments together until a picture of the meaning of utterances and behavior appeared. This was like completing a puzzle.

AGENCY AND COMMUNION

Agency and communion have been described as fundamental modalities in human beings' lives (73). Communion is the urge to be connected and unified with others. The positive themes of communion are love/friendship, dialogue, caring/help, and unity/togetherness, whereas the negative themes are separation, rejection, disillusionment about people, and another's misfortune (74). Agency implies a quest for autonomy, self-realization, and separation from other people. The positive themes of agency are self-mastery, status/victory, achievement/responsibility, and power/impact, and the negative themes are, failure/weakness, losing face, ignorance, and conflict (75). For a positive sense of self, we need agency (individuality) and communion (togetherness). Experiences of agency and communion have been assessed among persons with dementia (76). Although there are no clear-cut borders between the modalities, it seems as communion is more relevant for Self 1 and Self 3 and agency for Self 2.

Strengthening Self 1 communion

Being treated and even feeling as a non-person reasonably means suffering. Therefore, it is important to help persons feel as *persons* with a sense of self. Research has shown that the Self 1 is preserved among persons with advanced dementia. Even when they almost entirely answer "yes" or "no" to questions, they still show that they can experience themselves as "I" (32, 60). Still it seems reasonable to suggest that we can help persons preserve their feeling of being an I by making them feel that they are seen and listened to, that is that they are. This kind

of behavior has often been labeled confirming actions and seems a type of communion.

The concept *confirmation* is based on Martin Buber's philosophy and is described by Cissna and Sieburg (77, p. 254–260) as the process through which we endorse others by showing them recognition, acknowledgement and acceptance of their self-definition. Thereby they get help forming and maintaining human relationship. Cissna and Sieburg emphasize that confirmation includes four key elements: (i) The element of existence (the individual sees self as existing). (ii) The element of relating (the individual sees self as being-in-relation with others). (iii) The element of significance, or worth. (iv) The element of validity of experience. Observations at a small group living for persons with advanced dementia revealed that staff confirmed persons by accepting the ways they spoke and acted by making them feel accepted and allowed to be just as they were. A person who thought the ward is a church was not corrected as long as he appeared to feel good. Another person who found it meaningful to carry things around was allowed to do that as long as no one else was disturbed (78). It seems reasonable that confirmation could be seen as strengthening persons' Self 1.

Strengthening Self 2 agency

Experiences of using motoric and other abilities can be understood as part of agency. Because Self 2 concerns persons' perceptions of their abilities, it seems logical that there is a need that they both get opportunities to use their abilities and also get help to remember how they previously used their abilities. They most easily remember what happened during their childhood (54) and often express they are proud of these memories. In articles about needs of persons with advanced dementia, agency is mentioned (51, 78). To my knowledge, there are few studies presented about agency among persons with advanced dementia. There are, however, articles about topics that could be seen as agency. Together with their respective co-workers Kihlgren (79) and Ekman (80) analyzed video-tapes of morning care sessions with persons with advanced dementia and carers. The carers were taught about the Erikson (81) theory of eight stages of man and encouraged to, in a concrete way, promote the persons' experiences of trust, autonomy, initiative, industry, identity, intimacy, generativity, and integrity during morning care sessions. The comparison of behaviors and speech before and after the intervention showed that the persons with dementia displayed more and more ability (79) and that carers who spoke the persons' mother tongue (Finish) were most successful in helping them use their latent abilities than carers who only spoke Swedish (80).

Persons with advanced dementia may get help to recognize and remember important themes or episodes from their life history. As the ability to recognize is better preserved than the ability to recall, they might remember a phenomenon when reminded although they cannot recall it (17). They can have an unconscious or implicit memory of past experiences (38) and often remember emotions better than facts (81). As persons with dementia best remember their life before the debut of dementia and later their earliest memory, they most easily can express their experiences by referring to memories from their childhood (54). They may for example call their mother when they feel unsecure (82). When they perceive the emotions in a conversation, they can go back in memory to an experience with the same emotions to understand what the conversation is about (83).

Thus, when a person with advanced dementia asks a carer: You are my mother, aren't you, this does not have to mean that she thinks the carer really is her mother. Instead it might mean that the interaction with the carer made the person feel being loved and when she sought an experience with the same emotional tone from the past, she found memories of her mother.

At the last stages of life, persons with advanced dementia often experience eating difficulties, especially swallowing problems (84–85). By participant observations of meals Eggers (86) described fragmentation when the persons with advanced dementia did not seem to recognize what was going on, the persons involved, the things used, or recognize themselves in the meal situation. Carers counteracted fragmentation by showing attentive interest in the interaction, valuing the persons as human beings, considering the symptoms of the dementia, and striving for mutual interpretation of the meal situation.

Strengthening Self 3 communion

Strengthening persons' Self 3 seem to mainly concern themes of communion. Self 3 has been found especially vulnerable when persons with dementia are negatively positioned and do not get support of others (17, 28). This means that actions that promote the wellbeing of these persons are strengthening their Self 3. Few articles about *well-being* concern persons with advanced dementia due to the fact that they cannot take part in studies that require answering complicated questions. They can, however, take part in easy conversations and become observed, thus in qualitative research (87). Kaufmann and Engel (51) included persons with advanced dementia in a study based on a Tom Kitwood's model of needs and described well-being according to the themes *comfort* (small pleasures of life providing relaxation, consolation); *attachment* (company with human beings, animals and objects, support); *inclusion* (being part of a community, feeling recognized); *occupation* (e.g., listening to the radio, exercise, participation in activities); *identity* (role maintenance, recognition, familiar rhythms and habits). Jetten et al. (12) reported that life satisfaction that was lower among persons with mild dementia than among persons with advanced dementia. Reasonably this could be related to anagnosia among person with advanced dementia (54). There are several means to improve the sense of well-being among persons with advanced dementia such as using multisensory stimulation for example including music and massage (88), singing (89), dancing (90), animals (91) and dolls (92). Listening to well-known songs or music and to positive stories from their own lives can strengthen the feeling of being important. Music, touch, dance and rocking can mean comfort for persons with advanced dementia (43, 69). The stimulation of the senses can be combined with ordinary nursing actions. A review of 21 intervention studies on persons with advanced dementia, in which aromatherapy, music, simulated presence (for example, listening to a tape recording of their partner), touch and multisensory stimulation, have been used, showed no proven scientific evidence but carers' proven experience that the methods are effective, sometimes they fit, sometimes not (93).

As a positive Self 3 means that the persons with advanced dementia feel proud of themselves, loved and acknowledged other persons' acts toward them are of utmost importance, actions that promote the persons feeling dignified certainly would strengthen self 3. Manthorpe et al. (94) described *dignity* as a phenomenon involving an inherent self-respect and feelings of worthiness, and being respectfully recognized

and confirmed by others. Nordenfelt (95) wrote about four variants of dignity: *Menschenwürde* (human dignity), which is overall other variants of dignity, that is as it is part of being human it is the same for all people; dignity as merit (e.g., being a leader), dignity as moral stature (e.g., being an altruistic person) and dignity of identity (concerns self-image, self-respect, worth and value ascribed by oneself or others). Persons' dignity of identity can change over time, for example depending on if the persons are afflicted by dementia and how they are treated of others, which can result in physical, psychological, or emotional change or harm. Dignity of identity is connected to sense of self, and it is threatened if the persons have forgotten who they are.

The dignity as moral stature is about our moral actions. We can show that we know about their previous good properties and actions as persons with advanced dementia cannot upgrade their identity (54). Persons with advanced dementia should be cared so they can keep their experiences of human dignity, dignity as merit, dignity as moral stature and dignity of identity. When persons with advanced dementia are seen as having lost their self (4), their human dignity is questioned and there is a risk that they become treated as objects.

SPIRITUAL AND CONSOLING CARE AT THE END OF LIFE

There is so far, no cure for AD. Within approximately 4 to 8 years, dementia usually leads to *dying and death*, although some persons live up to 20 years after being diagnosed (96). Persons may *die with dementia* due to various causes (97) or *due to dementia* as it is a lethal disease (98).

There are few reports about needs during end of life among persons with advanced dementia. A review of 10 articles published 1993–2013 mentioned physical, social, psychological, spiritual, supportive, environmental needs and needs related to individuality. The authors emphasized that as persons with advanced dementia have severe communication difficulties, we need more research about views of stakeholders (99). Analyses of focus-group discussions at four nursing homes showed that dying was silent and silenced, emotions were put into the background and death was talked about after a person's death. The staff did not talk about death neither with each other nor with the residents (100). This seems unfortunate as several residents have revealed that they were aware of the fact that they soon would die. One person emphasized that she was waiting to go to her real heavenly home. Another resident said that she was only living at the ward temporarily until she would meet her deceased spouse again and another one said that she wanted to listen to gospels while dying. Some did not speak about death and dying but reasoned about their funeral (60). At the last stages of life persons with advanced dementia often experience eating difficulties, especially swallowing problems (84–85). Several qualitative studies have reported that persons with advanced dementia at the end of life often exhibit aversive refuse-like eating behavior (101). There have been discussions about whether tube-feeding or comfort feeding should be used (102–103). The American Geriatrics Society (96) has recommended comfort feeding.

Spirituality has been regarded as “an integral, even fundamental, element of what it is to be a human being” (93, p. 765) and if we regard persons with advanced dementia as human beings it follows that they have spiritual needs. Spirituality among persons with advanced dementia has not, however, been

extensively studied. A literature review of scientific articles about spirituality did not report any study about persons with dementia (104) and another review study found expressed spiritual needs in 2 out of 10 articles (99). According to Kverno (93) there is a diversity of definitions of *spirituality* such as being connected to meaning-making. Spirituality should be understood as involving the dimensions of time and/or social space and stresses its longitudinal, habitual dimension, that is, “the values, meaning and practices most deeply ingrained at the heart of ‘who we are’ are those which have been repeated and reinforced over and over again from our infancy” (p.773) and held together with other persons. Perkins et al. (105) reported that even persons with advanced dementia were able to engage in *spiritual practices* that provide life meaning in accordance with their values. Observations in a nursing home showed that some persons expressed a need for religious expression or participating in religious rituals (106).

Thinking about or even experiencing that one interacts with deceased dear loved ones can provide satisfaction (60). This finding seems to represent a tendency to gerotranscendence (107) and can be understood as related to the fact that among persons with advanced dementia memory for past events is better preserved than memory of recent events (12). Swinton (108) argued that spiritual practices can be beneficial for Christian persons with advanced dementia. When their memory fails their bodily memory can be reclaimed. He referred to Bergson’s writing about a memory synonymous with recollection that represents particular things that have happened in the past and inscribes the past in the present (54). Swinton emphasized that we are embedded in our memories even when we cannot recall them, we are our memories. Persons with other religions or life views of course also need spiritual care adopted to their needs. Nursing home residents with moderate dementia expressed that religion is consolation for them (109). Persons with advanced dementia need consoling care (69, 110). The most important ingredient in consolation for these persons certainly is communion (69, 111) and it may provide them a feeling of being at home (112). However, it is most probable that they can get some moments of homecoming (60).

CONCLUSION

Persons with dementia lose parts of their self which can be noticed when considering symptoms such as amnesia, agnosia, aphasia, and apraxia. Their own sense of self can be preserved during the entire course of dementia partly due to the fact that their amnesia makes it difficult for them to upgrade their life story. Of utmost importance is that other persons understand that persons with advanced dementia still are persons and support them to feel valuable.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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Depression in Alzheimer's Disease: The Roles of Cholinergic and Serotonergic Systems

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch14>

Abstract: Although depression and Alzheimer's disease fundamentally result from distinct pathophysiological events, their coincidence is far from a rare occurrence. In addition to the difficulty in the diagnosis of depression in the patients with a cognitive impairment, care givers and even physicians are mostly unaware that depression and Alzheimer's disease can coexist. While depression has already a devastating impact on quality of life by itself, coinciding depression and Alzheimer's disease may advance to a cataclysmic magnitude. This chapter underlines obstacles in the recognition of depression in the Alzheimer's patients following a brief introduction to the concept of depression. Depression and Alzheimer's disease appear to intersect in the cholinergic and serotonergic systems which may engender an exquisite strategy in the treatment of both disorders. Therefore, potential cholinergic and serotonergic targets are also emphasized.

Keywords: Alzheimer's disease; cholinergic system; coincidence; depression; serotonergic system

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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INTRODUCTION

Depression is an affective disorder as old as mankind. Hippocrates has defined depressive psychological state as “melancholia,” which means “black bile” in Greek, by the words of “despair, apathy, unwillingness, insomnia, anxiety, incompetence, gloominess, sadness and fear” in around 400 BC (1). The brief description of depression is being possessed by unhappiness, moodiness and unwillingness (2). However, its description as a medical condition is continually evolving with the efforts of classification to make differential diagnosis clearer. Depression is an additional mental burden in Alzheimer’s patients who already struggle with cognitive impairments. Both depression and Alzheimer’s disease lower quality of life and harden daily activities of the patients who are mostly elders. Alzheimer’s disease often does not have a good prognosis whereas depression is a reversible, but recurrent disorder. Almost one-third of the Alzheimer’s patients suffer depression (3, 4). This chapter focuses on the interrelation between depression and Alzheimer’s disease, and discusses common properties of these neuropsychiatric disorders.

HOW DO WE RECOGNIZE DEPRESSION?

Diagnostic and Statistical Manual of Mental Disorders (DSM) by the American Psychiatric Association is the main guideline to diagnose depressive disorders whereas *International Classification of Diseases* (ICD) by the World Health Organization is the global system for reporting health conditions. According to the fifth edition of DSM, depressive disorders are categorized as major depressive disorder, dysthymic disorder, disruptive mood disorder, premenstrual dysphoric disorder, substance or drug related depressive disorder, depressive disorder due to a medical condition, and otherwise undifferentiated depressive disorder (5). With the system of ICD, the most commonly diagnosed depressive disorders are single depressive episode, recurrent depressive disorders, and persistent mood disorders (6). Depression is the most prevalent psychiatric disorder among general population (7). The patients with depression often have low self-esteem, suffer overwhelming unwillingness, and are afflicted by attention and concentration deficits which result in cognitive impairments (6, 8). Depression may exceed being an affective problem and lead to physical abnormalities. It can coincide with and aggravate existing physical pathologies (2, 6, 8). On the other side, chronic diseases can also generate depressive disorders (2, 9, 10). Together with its complications including the aggravation of physical health conditions, depression is a serious public health concern which also creates an important economic burden (10–12). Concerningly, depression has become the leading cause of disability (13). This insidious pandemic urges a better understanding of its pathophysiological mechanism and so, development of more advanced treatment options.

COGNITIVE DYSFUNCTION MAY LOOK ALIKE DEPRESSION

Although depression occurs frequently, it should not be mistaken as its diagnosis is unchallenging, particularly for the patients with cognitive impairment. Depressive symptoms are summarized above; however, the cognitive impairment can easily be confused with depression and *vice versa*. Lowered self-esteem, self-blame, forgetfulness and indecisiveness are shared behavioral symptoms of depression and cognitive impairment. Furthermore, hypomimia, apathy, psychomotor slowness, fatigue, and reluctance to communicate are the signs a physician may notice in a depressive patient which again resemble cognitive dysfunction (14, 15). Therefore, in the patients with cognitive impairment, diagnosis of depression often requires scrutinization of medical history and discrimination of the affective disorder with overlapping signs of cognitive inability. Depression can emerge at any age, but its prevalence is higher in adults, especially between 55 to 74 years old (16). Also, women are reported to experience depression about two times more than men (11, 16), indicating that sex is a risk factor for depression (17). Besides, there are numerous other factors that create a tendency toward depression such as divorce, separation, loneliness, and low socioeconomic status. (18).

THE COINCIDENCE OF DEPRESSION AND ALZHEIMER'S DISEASE

Epidemiological and longitudinal studies indicate that there is a relation between Alzheimer's and depression. However, it is debatable whether depression is a symptom arisen from the neurodegeneration or a reaction against cognitive inabilities. Some authors are defending that depression is a preceding pathology and a risk factor for Alzheimer's disease whereas some others suggest that depression co-occurs in Alzheimer's disease, and it becomes apparent as a component of Alzheimer's (4, 19).

A yearly increase in elderly population is predicted in almost all countries (20). Because age is an individual risk factor for Alzheimer's disease (3), an aging population means more patients with Alzheimer's disease. About 5% of the people over 65 years have dementia and an additional 5% increases every 5 years. Thus, the prevalence of dementia is as high as 40% after 95 years of age (21). Today, it is estimated that there are 35 million demented people all around the world and this number is projected to be 115 million in 2050 (22).

Alzheimer's disease is the most common form of dementia (23). One-ninth people over 65 years of age and one-third over 85 years struggle with Alzheimer's disease (3). Alzheimer's disease affects more than 5 million people only in the United States and it is reported to be the fourth cause of death (24). Furthermore, coinciding pathologies can significantly increase the incidence of the disease. For example, the risk for Alzheimer's disease is 3 to 5 times more in Down's syndrome (25).

Depression is an affective disorder that can afflict who takes a medical treatment and also, it is more prevalent in inpatients and elders under nursing care (3). Depression is a notable problem for overall elderly health. It has higher recurrence rates in elders than middle-aged people (26). Depression soars the death ratio independently of any medical interventions in patients under the nursing care (27). Suicide is the gravest consequence of depression and depressive elders have the highest suicide rates in all ages (28). Startlingly, suicidal ideation has been reported in 45% of the patients with concurring depression and Alzheimer's disease (29).

Depression is considered to be a “syndrome” rather than a “disease” which presently lacks a definitive biomarker and hence, is diagnosed by subjective questionnaire inventories. These inventories mainly aim to inspect neuropsychiatric symptoms such as negative emotional state, changes in personality and psychotic signs. The emotional and psychotic symptoms are relatively common in the Alzheimer's patients (30). Dysphoria, anxiety, aggressiveness, psychomotor agitation, loss of interest, and sleep disorders are the most frequent depressive symptoms. These symptoms encumber the care of Alzheimer's patients which is already difficult without them (Figure 1).

Clinical studies suggest that depression coincides with Alzheimer's disease in more than a half of the patients (29). Besides, depression in Alzheimer's disease often resembles severe depression, but with a variety of ambiguous symptoms.

DEPRESSION AND ALZHEIMER'S DISEASE SHARE NEUROPSYCHOLOGICAL SIGNS

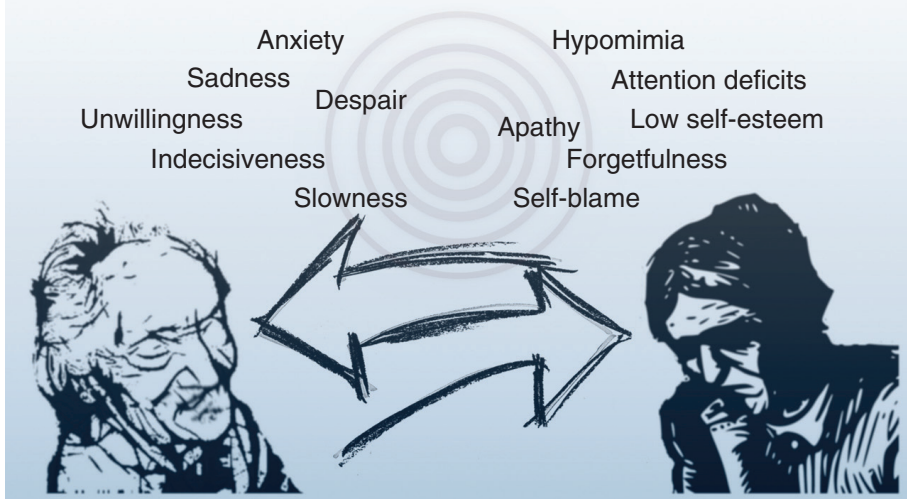


Figure 1 Depression and Alzheimer's disease are often manifested with similar neuropsychological symptoms and signs.

For example, depression in Alzheimer's disease can be represented with social isolation, self-abnegation or aggressiveness (3, 4). However, apathy and loss of interest remains to be the most common symptoms in coinciding depression and Alzheimer's disease (4, 31).

Diagnosis of depression in Alzheimer's disease is a strenuous task due to the lack of an objective and repeatable laboratory test to identify depression. Because of similarities with the patients with Alzheimer's disease, depression inventories can be misleading. Accordingly, it is important to emphasize that the incidence of depression gradually increases from mild to moderate cognitive impairment whereas decreases sharply in severe dementia (32). This decrease in incidence is a clear indicator of the obstacle in the diagnosis of coexisting depression in Alzheimer's disease.

WHAT DOES LIE BEHIND COINCIDING ALZHEIMER'S DISEASE AND DEPRESSION?

As mentioned above, the coincidence of Alzheimer's and depression is not a rare occurrence, and it creates a serious challenge to the diagnosis and quality of life. Although the two pathologies converge on behavioral and cognitive disturbances, they apparently do not originate in a common pathophysiological basis. However, they have a number of overlapping features that may explain the high comorbidity of Alzheimer's disease and depression.

The first report hinting the relation between Alzheimer's and depression dates back to late 1920s. Herz and Fünfgeld (33) have described depression as a preceding disorder that is immediately followed by deteriorations in memory in Alzheimer's patients. Numerous subsequent researches confirmed this link up to now, but post-mortem studies are peculiarly important since there is not a definitive ante-mortem diagnostic tool for Alzheimer's disease (34). Because longitudinal studies are invaluable means to reveal if there is a relation between seemingly distinct conditions, we will briefly discuss the prominent longitudinal studies in which post-mortem diagnosis was established.

In 2004, Milwain and Nagy (35) examined 89 histopathologically confirmed Alzheimer's patients with depression and found that the patients in the intermediate stage of the disease scored lower in CAMCOG, a neuropsychological battery to assess cognition (36), than the patients without depression. The worsened cognition in depressive Alzheimer's patients was implying a deterioration in the neuropathology, although this was not evidenced in that report. Rapp et al. (37) have investigated the post-mortem brains of 95 patients with clinically diagnosed Alzheimer's disease, of which 44 had a life-time history of major depressive disorder and 51 without depression. They noted that the Alzheimer's patients who suffered a life-time depression had about two times more amyloid plaques and neurofibrillary tangles in their hippocampi. In another longitudinal study that presents patient data from almost 40 years, Brunnström et al. (38) emphasized that the onset of dementia is lower in the depression sufferer Alzheimer's patients compared to those without depression.

Alzheimer's disease and depression appear to have a reciprocal relationship. Depression is an individual risk factor for Alzheimer's disease (39) even when the latency between the two pathologies is as late as more than 25 years (40). Preceding depression is a specifically notable predictor of Alzheimer's disease for the patients who do not carry apolipoprotein E (ApoE) $\epsilon 4$ allele which is an Alzheimer's-associated polymorphism (41). Thereby, non-ApoE4 allele carriers with depression have higher risk for Alzheimer's disease when compared with whom without depression. Furthermore, depression can have an outrageously high frequency in Alzheimer's disease. Usman et al. (42) have reported that depression was observed in three-fourths of the Alzheimer's patients without considering sex as a variable, and the prevalence was as high as 90% in females. This is particularly important because depression does not only aggravate amyloid pathology, but also worsens the clinical progress in Alzheimer's disease (43).

The mentioned interrelation points out some shared molecular features in Alzheimer's and depression even though they apparently originate from diverse pathological processes. Disturbances in the neurotransmitter systems and hypothalamic-pituitary-adrenal axis are prevailing peculiarities shared in the two pathologies. Indeed, the functions of the brain cannot be accredited to any individual neurotransmitter or neuromodulator because all systems should be operational in a stupendous harmony to achieve an efficient function. However, aberrations in the cholinergic, monoaminergic and serotonergic transmission are evident in both Alzheimer's disease and depression which compose a pathophysiological intersection.

Cholinergic system in the central nervous system consists of two sub-systems as nicotinic and muscarinic. Although cholinergic projections are clustered in distinct regions, both nicotinic and muscarinic receptors are widely distributed throughout the brain and hence, cholinergic transmission involves in numerous brain functions that are carried out by diverse brain areas (44). The nicotinic system works out through the neuronal nicotinic acetylcholine receptors which are simply cation channels (45) whereas the muscarinic system employs any of the five muscarinic acetylcholine receptors (M1-5) which all are G-protein coupled receptors (46). It is long known that cholinergic dysfunction is a problem in Alzheimer's disease (47). The cholinergic hypothesis of Alzheimer's disease proposes that the deterioration in the cholinergic signaling is responsible for learning and memory deficits, a condition which also can be experimentally mimicked by the administration of anti-cholinergic drugs (48). This hypothesis is supported by symptom relieving effects of acetylcholine esterase inhibitors whereas disapproved by the presence of cholinesterase inhibitor-resistant patients (48). Nevertheless, the cholinergic system is evidently disturbed in a remarkable portion of the patients and it shows a correlation with cognitive inabilities (49). This is probably because the cholinergic neurons are particularly affected by the amyloid accumulation (50). With regard to the cholinergic system, the relation between Alzheimer's and depression seems to be paradoxical, considering that reduced cholinergic signaling is linked to cognitive decline. The involvement of the cholinergic system in depression is known for almost 50 years (51) and preliminary studies have underlined the hyperactivity in the cholinergic signaling in depression (52). Consecutive researches have noted that enhanced cholinergic transmission leads to depression (53, 54) and

antagonizing nicotinic signaling can exert an anti-depressant-like effect (55). Contrarily, the activation of a sub-type of nicotinic receptors, alpha7 receptor, has been shown to alleviate depression in mice through restoring the hippocampal function (56). Therefore, instead of a widespread contribution of the cholinergic system to depression, its influence on hippocampus should be taken into account. As illustrated in Figure 2, decreased cholinergic innervation diminishes the hippocampal neurogenesis and function, and improving the cholinergic transmission by means of cholinesterase inhibitors reverses this consequence (53). In regard to alterations in the cholinergic system, the hippocampus is the crossroad where cognitive deficits meet with depressive behaviors. This probably explains the finding of that cholinesterase inhibitors improve neuropsychiatric symptoms in some Alzheimer's patients (57, 58). On the other side, it should be kept in mind that cholinergic hyperactivity created by cholinesterase inhibitors can result in depression (59) and hence, fine dose adjustment and a strict follow-up are particularly important issues in the Alzheimer's patients with a history of depression.

The other neurotransmitter system that bridges between Alzheimer's disease and depression is the serotonergic system that is named after its neurotransmitter, serotonin (5-hydroxytryptamine; 5-HT). Serotonin has 7 families of receptors (5-HT₁₋₇) which are all G-protein coupled except for the ionotropic 5-HT₃

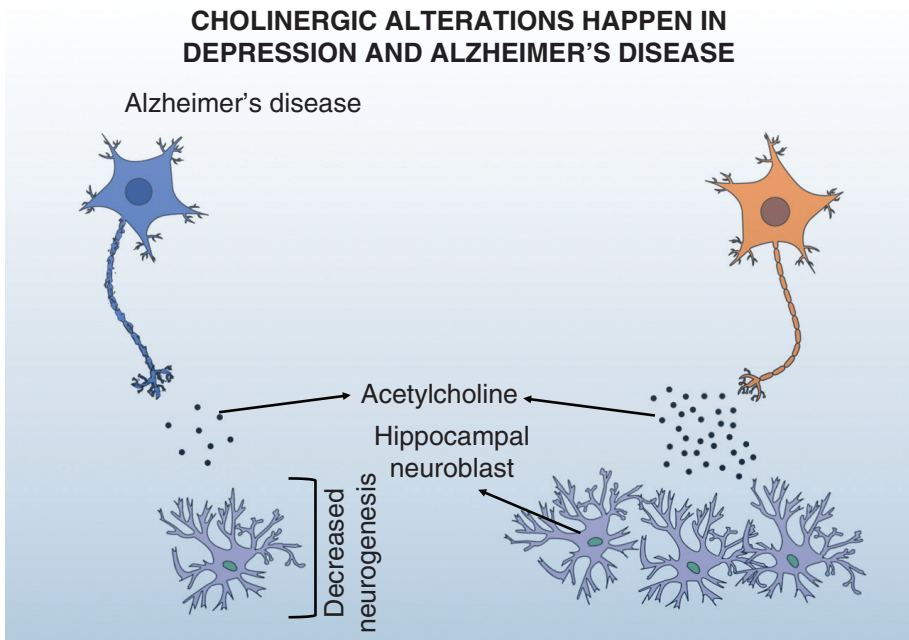


Figure 2 The cholinergic depletion reduced hippocampal neurogenesis that contributes to cognitive impairments.

receptor (60). The most commonly prescribed anti-depressants, selective serotonin reuptake inhibitors (SSRIs), aim the restoration of serotonin in the central nervous system. The alleviation of depression with SSRIs constitutes the foundation for the serotonin hypothesis of depression in which depressed mood and its complications are accredited to reduced serotonergic neurotransmission and neuromodulation (61). Besides the serotonin transporter (SERT), three sub-types of serotonin receptors, 5-HT_{1A}, 5-HT_{1B} and HT_{2A}, which are mainly localized in the limbic system, appear to bear higher importance in depression (61). Recently, 5-HT₄ and 5-HT₆ receptors have been suggested to have a role in depression. The stimulation of 5-HT₄ receptors has been shown to lead to an anti-depressant-like effect that is similar to fluoxetine (62, 63). Moreover, 5-HT₄ stimulation has been found to restore cognitive abilities that are altered in depression (63). An opposite link has been revealed for 5-HT₆ receptors which are abundant in the hippocampus (64). The inhibition of these receptors has been suggested to exert an anti-depressant-like effect (65). Indeed, the strongest relation between Alzheimer's disease and depression may lie behind the serotonergic system. The patients with Alzheimer's disease display depleted serotonin and 5-hydroxyindoleacetic acid, the main metabolite of serotonin, in their frontal and temporal cortices (49). Amyloidogenic activity increases in the post-menopausal period and this may be originated in decreased serotonergic signaling due to decreased estrogen (66) which is in accordance with the epidemiological data of higher prevalence of Alzheimer's disease in women (67). The Alzheimer's patients have a decreased 5-HT_{1A} receptor expression particularly in their hippocampi and raphe nuclei, and the hippocampal receptor decrement is correlated with worsened clinical symptoms (68, 69). Similarly, 5-HT₂ receptors decrease up to 69% in Alzheimer's disease as documented by decreased setoperone binding, a 5-HT₂ ligand that has particular affinity to 5-HT_{2A} receptors (70), and by decreased altanserine binding, a 5-HT_{2A} ligand (71). More recently discovered 5-HT₄ and 5-HT₆ receptors, which are novel anti-depressant treatment targets, also involve in the pathophysiology of Alzheimer's disease. Similar to that for depression, 5-HT₄ agonism alleviates Alzheimer's amyloidogenic pathology whereas 5-HT₆ antagonism augments memory and learning in the Alzheimer's patients (72). Moreover, a decrease in SERT accompanies the decrease in the receptors of interest which results in an extensive disruption in the serotonergic signaling in Alzheimer's disease (73). Overall, the serotonergic system, as summarized in Figure 3, plays a crucial role in both Alzheimer's disease and depression and constitutes a highly promising treatment target which may ease depressive mood while soothing cognitive deficits in the Alzheimer's patients with depression.

In addition to current treatment targets of cholinergic and serotonergic systems in Alzheimer's disease and depression, they share some other pathophysiological features such as disturbances in the hypothalamic-pituitary-adrenal axis, inflammation and oxidative stress (74). However, it is not clear whether these disorders are reasons or consequences. Nonetheless, it is evident that the treatments targeting either cholinergic or serotonergic systems can reduce coinciding immunohumoral and oxidative disruptions to some degree in both diseases (75, 76).

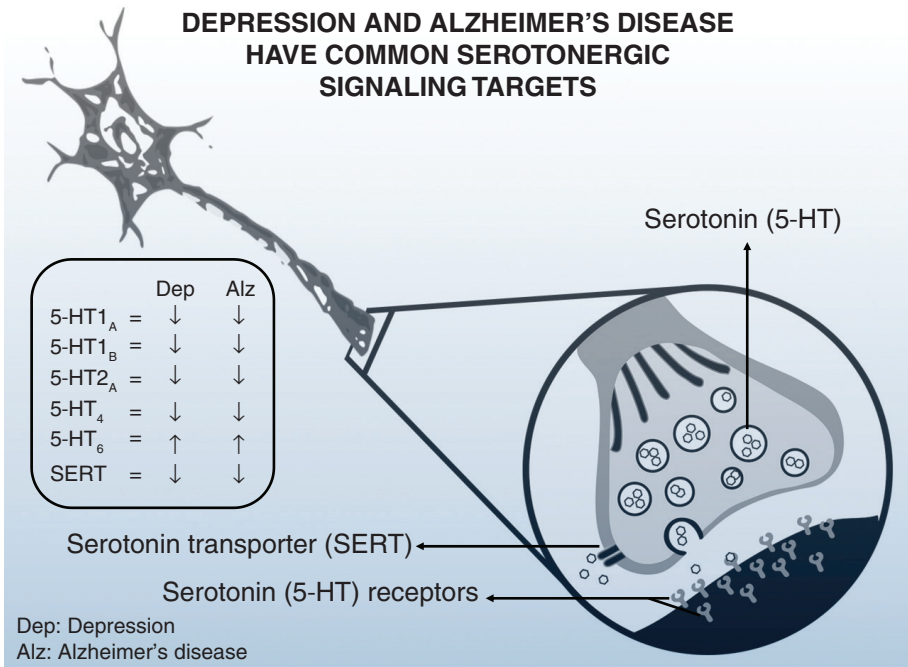


Figure 3 The serotonergic system is similarly altered in both depression and Alzheimer's disease.

CONCLUSION

Alzheimer's disease and depression are debilitating disorders which need further scrutinization to understand their pathophysiological properties and to develop novel treatment options. Alzheimer's disease is an incurable neurodegenerative disorder, at least for now, and undiagnosed/untreated depression in Alzheimer's patients creates a serious problem since it worsens neurodegeneration while causing further cognitive deficits and lowering quality of life. Considering abovementioned shared molecular features of both disorders, awareness among clinicians of the possibility of depression in Alzheimer's patients would let them prescribe not only against cognitive symptoms, but also affective disturbances which can benefit to both Alzheimer's disease and depression.

Acknowledgments: Images used in the figures have been labeled for "reuse with modification" according to Google Search by Google LLC.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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A Collaborative Approach to Treatment of Alzheimer's Disease from a Psychological Perspective

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Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019.ch15>

Abstract: After the age of 60, earlier in many cases, patients who experience perseverations, forgetfulness, and difficulties with daily living are often referred by their physicians for a neuropsychological evaluation. A neuropsychological evaluation consists of a variety of tests that illustrate a patient's cognitive functioning that include attention, concentration, verbal memory, visual memory, problem-solving, and cognitive flexibility. It further clarifies a range of diagnostic criteria that distinguish Alzheimer's disease (AD) from other mental health-related disorders. Depression presents in a very similar pattern to early stages of AD. Therefore, the neuropsychological evaluation will rule in or out diagnostic criteria and pinpoint which medication should be recommended. A collaborative approach between psychologists, physicians, and caretakers is crucial in obtaining an accurate diagnosis to develop an appropriate treatment plan. Results from the neuropsychological assessment provide physicians with information to develop a medication regimen that helps treat a patient's cognitive and behavioral symptoms. Additionally, this information provides caretakers with psychoeducation to help understand the current functioning of their loved ones.

In: *Alzheimer's Disease*. Thomas Wisniewski (Editor), Codon Publications, Brisbane, Australia. ISBN: 978-0-646-80968-7; Doi: <http://dx.doi.org/10.15586/alzheimersdisease.2019>

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The neuropsychological test findings coupled with a medical intervention is imperative to help patients and their families to develop adaptive methods that may help minimize the difficulties of daily living.

Keywords: Alzheimer's; attention; cognitive rehabilitation; dementia; emotional functioning; memory; neuropsychology

INTRODUCTION

Evaluating dementia, particularly Alzheimer's disease (AD), varies across settings. In this chapter, we will introduce what is neuropsychology, neuropsychological testing for possible or probable AD, as well as the importance of collaboration between the doctors involved in treatment of the patient with AD. In particular, we will describe what a medical doctor can expect from neuropsychological testing. Among countless batteries that are performed by neuropsychologists, we will emphasize the following phenomena: depression, substance use, decision-making, co-occurring mental health disorders, as well as the role that technology plays in neuropsychological testing. The importance of neuropsychological testing is priceless to patients. Results from neuropsychology testing can aid in confirming and/or ruling out often otherwise misdiagnosed syndromes that may require a different treatment plan and hence may impede and/or lead to success for appropriate treatment. For instance, neuropsychological testing may confirm AD and rule out depression and vice versa. Our hope is that readers will be more familiar with neuropsychological testing and its role in treatment for patients as well as their loved ones.

WHAT IS NEUROPSYCHOLOGY?

Neuropsychology is a scientific term that encompasses studying the central nervous system, including the brain and spinal cord, and how it influences an individual's cognitions and behaviors. This field within psychology has experienced a growth for over the last 40 years, with interest for about 120 years within the modern scientific psychology (1). Neuropsychology utilizes specialized knowledge of foundational neuroanatomy, principles of neuroscience, brain development, neurological disorders and etiologies, neurodiagnostic techniques, normal and abnormal brain functioning, and neuropsychological and behavioral manifestations of neurological disorders. In addition to this diverse amount of knowledge, neuropsychologists gather relevant historical information, conduct a neuropsychological examination, analyze and integrate data and findings, and provide feedback to the referral source. Neuropsychologists attempt to answer the question of "What mechanisms are responsible for human thinking, learning, and emotion, how do these mechanisms operate, and what are the effects of changes in brain states upon human behavior?" (1). This specialty applies principles of assessment and evidence-based interventions to the study of human behavior as it relates to normal and abnormal functioning of the central nervous system. The combination of extensive

training, knowledge, and education with the process of obtaining and analyzing information allows for neuropsychologists to solve questions about the mind that otherwise cannot be solved.

As the main focus for neuropsychology is to determine the brain and behavior relationship with each patient exhibiting their own unique presentation, this has pushed to develop the field toward becoming an essential discipline for diagnosing and treating cognitive mental health disorders. Neuropsychology utilizes mechanisms to elicit activation in the multiple areas of the brain to determine their individual levels of functioning. In particular, these areas are referred to as cognitive domains. These cognitive domains studied by neuropsychologists include “perception, attention, learning, memory, processing of spoken and written language, thinking, reasoning, or belief formation, with the aim of learning more about the normal functional architectures of the cognitive processing systems used to carry out these activities” (2). As a result of testing the functioning in all the above-mentioned domains, there are a wide range of disorders that may be diagnosed including dementia, vascular disorders, Parkinson’s disease, and other neurodegenerative disorders, traumatic brain injury, seizure disorders, learning disabilities (LD), neuropsychiatric disorders, infectious disease affecting the central nervous system (CNS), neurodevelopmental disorders, metabolic disease and neurological effects of medical disorders or treatment. Achieving a diagnosis allows individuals, their loved ones, their caretakers, and their physicians to gain awareness of the presenting problem and understand effective treatment recommendations to manage the diagnosis.

It is important to understand the direct correlation between cognitions and behaviors for neuropsychologists. This relationship that is observed is an individual’s natural response to their environment, which may experience fluctuations. Neuropsychologist’s main role is to attempt to distinguish where there are abnormalities and how it may cause dysfunction that may impact an individual’s ability to properly function in their daily lives. Dysfunctions that a patient may experience may present in one or more of the domains of cognitive functioning. Each domain plays a crucial role in how individuals function in their personal and professional lives. These dysfunctions may present at different severities. In general, the minimal symptoms are not noticed by the patients; however, the more pronounced are usually noticed by their significant others. Many times, when a cognitive domain begins to decline, the patient may have minimal or no presenting symptoms, while others may have a severe presentation from the beginning. Such presentation depends on the domain that is impacted and possible other co-occurring medical complications. While there may be an overlap between the areas that present with similar problems, each has their own focus on how they contribute to the brain and cognition relationship.

One of the main impacts to the cognition and behavior relationship is a type of brain damage or trauma. The damage or trauma can range from a direct impact to the head to an organic occurrence in the brain. Regardless of the type of brain trauma, when it occurs, it can be localized or generalized throughout the brain. The area of where the impact occurs will influence the patient’s presentation. It may be difficult to pinpoint where the impact occurred, but the neuropsychological evaluation will pinpoint impairments within each cognitive domain. The neuropsychological evaluation is pertinent as it will discern clusters of symptoms that may belong to psychiatric symptoms, medical conditions, as well as emotional presentation.

The primary reason for a neuropsychological evaluation is to create a diagnosis and eliminate other disorders that may seem relevant but may not apply to the individual's presentation. Neuropsychological assessments specifically target parts of the brain through measuring the different cognitive domains of functioning. Cognitive functions are processes that help individuals carry out tasks requiring attention, memory, language, judgment, and problem solving. While it is well known that certain domains of cognitive functioning have their main centers, they also may be spread across several parts of the brain. Neuropsychological assessments elicit activity in different parts of the brain when activated with test tasks. A thorough analysis of the integrated data from the neuropsychological evaluation, will not only pinpoint given cognitive strengths but also weaknesses. Such analysis is most likely driven by patterns within the testing battery which as a result renders a diagnosis. This is why a neuropsychological evaluation contains a set of tests that measure similar cognitive functioning, rather than utilizing screening assessments. On that note, the neuropsychological evaluation is a lengthy process which oftentimes requires several hours of testing. While the several hours may seem long and daunting, it presents accurate data, rather than screening alone. Each neuropsychological battery is designed for an individual's ability to withstand long testing hours. In those situations a focused neuropsychological battery is conducted and a single cognitive domain may be tested (i.e., attention). Hence it is not uncommon that testing may vary in length from one to several hours, depending on the setting. For instance, testing may be shorter within an inpatient bedside setting and longer for a patient seeking an evaluation for a high-profile employment position, in an outpatient setting. In spite of the long hours of testing, it is our experience that patients and their family members appreciate the time that they engage in the testing, as this allows for a thorough evaluation. Patient's family members especially their children, appreciate the knowledge as they may carry similar genetic load and hence can utilize measures for prevention.

Individual results of the neuropsychological evaluation are compared to norms that will then indicate the level of functioning of this individual. The neuropsychological evaluation will render normative data that will indicate whether a patient is in the above average, average, or impaired range of functioning. The neuropsychological evaluation provides the clinician with twofold data. First, it delineates the pre-morbid functioning level that allows the neuropsychologist to understand whether the impairment is significant, as this may vary from one individual to another. For instance, if the tested individual has never experienced difficulties in school, it is expected that their premorbid functioning would demonstrate intact cognitions that are impaired during the time of testing. It is crucial to highlight here, the importance of having accurate norms to which the results are compared. The neuropsychological testing norms on several tests include norms not only for AD but also for patients with stroke, head trauma, LD, PTSD, and schizophrenia as compared to a control group. To further delineate neuropsychologists' work it is also important to note that each neuropsychological assessment presents not only an understanding of the cognitive domains in the human brain but also its characteristics that then determine diagnostic criteria and the appropriate treatment plan.

For the purpose of diagnosing probable AD, clinical neuropsychology is the main discipline to determine its presentation and severity. As aforementioned, AD impacts several areas of the brain and may present as several different diagnoses. It is imperative then to utilize the neuropsychological assessment results to determine an appropriate diagnosis and rule out other possibilities, as those treatment recommendations may be drastically different.

NEUROPSYCHOLOGICAL TESTING FOR POSSIBLE OR PROBABLE AD

AD is a neurodegenerative disorder. It is the most common type of dementia, with an estimate of 5 million individuals in the United States (65 or older) who were diagnosed with AD and related dementias in 2014 and an estimated 13.9 million projected to be diagnosed with the disease by the year 2060 (3). According to the World Health Organization, worldwide there are an estimated 47 million individuals affected by the disease currently (4). According to Braak and Braak (5), AD is “characterized by neuronal atrophy, synapse loss, and the abnormal accumulation of amyloidogenic plaques and neurofibrillary tangles in medial temporal lobe limbic structures (e.g., entorhinal cortex and hippocampus) and the association cortices of the frontal, temporal, and parietal lobes” (6). Several brain regions are affected by AD including the anterior cingulate cortex, the frontal lobes, as well as the medial temporal lobes (7).

According to Groth-Marnat (8), AD is referred to as a “cortical” dementia due to it affecting the cortical regions in the brain, as opposed to other types of dementia that affect the subcortical regions in the brain and cause impairments in attention and visuoconstruction. To further explain, the cortical dementias are characterized by more difficulties with memory and learning and sub-cortical effect more problems within attention and visuoconstruction.

The first cognitive symptom of AD is an impairment in episodic memory functioning, and later on as the disease progresses it impacts the frontal cortex, which impairs executive functioning (9). Based on a study conducted by Reed and colleagues (9), it was found that “Pathologically defined cases of Alzheimer’s disease had verbal and non-verbal memory scores that averaged about 1 SD lower than their executive function scores.” According to Smith and Bondi (10), the types of cognitive deficits observed in AD include impairments in areas such as memory and episodic learning, language and semantic knowledge, visuospatial, and executive functioning such as difficulties with problem-solving and abstract thinking as well as set-shifting. According to the Diagnostic and Statistical Manual of Mental Disorders (5th Edition), procedural memory and social cognition may be preserved for a longer period of time. Smith and Bondi further indicate that individuals with AD can experience anosognosia, in which they lack awareness of the cognitive problems they may experience (10). This lack of awareness may result in delayed diagnosis and treatment. Most patients are tested due to family concerns who notice the most salient characteristics such as perseveration and lack of new learning.

Physicians may refer patients who experience forgetfulness, changes in their behavior and functioning, and/or a decline in the ability to complete activities of daily living independently, for a neuropsychological evaluation. When the referral question is for memory decline, it is important to conduct a thorough and detailed clinical interview. In such cases where the referred individual may have difficulties reporting relevant information and is deemed to be an unreliable historian, it is important when possible that the clinician attempts to obtain collateral information. This information may be obtained from the referred individual's caregiver or family member regarding the onset/frequency/severity of the individual's symptoms and functioning. Information obtained from the clinical interview guides the clinician to choose which test or series of tests need to be administered to the referred patient to address the referral question.

A standard neuropsychological testing battery to assess for possible or probable AD should include measures assessing several domains of functioning including: Attention, Processing Speed, Memory, Language, Executive Functioning and Dementia Severity (11). Simple attention continues to remain intact as patients with intact verbal skills, who present with severe impairments, are able to repeat 5 digits forward correctly (12). With regards to language abilities, individuals with AD often demonstrate impairments in verbal fluency, semantic fluency, and naming objects. Tests are administered to assess areas of visual and verbal memory, as well as the individual's performance in areas of immediate and delayed memory, and ability to learn new information. With regards to memory, patients with AD have difficulty encoding new information, the learning curve is flat across trials, and new information is not consolidated (13). Additionally, recognition is impaired and delayed recall of information is also poor, even after a short period of time (13). According to Delis et al. 1991, "...AD patients rapidly forget information over time and are equally impaired (relative to age-matched controls) on recognition and free recall components of the tasks. This pattern of performance is consistent with impaired consolidation rather than ineffective retrieval of new information" (14).

In addition to other criteria that must be met for a diagnosis of Major Neurocognitive Disorder Due to AD, the Diagnostic and Statistical Manual of Mental Disorders (5th Edition) indicates that there must be "clear evidence of decline in memory and learning and at least one other cognitive domain (based on detailed history or serial neuropsychological testing)" (15).

DEPRESSION AND AD

Neuropsychological tests help with determining if the patients have symptoms of dementia, depression, or both. As discussed above, depression and dementia share similar characteristics, but neuropsychologists know the differences. Neuropsychologists have the clinical capacity to rule out and state either diagnosis. Such luxury helps medical doctors and/or prescribing psychologists to design the most efficient treatment plan available for a patient.

There are many alternate diagnoses that may interfere with an accurate assessment of probable or possible AD. Depression is among one of the most common misdiagnoses due to the number of overlapping symptoms it shares with AD.

The most common overlapping symptoms include loss of interest in enjoyable activities and hobbies, social withdrawal, problems with memory, lack of sleep or over-sleeping, and impaired concentration (16). The difficulty in differentiating AD from depression depends on several factors, which may include inaccurate information provided by the patient and/or family members, normal effects of aging, dementia and depression comorbid conditions (17). The causal relationship between dementia and depression is supported by findings that people with dementia appear to have a higher prevalence of depression (18). However, in many cases patients may not have AD or dementia and may just have depression. In such cases, particular attention is placed on depressive symptoms which are less common in dementia alone. These symptoms may include feelings of hopelessness, expressions of guilt, feelings of worthlessness, and thoughts of self-harm (19).

There have been correlations found between mild, moderate, and major depressive disorder and insomnia with regard to AD risk (20). Insomnia and depression share a complex relationship. Depression may cause sleep problems and sleep problems may cause or contribute to depressive disorders (21). However, in terms of diagnosing AD when lack of sleep and depression occurs, the challenge becomes greater, as the symptoms overlap. Some of the symptoms such as memory loss, poor judgment and taking longer to complete normal daily tasks, all may contribute to lack of sleep, depression, and/or AD itself. Again this is why a full neuropsychological evaluation is necessary as it encompasses evaluating sleep patterns, symptoms of depression, as well as highlights hallmarks of AD. It is also crucial to state here that a neuropsychologist needs to work very closely with the patient's primary care physician, psychiatrist, and/or prescribing psychologist, as the medications that the patient is taking may also have a crucial impact on his/her functioning. "A survey in the United States of a representative sampling of 2206 community dwelling adults (age 62–85 years) was conducted by in-home interviews and use of medication logs between 2010 and 2011" (22). "At least 1 prescription medication was used by 87%, 5 or more prescription medications were used by 36%" (22). In summary, it is well known that an adult population that is most susceptible to AD takes about 1–5 different medications a day. Those medications include not only medication related to systemic failures and/or inadequacies including steroids, diabetes medication, vascular problems, to list a few and they may cause side effects stimulating not only metabolic system problems, arrhythmias, but also sleep problems.

In summary, a crucial part of the neuropsychological evaluation is evaluating sleep habits and to differentiate sleep difficulties related to emotional problems, side effects of medications, as well as poor sleep hygiene as they all require different interventions. Furthermore, Alhola and Polo-Kantolastate that attention, working memory, long term memory and decision making abilities can be impaired due to sleep deprivation (23). Moreover, metabolic functioning may also be impaired due to lack of sleep. While the body sleeps, a plumbing method called the glymphatic system opens up channels in the brain and allows fluid to flow rapidly throughout the brain, in order to flush out toxins or interstitial protein deposits (24) that may be accumulating in the brain (25). During sleep deprivation this accumulation of proteins or toxins may cause cognitive impairments, as our brain is unable to function at an optimal level. Although AD may not be the actual cause of these cognitive impairments for patients who lack

sleep, the diagnosis of dementia becomes a viable conclusion. Most likely, this is due to the fact that when older individuals do not have quality sleep as well as struggle with other medical complications, they may simply develop functional impairment that may constitute dementia.

Anxiety can interfere with a person's everyday life and it is also the most common symptom throughout the different stages of dementia (26). Anxiety and agitation become more apparent in the early stages of AD as people begin to recognize their losses and the seriousness of the disease. They may become anxious about being left alone or abandoned, while any changes in the daily routine can also trigger anxiety and agitation (27). The prevalence of depression in AD is fairly high, with rates reported as high as 87% and averaging 30%. Therefore, it is conceivable that comorbid anxiety and depression may affect a large percentage of patients with AD (28). The correlation is unknown between AD and anxiety; however, a recent study has shown that anxiety predicts risk of Alzheimer's disease ($n = 26,193$ out of seven studies, hazard ratio 1.53, 95% CI 1.16–2.01, $P < 0.01$) and vascular dementia ($n = 4916$ out of two studies, odds ratio 1.88, 95% CI 1.05–3.36, $P < 0.01$) (29). Although anxiety does not directly associate with the likelihood of having dementia or AD, it may reflect neurodegeneration in patients who experience symptoms of AD or dementia.

WHAT DO NEUROPSYCHOLOGISTS HAVE TO OFFER MEDICAL DOCTORS AND HOW IMPORTANT IS THEIR COLLABORATION

Neuropsychologists are able to collaborate with primary care physicians and other specialty driven doctors in a variety of ways, including answering referral questions and establishing and clarifying diagnostic criteria related to dementia. Neuropsychologists use countless tests that are established to be a crucial part of dementia assessments in various situations. A few are described below.

The most common question with which patients, their family members, and their doctors come to neuropsychologists on an outpatient basis is regarding the gravity of dementia. In most cases, medical doctors complete the Mini Mental Status Exam (MMSE) to screen a patient's memory and attention. Typically, patients with dementia fail such questions. In other words, when patients are provided three words to learn and later recall, they do not remember the three words or they remember only one of the three words provided. In most situations, the patient that failed the memory and/or orientation tests are sent to a neurologist so an MRI and/or CT scan can be ordered to indicate the presence of any notable changes in the patient's brain scan. Sometimes, impaired patients may have normal MRIs or an MRI may show significant changes even while the patient's cognitive functioning seems intact. This is most likely explained by neuroplasticity. In such situations when the MRI and/or CT results do not correlate with the patient's self-report, neuropsychological testing is taken into consideration.

Another well-known issue establishing the need for completion of neuropsychological testing is the fact that patients remember previously learned tasks from the Mini-Mental Status Exam administered by their doctors. Repetition of similar

tasks, for instance remembering three words, results in inconclusive data as the screening does not evaluate new learning but rather recall of previously learned information. Similar phenomenon is observed when adult children do not recognize symptoms of dementia in their parents. This happens due to repetition of similar conversations concerning daily tasks and/or activities that do not change.

Patients also tend to minimize their impairments when explaining them to their doctors, and their family members are unable to provide correct information about the patients' functioning because their loved ones have their routines. Usual rituals for family members often include calling the patient and asking them the same questions over and over. The questions they ask are most likely about the patient's eating habits and medication-taking rituals. Since going for a walk with the dog is not a novel task, the patients appear healthy and free from any cognitive problems. Neuropsychologists spend a lot of time with a patient's family, explaining to them that such routine is a very common phenomenon that promotes lack of accurate judgment about a family member's cognitive functioning. In fact, if the medical doctor and/or neuropsychologist hear any complaints relating to a family member's decreased cognitive functioning, such as perseverations and forgetfulness, the patient is most likely already in the advanced stages of dementia. Unfortunately, many patients reside alone and their beginning signs of dementia are not detected or are explained away as part of the normal aging process.

THE ROLE OF ALCOHOL CONSUMPTION IN DEMENTIA

Not all medical doctors choose to speak to their patients about their alcohol consumption. Most doctors that treat AD are younger than their patients. Both of these factors may often result in ambiguity and discomfort that may impede the doctor-patient dialog about alcohol use. However, most doctors of clinical psychology are well-equipped and clinically trained to discuss the topic of alcohol use with their patients.

Despite the toughness of this issue, it is well known that patients with AD are not immune to drinking alcohol. In fact, many dementia patients drink. Drinking causes falls, broken bones, and brain injuries. It also causes cognitive problems such as poor planning and organizational skills, poor decision-making and judgment, problems with impulsivity, difficulty controlling emotions, problems with attention and slower reasoning, lack of sensitivity to others' feelings, and behavior that is socially inappropriate. On the other hand, a systematic review by Peters and colleagues indicates that "in older people, small to moderate amounts of alcohol consumption are associated with reduced incidence of dementia and Alzheimer's disease (AD)" (30).

While there are more problems related to alcohol consumption, dementia and AD patients are getting contraindicated recommendations about drinking alcohol from their primary care physicians. In contrast, clinical psychologists with neuropsychology specialties are not only trained to treat alcohol use but are also able to perform neuropsychological tests that can characterize the type and extent of a patient's cognitive deficit as well as denote which symptoms belong to AD and which ones to alcohol use. In this way, rehabilitation efforts are maximized.

The importance of neuropsychological testing in matters of AD and alcohol consumption was delineated by Robert Heirene, Bev John, and Gereth Roderique-Davies. The authors reviewed the available data and agreed that cognitive screening is limited and is trumped by far by comprehensive neuropsychological testing following screening to ensure a correct diagnosis (31). The authors stated that neuropsychological testing establishes crucial characteristics of alcohol related cognitive decline that mostly includes a decline in executive functioning and episodic, autobiographical, procedural, and working memory. They also discussed the issue of confabulation that may be related to both dementia itself and an alcohol related impairment (30).

AD AND DECISION-MAKING CAPACITY

Another type of neuropsychological referral encompasses denoting the gravity of AD symptoms, as well as the patient's decision-making capacity. Indeed, the vast majority of outpatient referrals relate to the individual who resides at home, and his/her family members worrying about their cognitive functioning. Patients with detected and undetected AD spend time alone at home. During those moments, they are vulnerable to burglary, deceit, and even death because their judgment is impaired. For instance, there have been individuals who opened the door to a stranger, soliciting them to withdraw money from the bank; as well as patients selling health insurance, buying homes, and even moving to another state without having a previous discussion or agreement with the rest of their family members about their plans. This demonstrates the lack of judgment, rational thinking, and insight which may be characteristic of individuals with dementias.

Another very important aspect for the need to complete neuropsychological testing regarding decisional capacity is the fact that many AD patients are in the hospital and are unable to make decisions regarding their health. Unfortunately, without completion of neuropsychological tests, many AD patients seem to cognitively function well to not only their family members but also to their doctors. Those are the patients that refuse certain treatments that may be very vital to their life. Those are the patients that lie in their hospital beds, seem unconcerned about their health, and lack an understanding about the gravity of their illnesses. Those are the patients that have shallow humor and tend to answer their doctors' questions with short answers that indicate their disinterest. For example, they tend to state that they do not care for politics hence they do not know who is the current president, and they tend to fail orientation tests even when the correct date was written by a nurse in front of them.

Families of AD patients have the tremendous task of accepting that their parents, uncles, aunts, and other family members who used to be sharp, have lost the ability to make decisions. The family members also vicariously deal with their own stress responses, facing the possibility that they may have similar genetic loads and that they may also develop AD. All of the above mentioned constraints lead to missing the symptoms, which then leads to the most dangerous problem: not doing anything.

After completion of the neuropsychological testing, the report and recommendations are delineated. One of the possible recommendations may be cognitive rehabilitation. Another recommendation may encompass an evaluation for a

cognitive enhancer. Recommendations may also include possible counseling/psychotherapy and or a support group for the family members/caregivers to process their fears, help them develop skills to deal with their family member that has AD, and start the process of establishing a power of attorney.

AD AND OTHER MENTAL HEALTH PROBLEMS

Doctors of psychiatry often refer their patients for neuropsychological evaluations to rule out AD and possibly diagnose depression. They also seek neuropsychological evaluations to determine possible attention problems and undiagnosed LD that can all resemble early dementia.

It is our experience that more than a few referrals from psychiatrists include ruling out stress in patients as young as 50 years old that presented with dementia like symptoms. Those patients seem to have dementia, but neuropsychological evaluations are able to detect severe stress that results in their poor job performance. In such situations a conclusive diagnosis is crucial, as the treatment for stress as well as burnout differs from treatment for dementia.

Neuropsychological evaluations can also detect LD that have not previously been diagnosed. Nowadays, with more and more jobs requiring computer skills, this phenomenon occurs, even with those jobs that are considered computer-free. For instance, a 55-year-old janitor is now required to login to the computer to check memos, request days off, or perform required training. In this situation, a LD may mirror early dementia and hence lead to inappropriate treatment. Again, a neuropsychologist will not only test this individual's cognitive functioning but also recommend training, teach compensation skills, etc.

AD AND TECHNOLOGY

Typically, the older population does not do well with computerized testing, even though these kinds of tests are well-prepared for inexperienced computer users. Since computers were first used at schools in the eighties in the USA, patients that have never used a computer to study or work are included in this population. Hence, most patients that are at least 50 years old who lack the required computer skills, may be considered in this group. At our clinic, any time a computerized test was administered to an older population member, it has been observed that the cognitive abilities tested on the computer were lower than on paper and pencil tests. Hence, doctors using computer screening tests for cognitions may obtain inaccurate results. When in doubt about a patient's results, it is recommended that the patient be referred for a full neuropsychological testing battery.

AD AND MARIJUANA USE

Much of the older population in the United States recreationally consumes and/or smokes marijuana, as it is now prescribed as well as highly available. When asked what their purpose, as for smoking is, most people state that it is healthy and

that it helps them with sleeping and managing their pain. Research on smoking marijuana and its effects on cognitions vary, but in our practice it has been observed on several occasions, that severe delirium followed ingestion of cannabis. Cannabis use can result with hallucinations, as it is a hallucinogenic agent. It may also quicken cognitive decline, especially memory problems. While this has little to do with neuropsychological testing and AD, it is crucial to state here that all healthcare providers should consider referring any, but especially older patients, to neuropsychologists because the underlying causes of marijuana ingestion can be detected, processed, and potentially diminished; all of which would better their patient's quality of life. In other words, it is our belief that if an individual decides to smoke marijuana, he or she has reasons to do so. Those reasons may be depression, anxiety, withdrawal, loneliness, or many other problems. No matter the reason, in the therapeutic room of a skilled psychologist, those problems can be addressed, diminished, and/or possibly resolved.

AD AND THE N-648

The N-648 is a form that is used by medical doctors and psychologists to help immigrants obtain United States citizenship without passing the English proficiency and United States history exams. We believe that this form cannot be completed without normative data concerning the patient's memory. It is the neuropsychological testing that can actually determine whether an individual with probable or possible AD is capable of learning English and United States history, which are required to become a United States citizen.

CONCLUSION

Neuropsychological testing is underutilized and it is our hope that its use will be prevalent and treated as a necessity especially in patients with AD. Time spent on neuropsychological testing can change the patient's life tremendously. For instance, a depressed patient that actually has dementia after a neuropsychological assessment will not be prescribed anti-depressants. Conversely, a patient with dementia will be prescribed cognitive enhancers rather than anti-depressants. As mentioned above, testing may last from an hour to several hours, but the knowledge after it is completed is priceless and appreciated by the families we have served thus far. The neuropsychological testing not only helps the patient but also their families. We have spent countless hours working with our patients' families to not only help them with appropriate care, but also with the fact that they may be facing similar future presenting concerns. Those family members that worked with us had a tremendous advantage over their parents, as their anticipation and the possibility to carry similar genetic load allowed them to plan for the future and to initiate anything they can to avoid and/or delay AD. The neuropsychological reports written in our clinic are not only for the patients and their doctors, but also caregivers who can better understand the level of

impairment, as well as learn skills to be a better support system. In other words, a few hours of neuropsychological testing is worthwhile for everyone that is involved with the AD patient.

Conflict of interest: The authors declare no potential conflicts of interest with respect to research, authorship, and/or publication of this chapter.

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