The ABC transporter YejABEF is required for resistance to antimicrobial peptides and the virulence of *Brucella melitensis*

Zhen Wang[1], Pengfei Bie[2], Jie Cheng[1], Lin Lu[1], Buyun Cui[3], Qingmin Wu[2]*

[1]*Beijing Key Laboratory of Traditional Chinese Veterinary Medicine, Animal Science and Technology College, Beijing University of Agriculture, Beijing 102206, China*

[2]*Key Laboratory of Animal Epidemiology and Zoonosis of the Ministry of Agriculture, College of Veterinary Medicine, China Agricultural University, Beijing 100193, China*

[3]*State Key Laboratory for Infectious Disease Prevention and Control, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing102206, China*

*Corresponding authors. Tel.: +86-10- 6273-3901

E-mail address: wuqm@cau.edu.cn(Q.M. Wu)

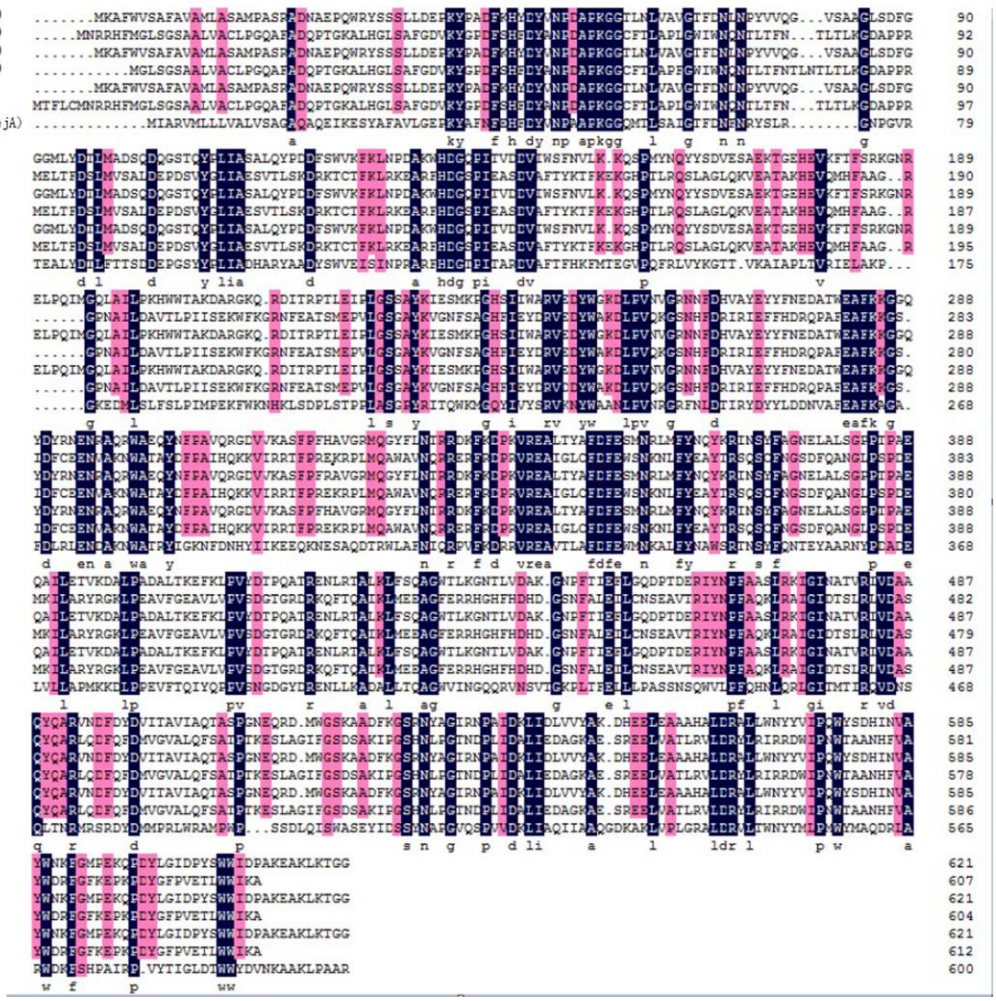
Supplemental Materials

Supplemental Table S1 Primers used in this study.

Primer Name	Sequence (restriction enzyme used)（5'-3'）	Locus (gene)
Primers used for RT-PCR		
pWU 855F	TACCAGCCCTTGACATCC	16S rRNA
pWU 856R	TCATCCCCACCTTCCTCT	
RT-061	AGAAGGCGAAACCGTAGC	BMNI_I0006
RT-062	GTGAAGCGGATTGAGCGAT	
RT-071	GTTACTGGTCGCTGTGGATT	BMNI_I0007
RT-072	TCGTTATTGACGGTGTTGT	
RT-081	ATTCCACTCGGCATTCG	BMNI_I0008
RT-082	GAAATCGGGCGAGGTG	
RT-091	CGGTGCTTACAAGGTCG	BMNI_I0009
RT-092	CGATGCTGCCTTTCTTG	
RT-101	GTGGCGGGATGCTTTA	BMNI_I0010
RT-102	GCACATTGAACGACCAGA	
Primers used for gene deletion		
WD0285	AACTGCAGCCCCGCCGTGATAGGTCTT	BMNI_I0006
WD0286	GCGGATCGGCGATACGAAGGGAAATA	
WD0287	CGATCCGCTACTCATTG	
WD0288	CG GGATCC TGGTCGTCAATCCCAG	
WD0289	AACTGCAG AGCAGTTTGGGCTTGTTG	BMNI_I0007
WD0290	GACGTGTGATGGGTCAATGAGTAGC	
WD0291	CACACGTCCCTCCGGTC	
WD0292	CG GGATCC GGCGGTTCCTTCTTTGAC	
WD0297	AACTGCAG AATGCGGAAGCCATAGAG	BMNI_I0008
WD0298	TCCAGCTGTGACCGACACCGCACTC	
WD0299	CAGCTGGACCTTATCCG	
WD0300	CG GGATCC TGCGAGCCAGTATCAG	
WD0293	AACTGCAG CTTGCGAATGCCGAGTG	BMNI_I0009
WD0294	TCCTTTGCTTACCGGAAAGTGGCGA	
WD0295	GCAAAGGAATGTCATTC	
WD0296	CG GGATCC GGCAATCCGTTCACCA	
WD0301	AACTGCAG GGCAGACGATTACAAAG	BMNI_I0010
WD0302	TTCAGGCCCCAGTTTCTCCACGTTTTG	
WD0303	GGCCTGAACGAGAATG	
WD0304	CG GGATCC AGGTGAATGCCACATCG	

WD0097	GGGGTACC GCGATACGAAGGGAA	BMNI_I0006-10
WD0098	CGAAGGTGCCGCCGTGATAGGTCTT	
WD0099	CACCTTCGGTTTTGCTCCTG	
WD0100	CG GGATCC GGGATCGAACCTGAAGAC	
Primers used for gene complementation		
C0007-1	CGGGATCCATGACCGACACCGCACTC	BMNI_I0007
C0007-2	AACTGCAGTCATAAAAATGCCTTTCGC	
C0007-P1	TCCCCCGGGCTTTACGGCTGGAATTTTC	BMNI_I0007 promoter
C0007-P2	CGGGATCCTCTCCACGTTTTGTTCCAG	

A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BMNI_I0009
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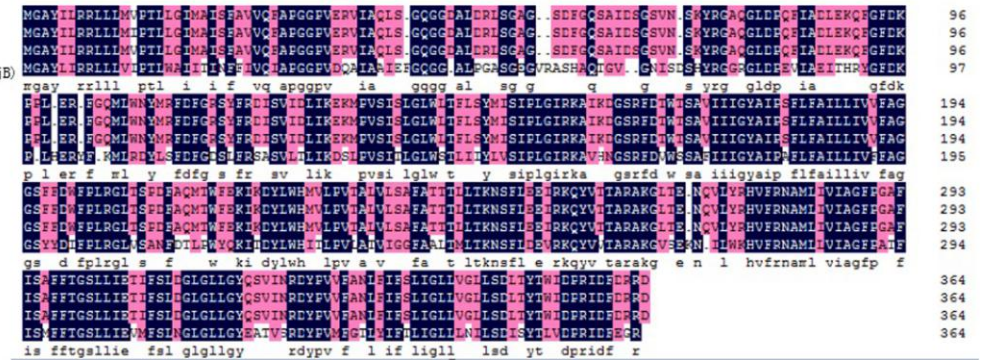
BABI_I0009
BMEI1934
BMEI1935
STM2216 (YejA)

B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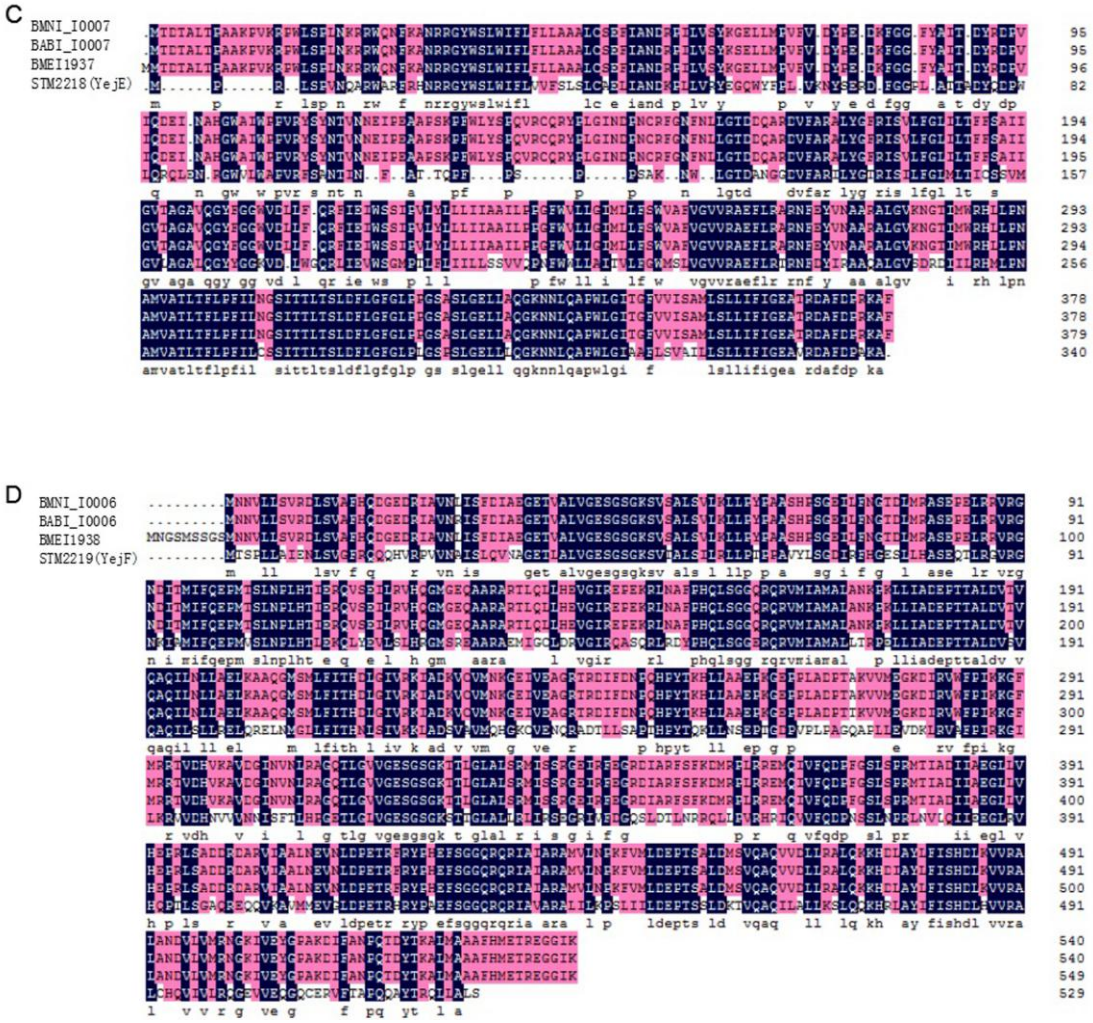

Figure S1 Alignment of the amino acid sequences of Yej proteins of *Brucella* with them in *S. Typhimurium* LT2. (A) YejA, (B) YejB, (C) YejE, (D) YejF. Shadows of navy and pink indicated the amino acid sequence identities are 100％and 75%, respectively.The accession numbers of the *yej* operon genes in *B.melitensis* NI are, *yejA1*:GI:384444099, *yejA2*:GI:384444098, *yejB*:GI:384444097, *yejE*:GI:384444096, and *yejF*:GI:384444095, respectively; in *B.melitensis* 16M are, *yejA1*:GI:17988217, *yejA2*:GI:17988218, *yejB*:GI:17988219, *yejE*:GI:17988220, and *yejF*:GI:17988221, respectively; in *B. abortus* 2308 are, *yejA1*:GI:82698942, *yejA2*:GI:82698941, y*ejB*:GI:82698940, *yejE*:GI:82698939, and *yejF*:GI:82698938, respectively; the accession numbers of the *yej* operon genes in *S. Typhimurium* LT2 are, *yejA*:GI:16765545, *yejB*:GI:16765546, *yejE*:GI:16765547, *yejF*:GI:16765548,respectively.