

Supplementary

***Mycoplasma genitalium* protein of adhesion promotes the early proliferation of human urothelial cells by interacting with RPL35**

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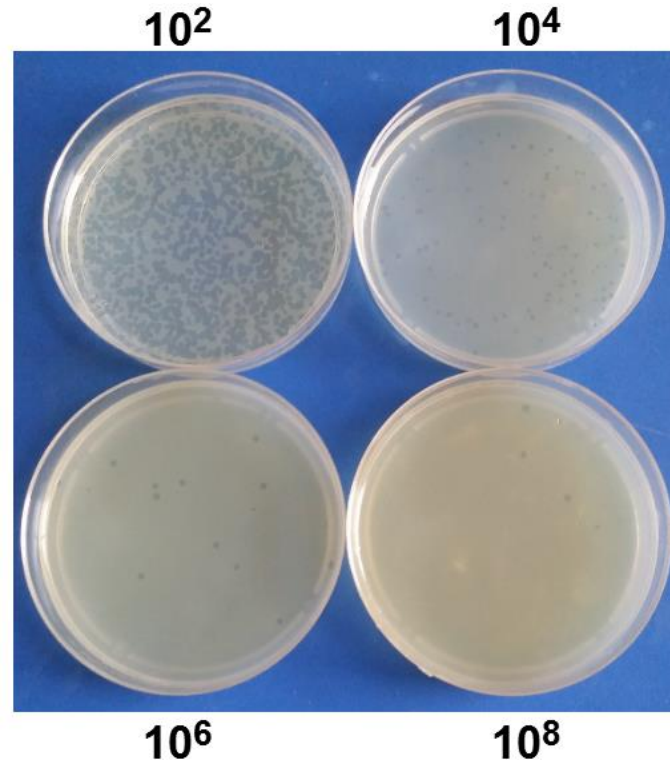
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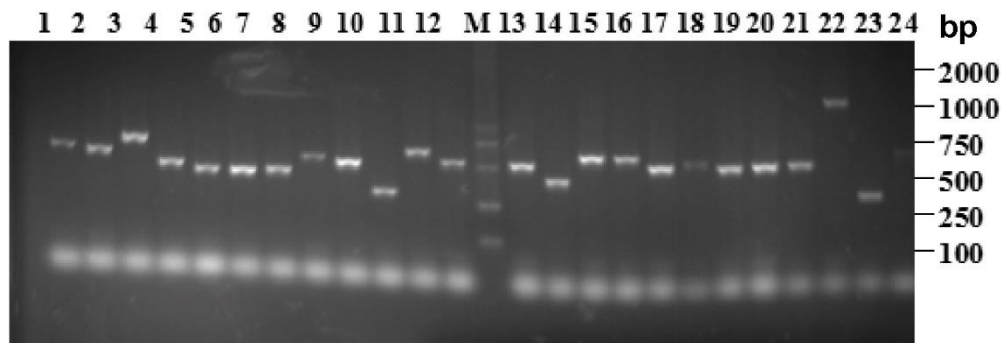
Yanhua Zeng: Institute of Pathogenic Biology, Hengyang Medical College, University of South China; Hunan Provincial Key Laboratory for Special Pathogens Prevention and Control; Hunan Province Cooperative Innovation Center for Molecular Target New Drug Study, Hengyang 421001, P.R.China.

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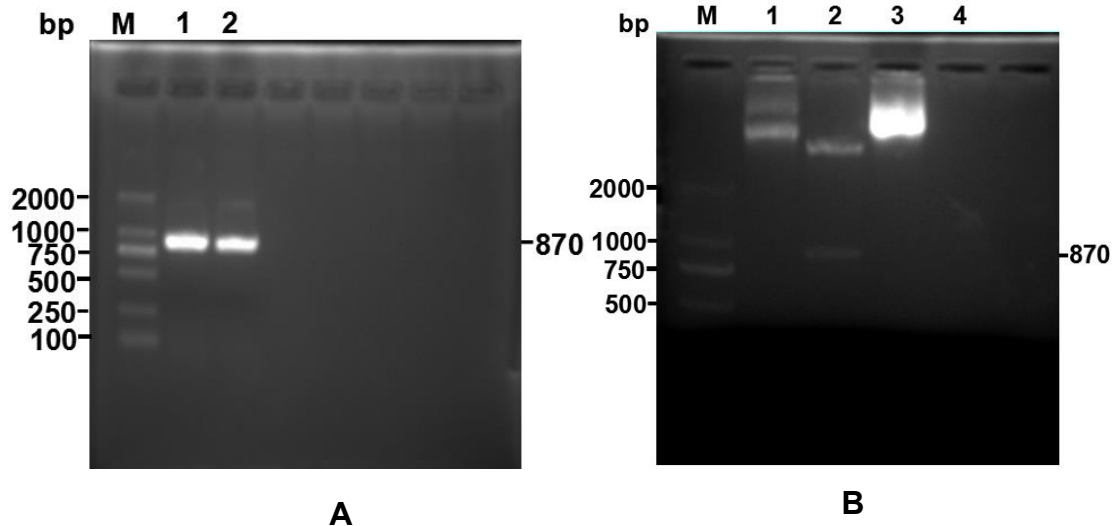
Running title: The interaction between the *Mycoplasma genitalium* protein of adhesion and RPL35.



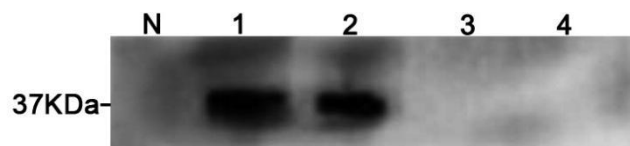
Supplementary Figure S1. The detection of titer for SV-HUC-1 T7 phage display cDNA library. The SV-HUC-1 T7 phage display cDNA library constructed by our research group was amplified in the host strain BLT5403. The phage library was diluted into different multiples and cultured overnight in 37°C. incubator in LB-SRB medium containing Carbenicillin. The calculated titer is 3×10^8 pfu. The result is shown in figure 1. Lanes: The 10^2 , 10^4 , 10^6 and 10^8 represents different phage dilution times.



Supplementary Figure S2. Agarose gel electrophoresis analysis of PCR products of the displayed phages. After four rounds of panning, the final enriched specific clones were plated and single pure plaque was isolated. The cDNA inserts in these plaques were amplified by PCR using primers and 50 clones were randomly picked and out of which 32 clones got clear amplified products and Agarose gel electrophoresis analysis of PCR products for partial phages as figure 2 showed. Note: M, DNA marker; Lane1~24, Number of different phage plaques.



Supplementary Figure S3. Construction of pcDNA3.1(+)/rMgPa. Mycoplasma TGA codons were substituted with TGG (3223~4092aa). *XhoI* and *EcoRI* restriction enzymes were purchased from ThermoFisher Scientific). According to the primer design guidelines (Sangon Biotech Co, Ltd, Shanghai, China). (A) Agarose gel electrophoresis analysis of PCR products of MgPa. Note: M, DNA marker; Lane1-2, PCR product of MgPa. (B) The recombinant plasmid was verified by double-enzyme cleavage. Note: M, DNA marker; Lane1, pcDNA3.1(+)/rMgPa Products; 2, pcDNA3.1 (+) /rMgPa was digested with *EcoRI* and *XhoI*; 3, pcDNA3.1 (+) null plasmid.



Supplementary Figure S4. Expression of the rMgPa proteins as detected by western blotting. The western blotting results revealed that rMgPa was detected in SV-HUC-1 cells transfected with pcDNA3.1(+)/rMgPa. By contrast, no rMgPa expression was observed in control groups. Note: N, Normal; Lane1and Lane2 transfection of SV-HUC-1cells with pcDNA3.1(+)/rMgPa. lane3, pcDNA3.1(+); Lane4, lip2000 (invitrogen). There was a distinct band observed at approximately 37kDa such as 1 and 2, whereas no band was observed for the control group as N, 3 and 4.

Homo sapiens ribosomal protein L35, mRNA (cDNA clone MGC:88597 IMAGE:4896387), complete cds

Sequence ID: [BC071915.1](#) Length: 457 Number of Matches: 1

Range 1: 1 to 445 [GenBank](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
817 bits(442)	0.0	444/445(99%)	0/445(0%)	Plus/Plus
Query 36	GCGGCTTGTGCAGCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAG	95		
Sbjct 1	GCGGCTTGTGCAGCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAG	60		
Query 96	GAGCTGCTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCAGCTGCGCGTGGCCAAA	155		
Sbjct 61	GAGCTGCTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCAGCTGCGCGTGGCCAAA	120		
Query 156	GTGACAGGCGGTGCGGCTCCAAGCTCTCTAAGATCCGAGTCGTCCGGAATCCATTGCC	215		
Sbjct 121	GTGACAGGCGGTGCGGCTCCAAGCTCTCTAAGATCCGAGTCGTCCGGAATCCATTGCC	180		
Query 216	CGTGTTCACAGTTATTAACAGACTCAGAAAGAAAACCTCAGGAAATTCTACAAGGGC	275		
Sbjct 181	CGTGTTCACAGTTATTAACAGACTCAGAAAGAAAACCTCAGGAAATTCTACAAGGGC	240		
Query 276	AAGAAGTACAAGCCCTGGACCTGCGGCTAAGAAGACACGTGCCATGCGCGCGCGGCTC	335		
Sbjct 241	AAGAAGTACAAGCCCTGGACCTGCGGCTAAGAAGACACGTGCCATGCGCGCGCGGCTC	300		
Query 336	AACAAGCAGCAGGAGAACCTGAAGACCAAGAAGCAGCAGCGGAAGGAGCGGCTGTACCG	395		
Sbjct 301	AACAAGCAGCAGGAGAACCTGAAGACCAAGAAGCAGCAGCGGAAGGAGCGGCTGTACCG	360		
Query 396	CTGCGGAAGTACGCGGTCAAGGCTGAGGGCGCATTGTCAATAAAGCACAGCTGGCTGA	455		
Sbjct 361	CTGCGGAAGTACGCGGTCAAGGCTGAGGGCGCATTGTCAATAAAGCACAGCTGGCTGA	420		
Query 456	CGAAAAAAAAAAAAAAAAAAAAA	480		
Sbjct 421	CAAAAAAAAAAAAAAAAAAAAAA	445		

Sequence ID: Query_44843 Length: 996 Number of Matches: 1

Range 1: 49 to 408 [Graphics](#)

[BC094828.1](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
593 bits(321)	7e-174	347/360(96%)	0/360(0%)	Plus/Plus
Query 1	GCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAGAGCTGCTGAAA	60		
Sbjct 49	GCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAGAGCTGCTGAAA	108		
Query 61	CAGCTGGACGACCTGAAGGTGGAGCTGTCCAGCTGCGCGTCGCCAAAGTGACAGGCGGT	120		
Sbjct 109	CAGCTGGACGACCTGAAGGTGGAGCTGTCCAGCTGCGCGTCGCCAAAGTGACAGGCGGT	168		
Query 121	GCGGCTCCAAGCTCTCTAAGATCCGAGTCGTCCGGAATCCATTGCCCCGTGTTCTACA	180		
Sbjct 169	GCGGCTCCAAGCTCTCTAAGATCCGAGTCGTCCGGAATCCATTGCCCCGTGTTCTACA	228		
Query 181	GTTATTAACCAAGTCAAGGAAACCTCAGGAAATTCTACAAGGCAAGAGTACAAG	240		
Sbjct 229	GTTATTAACCAAGTCAAGGAAACCTCAGGAAATTCTACAAGGCAAGAGTACAAG	288		
Query 241	CCCCGACCTGCGGCTAAGAAACACACGTGCCATGCGCGCGCTCAACAAGCACGAG	300		
Sbjct 289	CCCCGACCTGCGGCTAAGAAACACACGTGCCATGCGCGCGCTCAACAAGCACGAG	348		
Query 301	GACAACTGAAGACCAAGAAGCAGGACCGGAAGGACGGGTGTACCGCTGCGGAACTAC	360		
Sbjct 349	GACAACTGAAGACCAAGAAGCAGGACCGGAAGGACGGGTGTACCGCTGCGGAACTAC	408		

Sequence ID: **Query_47811** Length: **996** Number of Matches: **1**

Range 1: 23 to 408 [Graphics](#)

BC000348.2

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
636 bits(344)	0.0	372/386(96%)	0/386(0%)	Plus/Plus
Query 5	GGGCGCGCGCGTTGGCGGCTTGTGCAGCAATGGCCAAGATCAAGGCTCGAGATCTTCGCG	64		
Shjct 23	GGGCGCGCGCGTTGGCGGCTTGTGCAGCAATGGCCAAGATCAAGGCTCGAGATCTTCGCG	82		
Query 65	GGAAGAAGAAGGAGGAGCTGCTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGC	124		
Shjct 83	GGAAGAAGAAGGAGGAGCTGCTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGC	142		
Query 125	TGCGCGTCGCCAAAAGTGACAGGCGGTGCGGCCTCCAAGCTCTCTAAGATCCGAGTCGTCC	184		
Shjct 143	TGCGCGTCGCCAAAAGTGACAGGCGGTGCGGCCTCCAAGCTCTCTAAGATCCGAGTCGTCC	202		
Query 185	GGAATCCATTGCCCGTGTCTCACAGTTATTAACCAGACTCAGAAAAGAAAACCTCAGGA	244		
Shjct 203	GGAATCCATTGCCCGTGTCTCACAGTTATTAACCAGACTCAGAAAAGAAAACCTCAGGA	262		
Query 245	AATTCTACAAGGGCAAGAAGTACAAGCCCTGGACCTGCGGCCTAAGAAACACACGTGCCA	304		
Shjct 263	AATTCTACAAGGGCAAGAAGTACAAGCCCTGGACCTGCGGCCTAAGAAACACACGTGCCA	322		
Query 305	TGCGCGCGCGCTCAACAAGCACGAGGAGAACCTGAAGACCAAGAAGCAGCAACCGGAAGG	364		
Shjct 323	TGCGCGCGCGCTCAACAAGCACGAGGAGAACCTGAAGACCAAGAAGCAGCAACCGGAAGG	382		
Query 365	AGCGGCTGTACCCGCTGCGGAAGTAC	390		
Shjct 383	ATCGGATGTACCCGCTGCGGAAGTAC	408		

Supplementary Figure S5. Blast mapping of BC071915.1, BC094828.1 and BC000348.2 of RPL35 subunits with exogenous sequences.