

Supplementary

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

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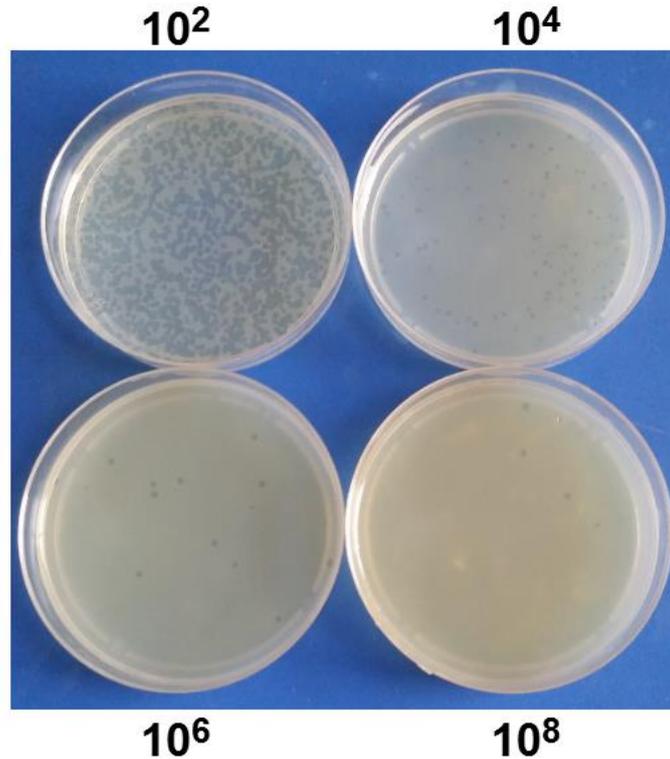
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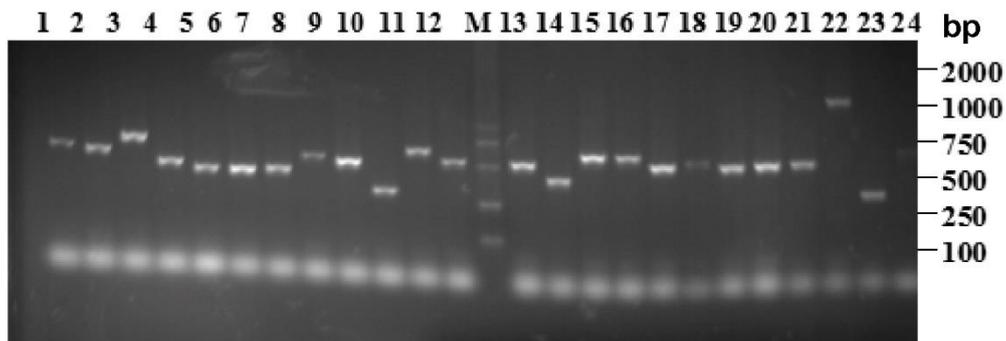
Yanhua Zeng: Institute of Pathogenic Biology, Hengyang Medical College, University of South China; Hunan Provincial Key Laboratory for Special Pathogens Prevention and Control; Hunan Province Cooperative Innovation Center for Molecular Target New Drug Study, Hengyang 421001, P.R.China.

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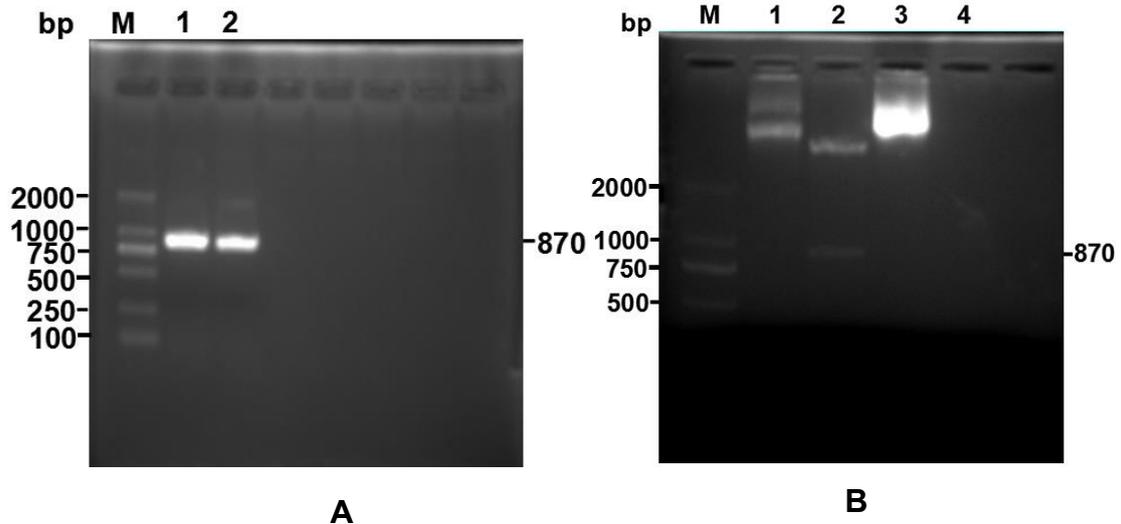
Running title: The interaction between the *Mycoplasma genitalium* protein of adhesion and RPL35.



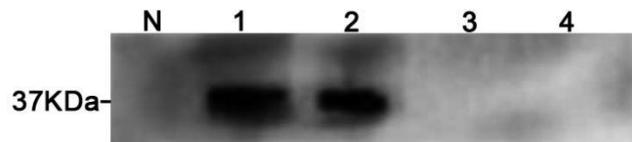
Supplementary Figure S1. The detection of titer for SV-HUC-1 T7 phage display cDNA library. The SV-HUC-1 T7 phage display cDNA library constructed by our research group was amplified in the host strain BLT5403. The phage library was diluted into different multiples and cultured overnight in 37°C. incubator 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; Lane 1~24, 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; Lane1 and Lane2 transfected of SV-HUC-1 cells 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	CGCGCTTGTGCAGCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAG	95		
Sbjct 1	CGCGCTTGTGCAGCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAG	60		
Query 96	GAGCTGCTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGCTGCGCGTGCOCAAA	155		
Sbjct 61	GAGCTGCTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGCTGCGCGTGCOCAAA	120		
Query 156	GTGACAGGCGGTGCGGCCTCCAAGCTCTCTAAGATCCGAGTCTGTCGGGAAATCCATTGCC	215		
Sbjct 121	GTGACAGGCGGTGCGGCCTCCAAGCTCTCTAAGATCCGAGTCTGTCGGGAAATCCATTGCC	180		
Query 216	CGTGTTCACAGTTATTAACCAGACTCAGAAAGAAAACCTCAGGAAATCTACAAGGGC	275		
Sbjct 181	CGTGTTCACAGTTATTAACCAGACTCAGAAAGAAAACCTCAGGAAATCTACAAGGGC	240		
Query 276	AAGAAGTACAAGCCCTGGACCTGCGGCCTAAGAAGACACGTGCCATGCGCGCGCGGCTC	335		
Sbjct 241	AAGAAGTACAAGCCCTGGACCTGCGGCCTAAGAAGACACGTGCCATGCGCGCGCGGCTC	300		
Query 336	AACAAGCACGAGGAGAACCTGAAGACCAAGAAGCAGCAGCGGAAGGAGCGGCTGTACCCG	395		
Sbjct 301	AACAAGCACGAGGAGAACCTGAAGACCAAGAAGCAGCAGCGGAAGGAGCGGCTGTACCCG	360		
Query 396	CTGCGGAAGTACGCGGTCAAGGCTGAGGGGCGATTGTCAATAAAGCACAGCTGGCTGA	455		
Sbjct 361	CTGCGGAAGTACGCGGTCAAGGCTGAGGGGCGATTGTCAATAAAGCACAGCTGGCTGA	420		
Query 456	CGAAAAAAAAAAAAAAAAAAAAAAAAA 480			
Sbjct 421	CAAAAAAAAAAAAAAAAAAAAAAAAAA 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	GCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAGGAGCTGCTGAAA	60		
Sbjct 49	GCAATGGCCAAGATCAAGGCTCGAGATCTTCGCGGGAAGAAGAAGGAGGAGCTGCTGAAA	108		
Query 61	CAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGCTGCGCGTGCOCAAAAGTGACAGCGGT	120		
Sbjct 109	CAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGCTGCGCGTGCOCAAAAGTGACAGCGGT	168		
Query 121	GCGGCCTCCAAGCTCTCTAAGATCCGAGTCTGTCGGGAAATCCATTGCCCGTGTCTCACA	180		
Sbjct 169	GCGGCCTCCAAGCTCTCTAAGATCCGAGTCTGTCGGGAAATCCATTGCCCGTGTCTCACA	228		
Query 181	GTTATTAACCAGACTCTAAGAAAACCTCAGGAAATCTACAAGGCAAGAAGTACAAG	240		
Sbjct 229	GTTATTAACCAGACTCTAAGAAAACCTCAGGAAATCTACAAGGCAAGAAGTACAAG	288		
Query 241	CCCCTGGACCTGCGGCCTAAGAAAACACAGTGCATGCGCGCGCTCAACAAGCACGAG	300		
Sbjct 289	CCCCTGGACCTGCGGCCTAAGAAAACACAGTGCATGCGCGCGCTCAACAAGCACGAG	348		
Query 301	GAAACCTGAAGACCAAGAAGCAGGACCGGAAGGACGGGTGTACCCGCTGCGGAACTAC	360		
Sbjct 349	GAAACCTGAAGACCAAGAAGCAGGACCGGAAGGACGGGTGTACCCGCTGCGGAACTAC	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
Sbjct 23	GGGCGCGCGCGTTGGCGGCTTGTGCAGCAATGGCCAAGATCAAGGCTCGAGATCTTCGCG			82
Query 65	GGAAGAAGAAGGAGGAGCTGTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGC			124
Sbjct 83	GGAAGAAGAAGGAGGAGCTGTGAAACAGCTGGACGACCTGAAGGTGGAGCTGTCCCAGC			142
Query 125	TGCGCGTCGCCAAAAGTGACAGGCGGTGCGGCTCCAAGCTCTCTAAGATCCGAGTCGTCC			184
Sbjct 143	TGCGCGTCGCCAAAAGTGACAGGCGGTGCGGCTCCAAGCTCTCTAAGATCCGAGTCGTCC			202
Query 185	GGAATCCATTGCCCGTGTTCACAGTTATTAACCAGACTCAGAAAAGAAAACCTCAGGA			244
Sbjct 203	GGAATCCATTGCCCGTGTTCACAGTTATTAACCAGACTCAGAAAAGAAAACCTCAGGA			262
Query 245	AATTCTACAAGGGCAAGAAGTACAAGCCCTGGACCTGCGGCTAAGAAACACACGTGCCA			304
Sbjct 263	AATTCTACAAGGGCAAGAAGTACAAGCCCTGGACCTGCGGCTAAGAAACACACGTGCCA			322
Query 305	TGCGCGCGCGCTCAACAAGCAGGAGAAACCTGAAGACCAAGAAGCAGCAACCGGAAGG			364
Sbjct 323	TGCGCGCGCGCTCAACAAGCAGGAGAAACCTGAAGACCAAGAAGCAGCAACCGGAAGG			382
Query 365	AGCGGCTGTACCCGCTGCGGAAAGTAC 390			
Sbjct 383	ATCGGATGTACCCGCTGCGGAAAGTAC 408			

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