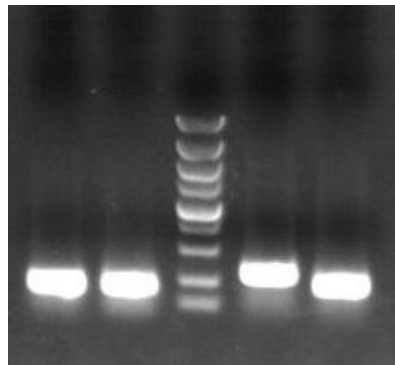


fabI 基因及 pmxA 基因 5'race 实验进展报告

合同编号: PG1-1601001

1. 根据 fabI 基因及 pmxA 基因序列, 我们分别设计两对引物, 依据引物进行 RT-PCR,
2. 以提取的 RNA 逆转录后的 cDNA 为模板, 进行 RT-PCR, 电泳检测结果如下:

FabI-1 fabI-2 M pmxA-1 pmxA-2



3. 并将测序结果进行比对, 比对结果如下:

Paenibacillus polymyxa SQR-21, complete genome
Sequence ID: [gb|CP006872.1](#) Length: 5828436 Number of Matches: 1

Range 1: 81030 to 81202 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
283 bits(153)	7e-73	169/176(96%)	4/176(2%)	Plus/Plus
Query 16	GGCTGCGTCCCTCT-CGTACTTTTGGCCGCCTTCTGGCATTCAAGATTTTAACACAATGCT	74		
Sbjct 81030	GGCTG-GTCCTATACGTAC-TTTGGCCGCC-TATGGCATTAAAGATTTTAACACAATGCT	81086		
Query 75	AAAGCATATTGAAGAACTACGCCCTACGCAAGACGGTCGATACGCTGAAGTCGGAGA	134		
Sbjct 81087	AAAGCATATTGAAGAACTACGCCCTACGCAAGACGGTCGATACGCTGAAGTCGGAGA	81146		
Query 135	TACGGCGTTATTCCTATTTTCCCATTTATCGAGAGGCATTACGGGTGAAGTTATCC	190		
Sbjct 81147	TACGGCGTTATTCCTATTTTCCCATTTATCGAGAGGCATTACGGGTGAAGTTATCC	81202		

Paenibacillus polymyxa SQR-21, complete genome
Sequence ID: [gb|CP006872.1](#) Length: 5828436 Number of Matches: 1

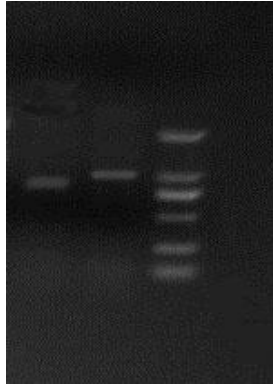
Range 1: 5061826 to 5062012 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
335 bits(181)	2e-88	186/188(99%)	2/188(1%)	Plus/Plus
Query 14	GGA-GCGCTGCGCCACTTTCTCCGAAAGCGTTCCACCGACGGTTGTCATAATGGGCGTC	72		
Sbjct 5061826	GGACGCGCTGCGCCAC-TTCTCCGAAAGCGTTCCACCGACGGTTGTCATAATGGGCGTC	5061884		
Query 73	AGGGAGCTTGGAGCTTTGCTGTAAGGTAGCCGCGTCAAGGTATAATCGTCGCTACCGAAT	132		
Sbjct 5061885	AGGGAGCTTGGAGCTTTGCTGTAAGGTAGCCGCGTCAAGGTATAATCGTCGCTACCGAAT	5061944		
Query 133	TTTTCGTCCAAAACGTTTCTTTTCAAAAGCCATCTGGATCGTTCCCTCTCTTCA	192		
Sbjct 5061945	TTTTCGTCCAAAACGTTTCTTTTCAAAAGCCATCTGGATCGTTCCCTCTCTTCA	5062004		
Query 193	TCGGTAAA	200		
Sbjct 5062005	TCGGTAAA	5062012		

4. 比对结果正确, 根据 RACE 试剂盒进行两个基因 5'端的 PCR 扩增, 扩增结果如下:

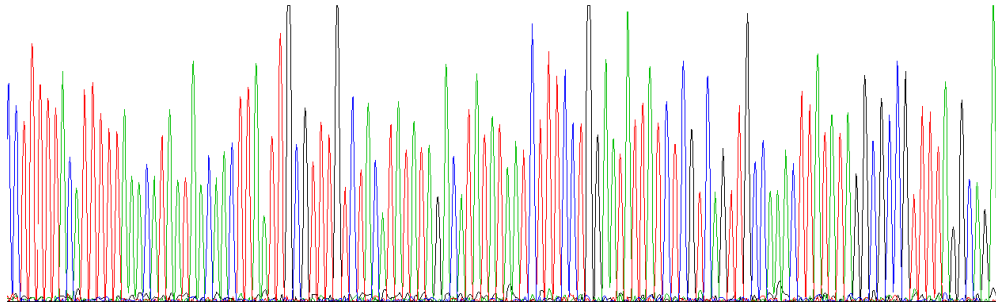
fabl pmxA M



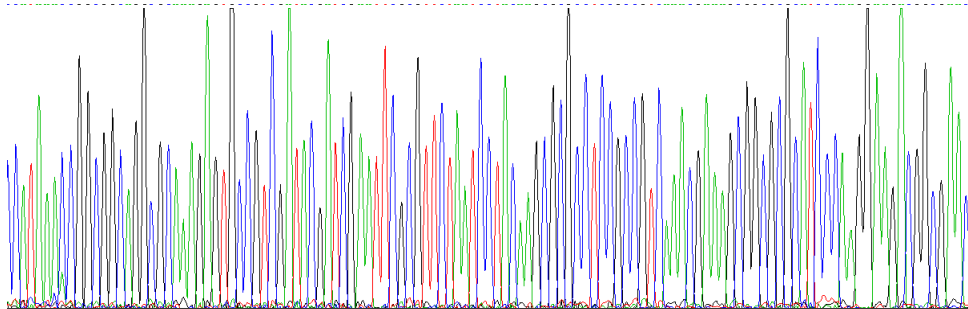
注：Marker 大小采用 DL2000，从上到下大小依次为：2000、1000、750、500、250、100bp

- 根据 RACE 扩增结果，凝胶电泳检测结果可以看到扩增出条带大小在 1K 左右的片段，将片段进行切胶回收送测序，测序峰图结果如下：

Fabl:



PmxA:



- 根据测序结果在 NCBI 上进行比对，比对结果如下：

Fabl:

Score	Expect	Identities	Gaps	Strand
1203 bits(651)	0.0	666/673(99%)	1/673(0%)	Plus/Minus
Query 8	CAGTGCATCTATTTCTTCATCGCTCTGTACATTGCAAGGACAGACAATGGAACCCGGAAT	67		
Sbjct 80691	CAGTGCATCCAATTCTTCATCGCTCTGTACATTGCAAGGACAGACAATGGAACCCGGAAT	60632		
Query 68	GGTTTCAGCGAGCTTTAGCACCCGTTCTGCAACCCCTCTCATTTTCGTAAGTAAAAATGAG	127		
Sbjct 80631	GGTTTCAGCGAGCTTTAGCACCCGTTCTGCAACCCCTCTCATTTTCGTAAGTAAAAATGAG	80572		
Query 128	ATTTGCTCCTTCGCGAGCTAAAGATTGGGCTGTCCCCAGGCAATACCTCTGTTATTAGC	187		
Sbjct 80571	ATTTGCTCCTTCGCGAGCTAAAGATTGGGCTGTCCCCAGGCAATACCTCTGTTATTAGC	80512		
Query 188	CACACCCATAATCAAAATGTTCTTTCCACTCAGTAGTACTGCCACAGAAACACCTTTCC	247		
Sbjct 80511	CACACCCATAATCAAAATGTTCTTTCCACTCAGTAGTACTGCCACAGAAACACCTTTCC	80452		
Query 248	TTTTTACATTTTAAACATAAATACCACTTAATTCGCTTTGCTACATATATAGACATAT	307		
Sbjct 80451	TTTTTACATTTTAAACATAAATACCACTTAATTCGCTTTGCTACATATATAGACATAT	80392		
Query 308	ATAATCTTTTCTGGAATATTATCTCGTCAGTTGCCAACTTATATAGCGCCGTTTATAG	367		
Sbjct 80391	ATAATCTTTTCTGGAATATTATCTCGTCAGTTGCCAACTTATATAGCGCCGTTTATAG	80332		
Query 368	CAGATGGCAGAAATATTTTAAAAATGTGAATGTGGTTCTGTTGATCTGTGTTCAATC	427		
Sbjct 80331	CAGATGGCAGAAATATTTTAAAAATGTGAATGTGGTTCTGTTGATCTGTGTTCAATC	80272		
Query 428	GAAAGGAGTCCATGCTGTGAAAAAAGTGGTGAGGCAACGATAAGATGACTGTCAAGCG	487		
Sbjct 80271	GAAAGGAGTCCATGCTGTGAAAAAAGTGGTGAGGCAACGATAAGATGACTGTCAAGCG	80212		
Query 488	ATTTTAATATAAAAAATATCATACTCTTATAAAATATTTCCATTATGACGATAGACTATCC	547		
Sbjct 80211	ATTTTAATATAAAAAATATCATACTCTTATAAAATATTTCCATTATGACGATAGACTATCC	80152		
Query 548	CACATTCGAAAGTAACCACTTCATTTACCGCTCAATGACTCTCCCGATTGGAACATCCTG	607		
Sbjct 80151	CACATTCGAAAGTAACCACTTCATTTACCGCTCAATGACTCTCCCGATTGGAACATCCTG	80092		
Query 608	ATTCGTTTCAAGCTTGAGGCTCTCTTCCCTTGGCTAAGCCTTATGTTTATGTTAGGTAG	667		
Sbjct 80091	ATTCGTTTCAAGCTTGAGGCTCTCTTCCCTTGGCTAAGCCTTATGTTTATGTTTATAG	80032		



PmxA:

Score	Expect	Identities	Gaps	Strand
1291 bits(699)	0.0	702/703(99%)	1/703(0%)	Plus/Minus
Query 14	GGATTATCCATTTCGAGGAGCTCGTGGAGCGTTTGAATGTGAAGCGGAGCGCGGCGGT			73
Sbjct 5047457	GGATTATCCA-TTCGAGGAGCTCGTGGAGCGTTTGAATGTGAAGCGGAGCGCGGCGGT			5047429
Query 74	TCCCGCTGTTCCGATGCCGTTTTTCGACTTGC AAAATATCGAAGAACGAGACGCCGAGCTGG			133
Sbjct 5047428	TCCCGCTGTTCCGATGCCGTTTTTCGACTTGC AAAATATCGAAGAACGAGACGCCGAGCTGG			5047369
Query 134	AAAGGGCTACGCTGAGACCTTACGAGCTTGACGATTTAGAGAGAACGAGCTTCGATCTGA			193
Sbjct 5047368	AAAGGGCTACGCTGAGACCTTACGAGCTTGACGATTTAGAGAGAACGAGCTTCGATCTGA			5047309
Query 194	CACGTGTTTATGTATGAAAACAACGGGGCGCTGAGTGGGGGCTTCTCTACGCCACCAAGC			253
Sbjct 5047308	CACGTGTTTATGTATGAAAACAACGGGGCGCTGAGTGGGGGCTTCTCTACGCCACCAAGC			5047249
Query 254	TGTTCAAAAGAGCGATGATCCGCGAGCTTGACCGAGGATTACGTGGCGGTACTGTGTGAAA			313
Sbjct 5047248	TGTTCAAAAGAGCGATGATCCGCGAGCTTGACCGAGGATTACGTGGCGGTACTGTGTGAAA			5047189
Query 314	TTCCGGAAAAATCCACAACTCGAGCTAAAGCCGGATTGAAATGCGATAAACCGCGCGAGCGC			373
Sbjct 5047188	TTCCGGAAAAATCCACAACTCGAGCTAAAGCCGGATTGAAATGCGATAAACCGCGCGAGCGC			5047129
Query 374	CAAGAGTGGCGCTCGATACGATCGAATTCGGTTCTAATGCTACAAAGCGCGCTCGCGCG			433
Sbjct 5047128	CAAGAGTGGCGCTCGATACGATCGAATTCGGTTCTAATGCTACAAAGCGCGCTCGCGCG			5047069
Query 434	TCAAAAGCAAAAGCGCGCGGATCCCAAGGAAGACGGCGAAGAACGTCCAAGCGCGTAAAGC			493
Sbjct 5047068	TCAAAAGCAAAAGCGCGCGGATCCCAAGGAAGACGGCGAAGAACGTCCAAGCGCGTAAAGC			5047009
Query 494	CGCAGGCGCAAAAGCAAGCTTTTTTCGACCTGCGCGCGGGGATGCGGTGACTTTCATTTTA			553
Sbjct 5047008	CGCAGGCGCAAAAGCAAGCTTTTTTCGACCTGCGCGCGGGGATGCGGTGACTTTCATTTTA			5046949
Query 554	GGGAGGTAAGAAATGAAATCTTTTTTTTAAAAAGAAAGATGTAATCGAGGCGCAATTTT			613
Sbjct 5046948	GGGAGGTAAGAAATGAAATCTTTTTTTTAAAAAGAAAGATGTAATCGAGGCGCAATTTT			5046889
Query 614	GACGCGGATGACAGCGCTGAGGTTTCCCTACAGTCAATGCTCCAAATTTTCGCGCGAC			673
Sbjct 5046888	GACGCGGATGACAGCGCTGAGGTTTCCCTACAGTCAATGCTCCAAATTTTCGCGCGAC			5046829

7. 下一步进行克隆测序，等待克隆测序结果。