

Table S1 The sequencing results of selected *V. parahaemolyticus* isolates and NCBI blast similarity

Isolate name	Targeted Gene	Consensus Sequence	Sequence Length	Blast Similarity Results	
				Hit Strain	Similarity Percentage
FVP26	<i>toxR</i>	ACGCAATCGTTGAACCAGAAGCGCCAGTAGTACCT GAAAAAGCACCTGTGGCTTCTGCTGTGAATCCTTG GATTCCACGCGTTATTTTATTTTGGCACTATTACTA CCGATTTGCGTACTGCTGTTTACAAACCCGCGGA ATCTCAGTTCCGTCAGATTGGTGAGTATCAGAACG TACCAGTGATGACACCTGTAAATCACCCGCAAATC AACAAC TGGTTGCCTTCTATTGAGCAGTGCAATGA ACGCTACGTTAAGCACCATGCAGAAGACTCGTTAC CAGTGGAAGTAATTGCCACTGGCGGACAAAATAAC CAGCTGATTTTGAAC TACATTCATGACAGCAA	349	<i>Vibrio parahaemolyticus</i> strain ATCC 17802, (CP014046.2)	100%
FVP35	<i>toxR</i>	TTCTGCTGTGAATCCTTGGATTCCACGCGTTATTTT ATTTTGGCACTATTACTACCGATTGCGTACTGCT GTTTACAAACCCGCGGAATCTCAGTTCCGTCAGA TTGGTGAGTATCAGAACGTACCAGTGATGACACCT GTAAATCACCCGCAAATCAACAAC TGGCTGCCTTC TATTGAGCAGTGCAATGAACGCTACGTTAAGCACCC ATGCAGAAGACTCGTTACCAGTGGAAGTGATTGCC ACTGGTGGACAAAATAACCAGCTGATTTTGAAC TA CATT CATGACAGCAACCA	300	<i>Vibrio parahaemolyticus</i> strain VP4 ToxR regulatory protein ( <i>toxR</i> ) gene, (MF983557.1)	99%
FVP47	<i>trh</i>	TACTTCGCGATGATCTGCATCATACCTTTTCCTTCT CCAGGGTCGGCTGAAC TGTATTGTTGTTAGAAAT ACAACAATCAAAACTGAATCCCCGGTTAAGGCAAT TGTGGAGGACTATTGGACAAACCGAAACATAAAAA GAAAACCATACAAAGATGTATACGGTCAATCGGTT TTCACAACAGCAGGTTCAAAGTGTTAAGCGCCTA TATGACAGTAAACATCAATGGTCATAACTATACGA TGGCAGCTCTTTCTGGTTATAAAGATGGTATTTCTA CGGTCTTCACAAAATCAGAGAAAAACAAGCCTAAA GCAAGACTATTCTCGGTAAAAATATTTTGTGATGA CAACGAAGAATCAATACCAAGTGTAAC TTATTTAG ATGAAACATCAGAATACTTTGTTACTGTCGAGGCA TATGAGAGCGGAAATGGGCATAGTTTGTATGA	457	<i>Vibrio parahaemolyticus</i> strain ATCC 17802 thermostable direct hemolysin-related hemolysin ( <i>trh</i> ) gene, (GU971654.1)	98%