

Supporting Information

Antigenic epitopes and cross-reactivity analysis of tropomyosin from *Oratosquilla oratorio*

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Table S1. Antigenic epitopes of *O.oratoria* TM were predicted by bioinformatics tools

No ^a	Server	Position
1	NetMHCII pan4.0	4~24, 47~75, 82~128, 138~215, 217~245, 250~278
2	NetMHCII 2.3	1~19, 87~125, 163~200, 220~243
3	SYFPEITHI	2~30, 54~68, 75~117, 123~152, 159~183, 194~208, 222~240, 250~264
4	Rankpep	3~78, 85~99, 112~126, 128~142, 153~190, 197~214, 221~255, 266~280
5	DNA star	20~42, 47~84, 96~113, 117~140, 156~164, 177~189, 209~233, 244~259, 262~281
6	ABCpred Server	10~25, 19~34, 26~41, 33~48, 44~59, 57~72, 64~79, 75~90, 93~108, 100~115, 106~121, 117~132, 123~138, 132~147, 153~168, 169~184, 179~194, 191~206, 209~224, 215~230, 221~236, 232~247, 248~263, 258~273, 267~282
7	BepiPred 3.0 server	5~280
8	Immunomedicine Group	56~67, 83~96, 110~118, 149~155, 161~174, 187~193, 195~202, 221~231, 242~255

^aNo.1~4 mean as predicted T-cell epitope peptides. No.5~8 mean as predicted B-cell epitope peptides.

Figure S1

<i>O. oratoria</i>	MDA IKKKMÇAMKLEKDNAMDRADTLEQQNKEANNRAEK AEEVHNLQKRMÇQLENDLQVQEQ LLIKANTIQL EFKKALÇN	80
<i>L. vannamei</i>	MDA IKKKMÇAMKLEKDNAMDRADTLEQQNKEANNRAEK SEEEVHNLQKRMÇQLENDLQVQEQ SLIKANTIQL EFKKALÇN	80
Consensus	mdaikkkmqamklekdnamdradtlegqnkeannraek eeevhnlgkrmqqlendldqvqe llkan ql ekdkal n	
<i>O. oratoria</i>	AEGEVAALNRRICLI EEDLERSEERLNTATTKLAEFASÇAADESERMRKVLENRSLSDEERMDALENÇL KEARFLAEEADR	160
<i>L. vannamei</i>	AEGEVAALNRRICLI EEDLERSEERLNTATTKLAEFASÇAADESERMRKVLENRSLSDEERMDALENÇL KEARFLAEEADR	160
Consensus	aegevaalnrriglleedlerseerlntattklaeasqaadesermrkvlenrslsdeermдалenqlkearfлаееadr	
<i>O. oratoria</i>	KYDEVARKLAMVEADLERAEERAETGESKIVELEEEELRVVGNNLKSLEVSEEKANÇREEAYKEÇIK LTNKLKAAEFARAE	240
<i>L. vannamei</i>	KYDEVARKLAMVEADLERAEERAETGESKIVELEEEELRVVGNNLKSLEVSEEKANÇREEAYKEÇIK LTNKLKAAEFARAE	240
Consensus	kydevarklamveadleraeeraetgeskiveleeeelrvvgnnlkslevseekanqreeaykeçik ltnklkaaeарае	
<i>O. oratoria</i>	FAERSVÇKLQKEVDRIEDELVNEKEKYKSITDELQÇTFSEL SGY	284
<i>L. vannamei</i>	FAERSVÇKLQKEVDRIEDELVNEKEKYKSITDELQÇTFSEL SGY	284
Consensus	faersvçklqkevdrledelevnekekyksitdelqçtfselsgy	

Figure S1. Sequence alignment of TM in *O. oratoria* and *L. vannamei*. The sequence alignment result was analyzed by DNAMAN. The homology with 100% is colored dark blue and the homology $\geq 50\%$ is colored light blue. The result of sequence alignment was 97.89%.

Figure S2

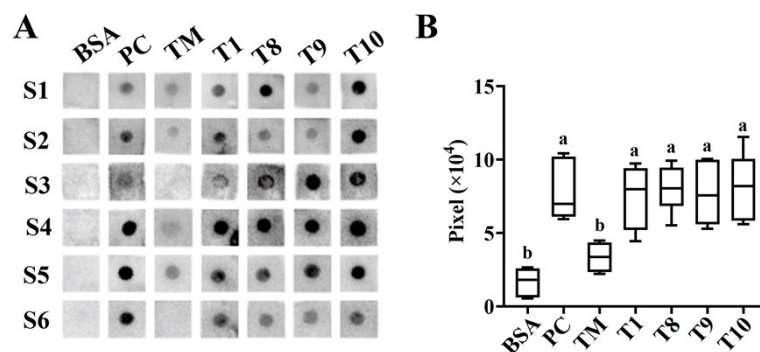


Figure S2 Analysis of IgE-binding activity in four T-cell epitopes from *O. oratoria* TM. (A) IgE-binding activity of four T-cell epitopes was analyzed by inhibition dot blot assay; Primary antibody, the sera from shrimp-sensitive individuals (S1~S6) of Table 1 with a dilution of 1:2. BSA, BSA was spotted on the nitrocellulose membranes and acted as a negative control group; PC, the primary antibody is the sera from shrimp-sensitive individuals without inhibitor; TM, TM used as an inhibitor was pre-incubated with the primary antibody; T1, T8~T10, four T-cell peptides used as inhibitor were pre-incubated with the primary antibody; Secondary antibody, the goat anti-human IgE antibody with a dilution of $1:2 \times 10^4$. (B) The IgE-binding activity of T-cell epitopes was quantitatively analyzed using the ImageJ software. Data were presented as mean \pm standard deviation (SD) and they were compared with a one-way ANOVA based on the Tukey test. Significant differences ($p < 0.05$) between the samples were labelled as “a, b, c...”, the difference of different marked letters is substantial.

Figure S3

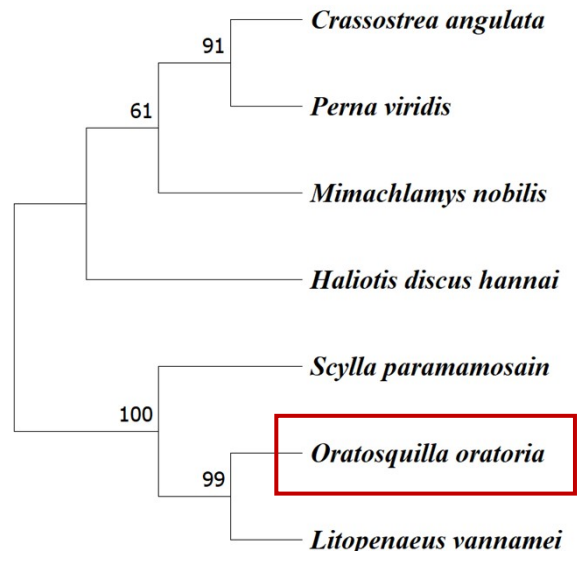


Figure S3 Phylogenetic tree analysis of TM between *O. oratoria* and other shellfish.