Accepted Manuscript

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PII: S1050-4648(16)30623-4

DOI: 10.1016/j.fsi.2016.09.056

Reference: YFSIM 4219

To appear in: *Fish and Shellfish Immunology*

Received Date: 7 August 2016

Revised Date: 25 September 2016

Accepted Date: 30 September 2016

Please cite this article as: Siva VS, Wang L, Qiu L, Zhou Z, Liu C, Yang J, Yang C, Song L, Polymorphism in a serine protease inhibitor gene and its association with the resistance of bay scallop (*Argopecten irradians*) to *Listonella anguillarum* challenge, *Fish and Shellfish Immunology* (2016), doi: 10.1016/j.fsi.2016.09.056.

Polymorphism in a serine protease inhibitor gene and its association with the resistance of Bay Scallop (*Argopecten irradians)* to *Listonella anguillarum* challenge

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Abstract

Serine protease inhibitors (SPIs) play a crucial role in regulation of both host and bacterial serine protease. They are classified into several protein families, where Kazal-type inhibitors are one of families with multi-domain. In the present study, the polymorphism of *Ai*SPI from Bay scallop *Argopecten irradians* was found to be associated with disease resistance of bay scallop against *Listonella anguillarum*. Nine single nucleotide polymorphisms (SNPs) were identified in the exon region of *Ai*SPI, where five SNPs were non-synonymous mutation. Three of these mutations were located in "kazal-like 3"domain, two SNP loci positioned at +536, +1312 were selected for further association studies. For the locus +536, the genotype frequency of A/G in the resistant stock (12.8%) was significantly lower (p<0.05) than that in the susceptible stock (35.1%), while, the genotype A/A