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Cloning and molecular modeling of *Litopenaeus vannamei* (Penaeidae) C-type lectin homologs with mutated mannose binding domain-2

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ABSTRACT. C-type lectins are animal proteins that contain at least one carbohydrate recognition domain (CRD) capable of mediating sugar and calcium binding. Carbohydrate recognition is directly required for some biological functions, including the innate immune response. We cloned two novel C-type lectin (CTL) precursors from the commercial marine shrimp *Litopenaeus vannamei*. The cloned cDNAs encompass ORFs of 1044 nucleotides and encode highly similar two-

domain polypeptides of 347 residues. The predicted proteins, LvCTL-br1 and -br2, contain the consensus triad that recognizes galactose (-GlnProAsp-) in CRD1 but also contain a mutated mannose-binding site (-GluProAsn-) in the second domain (CRD2). Phylogenetic analysis of LvCTL-br1 and -br2 and hundreds of CTL-like domain-containing proteins have allowed grouping of penaeid shrimp CTLs into three functional clusters. Reverse transcription coupled to PCR indicated that LvCTL-br1 expression is induced in shrimp gills upon IHHNV infection. Computational molecular modeling of LvCTL-br1 and -br2 revealed that three amino acid substitutions in CRD1 occur near the sugar binding site. Also, the 3-D models show a long loop of LvCTL-br1 CRD2 that might accommodate complex sugars. The structural data, evolutionary history and functional analysis support the hypothesis that gene duplication and accelerated evolution have caused functional diversification of penaeid shrimp C-type lectins.

Key words: C-type lectin-like domain; Invertebrate C-type lectin; Innate immune-related gene; Molecular phylogenetic analysis; Molecular modeling; Penaeid shrimp

