Hard-clam genome provides insights into the adapative evolution of molluscan IAP gene family

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Résumé

Inhibitors of apoptosis (IAPs) are critical regulators of programmed cell death that is essential for development, oncogenesis, immune and stress responses. While IAPs are extensively studied in humans and model organisms, their distribution and function are poorly understood in many taxa including Mollusca, the second most species phylum of Metazoa. We conducted genomic and transcriptomic studies of IAPs in the hard clam *Mercenaria mercenaria*, an economically important bivalve well-known for its 'hardiness' or resilience against environmental stress. The chromosome-level assembly of the hard clam genome encoded 34,283 genes with significant enrichment for domains and genes related to immune and apoptosis pathways. Comparative analysis identified massive expansion of IAPs in molluscs, especially in stationary bivalves, including 159 in hard clam, the largest number of IAPs observed in any metazoan. Further analysis uncovered a unique evolutionary process of molluscan IAPs where most genes originated in early metazoans and greatly expanded in Bivalvia through lineage-specific tandem duplication and retroposition, with 37.1% of hard clam IAPs located on one chromosome. The expanded IAPs exhibited great diversity in domain architecture and expression profile indicative of functional diversification and gene co-potion. Most expanded IAPs are highly expressed in immune-related organs or upregulated under abiotic challenges (84%), suggesting they are important for stress response. The expansion of IAPs in multiple molluscan lineages supports convergent evolution under common selection force. Our results indicate that sophisticated regulation of apoptosis enabled by the massive expansion and diversification of IAPs is crucial for stationary bivalves to cope with environmental stress.

Mots-Clés: IAP gene family, molecular evolution, Mollusca, gene duplication, divergence

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