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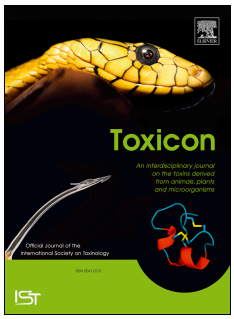

Neurotoxin stress-driven evolution in scallop genome

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Neurotoxin stress-driven evolution in scallop genome

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Understanding the molecular mechanisms underlying the resistance of organisms to specific environmental stressor is fundamental to understanding the deepest relationships between evolution and adaptation. Among environmental stressors, the exposure to contaminants and/or toxins could positively select specific and efficient adaptations providing advantages for resisting and surviving[1]. Few organisms, such as filter-feeding bivalves, can tolerate and accumulate remarkably high amounts of potent natural neurotoxins such as paralytic shellfish toxins (PSTs, produced by marine dinoflagellates)[2,3], although the specificity and molecular mechanism of this toxin resistance is not well apprehended.

Writting in *Nature communications*, Li et al. (2017)[4] recently take us an additional step forward in understanding adaptation and evolution processes, reporting how scallop genome evolution can be driven by environmental and ecological pressures (Fig. 1). Among all the investigations performed by the authors in this manuscript - comprising also impressive datasets on byssus, adductor muscle and sophisticated eyes evolution - specific attention has been provided to describing specific molecular mechanisms aim at handling PST production by blooming phytoplanktonic micro-algae. Indeed, this manuscript admirably shows that scallop uses its hepatopancreas to accumulate neurotoxins and its kidney to transform them into even more toxic forms through an expansion of sulfotransferases in the genome and the specific regulation of their expression processes, probably also as deterrence against predation, while it achieves neurotoxin resistance through point-mutations in sodium channels.

This research begs the questions of how environmental stressors are susceptible to select specific adaptative events from genome evolution? How resistance mechanisms are co-evolving with the development of toxic pressures, such as environmental toxin production? Indeed, the examples of the molecular adaptations managing specific ecotoxicological pressures remain critically rare[1], and this manuscript push forward our understanding of how it may have emerged in the scallop genome.

To our knowledge, the original integrative approach developed by Li and co-workers, combining genomic, transcriptomic and ecotoxicologic investigations constitutes the first evidence of the effective influence of a natural ecotoxicological environmental stress (*i.e.* the proliferation of PST producing *Alexandrium minutum*) to the genome evolution (through the selection of gene-specific duplication or mutation mechanisms) increasing the overall organism resistance. Li and colleagues' method combining the characterization of the evolution pattern of sodium-channel mutations within eucaryote genomes and the investigation of the specific genome duplication events increasing the number of detoxication enzymes was originally intended for understanding the outstanding accumulation and transformation of PSTs within the scallop tissues.

The paper presents two sets of analyses performed at both genomic and molecular level for complementary toxicological investigations. The first genomic analysis reveals the