

{rokbox title=|Median-joining networks of TLR-7 coding DNA sequence haplotypes and composition of *P. rudis* alleles at microsatellites and TLR loci within introgressed individuals ::

Image: Authors|

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[The characterization of toll-like receptor repertoire in *Pinna nobilis* after mass mortality events suggests adaptive introgression](#)

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Abstract: The fan mussel *Pinna nobilis* is currently on the brink of extinction due to a multifactorial disease mainly caused to the highly pathogenic parasite

Haplosporidium pinnae

, meaning that the selection pressure outweighs the adaptive potential of the species. Hopefully, rare individuals have been observed somehow resistant to the parasite, stretching the need to identify the traits underlying this better fitness. Among the candidate to explore at first intention are fast-evolving immune genes, of which toll-like receptor (TLR). In this study, we examined the genetic diversity at 14 TLR loci across

P. nobilis

, *Pinna rudis*

and

P. nobilis × *P. rudis*

hybrid genomes, collected at four physically distant regions, that were found to be either resistant or sensitive to the parasite

H. pinnae

. We report a high genetic diversity, mainly observed at cell surface TLRs compared with that of endosomal TLRs. However, the endosomal TLR-7 exhibited unexpected level of diversity and haplotype phylogeny. The lack of population structure, associated with a high genetic diversity and elevated dN/dS ratio, was interpreted as balancing selection, though both directional and purifying selection were detected. Interestingly, roughly 40% of the

P. nobilis

identified as resistant to

H. pinnae

were introgressed with

P. rudis

TLR. Specifically, they all carried a TLR-7 of

P. rudis

origin, whereas sensitive

P. nobilis

were not introgressed, at least at TLR loci. Small contributions of TLR-6 and TLR-4

single-nucleotide polymorphisms to the clustering of resistant and susceptible individuals could be detected, but their specific role in resistance remains highly speculative. This study provides new information on the diversity of TLR genes within the

P. nobilis

species after MME and additional insights into adaptation to

H. pinnae

that should contribute to the conservation of this Mediterranean endemic species.

Keywords: adaptation, critically endangered, fan mussel, genetic diversity, *Haplosporidium pinnae*, hybrids,

introgression, pathogens, toll-like receptors