{rokbox title=| Pinna rudis (left) and P. nobilis (right) embedded in the sediment. Morphologically, P. rudis differs from P. nobilis by its tawny brown color and its large tubular, tile-shaped scales, arranged along 5–10 radial ribs. It usually doesn't exceed a size of 30–40 cm, but can occasionally reach up to 50 cm :: Image: Authors| thumb=|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-comparative-genomics-pinna-vazquez-2026-thumb-et-al.jpg|}images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-comparative-genomics-pinna-vazquez-2026-et-al.jpg{/rokbox}

Stéphane Coupé,Mathieu Foulquié, **Maite Vázquez Luis**, **Elvira Alvarez Perez**, Jean-Marc Prévot ,Nardo Vicente, Robert Bunet, 2026.
Comparative Genomics of Pinna rudis and Pinna nobilis Reveals Conserved and Divergent Features of the Bivalve Defensome
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Abstract:The fan mussels *Pinna nobilis* and *Pinna rudis* have received increasing attention due to the mass mortality events (MMEs) that have severely impacted *P. nobilis* populations in the last decade. Strikingly, *P. rudis* was not affected by these events. Given that the two species can interbreed and that adaptive introgression has recently been suggested, it is essential to further investigate the genetic traits that may confer resistance to MMEs. This requires access to high-quality, annotated genomes for both species. Here, we present the first high-quality annotated genome of *P. rudis*, along with an updated genome assembly for *P. nobilis*. Comparative genomic analyses of gene sets associated with the “defensome” show that these genes are largely functionally conserved between the two species. Nevertheless, subtle differences in the number of annotations related to detoxification, stress response, and inflammation, along with variation in certain gene family expansions, suggest potential differences in susceptibility to environmental challenges. We also provide an updated characterization of the Toll-like receptor (TLR) repertoire based on the classifications proposed for bivalves. Both species share a highly conserved set of TLRs, with most genes under purifying selection. Overall, these genomic resources represent a critical step forward for future research aimed at understanding the molecular mechanisms underlying disease resistance in *P. nobilis* and will ultimately support conservation efforts for this endangered species.

Keywords:Pinna nobilis, Pinna rudis,