

{rokbox title=| Map of the Mediterranean Sea showing sampling locations :: Image:
 Authors|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-wide-geographic-long-vazquez-2022-thumb-et-al.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-wide-geographic-long-vazquez-2022-et-al.jpg{/rokbox}

Amalia Grau, Antonio Villalba, José I. Navas, Beatriz Hansjosten, José M. Valencia, José R. García-March, Patricia Prado, Guillermo Follana-Berná, Titouan Morage, **Maite Vázquez-Luis**, **Elvira Álvarez**

, Pantelis Katharios, Christina Pavloudi,

Elisabet Nebot-Colomer

, José Tena-Medialdea, Monserrat Lopez-Sanmartín, Claire Peyran, Hrvoje Čižmek, Georgia Sarafidou, Yiannis Issaris, Inci Tüney-Kizilkaya, Salud Deudero, Serge Planes, Gaetano Catanese , 2022.

[Wide-Geographic and Long-Term Analysis of the Role of Pathogens in the Decline of *Pinna nobilis* to Critically Endangered Species.](#)

Front. Mar. Sci.17 March 2022.Sec. Marine Ecosystem Ecology.Volume 9 .

<https://doi.org/10.3389/fmars.2022.666640>

Abstract:A mass mortality event (MME) affecting the fan mussel *Pinna nobilis* was first detected in Spain in autumn 2016 and spread north- and eastward through the Mediterranean Sea.

Various pathogens have been blamed for contributing to the MME, with emphasis in

Haplosporidium pinnae

, *Mycobacterium* sp. and *Vibrio* spp. In this study, samples from 762 fan mussels (necropsies from 263 individuals, mantle biopsies from 499) of various health conditions, with wide geographic and age range, taken before and during the MME spread from various environments along Mediterranean Sea, were used to assess the role of pathogens in the MME. The number of samples processed by both histological and molecular methods was 83. The most important factor playing a main role on the onset of the mass mortality of

P. nobilis

throughout the Mediterranean Sea was the infection by

H. pinnae

. It was the only non-detected pathogen before the MME while, during MME spreading, its prevalence was higher in sick and dead individuals than in asymptomatic ones, in MME-affected areas than in non-affected sites, and it was not associated with host size, infecting both juveniles and adults. Conversely, infection with mycobacteria was independent from the period (before or during MME), from the affection of the area by MME and from the host health condition, and it was associated with host size. Gram (-) bacteria neither appeared associated with MME.

Keywords: *Pinna nobilis*, *Haplosporidium pinnae*, *Mycobacterium* sp, Gram negative bacteria, molecular biology, histology.