activity by hemocytes, and the absence of bactericidal activity in hemolymph serum.

The results provide a first insight on the immune responses of different bivalve species towards *Arcobacter* strains and the underlying mechanisms.

Inflammation events occurring upon bacterial infection in *Mytilus galloprovincialis*

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Bivalves, and in particular the Mediterranean *Mytilus galloprovincialis* are important sources of food in several countries in the world. Because of that, mussels farming has a strong economic impact. Due to their status as sessile and filter-feeding animals, bivalves accumulate in their tissues environmental pollutants and a larger amount of microorganisms and between these, a multitude of infective bacteria for higher vertebrates and humans, such as *Vibrio* species. Several immunological responses of *M. galloprovincialis* were investigated and described after *Vibrio* infection both, *in vitro* and *in vivo* conditions, such as hemocytes count and different cellular subpopulations. Particularly, intracellular signaling pathways are activated to trigger the synthesis of antimicrobial effectors Here, were investigated the modulation of immunological cellular markers of the Mediterranean bivalve *M. galloprovincialis* in response to in vivo exposure with *Vibrio splendidus*. The activation of inflammatory cascade was examined through immunolabeling with antibodies involved in the pathway: Toll-like receptors 4 (TLR4), myeloid differentiation factor 88 (MYD88), Allograft inflammatory factor-1 (AIF1) and ribonucleases RNASET2 (T2 family), that trigger the recruitment and activation of macrophages in vertebrates. Results confirmed the activation of TRL4 during bacterial infection and MYD88 adapter suggesting a role in recognition and intracellular signaling. Moreover, Gram-negative bacteria determine the recruitment by the ribonuclease RNASET2 of haemocytes and a huge migration of AIF-1+ cells. This approach is suitable to understand the molecular defense mechanisms in invertebrates during the exposure to possible pathogens, also in order to develop new technics and tools to evaluate mussel immunity response used in aquaculture to prevent mass mortality of these mollusks, economic loss and potential risks for consumers of seafood.

Investigating the role of viral infections in the population of the *Congeria kusceri*

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Congeria kusceri (Bole, 1962), a highly endangered freshwater bivalve endemic to the Dinaric Karst, belongs to the only extant genus of cave-dwelling bivalves. This cave clam lives in a unique habitat, which has been subjected to minimal environmental changes over the past five million years. Since the natural populations of *C. kusceri* have been quickly declining over the past few decades, a key question to be answered is whether the "living fossil" status of this species, i.e. the apparent lack of morphological and physiological changes compared with its fossil relatives, is linked with a scarce resilience to the impact of human activities on the subterranean environment. In particular, the alteration of the seasonal abundance of pathogens, linked with the modified influx of water in Karst caves, might pose a severe threat to the survival of this species. Here, through a transcriptomic approach, we describe the identification in the tissues of *C. kusceri* of 5 nearly-complete genomes of RNA viruses belonging to the Picornaviridae family, which displayed a strong tissue preference and a significantly changes in abundance over the summer season. RNA-seq data also allowed to investigate whether these viral infections had an impact on gene expression in different host tissues. Since numerous reports have previously implicated Picorna-like viruses in the mass mortality events observed in different bivalves, we suggest that the presence of the 5 identified viruses should be closely monitored, together with other biological and chemical parameters, to gather a better understanding of the causes underlying the quick decline of *C. kusceri* populations.

AMPylation: a new facet of host-virus crosstalk in mollusks

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FIC-domain-containing enzymes (FicD) performed post-translational protein modifications from bacteria to humans, known as AMPylations. As part of the toxin-antitoxin system, FicDs of pathogenic bacteria occasionally induce AMPylation to overcome host defenses, whilst vertebrates FicDs drive the Unfolded Protein Response (UPR) and act during neurogenesis. Mining genomic and transcriptomic data of protostome metazoans, with a focus on marine invertebrates and associated dsDNA viruses, we traced a single-copy FicD gene transversally conserved in metazoans and viral pathogens, with structural and functional traits suggesting a preserved AMPylation capacity. Extra-numeral FicD gene copies are present in rotifers, in some bivalves and in the isopod *Armadillidium vulgare* genomes. Less conserved protein features and no syntenic conservation suggested their recent