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The name of a model species: the case of *Orchestia cavimana* (Crustacea: Amhipoda: Talitridae)

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Abstract
The species commonly known as *Orchestia cavimana* belonging to the Talitridae family (Amphipoda) has been used as crustacean model species. Here, we point out that this talitrid amphipod species is related to species in the genus *Orchestia* but now falls under what is described as *Cryptorchestia garbinii*, which is a different species from the nominal species *Cryptorchestia cavimana* endemic to the Island of Cyprus. It is therefore important that future basic research and applied studies involving this model organism refer to it as *C. garbinii*. Its old assignment *O. cavimana*, or even *C. cavimana*, as still reported in the National Center for Biotechnology Information (NCBI) GenBank and in recent papers, may lead to confusion.

Keywords: Orchestia, Cryptorchestia, *taxonomy*, *phylogeny*

In recent years, basic studies have highlighted the utility of model species to perform a variety of research experiments, translating into significant contributions to theoretical and practical aspects (Liu et al. 2017; Sanz et al. 2017). Particularly noteworthy are certain amphipod species (Crustacea) that have become model organisms for biological investigations conducted in the laboratory setting. They are used in both fundamental research (e.g. in developmental genetics, Stamataki & Pavlopoulos 2016), and applied studies such as those for toxicology and genotoxicology assessment purposes (Davolos et al. 2015; Ronci et al. 2015, 2017; Di Donato et al. 2016). Indeed, these crustacean amphipods are both easy to keep in culture and easy to breed in a laboratory environment. They have a short generation time and produce embryos with salient features that have been well investigated (Hunnekuhl & Wolff 2012; Stamataki & Pavlopoulos 2016). Moreover, the relevance of these model organisms to the evolutionary tree is shown by several phylogenetic results as well as by the peculiarity of their genomes and mitogenomes – e.g. the occurrence of particular gene rearrangements (Davolos & Maclean 2005; Ito et al. 2010; Krebes & Bastrop 2012; Stokkan et al. 2016).

Orchestia cavimana belonging to the Talitridae family (Amphipoda) has been used as a crustacean model species both in cellular differentiation studies at the molecular level, and in the spatiotemporal expression of genes (Luquet et al. 1996; Gerberding & Scholtz 2001; Raz et al. 2002; Testenière et al. 2002; Wolff & Scholtz 2002, 2008; Hecker et al. 2003, 2004; Ungerer et al. 2011; Hunnekuhl & Wolff 2012). However, it is highly important for the scientific community to keep updated with the most recent taxonomic position of model species. *Orchestia cavimana* has not only been transferred to the recently described new genus *Cryptorchestia* (Lowry & Fanini 2013), but as a result of genetic evidence (Ketmaier & De Matthaeis 2010), followed by a taxonomic revision (Ruffo et al. 2014), the current accepted name for the species is *Cryptorchestia garbinii*. This new taxonomic position differentiates the species from the nominal

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species *Cryptorchestia cavimana* (Ruffo et al. 2014). The taxonomic revision in fact creates as a consequence the splitting of the formerly widely known *O. cavimana* into two species: *C. garbinii*, distributed in the Mediterranean and European regions, and *C. cavimana*, endemic to the Island of Cyprus (Ketmaier & De Mattaheis 2010; Ruffo et al. 2014). So although it might still be consistent with past and previous literature (see above), the species must not be referred to any more as *O. cavimana*.

In addition, our recent molecular and taxonomic analyses helped to clarify the evolutionary history of *C. garbinii* and the currently described *Cryptorchestia* species, including the new species *Cryptorchestia ruffoi* from the Island of Rhodes, Greece (Davolos et al. 2017). The study, conducted on the nuclear and mitochondrial gene sequences, validates most of the results from previous works (Davolos et al. 2004) but it also adds considerable novel information. The phylogenetic analysis revealed that in fact *C. garbinii* is closely related to the *Cryptorchestia* species of the east Mediterranean regions. Moreover, we have recently found low levels of both genetic differentiation and morphological variation between Turkish and European populations of *C. garbinii* (Davolos et al. submitted). New DNA sequences confirmed that the evolution of *C. garbinii* could have been a pattern of recent east-to-west dispersal, with a more recent northward expansion. Furthermore, our studies confirmed the importance of insular speciation in both the northeast Atlantic and east Mediterranean *Cryptorchestia* lineages (Davolos & De Matthaeis 2017; Davolos et al. 2017).

In conclusion, being a model species for research has both costs and benefits. A wider notoriety in the scientific community as a model species includes appropriate taxonomic and molecular analyses to evaluate the extent of phenotypic and species-level genetic variation, such as to identify also cryptic species (Major et al. 2013; Fišer et al. 2018). It is therefore important and necessary that future basic research and applied studies involving this species refer to it as *C. garbinii*. Its old assignment *O. cavimana*, or even *C. cavimana*, as still reported in the National Center for Biotechnology Information (NCBI) GenBank (e.g. GenBank accession number AY744907.1) and in recent papers (e.g. Ramm & Scholtz 2017), may lead to confusion and misjudgement.

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