

A NEW GENETIC ANALYSIS OF A LESSEPSIAN SPECIES AS A TOOL TO PREDICT THE INVASIVE FORCE OF A POTENTIAL ECONOMIC RESOURCE

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Abstract

The genetic variability of the lessepsian species *Fulvia fragilis* was analysed with samples from a Red Sea population and a Tunisian population. Genetic markers showed no genetic loss in the Mediterranean Sea population. This analysis provided a tool to identify the taxonomic position of this little known species. It also underlined a relatively high level of genetic diversity of this newly established population and revealed a likely good adaptability of its potential economic resource.

Keywords: Alien species, Mediterranean Sea, Genetics, Population Dynamics, Bivalves

The phenomenon of colonization of the Mediterranean Sea by fauna from the Indian Ocean was observed soon after the opening of the Canal and has increased with the low input from the Nile fresh water as the result of Aswan dam construction in 1969. The acceleration of this phenomenon is also due to the increased shipping activities that promotes the transport of living organisms via ballast waters, combined with warming impacts that facilitate the settlement and colonization of Lessepsian species [1]. In this context, all alteration of natural communities appears as a particular form of human impacts (shipping, over fishing, aquaculture and artificial water ways) which has affected the eastern basin and now extends to the western basin. Among colonized exotic species, some have potential commercial interest in either fishing or aquaculture. Among these, the bivalve *Fulvia fragilis* (Cardiidae) belongs to a little-known species complex and is widespread around the edge of the Indo-Pacific Ocean. It occurs naturally in the Red Sea and was observed early in the Suez Canal and the Mediterranean Sea. Very quickly, its location has appeared in the form of patches that tend to spread. On the Tunisian coast, it was first observed in the Gulf of Gabes and since 2001, it has crossed the Tunisian-Sicilian channel and develops in the Bizerte lagoon and the Gulf of Tunis (Fig 1).

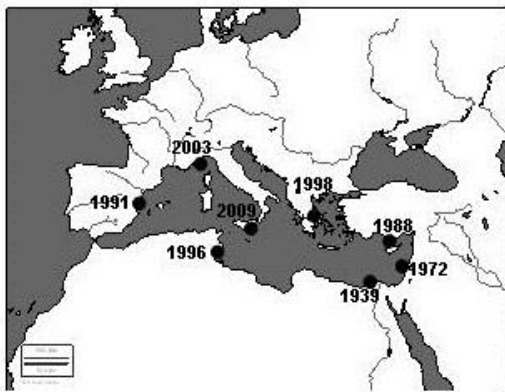


Fig. 1. Geographical distribution of *Fulvia fragilis* in the Mediterranean Sea (Ben Souissi, 2013)

Two populations of *F. fragilis* were sampled, one from the native area (Red Sea) and one from the colonized area (Gulf of Tunis). Molecular techniques were used for the first time on nuclear and mitochondrial genetic markers of this species and allowed us to characterize its genetic signature. They gave data about intraspecific genetic relationship [2]. Moreover, the phylogeographic information provided tools to establish monitoring the colonization of Mediterranean and understand the mechanisms of this process. The genetic analysis clarified the taxonomic position of this lessepsian species. It supplied a first assessment of the genetic diversity of this bivalve in its original area and in a new settled area and led to estimate

the impact of colonization of the Mediterranean Sea on its intrapopulation genetic diversity (Fig 2).

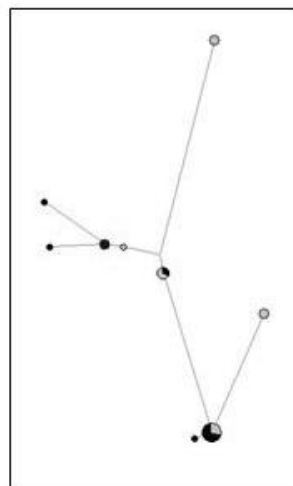


Fig. 2. Genetical relationship between a Mediterranean population (Black circles) and a Red Sea population (Grey circles) of *Fulvia fragilis* based on the ITS-1 sequence. The circle size is proportional to the number of the sequences

The first results suggested that no bottleneck processes reduced the genetic variability of *F. fragilis* populations established in the Tunis Gulf. On the nuclear non-coding region, most of variable sites are Indels ones. The estimation of the genetic diversity of newly established populations is a new tool for evaluating their adaptive capacity and thus their ability to grow facing new environmental characteristics. The level of genetic variability of the new population in the Gulf of Tunis underlined that it seems high enough to explain the success of this implementation. It can also explain that the populations of this invasive species are strong enough to almost eradicate a part of the native fauna [3]. Moreover, in the case of an exploitable invasive species like *F. fragilis*, determining the genetic heritage of the populations in the natural environment is a prognostic tool of its aquaculture potential.

References

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