

Letter to the Editor

Comments on “The Mediterranean Sea as a gateway for invasion of the Red Sea: the case of the Indo-West Pacific head-shield slug *Chelidonura fulvipunctata* Baba, 1938” by Manuel António E. Malaquias, Andrea Zamora-Silva, Dyana Vitale, Andrea Spinelli, Sergio De Matteo, Salvatore Giacobbe, Deneb Ortigosa and Juan L. Cervera, Aquatic Invasions, 2016

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Abstract

In a recent article, Malaquias et al. (2016) use molecular tools to test the conspecificity of the aglajid sea slug *Chelidonura fulvipunctata* Baba, 1938 populations from two sites in the Mediterranean (Cyprus, Italy) and the Indo-West Pacific (Mozambique, Lizard Island, Australia, and Marshall Islands). The authors then postulate that the species has entered the Red Sea from the Mediterranean Sea through the Suez Canal, the latter acting as a “revolving door” that can allow species of Indo-Pacific origin to enter the Mediterranean, and species established in the Mediterranean to move into the Red Sea. In this response evidence is offered that questions, if not refutes, the authors’ premises. The veracity and accuracy of the geographic origin and the pathways of introduction are of major importance for management of bioinvasions. For appropriate management measures to be prioritized, devised, and implemented, care should be taken to provide scientists, regulators and stakeholders with as accurate information as possible.

Key words: Mollusca, Aglajidae, DNA barcoding, COI, Suez Canal, non-indigenous species

In a recent article, Malaquias et al. (2016) hypothesize that since *Chelidonura fulvipunctata* Baba, 1938 has been widely recorded from the Indo-West Pacific and the Mediterranean Sea, but only once in the Red Sea, it had entered the latter from the Mediterranean through the Suez Canal. Furthermore, they argue that “...the Red Sea can also be a receiver of tropical species that have arrived in the Mediterranean by other routes than Lessepsian immigration, with the Suez Canal acting as a “revolving door” allowing both species of Indo-Pacific origin to enter the Mediterranean and species established in the Mediterranean resilient to tropical/subtropical environment conditions to move into the Red Sea.”

When assigning pathways/vectors and temporal sequence of introduction events caution should be exercised as, with the exception of documented intentional introductions, only rarely are they known

from direct evidence. Mostly, introductions are inferred from the habitats and localities a species occupies in its native and introduced range, patterns of dispersal (i.e. for a fouling species frequently recorded from ports, vessels are assumed to serve as the most probable vector, whereas a fouling species associated with shellfish farming is considered culture-introduced). As concerns “Lessepsian immigration”, a temporal succession of directional (“stepping stones”) records from the Red Sea, the Suez Canal, and along the coasts of the Levant confirms a species status as a naturally dispersing Erythraean NIS (Galil 2008). Questions arise, as in the present case, when we lack some of these records.

With these caveats in mind, we appraised the body of evidence offered by the authors in support of their proposition that the presence of *C. fulvipunctata* in the Red Sea may “...be more parsimoniously explained

by an expansion from the Mediterranean into the Red Sea rather than dispersal from the Indo-West Pacific to the Red Sea”.

A. The authors used the COI gene to test the conspecificity of *C. fulvipunctata* populations from two sites in the Mediterranean (Cyprus, Italy) and the Indo-West Pacific (Mozambique, Lizard Island, Australia, and Marshall Islands). They further claim that the results enabled them to “...show unequivocally that specimens of the W-shaped mark head-shield slug occurring in the Mediterranean Sea and those occurring in the Indo-West Pacific belong to the same species”. In fact their results reveal that the 3 Italian specimens display 3 COI haplotypes with substantial *p*-distances of 3.1% (KU183997 vs. KU184000), 2.7% (KU183997 vs. KU184001) and 1.9% (KU184000 vs. KU184001), forming 3 separate branches (using NETWORK analysis; Figure 1). Only one Italian sample (KU183997) was close to the Cypriot sample (KU183998) (0.4% *p*-distance value). The latter samples with the 4 COI sequences from Mozambique and the Marshall Islands (12 combinations) present very low distances (0–0.8% *p*-distance values) that are slightly increased with the addition of the Australian sample (6 combinations; 0.8–1.1% *p*-distance values), altogether show a group of COI sequences with small distances. These results suggest that the genetic repertoire of *C. fulvipunctata* is only partially represented.

The outcome of the molecular analysis in Malaquias et al. (2016) neither supports nor refutes the authors’ claim for a Mediterranean origin of the Red Sea population of *C. fulvipunctata*.

B. The authors state that Selimiye, Turkey, was a “former traditional boat-builders’ village popular with yacht owners”, suggesting that the occurrence in 1959 of *C. fulvipunctata* near its harbor could be regarded as evidence consistent with shipping from “...the Indo-West Pacific area of origin ...shipping routes may have been responsible for the introduction of this species in the Mediterranean basin”. However, in 1959 the inhabitants of the little fishing village were impoverished refugees from Crete, the nearest commercial port, Mersin, started operations in 1962 (<http://en.mersinport.com.tr>, viewed August 19, 2016), and the era of yacht tourism not yet began (Freely 1988). Selimiye is located in the Gulf of Antalya, not as shown in Figure 4.

C. The temporal sequence and geographical spread of *C. fulvipunctata* in the Mediterranean broadly

follows the “east to west” pattern of Erythraean NIS. The long hiatus between the first record collected in Selimiye, Turkey, in 1959 (Swennen 1961, as *Chelidonura mediterranea* spec. nov.), and the second one collected off Ashqelon, Israel, in 1986 (Mienis and Gat 1987), does not necessarily reflect the timeline of introduction, but quite possibly an asymmetrical research effort: the Netherlands Biological Expedition to Turkey stopped at Selimiye between 23 April and 5 May, 1959 (Anonymous 1963), whereas no comparable effort took place along the southern Levant. The importance of research efforts is starkly illustrated by the disparity in number of NIS recorded from adjacent Mediterranean countries: three times as many are known from the Mediterranean coast of Turkey as from Syria (Galil et al. 2016).

D. The authors state repeatedly that the recent single record of *C. fulvipunctata* from the Red Sea (“there is a single record from the Red Sea in the Gulf of Aqaba... yet there is but a single report for the Red Sea... the single observation (by Koretz 2005) of *C. fulvipunctata* in the Red Sea... It is also noteworthy that the Red Sea observation comes from Eilat in the Gulf of Aqaba in the northern part of the basin and was made nearly half a century after the species was first reported in the Mediterranean Sea”) conflicts with the hypothesis of “Lessepsian migration” *sensu* Por (1978). However, *Melibe viridis* (Kelaart, 1858), another Indo-West Pacific nudibranch introduced into the Mediterranean Sea, was also only recently recorded in the Red Sea (Yonow 2015).

As a matter of fact, species new to science have been described in the Mediterranean Sea as Erythraean NIS with either a single record or no record at all from the Red Sea, and were validated by subsequent research (e.g., *Alpheus migrans* Lewinsohn and Holthuis, 1978; *Rhopilema nomadica* Galil, 1990; *Marivagia stellata* Galil and Gershwin, 2010). The strikingly colored *Haminorea cyanomarginata* Heller and Thompson, 1983, had been described from a single specimen collected in the Sudanese Red Sea in 1980, and next from Greece (2001) and Turkey (2002) (Yokeş and Rudman 2004), before it was sighted again in the Red Sea (Lederman 2005). Species have been known to remain unrecorded for decades after their original description (e.g., the chromodorid *Hypselodoris dollfusi* (Pruvot-Fol, 1933), collected in the Red Sea in the 1920s and then again 80 years later (Gulf of Oman, Gosliner and Behrens 2000; Gulf

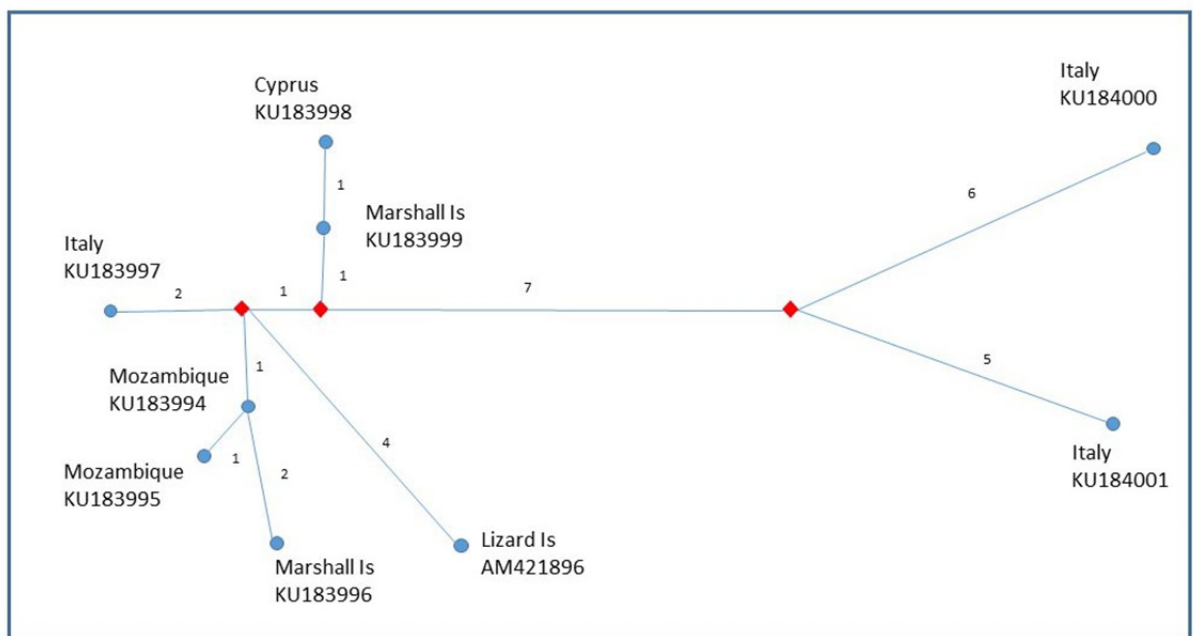


Figure 1. Haplotype network for the 9 cytochrome c oxidase subunit I (COI) sequences of *Chelidomura fulvipunctata*. Blue circles (specified by site collection names and accession numbers) denote the location of each haplotype in the network. Red squares refer to the median vectors (non-sampled yet haplotypes inferred from the data). Numbers above/beside the lines signify the number of mutations between haplotypes. Analysis was performed using Network ver 5.0.0.0 (Fluxus Technology, 1999–2016).

of Aqaba, Dafni 2006), or, like *C. fulvipunctata*, described from the Red Sea decades after they had been described elsewhere in the Indo-West Pacific (e.g., *Costasiella kuroshimae* Ishikawa, 1993, recently recorded from the Red Sea, which Yonow (2015: 535) suggests is “not an alien species to the Red Sea, but is so small that it has most likely been overlooked: its algal turf habitats are not a priority for photographer/divers”. Even larger nudibranchs may suffer the same fate (e.g., *Platydoris inframaculata* (Abraham, 1877), 180 mm long, is known from few recent records in the Red Sea (Yonow 2015: 539)).

According to Yonow (2008b) 51 heterobranch sea slug species have been recorded in the Gulf of Aqaba but not in the southern Red Sea, but that “anomalous” distribution may change “as numerous species are not yet formally described and others recently described may yet be found in the Indian Ocean or further afield.”

For the record, *C. fulvipunctata* was documented twice (not once) from the Red Sea: Koretz (<http://www.koretz.net/Eilat/Invertebrates/Molluscs/Opisthobranchs.htm>, viewed August 16, 2016) noted a single specimen 8 mm long, on a sandy flat in 2005. Yet, a photograph taken by a fellow sea

slug enthusiast, O. Lederman, documents another individual in Eilat (<https://lederman.smugmug.com/Underwater/Nudibranchs/The-Red-Sea/i-hfzKtS3>, viewed August 16, 2016; reproduced in Yonow 2008a).

- E. The authors state that “The Red Sea is a well-studied basin surveyed by a wealth of expeditions ... the Red Sea, a well-studied marine realm”. Yet, the pre-eminent scholar of Red Sea heterobranch sea slugs asserted unequivocally “The Red Sea is an important marine biogeographical region, but to date the opisthobranch fauna has only been described sporadically. No recent surveys have been carried out in the Gulf of Suez following the Cambridge and Dollfus expeditions in the 1920s”; “...none of the 21 species recorded only from the Gulf of Eilat are named. As many as 15 are possibly new species” (Yonow 2008b). The fact that “a further 73 species have been reliably recorded from the Red Sea” within a space of a few years emphasizes the dearth of current knowledge (Yonow 2015).
- F. The authors postulate that the Suez Canal “can act as a revolving door”, recapitulating Keller’s (1883). “Migrations-Schema” that charted the advance of the Red Sea and Mediterranean species from both ends of the Canal. A century

later, Barash and Danin (1987) listed three “antilessepsian” heterobranchs in the Red Sea (*Aplysia fasciata* (Poiret, 1789), *Pleurobranchaea meckeli* (Leue, 1813), *Tethys fimbria* (Linnaeus, 1767)). Hoenselaar and Dekker (1998) considered them incidental specimens or erroneous determinations and stated they “...do not know of any species of Mediterranean mollusk to be reported to really live in the Red Sea outside the Suez Canal system.” Some of the examples cited by the authors of Red Sea shelled mollusks which colonized the Mediterranean Sea but “bypassed” the Red Sea are erroneous too. Not only is *Saccostrea cucullata* (Born, 1778) commonly encountered throughout the Red Sea (Oliver 1992), it is also known from Pleistocene fossils from that area (Selli 1973); *Oscilla jocosa* Melvill, 1904 too was collected in the Red Sea (Mienis 2003). The authors’ bold claim that Mediterranean species of tropical affinities (native or otherwise) may be introduced through the Suez Canal into the Red Sea would have been better served by more robust examples.

Identifying the geographic origin and the pathways of introduction are of major importance for management of bioinvasions. Only when the source and the vector are established, can specific and appropriate measures be prioritized, devised and implemented. Therefore, care should be taken to provide scientists, regulators and stakeholders with as accurate information as possible.

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