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Comment

Comment on Kuplik et al. *Rhopilema nomadica* in the Mediterranean: Molecular Evidence for Migration and Insights into Its Proliferation. *Diversity* 2026, *18*, 94

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Based on COI analyses of three medusae collected in Dar es Salaam, Tanzania, and on a low-resolution photograph of a jellyfish swarm in Haifa Port, Kuplik et al. [1] assert that the invasive jellyfish *Rhopilema nomadica* Galil, 1990, had already been "documented" in the Levantine Basin 4–5 decades prior to its first collected specimen in 1976. They further suggest that construction of the Aswan High Dam may have facilitated its proliferation, while simultaneously stating that a scenario "whereby *R. nomadica* migrated from the Mediterranean to the Indian Ocean…cannot be entirely excluded." We contend that the data presented in their article [1] support neither these conclusions nor the proposed scenario.

Here, we provide factual evidence refuting the authors' assertions and address omissions regarding genetic data from Mediterranean populations of *R. nomadica*.

Kuplik et al. [1] antedate the presence of *R. nomadica* in the Mediterranean—"possibly soon after the Suez Canal was constructed"—on the suggestion of Prof. Andre C. Morandini, University of Sao Paulo, Brazil, who identified it from a 1938 photograph taken in Haifa port (Figure 2) [1]—no morphological details are given as none can be discerned. It is more than likely that the rhizostomid jelly is the superficially similar native *Rhizostoma pulmo*. Indeed, Bodenheimer [2] reported observing at the time "enormous shoals" of the latter species in Port Said (Egypt) and the Golden Horn (Turkey). Though the authors concede that the 1938 photograph provides no "taxonomic proof", they rely on the "the image from 1938" to "…propose that *R. nomadica* medusae were introduced into the Mediterranean over the last century, possibly soon after the Suez Canal was constructed". Furthermore, their central conclusions concerning "the establishment and colonization dynamics of *R. nomadica*" [1] hinge on its unsubstantiated identification to substantiate the proposition of a century-long cryptic population with "a slow initial establishment phase, followed by rapid dispersal, and probably a period of several decades from first observation in the Levant to a pan-Mediterranean distribution".

The authors repeatedly insist that *R. nomadica* "…was assumed to originate in the Red Sea, or in the Indo-Pacific region, but in the absence of additional reports of live specimens outside the Mediterranean, its origins have remained a mystery"; "…considering *R. nomadica*'s absence from the Red Sea, based on the lack of reports"; "yet there have been no published reports of its presence elsewhere in the Red Sea, nor anywhere else, aside from the Mediterranean". Only once do they concede "… it being considered a Lessepsian migrant", based on **a specimen** collected off Kamaran, Yemen, southern Red Sea, in 1939 (holotype, RMNH 7038)". In fact, **18 specimens**, collected in 1937 and 1939 by J.H. Ziesel,

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a collector based on the island of Kamaran in the southern Red Sea and identified by G. Stiasny, are preserved in Naturalis Biodiversity Center (RMNH 7036-39, 7043) [3].

The paper's title further claims to provide "... Molecular Evidence for Migration and Insights into Its Proliferation" [1]. Neither claim is substantiated in the text, and two molecular studies documenting long-term population genetics of Levantine *R. nomadica* populations (1091 specimens), based on COI haplotypes and microsatellite alleles [4,5], are omitted. In these studies, Levantine populations were analyzed using 490 bp COI fragments, revealing 89 haplotypes; most other GenBank sequences used are 433 bp long, with few others ranging from 660 to ~1220 bp. In contrast, Kuplik et al. [1] analyzed fragments just 316 bp long, which are too short and insufficient to resolve molecular distances between Tanzanian and Mediterranean haplotypes. Nevertheless, the three Tanzanian specimens exhibit two distinct haplotypes, both different from the 89 Mediterranean haplotypes, thereby refuting any inference of shared origin or connectivity and undermining the validity of the proposed invasion trajectory.

Relying on only three DNA samples from Tanzania, Kuplik et al. [1] expanded their manuscript with largely unrelated forms of "documentations". These include a drone image of a *R. nomadica* aggregation off Haifa, Israel (their Figure 1); the above-mentioned black-and-white photograph from 1938 (their Figure 2); photographs of medusae from Israel and Mafia Island (their Figure 3, with the latter sourced from the internet); and a generic life-cycle schematic (their Figure 4). None of these elements are directly relevant to the molecular findings presented in the paper. In addition, the authors include a phylogenetic tree demonstrating the monophyly of *Rhopilema*, while disregarding an extensive body of prior literature in which the monophyly of species within this genus has already been thoroughly examined and established, e.g., [6–9].

Kuplik et al. [1] make extensive use of semantic prosody, that is, evaluative language embedded in ostensibly supportive contexts, through frequent deployment of terms such as "probably," "interestingly," "may be related," "may remain," "may exist," "may have existed," "may have led" "potentially," "likely," "suggested", "perhaps" and more. These terms were employed to construct a speculative narrative regarding *R. nomadica* species' origin, the purported influence of the Aswan Dam impacts, and hypotheses such as a "cryptic reservoir of dormant podocysts", among others. This rhetorical framing, combined with reliance on extensive self-citations that are said to "concur with our assumption" (Discussion), stands in marked contrast to the limited empirical evidence actually presented (three COI sequences).

Kuplik et al. [1]'s restricted dataset and persistent omissions of the relevant literature are at a core of a narrative built on speculative discussion and "likely" conclusions not substantiated by the underlying data or analyses.

Accurate determination of geographic origin and introduction pathways is critical for effective bioinvasion management. Molecular tools are widely relied upon to address these issues, and the veracity and accuracy of published interpretations are therefore of crucial importance. In this context, the three short COI sequences presented by Kuplik et al. [1] do not add any meaningful or novel genetic information relevant to *R. nomadica* migration history, connectivity, or proliferation dynamics. Given the substantial implications for regulators, scientists, the public, and marine ecosystems, it is imperative that inaccurate, unsubstantiated or misleading statements and interpretations be identified and corrected.

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