Review

Title

"Refining a zoogeographic puzzle: Invasion history of the clinging jellyfish *Gonionemus* in the Northwest Atlantic Ocean"

> Considering the results and discussion of this article, I think that "invasion history" is not appropriate. This is a detailed article considering description and diagnosis of genetic/population delineation and taxonomy for *Gonionemus* in several Atlantic and Pacific Ocean localities. The article´s analysis is more related to these matters, and the discussion clearly stated that several hypothesis would be considered, even cryptic (native) lineages. Maybe a simpler statement would be more appropriate, like genetic delineation and taxonomy (as stated at the beginning of the discussion).

Author's affiliations
"United States" should be referenced as "United States of America"
"Rusia" (Semenchenko´s affiliation) should be referenced as "Russia"

Abstract

Line 16 > "…with multiple scenarios…" maybe "with alternative scenarios" would be more informative, because they are contrasting scenarios.

Last line > "…introduction of a new lineage has reinvigorated…" I don´t think "reinvigorated" is a proper word because it would be assuming some improvement or positive effect, which I think is not part of the text (it would be unnecessary confusing). A simpler word like "increase" or "extend" would be fine.

Main text

Introduction

Line 28 > "…inoculations…" This would should be changed (it is unnecessary confusing). A simpler word like "input" should be fine.

Lines 35-38 > Besides the sampling (individuals, molecular) the methods applied for this kind of animals would be very challenging as well (eg, 10.1093/cz/zow107).

Lines 86 > "…mitochondrial cytochrome oxidase (COI)…" should be referenced as "mitochondrial cytochrome oxidase I (COI)".

Methods

Line 100 > ". A portion of…" As a suggestion: for this type of description, it is common to use the sentence "part of" or the word "partial".

Line 103 > Detail the approximated expected bp length of the PCR amplification.

Line 108 > Before assembled "sequences" we will work with the "chromatograms".

Line 110 > "…As Kimura 2-parameter (K2P) distances are commonly employed in DNA barcoding studies, mean KP2…" This is not a proper justification to use an evolutionary model. If it´s considered as necessary to detail (I think it is), an improved sentence should clarify why we are using it. In fact literature has several criticism about these approaches. Examples:

On the inappropriate use of Kimura-2-parameter (K2P) divergences in the DNA-barcoding literature. Cladistics; doi: 10.1111/j.1096-0031.2011.00370.x

The Use of Mean Instead of Smallest Interspecific Distances Exaggerates the Size of the "Barcoding Gap" and Leads to Misidentification. Systematic Biology; doi: 10.1080/10635150802406343

However, considering the scope and dataset of this article, I think this is not a problem.

Line 111 > "Mega 7" should corrected to "MEGA 7" (is an acronym). Besides, to define an unique way to reference software, it should detail version in all cases (PAUP*, DnaSP, etc).

Results

Line 120 > Besides Table 1, it should be cited Figure 3 (the Map figure). Because this is an international article and journal, all localities from countries should be detailed (in other words, localities from USA). Another issue is that Figure 3 do not detail San Juan Island, USA, and the Iceland location. Both localities should be represented as well in the "geography figure".

Lines 140-157 > This section is quite confusing about how to present and reference the seven haplotypes, specially their distribution. A clearer and even simpler way would be better, like localities in lines 117-120. Maybe an initial approach, just informing basic information and distribution of haplotypes I to VII, and then briefly a remark of the most interesting shared haplotypes considering NWP, NWA and NEP-NEA…an approach somewhat similar as you did in the first part of the paragraph.

Discussion

Line 218 > "(ref Naumov?)" Citation missing.

Lines 312-313 > I recommend to replace words "inoculations" and "inoculating" for simpler ones, like input. The referenced phenomena is already well detailed in the text.

Lines 317-318 > "Could be" repeats in both lines. I suggest changing one of them.

Line 371-372 > The sentence "…speak to an urgent need for a better understanding of its invasion history, which can come from…" give us the idea that this phenomena is confirmed/corroborated, but I think this is not the case as already explained in the main text, where it is commented as hypothetical/speculative scenarios (e.g., discussion). The biological invasion concept is quite confusing, so I´m referring to it as "Biological invasions, although mechanistically related to other causes of rarity and abundance, are distinct in that they arise through human-mediated extra-range dispersal" (Wilson et al. 2009, doi: 10.1016/j.tree.2009.07.004).

So, the invasion hypothesis should not be presented as a "fact" in this sentence (or even in the main title).

Other details

> In Table 1 "San Jan" should be "San Juan"

> Table 2 should include NEP-NEA, and a specific column describing haplotype (from I to VII) and number of individuals. Example: for GB the column would be "II (5), IV (2)"

> Maybe a combined Figure from Figures 1 and 2, including NEP-NEA would be nice.

> I did not have access to full sequences' metadata, so I hope that all metadata (even samples´ collectors) are part of the GenBank submissions.