

RESPONSE LETTER TO ROUND #2

Resubmission MS Title:

Inference of the worldwide invasion routes of the pinewood nematode *Bursaphelenchus xylophilus* using approximate Bayesian computation analysis

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Submitted to: PCI Zoology

Dear Recommender,

Thank you for your comments and criticisms. We have incorporated your suggestions in the new version of the manuscript. We hope that you will now find it appropriate for recommendation in PCI Zoology.

Please find below our detailed responses (in italic characters) to your comments (in bold characters).

Best wishes,

Eric Lombaert on behalf of all authors

Round #2

by Stéphane Dupas, 2021-04-01 23:44

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Evaluate one versus multiple bottleneck sources in the native area

I would like to thank the authors for the quality of the new analyses performed. A lot of work responding to almost all reviewer issues, and many improvements in the analysis have been included in this second version.

I would have only one issue to raise before recommendation. In the first version, I had pointed out the interest of the result that, based on the analyses not only there would have been several independent introductions from the native area in USA to the different regions in Asia, but that these introductions would come from the same one local population in the USA. The authors changed the analysis by including ghost populations between the USA source and the invasive populations. This is justified since the probability to have sampled the very population source is low. Yet, this removes from the present version the single population source results that had come out, since the authors group all the USA population and perform several independent bottlenecks after, to generate different introductions. Since there is a strong population structure in the USA, this result of a single pop source certainly had strong signals. In addition it has implications for quarantine efforts on this population, and for biological invasion theory in general. It may thus be of interest to address again the issue of a single versus multiple source populations in the USA. This can be easily combined with the ghost source hypothesis by performing a single bottleneck on the joint USA pop before the introductions (single pop hypothesis) versus multiple bottlenecks before the introductions (multiple pop hypothesis).

This request is very minor but might improve the impact of the paper that makes use of the most recent inference technologies to unravel invasion routes from population genetics data, and might be seminal for many students and researchers.

As proposed, we added a third scenario within Step 6 (page 11). This new scenario consists of simulating a single native population as the source of the three independent invasive populations (i.e. Japan1, Japan2 and China2). This scenario is thus very similar to scenario 2 (the "bridgehead" scenario), but with a single bottleneck instead of two (which incidentally explains the increase of the prior error rates, and confirming our poor ability to identify the exact native source population; see Table S2 for details). Scenario 1 remains the selected one in all situations (Table S2), and we therefore did not make any changes to the discussion section. The Zenodo deposits have been modified accordingly.

In addition some minor comments:

- remove "of" line 38

The text has been modified (page 1).

- Line 206. Number of independent introduction events instead of "independently" later.

The text has been modified (page 6).

- Line 251 not clear what is main and alternative in the text. Although it's clear on the table.

The text has been modified (page 7).

- Line 427 May have derived

The text has been modified (page 11).

- Line 528 Change “and being” by “which was”

The text has been modified (page 13).

- Line 628 : “For instance, if the native area is weakly diversified so that it exhibits a few very frequent alleles, it is probable that two independent introductions from this native area (native → invasive 1 and native → invasive 2) lead to samples closer to each other than to their native area.”

In the present case the native area is diversified. Only the source population if unique would be weakly diversified

We agree, but, as said above, it is not possible in our case to characterize the precise native origin(s) of the invasive populations. This sentence is only aimed at underlining one of the hypotheses that could explain the pattern we observe.