

Dear Miguel Navascues,

I first want to apologize for the long delayed resubmission. I have been taken by other work and family priorities that took over the PCI paper.

We are grateful for the thorough review of our work. And we appreciate that you highlighted small inconsistencies and issues in our work. These definitely helped us improve the manuscript.

We provide below a detailed point by point response to your comments and suggestions, all of which were considered with great care.

Best regards,

Jordi Salmons, for the co-authors.

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*Decision for round #2 : Revision needed*

*Revision required*

*Dear Jordi Salmons, Guillaume Besnard and coauthors,*

*Thank you for the thorough revision of your manuscript. You have satisfactorily addressed the concerns raised by the reviewers.*

*However, in the evaluation of your reply it has come to my attention an important problem that was overlooked in the previous round of review. At different parts of the manuscript you refer to “genetic diversity”, “heterozygosity”, “Ho”, “He”, and “% of polymorphic sites” regarding nuclear RADseq data. After carefully reading all the relevant text and supplementary materials I conclude that in all of these instances you are referring to the same measurement: the individual heterozygosity per base pair, that is, for each individual the number of heterozygous sites over the total of sequenced data (after application of relevant filters). First, the text needs to state this more clearly and use a consistent name for that measurement throughout the entire work. Second, individual heterozygosity is a poor measure of genetic diversity. For instance, it can be affected by the reproductive system (i.e. clonal or selfing reproduction). Expected heterozygosity (per bp, i.e.  $\pi$ ) calculated among individuals of the same forest patch (for comparisons among populations) or over all individuals (for comparisons with other species) is a more appropriate measure and what most readers expect as a measure for genetic diversity, please add this or an equivalent measure to your work. Since the levels of genetic diversity are one of the main results from the work this problem needs to be addressed before the work can be recommended.*

We are grateful to you for pointing out (i) the inconsistencies in which genetic diversity was referred to along the text and (ii) for suggesting additional more comparable measure. We have carefully revised the text to use consistent genetic diversity terminology. As suggested, we now estimated expected heterozygosity ( $H_E$ ) at the population level. The new estimates have been included in Tables 2 & S1 and in Figs S14, S15, S16, and where appropriate in the text. These new estimates also led to slight changes in the results and discussion.

*In addition to this main point there are some other minors points that I would like you to consider:*

*In the discussion you suggest that current landscape structure must have been in place “at least 40 generations” corresponding to “at least ~800 years”. I think there is little justification for those numbers even in the light of the results by Landguth et al., (2010) and Mona et al. (2014). The dynamics of how pattern change through time in non-equilibrium models depends on many unknown parameters (effective population sizes, migration rate...), giving such precise numbers seems misleading. While I agree with the general message and I understand that this sentence was intended to address a point Yurena Arjona raised in her review, I think it would be more appropriate to discuss that the number of generations for the period with data on forest cover (1953-present) represent less than 5 generations, which seems too low to erase the signal of previous population structure (or lack of).*

We indeed suggested such number to address the point Yurena Arjona. Although we based this number by roughly matching our population parameters with the results by Landguth et al. (2010) and Mona et al. (2014), their simulation-based studies have not been designed to answer our particular question. Consequently, the tested parameters and models may not match well *N. spinifolia*'s demography. We agree that this value can be misleading and took your advice to discuss that the number of generations for the period with data on forest cover (1953-present) represent less than 5 generations, which seems too low to erase the signal of previous population structure (or lack thereof).

*Please verify that the description of header for Table S1 is complete and accurate.*

The formatting issue in Table S1 has been corrected.

*In line 617, I suggest to write “geographical distance” instead of “Euclidean distance”.*

The suggestion has been considered.

*Last, I would like also to suggest you considering an alternative wording for fragmentation/forest fragments throughout the text. Since one of the conclusion of the work is that the landscape structure with open areas is a relatively old feature, it is unclear to me whether there was ever an ancient continuous forest in the region subsequently fragmented (presumably by humans). Thus forest patches might be just that, “patches” and not “fragments”.*

We agree with your wise and more accurate terminological suggestion, and changed all occurrences of “forest fragments” to “forest patches” as well as some descriptions of the present vegetation cover as “patchy” instead of “fragmented”. However, we kept the word fragmentation in several occasions where it better describes the process.