

Lille, October 8, 2022

Dear authors and editor,

I am reviewing the second version of this manuscript which has gained in clarity. My first review was already positive, it can only be that way. However, I still have some minor points to raise:

It may seem like nitpicking (or maybe a mistake on my part), whether I agree with the authors that there is clearly some recent introgression, I don't see what makes this introgression "ongoing". Couldn't a past secondary contact at some time generate the observed pattern? Such an intermediate period of migration that is neither "ancestral" nor "current" would allow species to continue to diverge. This does not change the paper at all, but it is to discuss (or reinforce) the fact that there is actually introgression between species whose net divergence is 2.5%. My opinion on the matter being biased, I think that one cannot conclude between "migration (more or less) recent" and "ongoing migration" without an explicit test. Even if in one extreme these two scenarios overlap, there may be some proportion of the current divergence that is due to an accumulation of mutations since the last contact.

There is a methodological point that I still don't fully understand. Box 1 on genomic landscapes of diversity, differentiation and divergence is very instructive on the effects of the proposed scenarios, deserving to be in a text book. However, the methodological application escapes me beyond the verbal explanation. Perhaps the test is explicitly described in a reference that I have not read. I can imagine that a significant/non-significant status + sense of relationship would be sufficient to classify scenarios 1, 2 and (3, 4). But I don't see how the authors distinguish scenarios 3 and 4 with a simple categorical approach.

Concerning the figures, I am still not convinced by the way populations are labelled: the letter p, next to the first 3 letters of the populations/species. This makes the pairs difficult to read, especially figure 2-A: *padepgra*, *palbpgra*, etc ... it must certainly speak to the *Populus* community, but it hinders the reading for outsiders.

In conclusion, the paper is a rigorous study of the evolutionary forces shaping intra/inter-specific genomic patterns, with data still impressive. I will only ask to add in the material and method a link to the reference genome used for the mapping to avoid any surprises if a rather different version is published.

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