

Editor comments (Paolo Giordani)

Thank you for submitting a revised version of your paper. I have still a couple of minor remarks to this version of your ms, that is generally improved.

Among others, the most relevant is the one posed by reviewer #2 when she/he says that "You must also incorporate a very clear statement where you explain that even though you are interested in gene flow, the studies you reviewed use various genetic metrics of genetic differentiation and structure".

Many thanks.

> Dear Paolo, thank you very much for the quick handling of our manuscript. We have now included the requested sentence in the methods section and addressed all additional issues raised by both reviewers. We look forward to your final decision.

Reviewer 1 (Anonymous)

Basic reporting

I am happy with the new version of the manuscript. I have gone through the authors' response to the reviewers and happy with the modifications incorporated. I accept the manuscript in its present form with a few minor suggestions mentioned below, which can be incorporated during proof-reading.

> We are happy that Reviewer is satisfied with our revised manuscript and thank her/him for the additional suggestions made.

P75-79: I suggest simplifying the sentence.

> The sentence has been simplified.

P89: Please check "specie's"

> We have now reworded to "species".

P185: I suggest explaining the term "Electrical resistance" in landscape genetics which is used as an analogy to resistance in a network. This will bring clarification to the readers of the manuscript.

> We have now cited the original paper by McRae (2006) where the term "isolation by resistance" was first introduced.

Reviewer 2 (Anonymous)

Basic reporting

Basic reporting is fine.

Experimental design

Study design is fine.

Validity of the findings

See my general comments below.

Comments for the Author

The new version incorporates most of the previous reviewer comments, but not all. The manuscript generally has improved, however, I still think that one main issue has not adequately been addressed, i.e., the inappropriate use of the term “gene flow”. In your reply to that comment, you basically say that many previous studies have used the term incorrectly, so it’s okay to continue to do so. That is obviously a horrible way to argue. I also don’t see why the definition of landscape genetics by Balkenhol et al justifies your terminology. After all, that definition describes a broad field (in which one process of interest is gene flow), while you are conducting a certain analysis (involving various genetic metrics that are influenced by gene flow, among many other factors) from which you then try to make very specific inferences (concerning gene flow). I am fine with leaving the term in the title, but I still think you should be much more careful in your use of the term throughout the manuscript. You must also incorporate a very clear statement where you explain that even though you are interested in gene flow, the studies you reviewed use various genetic metrics of genetic differentiation and structure; that these are often used as surrogates of actual gene flow estimates; and that genetic differentiation/structure is also influenced by many other processes. This statement should be either in the beginning of the discussion, or in the methods. In your reply, you actually acknowledge that equating genetic structure with gene flow is not straightforward by stating “Genetic structure, on the other hand, may not necessarily comprise gene flow, as it can result from drift acting on isolated populations, adaptive processes or both” – so then why do you think it is okay to act in your manuscript like gene flow and measures of genetic structure are the same?

> **We are happy that the Reviewer finds that our revised manuscript has been improved and thank her/him for the additional suggestions. As requested, we have now included a statement in the methods section, where we stress: “We note that these genetic distance metrics should be considered surrogates of actual gene flow, as they reflect the joint influence of genetic drift and dispersal (Prunier et al., 2017).”.**

Additional /new comments:

“Interestingly, several studies found an effect of habitat suitability on gene flow, suggesting that habitat suitability models are useful when proposing ecological corridors or forecasting the impact of future climate on gene flow (Franklin & Miller, 2009)” – But you should state that this is generally not the case, as many species will still move through habitat that is not suitable to live in. See Scharf et al. (2018, doi: 10.1186/s40462-018-0136-2), Keeley et al (2017, doi: 10.1016/j.landurbplan.2017.01.007), Abrahms et al. (2016; doi: doi: 10.1111/1365-2664.12714), Mateo-Sanchez et al (2015; doi: 10.1007/s10980-015-0194-4), ...

> **We thank the reviewer for highlighting this issue and for the recommended references. We have now modified our original sentence and cited the work by Mateo-Sánchez et al. (2015), as it seems the oldest and most relevant paper.**

“...a limit of two predictor variables that can be simultaneously analyzed (in partial Mantel tests)...” – this is still incorrect. A partial Mantel test can be used to partial out as many covariates as you want, but you can only assess the impact of one variable that you do not partial out. Please correct this statement.
> **We have now reworded this sentence to “ the inability to model the effect of multiple covariates simultaneously (as in a multiple regression)...”.**