Does the seed fall far from the tree? - weak fine scale genetic structure in a continuous Scots pine population

The present study describes the fine scale spatial genetic structure of *Pinus sylvestris* in two collection sites from the same population in south-eastern Finland. The study was well conducted and has a clear methodology appropriate to the question.

The text is clear and well written and presents a relevant and interesting discussion regarding the importance of knowledge on SGS for practical forest management issues.

Minor suggestions were made throughout the text.

Title:

The title says that the study is conducted on a continuous Scots pine population. However, the images of the landscape in Punkaharju area show several patches of land separated by water. Also, the two sampling sites seem to be located in different sides of a series of ridges. In each site, the area is continuous, but considering a bigger picture, it seems to be an area that is naturally subdivided and trees are located in different population patches separated by water.

This is genuine curiosity: could this be considered a continuous population?

I mean, genetically, the study demonstrates that it is a single population. But is that the intention in the title? Or the term "continuous" in the title is referring to the fact that both study sites are in the same area? Because it looks like a very discontinuous landscape, although the study showed that the physical discontinuity of the land does not promote a strong genetic structure.

Abstract

Line 26: While we detected some pairwise relatedness at short distances, the relatedness decreased with increasing distance, as expected.

R: I believe that this sentence would be better written by stating that the relatedness was restricted to a very short distance, and not that it has simply decreased with increasing distance, because it is expected indeed. But I think that the authors wanted to state that relatedness was weak and restricted to a few meters.

Line 32: Detailed empirical estimates of dispersal are necessary both in studying post-glacial colonization and predicting the response of forest trees to climate change.

R: I think this last sentence could be relocated to the beginning of the abstract. It is an important remark to give context to the relevance of the study but it's not a conclusion of this study.

R: No keywords?

Introduction

The introduction is well-written and provides the necessary context for understanding the issue being addressed.

Line 79: As a major source of timber, paper and pulp, Scots pine holds also high economic value.
R: Add reference.

Material and Methods

Statistical analyses are well described and carefully conducted. The chosen estimators are suitable to describe SGS and the marker has sufficient resolution to differentiate genotypes at the individual level.
Regarding spatial distribution of genetic variation, I find it interesting to use the term "gene flow" to describe the exchange of alleles between groups with estimators such as Fst and PhiST and the term "gene movement" to describe the intragroup (intrapopulation) spatial genetic structure.

Line 108: We sampled 469 adult (33–145 years) Scots pines approximately at 20 m distance, with shortest within sampling site distance of 10 and 14 m and longest 464 and 1164 m in Makra and Ranta-Halola, respectively.

R: How many samples were collected on each site?

Line 121: Figure 1. Maps of the sampling sites. Sampled trees are indicated as red dots.

R: Include source of the images in the figure legend. Include more details of the location of the study area.
Suggestion:
Maps of the sampling sites in Punkaharju intensive study site located in south-eastern Finland. Sampled trees are indicated as red dots.

Line 169: "first cousins once removed"

R: what do you mean by "First cousins once removed"?

Results

Line 248: Figure 2 – PCA analysis.

R: The percentage of total variance explained by PC1 And PC2 seems very low. From 0.35% to 0.42%.

Line 292: Figure 4 – Mantel test results

R: Authors chose to present Mantel test results on relatedness versus distance by plotting r^2 values of Mantel test versus each distance class. I find the graphic a bit confusing and hard to interpret. I understand this was done because the test was performed separately for each distance class. But wouldn't it be possible to plot the relatedness values (GRM) versus distance and show the significant r^2 values within the plot, next to the data point?

Lines 254 – 258: Parameters in Ranta appear to be twice as large as in Makra. What could be the reason for this difference? The larger area of the collection site in Ranta? Different population densities?

Line 300: Figure 5. The relation between family relationship classes and spatial distance. ==The pairwise distances of the second degree related individuals in a) Makra and b) Ranta-Halola are shown as red lines.== The distribution of all pairwise distances of individuals in different family relationship classes are shown in c) for Makra (turquoise) and Ranta-Halola (orange). Boxplots show the median (central vertical line), the lower and upper quantiles (boxes), and up to 1.5 interquartile range (whiskers) distances. The family relationships are classified based on pairwise GRM: second degree between 0.177–0.354
(e.g., half-sibling), third degree between 0.088–0.177 (e.g., first cousin), fourth degree between 0.044–0.088 (e.g., first cousin once removed), and unrelated below 0.044.

R: Is there supposed to be another part in this figure? I couldn't find any red lines.

Discussion

The discussion is well constructed and refers to many studies with pines and other tree species, providing a suitable overview for contextualizing the results. Authors refer to both classic studies on the spatial genetic structure of plants and more recent works in the field.
The work is relevant and brings an interesting discussion regarding the effect of dispersion on adaptive potential, which is not usually addressed in an objective way in studies describing the spatial genetic structure of plants.

Line 335: Fine scale genetic structure has previously been found in smaller fragmented Scots pine populations (Robledo-Arnuncio & Gil 2005; Sofletea *et al.* 2020) but here we show this pattern within a large continuous population for the first time.

R: Could this weak SGS be the result of the discontinuous landscape with vegetation patches separated by series of meandering waterways that create unsuitable habitats for seed germination? Therefore, either pollen or seeds can only thrive if they fall close to the parent plant or if they cross larger distances to land on a different ridge with proper conditions to succeed in finding another plant to pollinate or a place to germinate.