Interactive comment on “Dispersal distances and migration rates at the arctic treeline in Siberia – a genetic and simulation based study” by Stefan Kruse et al.

Anonymous Referee #2

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> **We thank the reviewer for reviewing the manuscript and for the helpful comments. We revised our manuscript at the corresponding positions for each specific comment below.**
> **Our response are placed in bold font below each of the reviewer’s comments in italics. Followed by a citation of changed text with a line statement that refers to the version of the manuscript with tracked changes.**

General comments:

> *This paper uses the LAVESI model to explore the rate of northward Larix migration on the southern portion of the Taimyr Peninsula in Siberia. The study uses recent field data collected in the area to drive the simulation work. The focus of the model parameterization/calibration was to improve the Larix dispersal functionality using genetic parentage, and then apply the model to understand how the Larix dispersal characteristics will play out in given some climate scenarios. The site of this modelling work is of particular interest, as it is near the northernmost forest stands where paleoecological records have indicated past presence of trees north of where they are currently found.*
> *Given the unique nature of Larix forests (deciduous conifers linked to continuous permafrost distribution) and the fact that across their broad spatial domain (central and eastern Siberia) this class of trees coincides with marked changes in climate, and the potential for changes in tree distribution to alter the dynamics of high latitude systems (through changes to albedo and permafrost), this study is of great interest. I think the paper is for the most part clear and well-structured. Perhaps there can be some modification of the Discussion based on my main critique.*

Main critiques:

> *1. At the scale of this study, are south-north assumptions of tree migration robust? At fine scales, the migrations may occur according to the patterns of favorable microsites, and primarily be confined to corridors with favorable active layer dynamics, and direct insolation. Such landforms seem important for explaining the current pattern of trees. A study with such an individual model that doesn’t account for the conditions that are associated with the germination, survival, and growth of those individuals that are being dispersed should probably discuss in some detail this issue of the micro-site constraints that may contribute to broad error bars associated with migration rates. In other words, would the velocity of migration change between different microsites? If so, what is the relative prevalence of such favorable sites across the landscape, and how are they connected to the seed sources? These may be questions for follow-up work, and may be beyond the scope of this study, but I think a section in the Discussion could serve as a link between this study and some potentially viable next steps (one that incorporates landforms and micro-sites details).*

We added a discussion about the important microsite effects and seedling survival rates to section 4.3. “Treeline migration rates”. Basically, we implicitly take account for them with our parameterization approach (Kruse et al., 2016). An explicit implementation would of course improve the realisticity of the model’s outcome, but also increase the already high demand of parameters and finding good estimates for them. Nevertheless, testing for microsite effects and implementing them in the model would allow for a detailed study of their impact, but this is out of the scope of this manuscript.

Same response as to comment R3 General comments.

Line 361ff:
“Furthermore, the probability of seeds surviving and forming a seedbank and the survival rates of seedlings strongly determine the colonisation speed. This is linked to the availability of microsites where seedlings benefit from shelter, thus lowering their mortality rates (e.g. Resler et al., 2005; Maher et al., 2006; Germino et al., 2011). These effects are not explicitly simulated but implicitly taken account of by our model parameterisation (Kruse et al., 2016). Migration corridors along rivers are not taken into account but they likely assist colonisation in these landscapes because of deeper active-layer depths close to the rivers and also from downstream seed dispersal (Neilson et al., 2005; Wieczorek et al., 2017). Nevertheless, the positive impact of an increased survivorship on migration rates can be observed in our migration simulation experiments.

The mortality rate ahead of the treeline is lower under homogeneous climate than in the linearly decreasing climate gradient scenario with the consequence that the migration enters the exponential phase earlier (Fig. 6 & 7). In addition, we based our model adaptations on an area that is only one hectare in size and with this we cannot directly assess the long-distance seed dispersal to which to fit our implemented kernel. To account for these cases, we implemented a Gaussian dispersal kernel combined with an exponential shaped with a fat tail (Kruse et al., 2016). In this study, this allows numerous seeds to be dispersed to far distances and led to a higher immigration into the simulated forest plot than observed. In consequence, the simulated migration rate tends to be overestimated.

This comprehensive study from genetic analyses to a model application is a first attempt showing the importance of undertaking these timely model parameterisation studies and should be enhanced by, for example, inferring the parentages for other positions in the treeline ecotone on the southern Taymyr Peninsula.”

2. This area is the northernmost forest ecotone. Some discussion for why this may be the case (paleoecological history) could be interesting and help contextualize predicttions of future treeline velocities.

We added a short history of the treeline at the Taymyr Peninsula and giving likely explanations for the northward expansion and rate, ending with the modern situation.

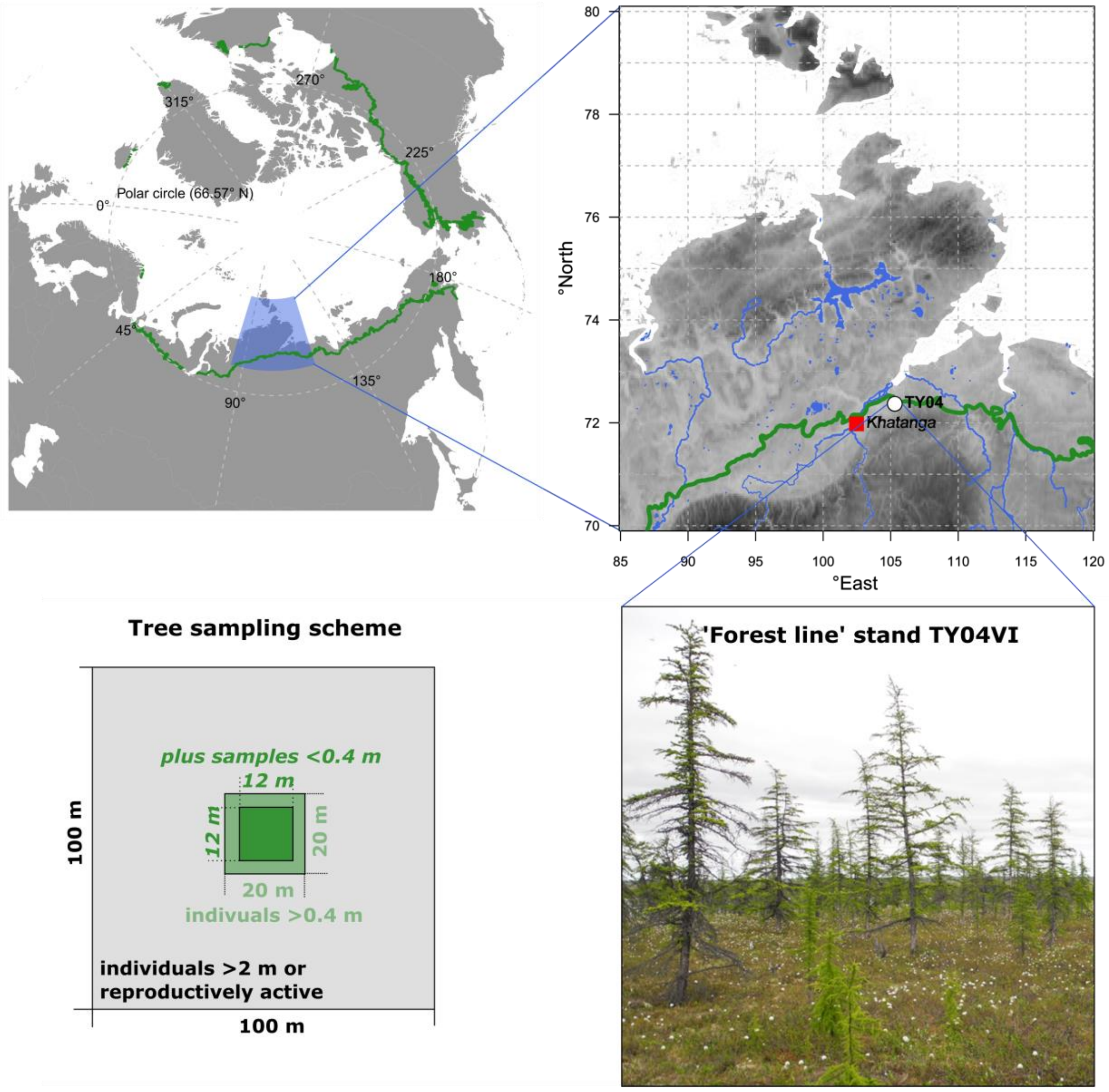
In lines 350ff:

"During the Holocene Thermal Maximum boreal forests expanded on the Taymyr Peninsula to their northernmost position during the Holocene, which was likely assisted by glacial refugial populations ahead of the treeline (MacDonald et al., 2000, 2008). The treeline responded with a centennial lag to environmental improvement, for example solar insolation, and reached its maximum position at ~8000 to 4000 yr BP, and subsequently declined to reach its modern limits around 3000 yr BP (MacDonald et al., 2000). Recently, global warming is ameliorating conditions for *Larix* forests in Siberia and evidence can be found that treeline stands are starting to respond, but at a slower rate than one might expect given the strong increase in temperatures (Wieczorek et al., 2017; Harsch et al., 2009)."

3. In Figure 1, a simple schematic of the sampling design could be useful.

We added a simple sampling scheme of trees for the study site in Fig. 1.

The figure now is in line 93:



Other comments:

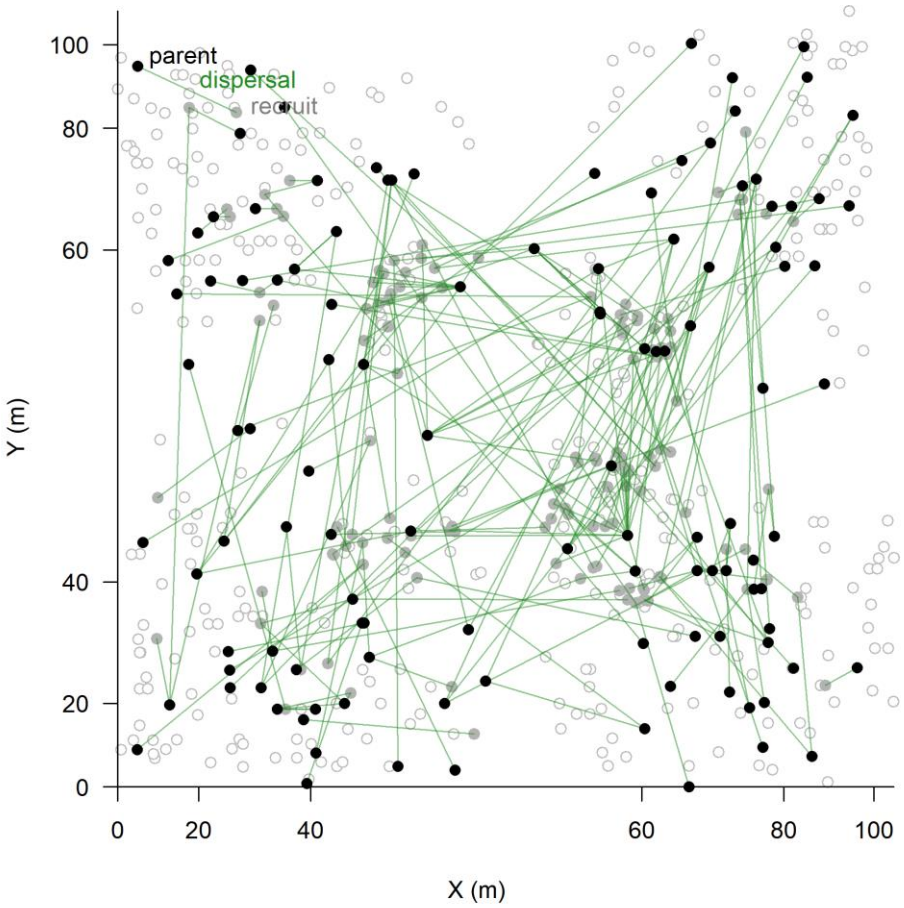
In the abstract, might it be possible to replace some of the technical wording associate with the genetic analysis with other more recognizable terminology that would be more likely to be understood by most of the readers of this journal?

This comment refers to the sentence in line 17. Following the suggestion of the reviewer, we edited this by deleting “highly polymorphic”, which is already a requirement for the parentage analysis that we meet with our eight microsatellite loci. Additionally, we exchanged the word “loci” and used the synonym “marker”.

The text in line 16ff is now:
“We inferred the effective seed dispersal distances of a typical open forest stand on the southern Taymyr Peninsula (north-central Siberia) from genetic parentage analysis using eight nuclear microsatellite markers.”

Figure 4. Nice figure that shows how a few individuals dominate the reproduction. I think it needs to be graphically enhanced. Suggestion: Put an alpha (i.e., transparency) on the green lines, and put the dots on top.

As suggested we changed the transparency of the dispersal connections. Furthermore, we use now lines instead of arrows for a clearer view on the connections. Bringing the dots to the front caused many connections to be hidden. So that we decided to modify the coordinate system by stretched it to zoom in to the plot centre where most recruits and their connection to the parents can now be seen.



Section 4.3 Line 336 - “However, further processes...and should therefore [NOT?] be neglected in simulation studies:...”

Yes, this is a critical point for us. We corrected this mistake in writing.