

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 #1

Received and published: 19 September 2018

We thank the reviewer for the review and 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:

The manuscript by Kruse et al. describes an empirical study of effective seed dispersal using molecular markers which is used to adapt and parametrize a simulation model on larch migration rates at the arctic treeline. The topic of this study is of general interest because estimates for the capability of species to shift their distribution ranges are important for assessing the impact of climate change on many ecosystems. Especially tree species are of interest since they are the foundation species of many ecosystems and exhibit life history traits, which make direct observations difficult. The study offers a nice example for a combined approach with empirical data and simulations although its direct implications are somewhat limited due to the lack of replications and the rather small study site. However, the authors acknowledge these limitations in their manuscript and it will be nice to see some replicates in the future to judge the range of migration rates possible at different locations.

The manuscript is overall well written and clearly structured. The applied methods are well chosen and experiments and data analyses are described in sufficient detail. The results are discussed in a concise way using the available body of literature and conclusions are well founded.

In general the manuscript is of high quality and I have not found any major flaws. Please find below a few specific comments.

Specific comments:

Page 2 lines 53 ff: These sentences are a bit hard to follow. Also it does not immediately become clear that the authors refer only to the Taymyr peninsula. Since there is so much literature on this available, it should maybe added somewhere that this region is well studied, which is a further argument for choosing this region for the study.

We added a reference to the region in focus here and tried to point out in the preceding sentence that this region was in focus for several treeline studies.

Now the text in line 52ff is:

“It represents an ideal study area because the treeline is formed of monospecific tree stands of *Larix Mill.* Taxa and was thus the focus of several treeline studies (IPCC, 2013; Naurzbaev et al., 2002; Sidorova et al., 2010). The response to warming seems to differ with time-scale:

while millennial-scale warming during the mid-Holocene is reflected by a treeline location 200 km further north on the Taymyr Peninsula (Andreev et al., 2002; Klemm et al., 2016; MacDonald et al., 2008), the decadal-scale ongoing warming generates no response (Niemeyer et al., 2015; Wieczorek et al., 2017), possibly because of low seed availability.”

Page 3, lines 70 ff: I suggest to elaborate a bit more on the specific aims of the study here at the end of the introduction. Some aspects have been mentioned in earlier paragraphs but rather indirectly and not specifically related to this study.

As suggested, we edited the final paragraph of our introduction to enhance the visibility of the specific aims of our study.

Lines 75ff are now:

“With this study, we aim at improving seed dispersal and establishment processes in the simulation model LAVESI to make it applicable for simulating treeline migration rates. Therefore, we undertook a genetic parentage analysis of a treeline stand on the southern Taymyr Peninsula by applying an assay of eight nuclear microsatellites to get a reliable estimate of the effective seed dispersal distance (1). This information was used to improve the individual-based model LAVESI (2), which we then ran to simulate treeline advances into the tundra and estimate migration rates (3).”

Page 9, lines 195 f: Is there an explanation how ramet pairs can occur 30 m apart in Larix? How about the chance for full sibs to have identical genotypes?

We carefully checked the possibility of having sampled the same tree again and are confident to not have such a sampling error in our data.

Indeed, it seems a rather far distance, however, further own observations support the existence of ramets even on a longer distance than under the crown.

1. Wind thrown trees can survive (own observations) and most probably produce adventitious roots from their branches when touching the ground (Kajimoto, 2010; Cooper, 1911). If the main stem rots, two separate individuals could be found if both survive.

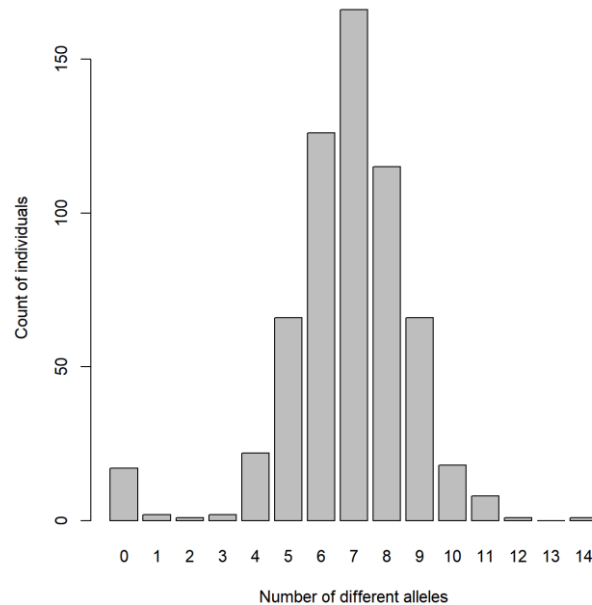
2. Under non-favorable conditions, larches can survive forming krummholtz individuals (Wieczorek et al., 2017, own observations). They grow by producing horizontal branches rather than an upright stem. At these, they could form adventitious roots and again after separating two individuals could be found sharing the same genotype.

Nevertheless, there is a chance that full siblings share the same genotype, but which is quite low especially because we used highly polymorphic nuclear microsatellites that are not in linkage disequilibrium (Kruse et al., 2018). Thus, the probability that two full siblings would have the same given genotype under pure Mendel inheritance (without mutations and recombination) is approximately $\frac{1}{4}$ per locus. In our case this leads to a low chance of 1 to ~ 65536 ($\frac{1}{4}^8$) that full sibs share the same genotype.

Additionally, we cannot rule out that selfing or back-crossing have occurred that could yield to offspring being genetically identical to one

of the parents. If those modes of inheritance occur regularly and would have caused a misidentification of full siblings as clones, we would expect to observe an continuously increasing number of transitional states from identical genotypes (0 different alleles) to sharing 50% of their alleles (8 different alleles). However, it drops from the identified clonal groups to a very low value and increases again beginning at 3 to 4 differences (Fig. R1). This gives us confidence to classify such identical individuals as clones.

Figure R1. For each individual the smallest number of different alleles, binned into 0 to a maximum of 16 alleles.



References:

Cooper, W. S., 1911. Reproduction by layering among conifers. *Botanical Gazette* 52(5):pp. 369–379.

Kajimoto, T., 2010. Root system development of larch trees growing on siberian permafrost. In A. Osawa, O. A. Zyryanova, Y. Matsuura, T. Kajimoto & R. W. Wein, editors, *Permafrost Ecosystems*, volume 209, pages 303–330. Springer Netherlands, Dordrecht.

Page 15, line 320: When I read this, I asked myself if the model includes the case of established individuals ahead of the treeline, which are not able to reproduce, yet, because conditions do not allow this at the moment. When the conditions change, the treeline might progress quite rapidly at first and then slow down. Since I am not familiar with the model in detail, I cannot judge if this is a point worth discussing or a scenario worth simulating.

For simplification and to clearly infer migration rates into tundra we did not allow in our transect simulation experiments survival of individuals ahead of the treeline until year 100.

At some places the presence of krummholtz may enhance migration if such tree island/refugials begin to reproduce sexually. Although not explicitly incorporated, this is partly covered by the homogenous forcing climate that allows long dispersed seedlings to survive with a higher chance ahead of the treeline than in the climate gradient scenario forming faster forest islands within the tundra (see simulation example

in Fig. 2). At the beginning of the simulations the migration rate is only slightly faster but this benefit accumulates over time until the positive effect can clearly be seen at the end of the simulation period (Fig. 6 & 7).

A detailed simulation study for a variety of latitudinal treelines might be worth considering in an extra study in which we could assess responses of different treeline types (e.g. sharp boundary vs. wide transition zone, and the presence/absence of krummholtz).

Page 15, lines 325 ff: The migration rates mentioned here, are they 20-60 m/20-50 m for the entire time period respectively or per year in these time periods? Is it possible to translate the elevational shift into a migration rate comparable to the model?

Migration rates at altitudinal treelines are hardly comparable to those of latitudinal treeline, the climate gradient is much steeper so that still seed sources are closer to the species limit so that climate improvements can lead to faster a migration response up the slope. In comparison, the same climate gradient is very likely thousand times longer on latitudes: 1 °C per ~150 m elevation compared to 1 °C per ~160.000 m latitude for the Taymyr Peninsula.

Because of not being strongly affected by dispersal limitations, they help to understand how treelines could ideally migrate when not limited by seed availability. Nevertheless, other restrictions might become more important for the migration process at these locations such as facilitation (e.g. Martínez et al., 2011).

References: Martínez, I., Wiegand, T., Camarero, J. J., Batllori, E. and Gutiérrez, E.: Disentangling the formation of contrasting tree-line physiognomies combining model selection and Bayesian parameterization for simulation models., *Am. Nat.*, 177(5), E136–E152, doi:10.1086/659623, 2011.

Page 15, line 330: Establishment will for sure be affected not only by density-dependent mortality but also by abiotic conditions and their stochasticity in this extreme region of the planet.

That is right, therefore establishment of seeds dependent on weather forcing and their survival (mortality) implemented as a stochastic process (see details in Kruse et al., 2016).

Technical comments:

Page 5, line 102: “inferred” Why are the microsatellite data described as inferred? To me they seem quite directly measured.

The reviewer is right, the fragment lengths were measured and the parentage was inferred from these data. Accordingly, we deleted the word “inferred”.

Figure 5: The x axis is quite cramped in this figure. Maybe it could be stretched out a bit?

For a better visibility of the plotted results, we show now lines instead of points and stretched the scale of the x-axis.

The figure in line 236 is now:

