Natascha Töpfer
Copernicus Publications
Editorial Support

Dear Natascha,

RE: MS No.: bg-2015-371

Thanks for the useful and constructive comments on the above-mentioned manuscript. Below, please find our response to the suggestions and concerns raised by the reviewer:

Point 1: Bad/complicated style

Response: we rewrote all the sentences required changes and will revise in the final version.

1. P14107L10:
It is controlled by the level of seed dormancy, whereby dormant seeds await germination cues for dormancy release.

2. P14111L4-6:
Germination parameters were estimated from cumulative germination curves fitting a mathematical function known as the four parameter Hill function.

3. P14114L27-28:
Ecosystem zones, representing ecological boundaries in geography, had a greater impact on the variation of seed weight than that of seed dormancy.

4. P14116L5-7:
AUC and phenotypic plasticity under chilling treatment had a moderate correlation (R^2 =0.53, $P < 0.0001$) (Fig. 4), indicating that seeds that germinated after chilling treatment were more plastic. However, when no treatment prior to germination was applied, they yielded a weak and not statistically significant correlation (R^2 =0.04, P =0.3479).

5. P14116L21-22:
Climate change is accelerating plant life-cycle transitions in relation to seasonal changes.

6. P14118L14-17:
The "abundant center" model, which deals with the spatial distribution for populations across species' ranges and its evolutionary potential, also has implications (Volis et al., 2014; Etterson and Shaw, 2001; Parmesan, 2006), that is, compared with core populations, locally adapted peripheral populations had lower adaptive potential and were outperformed in the novel environment.

7. P14118L19-29:
A number of ecologically and evolutionary relevant genes have been identified in Arabidopsis and some annuals, such as *FLC* (Flowering Locus C), *SCR/SP11* (S-locus Cysteine-Rich protein/S-locus Protein 11) (Shimizu et al., 2011; Amasino, 2010), as they provided genetic diversity in adaptive evolution. Moreover, both seed dormancy (genes in ABA and GA signalling circuit) and flowering (such as *FLC*) were modulated by epigenetic mechanisms (Müller et al., 2012; Chinnusamy et al., 2008; Bossdorf et al., 2008). This indicates that epigenetic changes play a significant role in evolution and ecology and the environmental signals acting on genes by epigenetic modification were crucial for life-history traits. In recent years, much progress has been made in uncovering genes operating on different seed compartments i.e., embryo, endosperm, and seed coat, which modulate seed development (Le et al., 2010).

8. P14120L10:

In the long run, only the species that can respond by phenotypic plasticity and/or genetically-based local adaptation can persist.

9. P14120L21:

An optimal balance between adaptive and non-adaptive (bet-hedging) plasticity may exist and possibly vary among populations.

10. P14121L12:

Taken together, we reinforced the importance of climatic signals during seed set to the formation of early life-history traits.

Point 2: In the introduction, I strongly suggest to either add a section on the underlying ecological theory or to introduce some subheadings.

Response: key words have been added to the beginning of main paragraphs in italics in the introduction section.
Paragraph 2- *Seed dormancy and climate.*
Paragraph 3- *Seed size and climate.*
Paragraph 4- *Adaptive and non-adaptive plasticity.*

Point 3: When introducing your statistical tests: I think you should clearly state what do you test (which hypothesis) with which method and why with that method.

Response: Table 1-3 are related to statistic tests. Table 1 is CCA and detailed hypothesis and tests were given in Table S2. Table 2 includes a MANOVA table (a) and an ANOVA table (b) where SOV (source of variance) indicates the target for test and F-value indicates test method. Hypothesis and test for MANOVA are also given in Table S2. Table 3 includes tests for the model (t-test for intercept (beta0) and F-test for other beta's).

Point 4: What are the implications of your findings?

Response: In this paper, the message we intend to deliver is that according to our results, future climate change will result in deeper seed dormancy in white spruce across BC. As per the predicted climate data, winters in 2050s will become warmer and shorter, and this is likely to make the decay of seed dormancy insufficient, thus bringing in adverse consequences for seed emergence and establishment along the seasons. This finding is a good example for the interaction between dynamic environment and phenotype variation and provide information to studies related to assessment of seed transfer and tree adaptation.

Point 5: other specific aspects

P14106L1-2: delete two times the "to"

Sorry, we could not to find this in the manuscript.

P14106L10-11: Aren't the climatic variables and the geographical variables strongly correlated? Did you test this?
This correlation is tested by CCA. Please refer to Table S2 for the test and hypothesis.

P14107L1: "life history traits such as...." give examples and provide a reference for this statement.
Examples and references have been added as follows:

"Life-history traits, known as fitness components due to their predictable monotonic relationship with fitness, are related to the timing and success of development, reproduction, and senescence throughout life cycles [Calow P. 1998. The encyclopedia of ecology and environmental management. New York, Blackwell Science]."

P14107L20: This paragraph seems without any logical connection to the previous one
A key-word subtitle is added to this paragraph.

P14107L23-34: Here you jump from paleoecolgical evidence to observations from the 1950... totally different things, I believe...
The core idea is that the environment plays an important role in seed size development. The paleontology data give evidence that climate change may account for seed size variation, followed by studies of how the impact of environment on seed size variation gradually brings our attention. We attempt to emphasize the importance of environment on seed size variation from the perspective of paleontology and previous studies.

P14108L23: "A continously..."
Modified as suggested.

P14110L12: I am really not convinced that you need so many climatic variables. they will be highly correlsted anyway, right?
ClimateWNA can easily generate many climate variables and each of them has its own specific meaning although many of them might be correlated. We wanted to take the full advantages of this program and let PLS to make selection among the climate variables. PLS is specifically suited for this purpose.

P14110L13: You should really explain what ClimateWNA does.
ClimateWNA has been widely used with over 200 citations according to Google Scholar over the past three years. The program downscales gridded PRISM climate data to scale-free point locations using partial derivative functions with respect to elevation. It also uses a delta method to downscale GCM climate data. Detail description of the methods can be found in Wang et al. 2012.

P14110L20: Since you are using only one GCM, which is always risky and actually not very robust in terms of uncertainty, you should at least explain where in the range of CMIP5 GCMs CCSM4 is located.
CCSM4 is near the average in both temperature and precipitation increases for BC, the study area.

P14114L1: Another very unclear sentence. how can climatic variables not be correlated with environemntal factors related to temperature? and what actually are environmental factors related to temperature if not climatic variables?
Here, we meant "environmental factors related to temperature" NOT "relative to temperature". Because environmental factors mainly include two categories, temperature and precipitation.

P14114L3-5: How do you explain the difference between PLS and PCA?
Please refer to the Methods section L14111L17-22.

P14114L210: providing these cryptical variable abbreviations that are explained in the online material only here and elsewhere in the text doesn't help much to understand your paper...
Explanation for the critical variables is provided in the Methods section (14110L25-27).

P14115L16: Why "presumably" if you put in climate data from a climate model and don't change anything else in your model, it must be a climate effect, right?
Thanks for pointing out. This word is deleted.

P14117L12: "reproduction"
Corrected as indicated.

P14117L18: it's Camille Parmesan, hence "she"
Corrected as indicated.

P14119L20ff: Are these numbers of climate effects across different RCPs? then better to provide the range over the RCPs rather than the mean...
I don't know which line you denote. I guess it should be some line between L16 and L28. Through Fig. S8, you can see the mean and variance for each population. It therefore makes sense if the mean is used for general comparison. Otherwise, I should provide three ranges as per three RCP scenarios.

P141120Ö1-4: Here another one sentence paragraph that seems totally disconnected from the one before.
Actually, in the Discussion, the last paragraph of each subtitled section is used to provide supplementary evidence from the aspect of molecular biology. Its role is parallel to the previously paragraphs.

P14120L12: "evolutionary"
Corrected as indicated.

Table 1: column headings seem to be shifted

Thanks for pointing out. We provided three-line table in the manuscript and this shift happened during typesetting. We will note this in final proof.

Table 3: explain the climatic variables
The full name is given in two places, 14110L25-27 and Table S1. However, have added the full name of the variables.

Figure 3: explain DI
The full name is provided, dormancy index. Detail explanation was given in 14111L7.

Figure 4a: should these not be better boxplots for control and chilling? how can you connect the dots? what do the lines mean?
We provided an explanation in 14115L25-26. This plot reflects reaction norm, and if no phenotypical plasticity exists, the lines should be parallel. We connected the dots for the same population with or without moist-chilling treatment.

Figure 5: lower left panel, should the "good year" part not be black? please explain in the caption what good and bad year mean
No, the black area in the lower left panel should be lower than the grey area, because this parameter is time to germination. Good year takes shorter time to germinate but has higher germination capacity. The meaning of good and bad years is given in 14113L15 (Methods section).