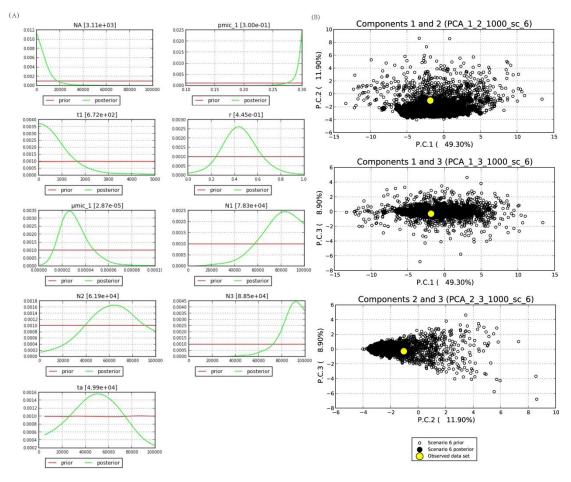Dear Editor,

We are very grateful for providing an opportunity for revising our manuscript (Manuscript -583284). We are also thank you and reviewer for your time and patience as well as your very helpful suggestions and comments. We have received the new comments posted by reviewer3, and we have studied these comments carefully and have made thoroughly corrections in the revised manuscript. We would like to response these comments directly via the review3 system forum, however, we found reviewer 3 review are closed. The followings are the corrections:

(1) The genetic patterns in the paper is similar with previous paper publication in Tree Genetics & Genomes, although two paper have different genetic marker. Therefore, I think the authors could focus mainly on discussion the contribution of environmental heterogeneity to species genetic pattern in the paper.

Reply: We really appreciate for reviewer's advice. In this study, we detected the genetic pattern of *Quercus fabri* based on the 17 nuclear microsatellite loci in 29 natural populations (490 individuals), and we used approximate Bayesian computation (ABC) to detect the demography of populations. In addition, we used the Mantel test and RDA analyses to test whether environment (geography and climate) isolation contributed to the current distribution, and detect the potential differences of ecological niche among the groups. Additionally, according to the reviewer's comments, we have revised this apart in the discussion of manuscript.

(2) As a dominant species in Northern Hemisphere forests, many studies focused on the effects of environment factors on oaks genetic patterns, including oaks from Europe, America and Asia. However, the authors not compare any one of these paper with present result.

Reply: Very thanks to reviewer's suggestions. In the revised manuscript, we have read some *Quercus* species papers carefully, according to the comments, and compared with our result about the effects of environmental heterogeneity on the genetic patterns of *Quercus* species in the California (Ortego et al., 2012; 2015),

and Aisa (Jiang et al., 2018; Gao et al., 2020). We have also discussed these contents in the newly revised version.

Gao, J., Liu, Z.L., Zhao, W., Tomlinson, K.W., Xia, S.W., Zeng, Q.Y., Wang, X.R., and Chen, J. (2020), Combined genotype and phenotype analyses reveal patterns of genomic adaptation to local environments in the subtropical oak *Quercus acutissima. J. Syst. Evol.* 00, 1-6. doi:10.1111/jse.12568

Jiang, X.L., An, M., Zheng, S.S., Deng, M., and Su, Z.H. (2018). Geographical isolation and environmental heterogeneity contribute to the spatial genetic patterns of *Quercus kerrii* (Fagaceae). *Heredity* 120: 219-233. doi: 10.1038/s41437-017-0012-7

Ortego, J., Riordan, E.C., Gugger, P.F., and Sork, V.L. (2012). Influence of environmental heterogeneity on genetic diversity and structure in an endemic southern Californian oak. *Mol. Ecol.* 21:3210-23. doi: 10.1111/j.1365-294X.2012.05591.x

Ortego, J., Gugger, P.F., and Sork, V.L. (2015). Climatically stable landscapes predict patterns of genetic structure and admixture in the Californian canyon live oak. J. Biogeogr. 42, 328-338. doi: 10.1111/jbi.12419

(3) In DIYABC, the upper limit of prior 100,000 is unreasonable for parameter "N3", which was estimated to 88500 (90 CI%: 64,800-98,000), was more closely to the max value. Unreasonable parameter constraints may affect the model selection. However, the authors just resort the Figure S5 in the revised manuscript.

Reply: Thanks very much for reviewer's carefully comment, we are very sorry for our negligence of incomplete picture. We have added model checking for the best model of scenario 6 as Figure S5 in the newly revised manuscript.

Besides, in the process of revision, we re-analyzed ABC according to the reviewer's suggestion. The prior parameter of N3 was increased, and we set the 1000,000 for parameter 'N3', the results seem unreliable (see below Figure). After that, we try to setting 'N3' prior parameter ('200,000' and '300,000'), the results still unreliable. However, our original setting 100,000 for prior parameter, the observed value is located in simulated data set, and the RMAE values for all

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68   Fig. S5

Components 1 and 2 (PCA_1_2_1000)

Components 1 and 3 (PCA_1_3_1000)

Components 2 and 3 (PCA_2_3_1000)

Logistic regression

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