Supplementary Material

# Supplementary Methods

To test for isolation by distance (IBD), Ritland’s method of moments based pairwise relatedness values were subtracted from one (1-relatedness coefficient) to convert the relatedness matrix to a distance matrix. A pairwise geographic distance matrix was calculated using the distm function as implemented in the package geosphere 1.5-18 (Hijmans, 2022) in R. The matrices were then tested for correlation and significance using the mantel function as implemented in vegan 2.6-4 in R, using a Pearson correlation.

# Supplementary Figures

# Supplementary Figure S. Results of STRUCTURE analysis as inferred with pophelper 2.2.9 based on Evanno’s method (Evanno, 2005). (A) Mean log-normal probability (±SD) and (B) Evanno’s Δ*K* in relation to the inferred clusters based on ten replicate runs per cluster.



**Supplementary Figure S2**. Genetic structure of 434 individuals inferred by 540 SNPs under different population models (K=2 to K=10). Plots within transect sites are arranged in decreasing elevation from left to right and separated with white dotted lines.



Supplementary Figure Relationship between genetic distance (1 - relatedness coefficient; y-axis) and geographic distance (x-axis). The inferred pattern is consistent with a scenario of isolation by distance (IBD).



Supplementary Figure S Schematic of the ddRAD sequencing approach following Parchman et al. (2012). Adaptors include adaptor sequence, barcode, cutsite and protector base. Adaptors in color; EcoR1 on the left, Mse1 on the right. The highlighted sequence show the index 1 primer and the read 2 sequencing primer, which corresponds to the reverse complement of the index 1 primer which may cause failure in sequencing the reverse reads. Figure adapted from Parchman et al. (2012), supplementary information RF\_seq\_protocol available at <https://datadryad.org/stash/dataset/doi:10.5061/dryad.m2271pf1>

# Supplementary Table

Table S1 is submitted as excel file.

**Table S1**. List of all samples included in this study and the corresponding metadata. The latter includes identifiers for each sample, the Stillinger herbarium (ID) and the NCBI Biosamples; assigned subspecies, experiments performed, flow cytometry (FCM) information and sampling location. Subspecies were assigned based on the results of the model-based clustering approach (STRUCTURE) under the best-fit model (K=4). Ploidy was assigned based on the relative fluorescence values (RF) and relationships between genome size and chromosome number inferred from Garcia et al. (2008).

# Supplementary References

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