

Figure S1 The shared SNPs among different populations. The black points represent shared SNPs detected in different populations.

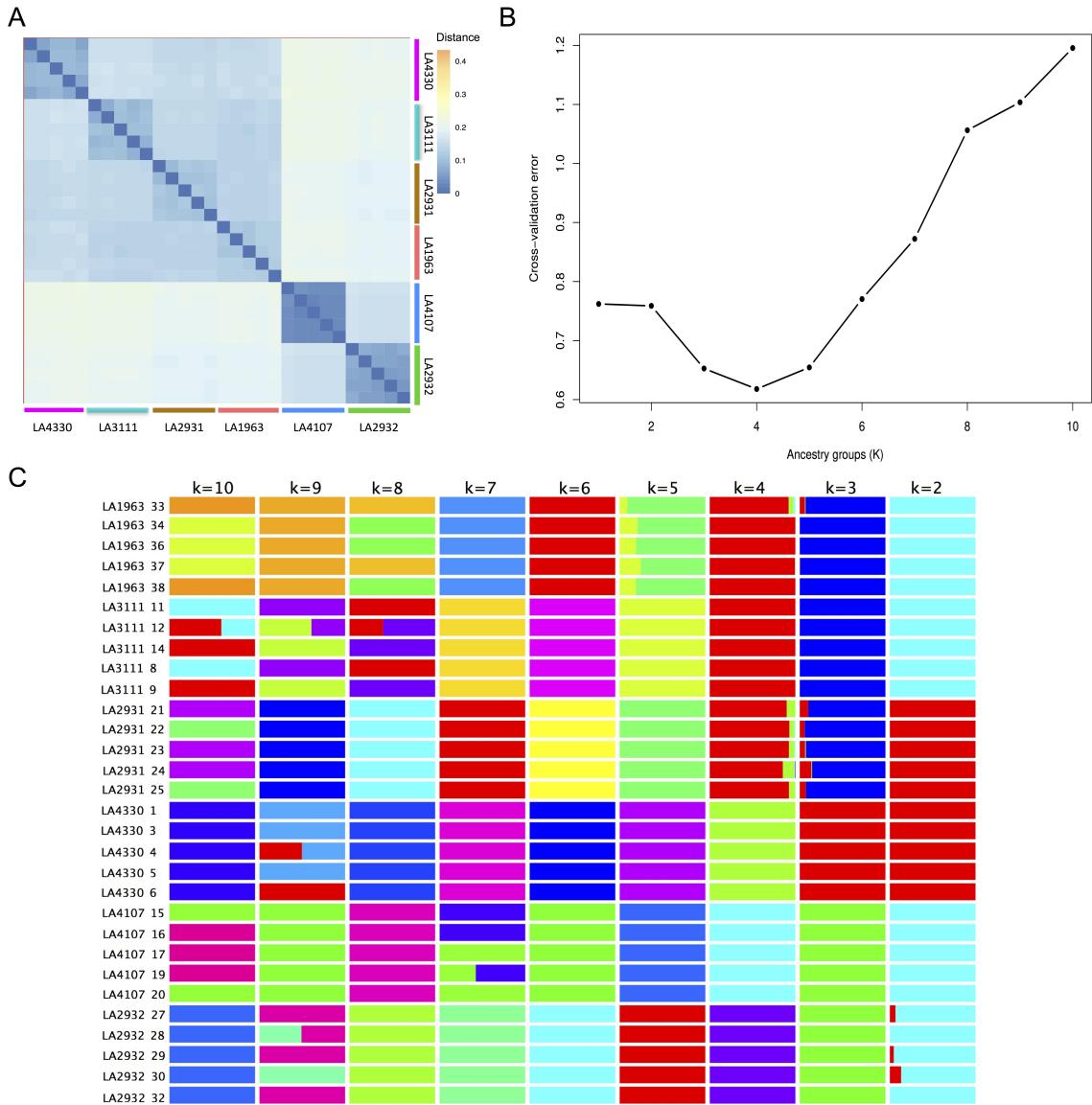


Figure S2 The relationship of different populations. (A) maximum likelihood (ML) phylogenetic tree, *S. pennellii* LA0716 is used as outgroup. (B) The accuracy of prediction for different number of co-ancestry (K). K refers to the number of presumed ancestral groups. (C) ADMIXTURE analysis showing clustering of samples from 30 individuals within K groups (2 to 10). (D) The heatmap inferring the genetic relationship using SNP data from 30 individuals. The genetic distances between pairwise individuals were calculated using Nei's distance by R package 'poppr'. (E) The correlation between genetic distance (Euclidean distance) and geographic distance (Pearson test, $r = 0.354$, $P = 0.281$).

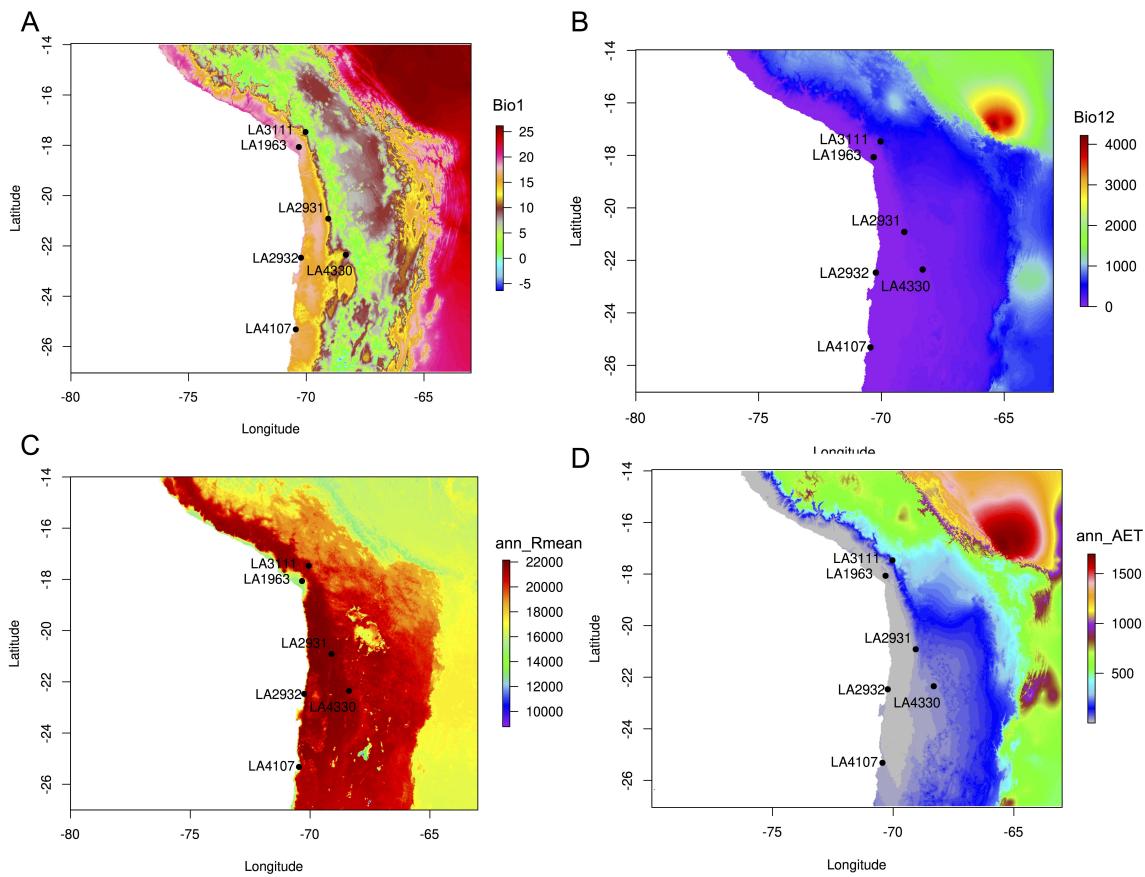


Figure S3 The maps of climatic variables in different populations. (A) annual mean temperature (Bio1). (B) annual precipitation (Bio12). (C) annual mean solar radiation (ann_Rmean). (D) annual actual evapotranspiration (ann_AET).

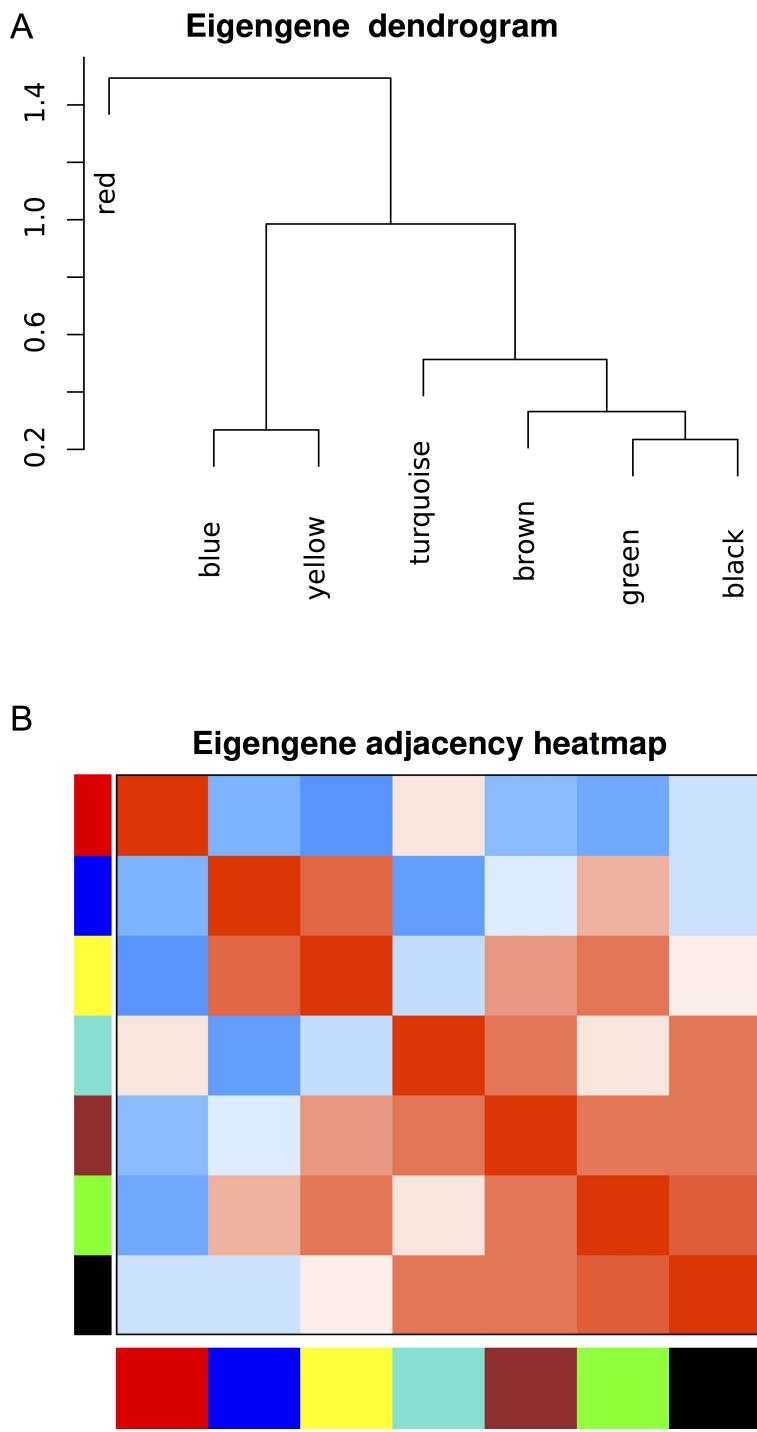


Figure S4 The relationship of different modules using eigengene of each module.