Supplementary material

Supplemental methods:

We used the AFLP data presented in Campitelli and Stinchcombe [1] to evaluate $F_{ST}$ and isolation by distance in the 20 populations used here. For a full analysis of population structure, differentiation, and autocorrelation in AFLP allele frequencies in a larger population sample (77 populations), see Campitelli and Stinchcombe [1]. We estimated $F_{ST}$ using Hickory [2], to obtain both pairwise $F_{ST}$ and credibility intervals. We used the theta-II values from the f-free model of Hickory, which are directly comparable to $F_{ST}$ from Weir & Cockerham’s [3] approach. For the set of 20 populations used here, Hickory utilized 170 AFLP loci. We found an overall average $F_{ST}$ of 0.024 (credibility interval: 0.017 – 0.032). To examine neutral population structure, we regressed pairwise $F_{ST}$ on pairwise geographic distance; $F_{ST}$ was transformed as $F_{ST}/(1- F_{ST})$ for these analyses, following Rousset [4]. We failed to detect any pattern of isolation by distance (P = 0.67; Figure S1).

References for suppemental methods:
**Figure S1:** Plot of isolation by distance, portrayed as $F_{ST}(1 - F_{ST})$ plotted against pairwise geographic distance between populations, based on 170 AFLP loci. The relationship is not significant.
Figure S2a-e: Latitudinal clines in quantitative traits. Plotted are inbred line means for phenotypes against latitude. (A) Anther-stigma distance, (B) Corolla width, (C) Days to flower, (D) Growth rate, and (E) Seed mass.