Global gene flow releases invasive plants from environmental constraints on genetic diversity

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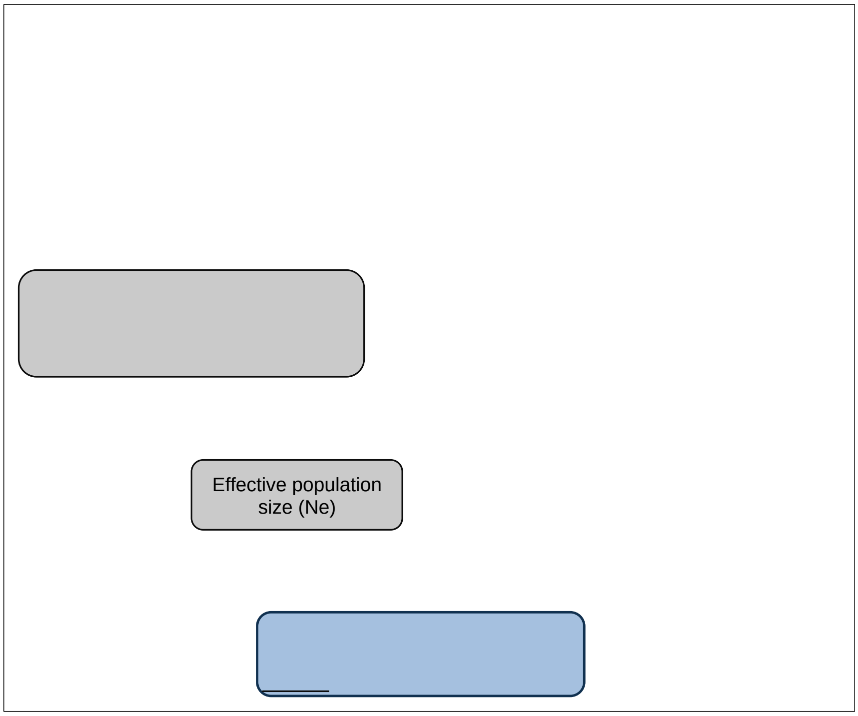
[illegible]


Effective population size (Ne)

Results and Discussion

Hypothesis 1: Dispersal between Populations Will Dilute Demographic Effects on Genetic Diversity. [illegible] ($\sigma = 0.1$ [illegible] 0.2) [illegible] ([illegible], $\Phi_F = 1$ [illegible] 100), [illegible] v v w v . w v , w

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(6, 44).

(42).

(45).

(46),

(36).

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(BayeScan) and two individual-level methods (PCAdapt and LFMM). BayeScan uses a Markov chain Monte Carlo algorithm to examine outlier loci against background values of population differentiation (F_{ST}) among predefined populations (65). PCAdapt and LFMM both define background population structure as K three variables that can influence genetic diversity (Table 1): population density (rosettes per meter^2), fecundity, and empirical population growth rate. For fecundity, we used reproductive effort estimated as the rosette-level inflorescence length × number of flowering stems per meter^2

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