

File S6

Stability and response of polygenic traits to
stabilizing selection and mutation.
Supplementary Information 6

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6 Admixed populations and genetic incompatibilities.

Assume that two populations that are genetically distinct, although with the same mean trait and genetic variance come into contact. The new, admixed, frequencies at each locus i are $p_i^{ad} = \alpha p_i^{(1)} + (1 - \alpha)p_i^{(2)}$, where the superscripts denote the source population, and α is the degree of admixture. Since the trait is additive, the admixed mean trait is the weighted average $\bar{z}^{ad} = \alpha \bar{z}^{(1)} + (1 - \alpha)\bar{z}^{(2)}$. The genetic variance, however, is not additive, thus:

$$\nu^{ad} = \alpha^2 \nu^{(1)} + (1 - \alpha)^2 \nu^{(2)} + 2\alpha(1 - \alpha) \sum_{i=1}^n \gamma_i^2 \left(p_i^{(1)} q_i^{(2)} + p_i^{(2)} q_i^{(1)} \right). \quad (24)$$

Necessarily, n_s and n_f are the same in both populations, and thus have the same genetic variance, $\nu^{(1)} = \nu^{(2)} = \nu$. By distinguishing those alleles that are at the same frequency in both populations, and those that have different frequencies across populations we get:

$$\nu^{ad} = \nu + 2\alpha(1 - \alpha) \left(\sum_{i \in \mathbb{I}} \gamma_i^2 - 2\tilde{n} \frac{\mu}{S} \right) \quad (25)$$

where the set $\mathbb{I} = \{i : p_i^{(1)} = q_i^{(2)}\}$ has \tilde{n} loci. Notice that \tilde{n} is the number of loci that have contrary alleles close to fixation in each population, i.e. $p_i^{(1)} = q_i^{(2)}$. Since $\gamma_i^2 > 2\mu/S$, then $\nu^{ad} > \nu$ the admixed population, has larger genetic variance, and is unfit with respect to any of the source populations (independently of the degree of admixture).