**Introduction**

Evolutionary clines—changes in the frequency of a measurable character (e.g. allele, genotype, phenotype) over a geographical area (Huxley 1938, 1939)—have long served as model systems in evolutionary biology (Endler 1977). Clines arise and are maintained via the interplay of natural selection generating spatial differentiation in morph frequencies, gene flow homogenizing morph frequencies between populations local genetic drift acting within populations (Haldane 1948; Felsenstein 1975; Slatkin and Maruyama 1975; Endler 1977; Saccheri et al. 2008; Volis and Zhang 2010; Takahashi 2015). The multiple evolutionary mechanisms structuring clines has prompted their continued use by evolutionary biologists seeking to explore the relative contributions of non-adaptive and adaptive evolutionary processes in structuring patterns of genetic and phenotypic diversity and differentiation within natural populations.

When clines occur in parallel along repeated environmental gradients, natural selection is often assumed to be the cause, as putative adaptations are unlikely to evolve repeatedly via stochastic forces (Samis et al. 2012). However, it is under appreciated that even parallel clines can occur via neutral processes. For example, local genetic drift in combination with spatially restricted gene flow (i.e. isolation by distance, Wright 1943) can generate clines in single locus traits (Vasemägi 2006). Similarly, serial founder events can generate clines in additive quantitative traits (Colautti and Lau 2015) and phenotypic clines can arise via multiple introductions from a species’ native range during invasion (Keller et al. 2009). Disentangling the relative importance of stochastic and deterministic forces in the formation of clines is thus essential prior to invoking the role of selection in generating adaptive differentiation between populations.