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The effects of linkage and gene flow on local adaptation: A two-locus continent-island model

We study a population-genetic model of evolution in a derived (island) population that experiences altered environmental conditions and maladaptive gene flow from the ancestral (continental) population. It is assumed that locally advantageous mutations have arisen on the island at two linked loci. Gene flow in concert with selection induces substantial linkage disequilibrium. This has a number of consequences for evolution. The central mathematical result is an explicit characterization of all possible equilibrium configurations. From this, we deduce explicit expressions for two measures of linkage disequilibrium. We determine explicitly how the maximum amount of gene flow that admits the preservation of the locally adapted haplotype depends on the strength of recombination and selection. We also study the invasion of beneficial mutants of small effect that are linked to an already present, locally adapted allele. As a consequence of linkage disequilibrium, mutants of much smaller effect can invade successfully than predicted by naive single-locus theory. This raises interesting questions on the evolution of the genetic architecture, in particular, about the emergence of clusters of tightly linked, slightly beneficial mutations and the evolution of recombination and chromosome inversions. Finally, the influence of linkage on the degree of local adaptation and the migration load is explored.

REFERENCES

- [1] Bürger, R., and A. Akerman. The effects of linkage and gene flow on local adaptation: A two-locus continent-island model. Submitted manuscript (2011)