The hybrid zone theory, a universal framework for population genomics

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Abstract

Most species are subdivided by hybrid zones. Overwhelming evidence support this claim and recent analyses of genome sequences have strengthened it as a ubiquitous result of population genetics. Surprisingly,the consequences for the interpretation of population genetics data have remained mainly ignored. I intend to highlight the generality of the hybrid zone framework for population genomics. First, I will argue that hybrid zones of the pre-genomic era, studied with a few markers, represented only a small fraction in the gradient of genomic differentiation between interacting genetic backgrounds. Genome analysis allowed identifying many new cryptic hybrid zones between more loosely differentiated lineages (younger divergence) or more loosely isolated taxa (more porous genetic barriers). Refraining to call them hybrid zones is unfortunate and distracts us from interpreting them in the light of the hybrid zone theory. Second, I will recall two important predictions of the hybrid zone theory that well explain how genetic diversity is structured in space and within genomes. (i) Hybrid zones are expected to be trapped by barriers to dispersal or by ecotones. This explains genetic-landscape associations, even when past vicariance and/or partial reproductive isolation best explain the genetic differentiation. (ii) Hybrid zones are expected to act as semi-permeable barriers to gene flow between heterogeneously differentiated genomes. This explains the usually much higher observed variance of differentiation than the neutral expectation, and the correlation with recombination rates. I will seize the opportunity to dispute against the mistaken belief that selection against migrants could be an effective genome-wide barrier to gene flow. Finally, I will argue that introgression tails emanating from hybrid zones should be accounted for to interpret population genomic data within apparently well-mixed biogeographic regions. There are good reasons why introgression gradients should better correlate with ecological variables or with least cost path connectivity maps than with geographic distance.

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