
Gene flow and landscape ecology

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Abstract

Connectivity is considered an inherent property of landscapes encapsulating gene flow across space. However, its operational use requires the understanding of why, where and how organisms disperse. Such movements, and hence landscape connectivity, will vary according to both organism properties and landscape features. We review whether landscape connectivity estimates could gain in both precision and generality by incorporating three fundamental outcomes of dispersal theory. Firstly, dispersal is a multi-causal process; its restriction to an ‘escape reaction’ to environmental unsuitability is an oversimplification, as dispersing individuals can leave excellent quality habitat patches or stay in poor-quality habitats according to the relative costs and benefits of dispersal and philopatry. Secondly, genetic variation among individuals can result in contrasting dispersal strategies. Finally, dispersal is a major component of fitness under strong selective pressure, which could generate rapid adaptation of dispersal strategies given the genetic variability underlying dispersal. We recommend the use of genetic/genomic tools to assess (i) gene flow intensity and direction among populations in a given landscape; and (ii) which landscape features impact gene flow. Such approaches will provide basic data for planning corridors or stepping stones aiming at (re)connecting local populations of a given species in a given landscape. Although this strategy clearly is species- and landscape-specific, we suggest that a general ecological network could be designed by stacking up such connections designed for several species living in different ecosystems.

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