
Insights from evolutionary genetics of invasive species: introduction routes, bottlenecks and admixtures

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Abstract

The reconstruction of invasion routes with population genetics-based methods has allowed, over the last years, to address fundamental questions in evolution and practical aspects of the management of biological invasions. After providing a brief description of the methods used to reconstruct invasion routes and describing their main characteristics, we will highlight some important features that have arisen from these analyses. In particular, we will focus on the genetic bottlenecks and population admixtures, and their impacts on rapid evolution of invasive species. We will discuss the general importance of genetic drift and its interaction with natural selection during the invasion process, and its peculiar consequences, especially when the mutation load is involved. These aspects will be considered in the light of a particular invasion scenario - the bridgehead invasion scenario -, which had been overlooked until recently. This scenario, in which an invasive population is the source of other invasive populations, is evolutionarily parsimonious and may have played a crucial role in determining the success of many invasive species.

Keywords: Biological invasion, genetic admixture, small populations, bottleneck, introduction routes, population genetics

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