Exploring the contemporary dynamics of gene flow through spatial connectivity: insights from passively dispersing marine coastal species

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Résumé

The living world can be viewed as a wide and complex network in which organisms mediate connections between populations by dispersing heterogeneously over space and time. Many sedentary species rely on the action of winds or oceanic currents for broad-scale dispersal through passively transported propagules (seeds, pollens, larvae, spores, fruits, etc.). As in most cases it is extremely difficult to directly quantify such processes empirically, especially in the marine environment, we can rely on biophysical models that simulate trajectories of virtual propagules among favourable habitat patches by integrating atmospheric or oceanic flow fields. This allows predicting the migratory component of spatial connectivity and appraising gene flow over consecutive dispersal events between subpopulations. Here, we test how modelled gene flow estimates explain genetic differentiation for various marine taxonomic groups, at the scale of both the Mediterranean basin and the global ocean. In particular, we demonstrate that the bimodal dispersal abilities of macroalgae accelerates

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gene flow, as rare long-distance dispersal events induced by rafting lead to pulses of migrants between distant populations, thereby reducing the number of consecutive generations required for effective gene transfer. Moreover, to improve gene flow predictions, we model for the first-time genetic cohesiveness among populations that share a common ancestor. Such spatial coalescent connectivity assesses the relative contribution of gene flow to observed genetic structures across various taxonomic groups (e.g., Teleostei, Mollusca, Crustacea, Anthozoa, Spermatophyta). Our results suggest that the best number of generations to predict gene flow and the spatial extent of observed genetic patterns are tightly linked, shedding light on the typical spatio-temporal scales of connectivity. Finally, we discuss how environmental variability and population dynamics, such as variations in effective population size, migration pulse or carrying capacity, could either mitigate or increase gene flow. In the context of climate-driven biodiversity redistribution, further interdisciplinary research is needed to better understand the eco-evolutionary forces that control the dynamical structuring of populations.

Mots-Clés: Ecological modelling, Oceanography, Macrogenetics, Dispersal