

A genomically-explicit evolutionary modeling approach to study metapopulation adaptive responses under arbitrary connectivity

Gutiérrez Jayson

Flanders Marine Institute (VLIZ), InnovOcean site, Wandelaarkaai 7, 8400 Oostende, Belgium
E-mail: jayson.gutierrez@vliz.be

The demographic connectivity of a metapopulation (*i.e.* an ensemble of populations of the same species distributed across habitable patches) is a crucial factor underlying the ability of the system to undergo evolutionary adaptation to rapid environmental changes, thus enabling evolutionary persistence. Over the last few years, this factor has been increasingly recognized in marine evolutionary ecology as a key optimization objective for the design of robust and adaptable marine protected areas (MPAs). Unfortunately, most methodologies in current use lack the ability to predict future states of metapopulation systems under rapidly changing environments. To quantitatively study this issue, we introduce a flexible, individual-based metapopulation evolutionary simulation framework, which enables explicit modeling of individual genomic features (*e.g.* quantitative trait loci) putatively associated with the development of ecologically important traits, as well as the simulation of age-structured populations of species with larval dispersal mechanisms. Based on this computational framework, we have been conducting numerical evolutionary experiments, under biologically realistic parameter settings inferred for reef-building corals, to investigate the adaptive responses to rising sea surface temperature of metapopulation systems with varying degrees of connectivity. Our results indicate that metapopulations with varying degrees of connectivity can display a great variety of adaptive responses to rapidly changing conditions, highlighting the evolutionary flexibility (*evolvability*) of such complex adaptive systems. For instance, we observe that the worst-performing subpopulation in a metapopulation system typically experiences a large drop in fitness as the temperature increases throughout the simulated evolutionary time window. By contrast, the best-performing subpopulation in a metapopulation system is typically able to successfully track the moving phenotypic optimum, after experiencing a relatively small drop in fitness within a short time period. In general, the overall fitness trend across a metapopulation system highlights its genetic rescue potential, which is likely to derive from the redistribution of pre-existing adaptive genetic variants (*e.g.* thermotolerant alleles) across the entire metapopulation system. Interestingly, under specific conditions, our simulations are able to recapitulate extinction-colonization dynamics for specific subpopulations within the metapopulation system. Overall, our results demonstrate that the size and the connectivity of a metapopulation system can have non-trivial influences on its potential to adapt to novel environmental conditions. The genericity of our genomically-oriented evolutionary simulation approach provides a powerful platform to make projections and forecast future adaptive responses to climate change scenarios of metapopulations of ecologically and economically important marine species from the North Sea, such as the emblematic European flat oyster (*Ostrea edulis*).

Keywords: Marine evolutionary ecology; Marine protected area; Evolutionary persistence; Evolvability; Individual-based simulation; Ocean surface warming