



RECOMMENDATION

Introgression from related species reveals fine-scale structure in an isolated population of mussels and causes patterns of genetic-environment associations

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Based on reviews by:
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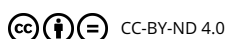
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A recommendation of

Fräisse C, Haguenaier A, Gerard K, Weber AAT, Bierne N, and Chenuil A. Fine-grained habitat-associated genetic connectivity in an admixed population of mussels in the small isolated Kerguelen island. *bioRxiv* 239244 (2018), ver. 4 peer-reviewed and recommended by *PCI Evolutionary Biology*. DOI: 10.1101/239244

Assessing population connectivity is central to understanding population dynamics, and is therefore of great importance in evolutionary biology and conservation biology. In the marine realm, the apparent absence of physical barriers, large population sizes and high dispersal capacities of most organisms often result in no detectable structure, thereby hindering inferences of population connectivity. In a review paper, Gagnaire et al. [3] propose several ideas to improve detection of population connectivity. Notably, using simulations they show that under certain circumstances introgression from one species into another may reveal cryptic population structure within that second species.

The isolated Kerguelen archipelago in the south of Indian Ocean represents a typical situation where the structure of coastal marine organisms is expected to be difficult to detect. In an elegant genomic study, Fräisse et al. [2] take advantage of introgression from foreign lineages to infer fine-grained population structure in a population of mussels around the Kerguelen archipelago, and investigate its association with environmental variables. Using a large panel of genome-wide markers (GBS) and applying a range of methods that unravel patterns



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of divergence and gene flow among lineages, they first find that the Kerguelen population is highly admixed, with a major genetic background corresponding to the southern mussel lineage *Mytilus platensis* introgressed by three northern lineages. By selecting a panel of loci enriched in ancestry-informative SNPs (ie, SNPs highly differentiated among northern lineages) they then detect a fine-scale genetic structure around the Kerguelen archipelago, and identify a major connectivity break. They further show an association between the genetic structure and environmental variables, particularly the presence of *Macrocystis* kelp, a marker of habitat exposure to waves (a feature repeatedly evidenced to be important for mussels). While such association pattern could lead to the interpretation that differentiated SNPs correspond to loci directly under selection or linked with such loci, and even be considered as support for adaptive introgression, Fraïsse et al. [2] convincingly show by performing simulations that the genetic-environment association detected can be entirely explained by dispersal barriers associated with environmental variables (habitat-associated connectivity). They also explain why the association is better detected by ancestry-informative SNPs as predicted by Gagnaire et al. [3]. In addition, intrinsic genetic incompatibilities, which reduce gene flow, tend to become trapped at ecotones due to ecological selection, even when loci causing genetic incompatibilities are unlinked with loci involved in adaptation to local ecological conditions (Bierne et al. [1]'s coupling hypothesis), leading to correlations between environmental variables and loci not involved in local adaptation. Notably, in Fraïsse et al. [2]'s study, the association between the kelp and ancestry-informative alleles is not consistent throughout the archipelago, casting further doubt on the implication of these alleles in local adaptation.

The study of Fraïsse et al. [2] is therefore an important contribution to evolutionary biology because 1) it provides an empirical demonstration that alleles of foreign origin can be pivotal to detect fine-scale connectivity patterns and 2) it represents a test case of Bierne et al. [1]'s coupling hypothesis, whereby introgressed alleles also enhance patterns of genetic-environment associations. Since genomic scan or GWAS approaches fail to clearly reveal loci involved in local adaptation, how can we disentangle environment-driven selection from intrinsic reproductive barriers and habitat-associated connectivity? A related question is whether we can reliably identify cases of adaptive introgression, which have increasingly been put forward as a mechanism involved in adaptation [4]. Unfortunately, there is no easy answer, and the safest way to go is to rely – where possible – on independent information [6], in particular functional studies of the detected loci, as is for example the case in the mimetic butterfly *Heliconius* literature (e.g., [5]) where several loci controlling colour pattern variation are well characterized.

References

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Appendix

Reviews by Tatiana Giraud and Thomas Broquet, DOI: 10.24072/pci.evolbiol.100059