Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges

Recent improvements in the speed, cost and accuracy of next generation sequencing are revolutionizing the discovery of single nucleotide polymorphisms (SNPs). SNPs are increasingly being used as an addition to the molecular ecology toolkit in nonmodel organisms, but their efficient use remains challenging. Here, we discuss common issues when employing SNP markers, including the high numbers of markers typically employed, the effects of ascertainment bias and the inclusion of nonneutral loci in a marker panel. We provide a critique of considerations specifically associated with the application and population genetic analysis of SNPs in nonmodel taxa, focusing specifically on some of the most commonly applied methods.

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Contributors: Helyar, S., Hansen, J. H., Bekkevold, D., Taylor, M. I., Ogden, R., Limborg, M., Cariani, A., Maes, G. E., Diopere, E., Carvalho, G. R., Eg Nielsen, E.
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