Optimising sampling design for the genomic analysis of quantitative traits in natural populations

Jefferson Paril[1], David Balding[1], and Alexandre Fournier-Level[1]

[1]The University of Melbourne

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Abstract

Mapping the genes underlying ecologically-relevant traits in natural populations is fundamental to develop a molecular understanding of species adaptation. Current sequencing technologies enable the characterisation of a species' genetic diversity across the landscape or even over its whole range. The relevant capture of the genetic diversity across the landscape is critical for a successful genetic mapping of traits and there are no clear guidelines on how to achieve an optimal sampling. Here we determine through simulation, the sampling scheme that maximises the power to map the genetic basis of a complex trait across an idealised landscape and draw genomic predictions for the trait, comparing individual and pool sequencing strategies. Our results show that QTL detection power and prediction accuracy are higher when performing a shallow sampling of more populations over the landscape which is done best using pool sequencing. Populations should be collected from areas of high genetic diversity and we recommend against sampling from the margins of the species' range. As progress in sequencing enables the integration of trait-based functional ecology into landscape genomics studies, these findings will guide study designs allowing direct measures of genetic effects in natural populations across the environment.

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