

Ex situ conservation of two rare oak species using microsatellite and SNP markers

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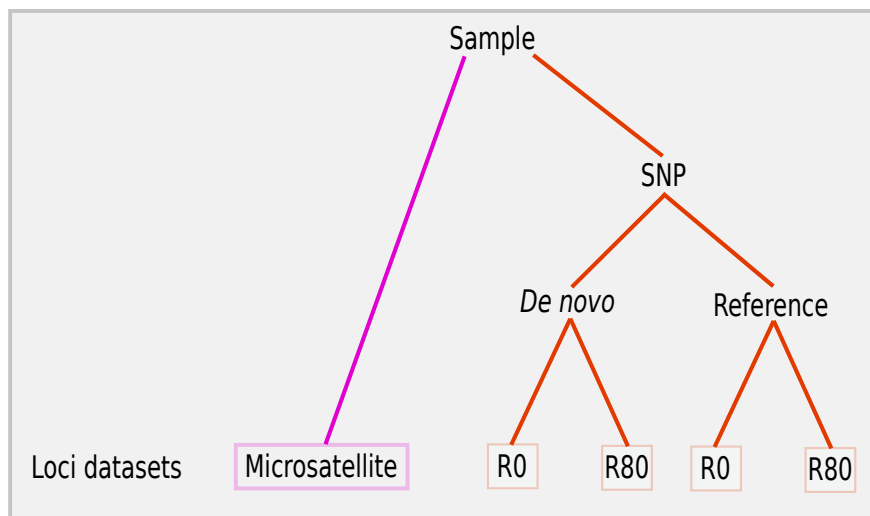
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Abstract

Plant collections held by botanic gardens and arboreta are key components of ex situ conservation. Maintaining genetic diversity in such collections allows them to be used as resources for supplementing wild populations. However, most recommended minimum sample sizes for sufficient ex situ genetic diversity are based on microsatellite markers, and it remains unknown whether these sample sizes remain valid in light of more recently developed next-generation sequencing (NGS) approaches. To address this knowledge gap, we examine how ex situ conservation status and sampling recommendations differ when derived from microsatellites and single nucleotide polymorphisms (SNPs) in garden and wild samples of two threatened oak species. For one species, SNPs show lower ex situ representation of wild allelic diversity and slightly lower minimum sample size estimates than microsatellites, while results for each marker are largely similar for the other species. Missing data filters tend to suggest higher ex situ representation, while the impact of different SNP calling approaches depends on the species and analysis. Measures of population differentiation within species are broadly similar between markers, but larger numbers of SNP loci allow for greater resolution of population structure and clearer assignment of ex situ individuals to wild source populations. Our results offer guidance for future ex situ conservation assessments utilizing SNP data, such as the application of missing data filters and the usage of a reference genome, and illustrate that both microsatellites and SNPs remain viable options for botanic gardens and arboreta seeking to ensure the genetic diversity of their collections.

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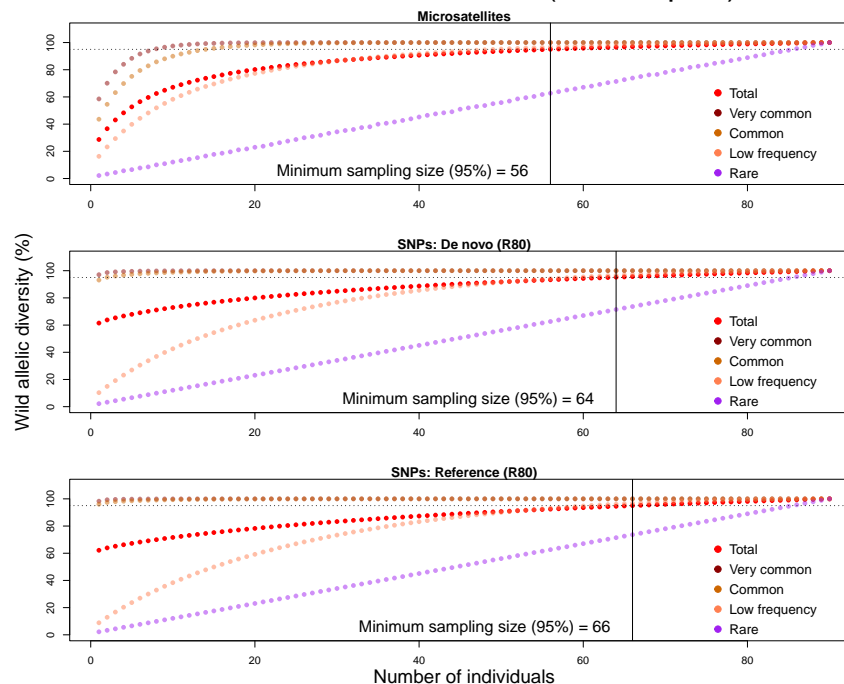
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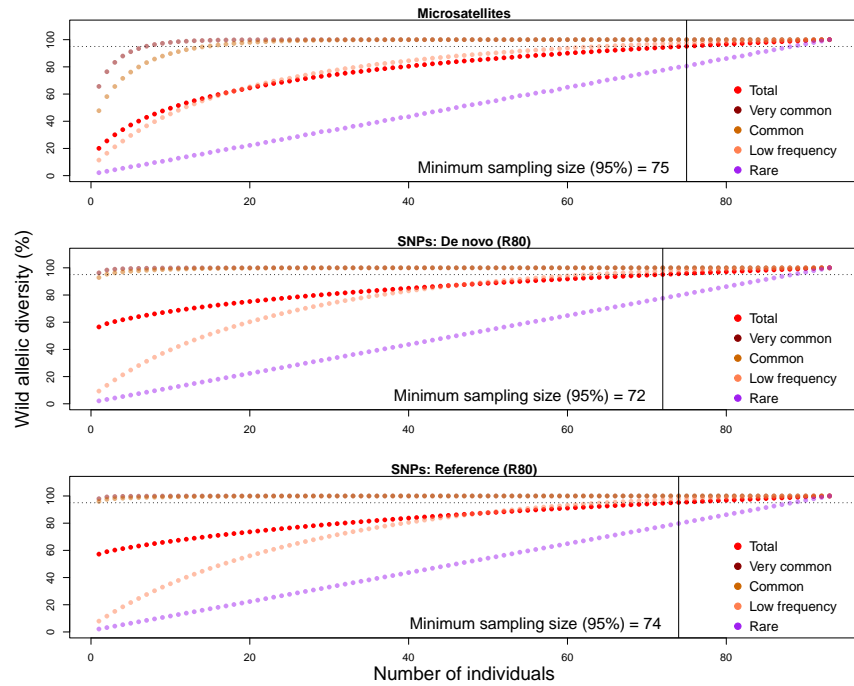
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QUAC: Subset Datasets (91 Samples)



QUBO: Subset Datasets (94 Samples)



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