Uneven genetic data limits biodiversity assessments in protected areas globally

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Résumé

Global conservation targets now include protecting genetic variation within species. Yet few studies examine whether protected areas (PAs) include genetically-diverse populations across multiple species at the global scale. A first step is understanding the availability of population genetic data that could be used in these assessments. We surveyed georeferenced population-level nuclear genetic data across continents and marine biomes (36,354 populations, 2809 species), and found substantial geographic and taxonomic gaps. Most sampled populations were concentrated in Europe and North America, with the largest gaps in Africa and Asia. For most major taxonomic groups, genetic data were only available for $<$ 1% of known species. Globally, 52% of PAs did not contain any genetically sampled populations. These major gaps highlight the need for targeted genetic data collection, harmonization, and sharing to facilitate integrating genetic data in PA assessments and area-based conservation initiatives like 30x30, and better support global genetic conservation targets.

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