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Editorial / Editorial

THE NEW GENERATION OF SEQUENCING AND ITS APPLICATION IN POPULATION GENETICS, PHYLOGEOGRAPHY, AND SYSTEMATICS

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Abstract
The advent of next-generation sequencing (NGS) has dismantled longstanding barriers in evolutionary biology. Once constrained by limited molecular markers, researchers now navigate vast genomic landscapes to reconstruct species histories, map adaptive loci, resolve taxonomic disputes, and investigate plant–microbe interactions. This special issue highlights how NGS tools—from ddRAD-seq to whole-genome skimming—are redefining population genetics, phylogeography, systematics, and ecology, offering insights at scales previously unimaginable.

Population Genetics: Unraveling Diversity and Adaptation

NGS has transformed population genetics by enabling genome-wide characterization of genetic structure. By distinguishing between neutral and adaptive regions, researchers can now describe how demographic processes—such as migration, gene flow, hybridization, and drift—have shaped species diversity. For example, Rodríguez-Gómez *et al.* (2025) used genotyping-by-sequencing to uncover hybridization between *Quercus affinis* and *Q. laurina*. Once demographic histories are inferred, statistical approaches can identify genomic outliers potentially under selection, revealing local adaptation. This information has been used to model population responses to climate change through genomic offset metrics (Fitzpatrick & Keller 2015). Aguirre-Liguori & Góngora-Ayora (2025) applied SNP arrays and climate data to detect adaptive loci in teosintes, identifying populations that may support maize conservation and improvement.

Metabarcoding: Revealing Hidden Microbial Communities

NGS has enabled metabarcoding techniques that uncover cryptic biodiversity and complex microbial interactions. López-Garrido *et al*. (2025) analyzed the phyllosphere of *Cordia dodecandra*, identifying 420 operational taxonomic units and nine consistently present bacterial genera. Sequences of the *nifH* gene confirmed nitrogen-fixing potential in at least six species, highlighting the ecological relevance of these microbial communities.

Phylogeography: Tracing Plant Migrations and Refugia

Early phylogeographic studies relied on Sanger sequencing of mitochondrial or chloroplast markers, limiting resolution (Avise 2000). High-throughput sequencing now allows detailed reconstructions of population histories, geographic barriers, and migration patterns. Aguirre-Dugua *et al.* (2025) used SNPs to investigate diversification and genomic differentiation in the highland conifer *Pinus greggii*, revealing the role of geographic isolation.

Systematics: Resolving Phylogenetic Relationships

From early studies using *rbcL* (Chase *et al.* 1993) and ITS (Baldwin *et al.* 1995), systematics has evolved toward phylogenomics. This methodological progression culminated in the current use of next-generation sequencing (NGS) to reconstruct angiosperm phylogenomics (Guo et al. 2023, Zhang and Ma 2024). NGS provides multilocus data that resolve longstanding taxonomic debates. Gernandt *et al.* (2025) examined *Pinus* subsect. *Ponderosae* using Hyb-Seq, confirming its monophyly despite cytonuclear discordance. Ruiz-Sanchez & Maya-Lastra (2025) revealed two clades in *Olmeca*, corresponding to tropical and montane habitats. Morales-Saldaña & Ornelas (2025) sequenced the complete mitochondrial genome of *Psittacanthus palmeri*, identifying 60 plastid sequences and genes under selection. Cuéllar-Garrido *et al*. (2025) sequenced the plastome of *Ipomoea dumosa*, placing it near *I. quamoclit* and highlighting shared morphological traits.

Challenges and Future Directions

Despite significant progress—NGS is now more accessible than microsatellite development—challenges remain. Sequencing costs and limited infrastructure can hinder research, especially in resource-limited regions. Fortunately, costs continue to decline, and expertise is growing. Computational demands for large-scale analyses are increasing, but more researchers are acquiring the necessary skills. Integrating genomic data with ecological and morphological information remains complex and time-consuming. Interdisciplinary collaboration is essential to standardize workflows and share genomic resources globally.

This special issue exemplifies how NGS is reshaping evolutionary biology. The studies presented offer tools and case studies to inspire future research. We thank the authors and reviewers for their contributions to this collective mission of decoding biodiversity.

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