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Unveiling Brazil's Plant Diversity: A Review of Neutral Genetic Variation

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INTRODUCTION & AIM

Genetic diversity is crucial for the long-term conservation of a species. The fate of a species and its population depends on its genetic variability and how it is distributed among natural populations (Siomos, 2009; Frankham et al., 2002). Various evolutionary forces, such as migration, mutation, genetic drift, and natural selection, influence the genetic variability of species and their natural populations over time, providing a source of adaptive variation (Charlesworth et al., 2017). However, in the short term, there is a lack of information on how the evolutionary process is accelerating and its consequences for many species regarding changes and disequilibrium in speciation and extinction rates (Thomas, 2015).

Brazil is a megadiverse nation with a wide variety of forests that cover many ecosystems and contain a rich diversity of plant life. However, there is still a need for studies on neutral genetic diversity (NGD). The advances in next-generation sequencing (NGS) present a challenge for biodiverse countries with limited funding or incentives for this research technique. In contrast, other countries' advances and funding make local research seem outdated. For instance, neutral traditional markers are considered obsolete as high-impact scientific journals do not accept this type of paper, which describes local genetic diversity and translates it into conservation management planning. However, the knowledge based on NGD from the literature could be used to uncover wild plant diversity.

In this study, we gathered published data on NGD in native Brazilian plant populations to assess the progress made in this field during the 2000s. Our aim was to analyze all available data and utilize this information to develop future strategies for biodiversity conservation in Brazil, taking genetic diversity into account.

METHOD

Scopus database search for published articles in English or Portuguese from 2001 until 2022 with the terms:
((ALL("genetic diversity") AND ALL(plant) AND ALL(Brazil))) AND (marker)

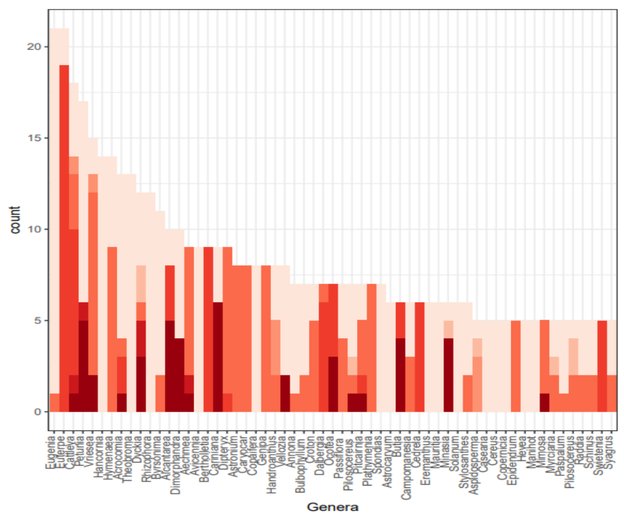
Exclusion criteria:

1) Articles in English and Portuguese;
2) Brazilian native species;
3) Molecular markers used in population studies.

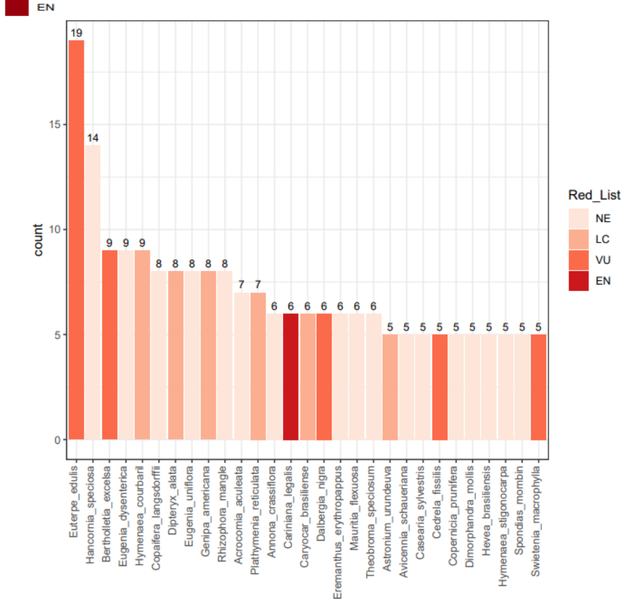
The species taxonomy and habit information were obtained from the Flora and Funga database (http://floradobrasil.jbrj.gov.br/). Conservation status data were obtained in the Flora and Funga database and the IUCN Red List of Threatened Species.
Graphics were created in R software.

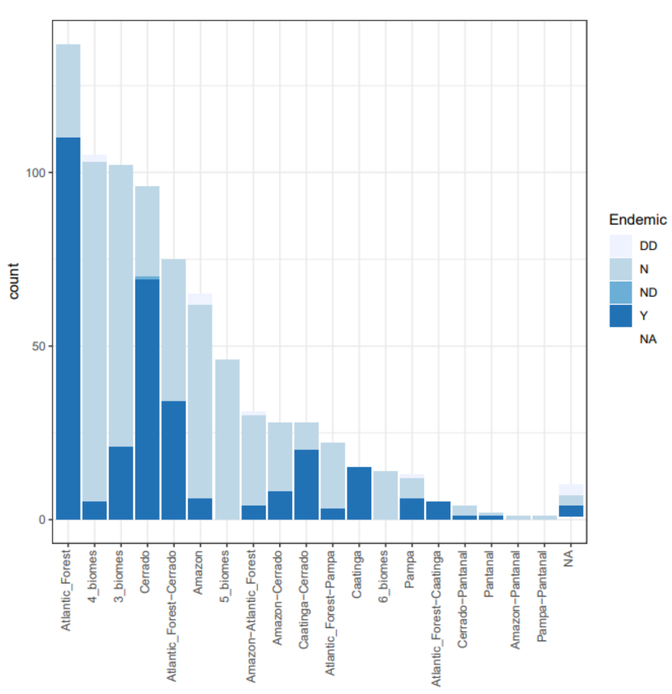
RESULTS & DISCUSSION

The results were based on 651 studies. The most used molecular markers were microsatellites (SSR; N = 340), followed by dominant markers such as ISSR and RAPD (N = 97 and 62, respectively) and SNP (N = 19).



Most studied families were Fabaceae (N = 107); Bromeliaceae (N = 72); and Arecaceae (N = 66). Species are classified as NE (N = 447); LC (N = 173); VU (N = 82); and EN (N = 67). Most species are trees (N = 371); herbs (N = 194); and shrubs (N = 72).





The biomes most studied exclusively were Atlantic Forest (N = 137), Cerrado (N = 96), and Amazon (N = 65). However, many studies encompassed species or populations from more than one biome.Brazilian endemic species were studied in 311 papers, and non-endemic species were studied in 477.

CONCLUSION

This work showed critical gaps in the knowledge of Brazilian plant genetic diversity. Researchers still underutilize the marker SNP. Much effort is directed to a few species, such as *Euterpe edulis* Mart. (heart of palm tree) and *Hancornia speciosa* Gomes (umbu tree), both economically important and broadly found in Brazil. Research efforts should focus on endangered and endemic species. For this, funding is crucial. This kind of information is essential for safeguarding Brazil's irreplaceable plant biodiversity, menaced by climate and landscape changes.

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