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# FROM DNA TO ECOSYSTEMS: WHY MOLECULAR TAXONOMY MATTERS IN ECOLOGY EDUCATION

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**Abstract.** Molecular Ecology has become a key field for understanding biodiversity, evolutionary processes, and ecological interactions. Despite its growing relevance, molecular taxonomy remains largely underrepresented in ecology education. This article argues for the urgent inclusion of molecular approaches in ecology curricula, highlighting how tools such as DNA barcoding, metabarcoding, and bioinformatics can enhance student understanding and professional preparedness. We present didactic strategies, low-cost alternatives, and interdisciplinary project ideas that link molecular methods to real ecological problems. Finally, we propose a research agenda to assess the educational impact of these methods and suggest policy and institutional pathways for broader integration. Including molecular taxonomy in ecology education is not only an academic advancement, but an essential step toward training professionals capable of addressing 21st-century environmental challenges.

**Keywords:** Bioinformatics, DNA Barcoding, environmental DNA - eDNA, Interdisciplinary Science Education, Molecular Ecology

The last few decades have seen the emergence and popularization of Molecular Ecology as an instrumental branch for answering important questions in population ecology, community ecology, behavioral ecology and conservation (Nielsen et al. 2022). The methodological advances in Molecular Ecology have been mainly due to the development of DNA and RNA sequencing techniques and bioinformatics algorithms and tools, which have allowed ecologists to obtain a large amount of biological data and explore complex biological relationships looking for evidence at the genetic level (Mascarenhas et al. 2020).

Among the main applications of Molecular Ecology, we can highlight: i) analyzing the relationship between evolutionary factors (natural selection, genetic drift, mutation and gene flow) and complex ecological interactions such as predation, parasitism and symbiosis (Gaggiotti et al. 2009, Hohenlohe & Phillips 2010, Clark et al. 2018); ii) assessing diversity and genetic structure to investigate the health and functioning of populations (Parsons et al. 2018, Weitemier et al. 2021); iii) detecting and monitoring invasive or endangered species (Le Roux & Wieczorek 2009, Dufresnes et al. 2019, Andres et al. 2023); iv) elucidating interaction networks, trophic ecology and food chains (Machado et al. 2019, Weitemier et al. 2021); and v) understanding the adaptive responses of organisms to environmental changes (Sork 2016, Machado et al. 2020). Among the range of applications of Molecular Ecology, molecular taxonomic identification has occupied a prominent position as an ally to traditional taxonomic methods. Traditional taxonomic methods are often based on the morphology of organisms, which can be a limiting factor in some cases, such as the identification of cryptic species, early or different life stages or the identification of damaged or incomplete specimens (Bickford et al. 2006, Ismailaj et al. 2024).

The use of molecular data, such as DNA sequences, allows for more accurate and reliable taxonomic identification, revealing hidden diversity and improving the understanding of biodiversity (Oualid et al. 2019). Nevertheless, despite its recognized potential, molecular taxonomy is not free of methodological limitations and potential pitfalls. Its correct application requires solid technical expertise, including careful laboratory procedures, appropriate marker selection, robust reference databases, and critical interpretation of results, as inadequate methodological choices may lead to biased or misleading conclusions. Thus, although our understanding of the importance and applicability of molecular methods in ecological taxonomy is indisputable, there is a worldwide shortage of professionals qualified to understand and use these techniques, even in regions with high biological diversity, such as Brazil (Prathapan & Priyadarsanan 2020).

Current ecology teaching still faces important gaps in integrating the technological and methodological advances of recent decades, particularly regarding the use of molecular methods for taxonomic identification and biodiversity analysis. Although comprehensive quantitative assessments of university curricula are still scarce, several studies and expert evaluations indicate that molecular ecology, bioinformatics, and related approaches remain underrepresented in many undergraduate and graduate ecology programs, especially in biodiversity-rich countries such as Brazil (Prathapan & Priyadarsanan 2020). Many courses continue to be strongly anchored in traditional approaches that are largely descriptive and observational in essence, with limited emphasis on analytical frameworks and modern techniques such as DNA sequencing, molecular markers, and computational analyses. This mismatch between the content taught in formal education and the tools routinely employed in contemporary ecological research has been repeatedly highlighted in the literature and results in a significant gap in the training of future ecologists, limiting their ability to keep pace with rapid methodological and conceptual advances in the field (Pevzner & Shamir 2009, Maloney et al. 2010, Pompanon & Samadi 2015, Porter & Smith 2019, Emery et al. 2021).

These curricular gaps result in professionals being trained with a partial and incomplete view of ecological phenomena. By neglecting molecular tools, the opportunity to deeply explore genetic diversity, structure effective conservation strategies and more accurately understand complex evolutionary and ecological processes is lost (Harrisson et al. 2014, Brodersen & Seehausen 2014). Furthermore, the absence of these methodologies limits the ability of future ecologists and teachers to respond adequately to contemporary ecological challenges, such as climate change, biological invasions and other global biodiversity crises (Momsen et al. 2022). The use of molecular methods for taxonomic identification in ecology teaching not only enriches students' knowledge, but also promotes the development of essential skills for biodiversity research and conservation. Another relevant issue is that the lack of practical training in molecular techniques significantly restricts students' technical skills, affecting their future employability and professional effectiveness. In a world increasingly demanding advanced analytical and interdisciplinary skills, this gap can jeopardize not only individual performance, but also the overall advancement of ecology and environmental conservation (Sundberg et al. 2011, Barraquand et al. 2014, Ellwood et al. 2019).

It is therefore crucial to rethink and update ecology curricula and teaching strategies, inserting modern laboratory practices and interdisciplinary approaches that fully integrate molecular methods (Chodkowski et al. 2022). This will provide students with a more robust, holistic and applicable view of ecological sciences, better enabling them to deal with current and future environmental challenges.

Integrating molecular methods into ecology teaching can be done gradually and affordably, even in contexts with limited resources. One practical proposal is the implementation of DNA Barcode species identification laboratories. This type of practice can involve understanding different methods such as PCR (Polymerase Chain Reaction), DNA extraction and sequencing, allowing students to understand in practice how to obtain and analyze genetic material from organisms. In contexts where it is not possible to access DNA extraction and sequencing laboratories, it is possible to use online platforms, open access databases (for example: Nucleotide from the NCBI - https://www.ncbi.nlm.nih.gov/nucleotide/ and BOLD - https://boldsystems.org/) and bioinformatics software (for example: Cipres - https://www.phylo. org/ and Galaxy - https://usegalaxy.org/), where students can analyze pre-existing data, compare DNA sequences from different organisms and build phylogenetic trees, learning to identify evolutionary relationships and classify species based on molecular data as long as they have access to a computer with internet (Venturini et al. 2018).

Another possibility is to use simplified metabarcoding protocols with environmental samples (such as soil, water or animal feces), followed by analysis on free bioinformatics platforms such as DNA Subway (https://cyverse.org/dna-subway) or using R scripts with the DADA2 package using simulated or previously published data (Callahan et al. 2016). These resources can be used to introduce concepts of microbial diversity, species identification and trophic networks, directly linking theoretical content to real scientific practice. Basic bioinformatics concepts and tools can also be learned using the Rosalind platform (https://rosalind.info/problems/locations/). The application of bioinformatics tools in biology and biotechnology teaching is also facilitated by the use of accessible data analysis environments such as Jupyter Notebooks, Galaxy, KBase or KNIME (Liebal et al. 2023). There are also didactic articles and tutorials published in teaching journals that guide the application of these techniques in the classroom, such as those published in The American Biology Teacher, Biochemistry and Molecular Biology Education (McNeil et al. 2018, Fernández et al. 2020, Rumfelt et al. 2020), or even Brazilian initiatives in journals such as Genética na Escola (https://www.geneticanaescola.com/revista), which also has a large collection of articles that involve everything from the proposal of new teaching materials to discussions of the implications that molecular methods can have on society.

In addition, interdisciplinary projects based on real problems, such as monitoring invasive species, diagnosing environmental quality using eDNA, or identifying endangered species in conservation units, can be integrated with Ecology, Genetics and Molecular Biology subjects. This promotes meaningful learning, while at the same time developing technical skills, critical thinking and the ability to work as part of a team. Such approaches contribute to training professionals prepared to deal with the complexity of contemporary ecological challenges, and should be encouraged by curricular policies and innovative pedagogical practices (Nunes et al. 2020, Wei et al. 2020).

Thus, we believe that the inclusion of molecular taxonomy in ecology education is not only a desirable innovation, but an urgency in the face of the environmental and scientific challenges of the 21st century. Genomic tools allow for a more precise and in-depth understanding of ecosystems, which reinforces their importance in training professionals prepared to work in research, teaching and environmental management applied to ecology. The absence of this approach in curricula limits both the training potential and the ability of graduates to respond to the demands of society and science.

For the future, it is essential to promote a research agenda in education that evaluates the effectiveness of teaching strategies based on molecular taxonomy methods at different levels of education. It is also necessary to develop even more accessible and contextualized teaching materials, as well as institutional policies that encourage interdisciplinarity and pedagogical innovation applied to solving real problems in ecology. Only in this way will we be able to train ecologists and teachers who are fully capable of facing contemporary ecological challenges with a solid and up-to-date scientific basis.

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