

Assessing Data Quality in Taxa Sampling: Implications for Evolutionary Biology

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keywords: Africa, phylogenetic data, Eugenia, hot spots, speciation

Main points

- Data Quality in Taxa Sampling
- improving-quality taxa sampling is essential for accurate evolutionary analyses.
- Focus on native vs. endemic species to determine which is more relevant for phylogenetic studies.
- Understanding Species Categories & evolutionary trends
- Speciation & Evolutionary Biology Processes
- Focus on Africa: Evolutionary History and Biogeography.
- African Myrtaceae & Eugenia Case Study
- Phylogenetic Research & Conservation
- I. Visual explanation for
 - Eugenia Distribution & Endemism in Africa
 - Study highlights percentage of native vs. endemic Eugenia species in Africa.
 - Endemism varies across different geographic regions, shaping conservation strategies.

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Question

Recently many studies have highlighted the critical role of the data quality, particularly in taxa sampling. This work explores the data quality problems associated with taxa sampling specifically. to better understand the distinctions between native and endemic species, with the goal of determining which group should be prioritised when reconstructing the evolutionary history of a taxon. It is adopted the software "ChatGPT" to explore the question, "Native vs. Endemism." and to create a comprehensive bibliography list relevant to this topic. We We limited our attention to English-language papers published over the past century and we meticulously verified the resulting publications with personal knowledges. All related papers underscore the importance of preserving global biodiversity for the sustainable use of natural resources.

Numerous reputable websites, such as the Royal Botanic Gardens, Kew species checklist (<https://powo.science.kew.org>), The Plant List (<http://www.theplantlist.org>), and the Missouri Botanical Garden species list (<https://www.missouribotanicalgarden.org>), provide valuable resources by cataloging the taxa of interest and provide valuable support by listing the taxa of interest and restricting research to specific geographical areas or specific taxa requirements, such as introduced, native, or endemic species. Although the distinction of these last categories is not always clearly explained,so these terms are elucidated here. The introduced species are defined as exotic and they naturally belong to a different ecological area. These “not indigenous” species can

be introduced intentionally, for several different utilisations by man as pest controllers, for beauty purposes, or more generally, for several different utilisations or accidentally. However, these species can either have a significant negative impact on the local ecosystem or minimal to no impact on the environment. Moreover, the terms endemic and native plants actually refer to distinct concepts in ecology and biogeography, although frequently used interchangeably. The classic definition of the native taxa reports these organisms to naturally occur and to have evolved in a particular geographic region, but also these types of species can be found in other parts of the world. As a result, native species may have broader distributions, showcasing wider ecological tolerance, or exhibit biogeographic disjunction by naturally occurring in two or more distant areas separated by barriers like oceans or deserts. Hence some taxa are extremely versatile and can live in a wide range of habitats. Their presence is frequently influenced by historical events, such as geological upheavals, climate change and species interactions [1]. Meanwhile, endemic taxa are treated as a subset of native species. The endemic taxa (taxa is a wider term here), which are often restricted to a specific geographic area and can not be nowhere else in the world. These forms have evolved and adapted to unique local conditions, often over long periods of isolation at diverse spatial scales, ranging from small isolated habitats like islands and mountains to larger regions. Understanding the evolutionary history and genetic diversity of endemic species is crucial for developing effective conservation strategies for their evolution[2]. Endemism frequently displays distinct evolutionary histories and adaptations, making these types of taxa highly vulnerable. In fact also, their restricted ranges make them more vulnerable and sensitive to any habitat loss, climate change and invasive species; then, in general, they are more susceptible to extinction [3].

Species concept

The formation of new species is referred to as the speciation process and it is the central concept in evolutionary biology. Mayer [4] described the first species definition, known as the 'biological species concept'

(BSC). Currently, numerous biologists embrace this concept, yet the theory of species formation remains intricate and often contentious. These basic units (species) are actually or potentially interbreeding populations, especially reproductively isolated from other taxa groups. Despite this, the BSC concept primarily focuses just on the morphological or typological aspects of a new species. Although, many models suggest that species evolve due to differences in environmental pressures and genetic changes, particularly evident in small populations. Furthermore, different evolutionists admit that species mostly evolve in either an allopatric mode, where taxa are geographically separated and morphologically differentiated, or a sympatric mode, where differences in organism features, not distance or geographic restrictions, cause species to evolve [5]. In fact, numerous theories emphasise that secondary sexual characteristics in species are responsible for explaining sympatric speciation and consequently, potential evolutionary radiation, followed by ecological adaptation [6]. On the other hand, the allopatric process is commonly categorised into vicariance, which involves geographic isolation and dispersal, where a few members move to new areas and establish different populations. Vicariance is described as a geographic isolation, while the dispersal event occurs when a few members of a species move to a new geographical area and colonise it. Moreover, allopatric speciation is typically subdivided into two major classes: vicariance and peripatric, on the basis of their population sizes and geographic isolating mechanisms (pre/post-zygotic) [7, 8]. Often, a gradual divergence of the taxonomic populations leads to reproductive isolation and the formation of distinct species [9, 10]. As a result, speciation is seen as a complex process influenced by genetic changes, natural selection, mutations and environmental shifts. There are different types of speciation mechanisms, such as allopatric, sympatric and paratactic [11]. In nature, many plants occupy the same habitat but with a strong adaptation to different parameters (like temperatures and soil competition), so the sympatry may restrict them to different niches [12, 13, 14]. This phenomenon could explain why new species are formed, which are genetically and ecologically distinct from their parental populations, allowing them to coexist without being in competition. An interesting study tested this last concept by examining two endemic ginger species on the island of Taiwan, which occupy similar ecological niches. Although the data indicate that these two gingers occupy similar

but not identical ecological niches, the results indicate these two species share the same areas but with altitudinal differentiation and separate dispersal strategies. As a consequence, these parameters are being underlined as potential main factors responsible for shaping and maintaining the island's biodiversity [15]. It has been reported that species overlap more often in sympatric ranges than in allopatric ranges [16], although it's still not clear how species form. Is it through allopatry, sympatry, or more adaptation to different habitats? When it is assumed, the speciation is due entirely to the genetic isolation and then gene adaptation forces; this described process has to be considered only because of an environmental evolution, often known as “the founder effect.” Interestingly, research also revealed that ecological differences, rather than reproductive isolation among species, can foster coexistence [4, 7, 17]. Another intriguing example is due to the remarkable diversity of flowering plants. Their high differences in appearance between closely related plant species have often been attributed to adaptation toward diverse pollinators. Because pollinators are often described as agents of gene flow or selectors [31, 32], it is often thought that the different animals' morphology could prevent cross-pollination of intraspecific plants. An alternative theory is that the wide range of angiosperms (flowering plants) in the world is because they adapt to different environments that have nothing to do with pollinators, so maybe the presence of different niches could be the main cause. Many researchers now believe that habitat isolation among species is a by-product of adaptation to the environment and maybe the primary cause of speciation [17]. Moreover, both the plant's morphology and DNA data can offer common indicators for identifying species. However, more taxon-specific knowledge and methods are needed to make the species distinctions clearer. Recently, it has been suggested that using molecular markers along with phylogenetic methods can give us at least two new types of information to explain the species problem in a new way: how closely related species are to each other and how fast they evolve (i.e., molecular clocks; [18]). Several authors have coined phylogenetic or genealogical species concepts that define species in terms of monophyly, without explicit regard to reproductive barriers, though a new species concept has been more often applied unambiguously to different kinds of taxa data for investigation, avoiding the difficulties associated with diagnosing reproductively isolated species [19; 20]. In fact, phylogenetic

studies play a crucial role in understanding the evolutionary relationships among species to elucidate the evolutionary history of organisms and infer their patterns of speciation, extinction and dispersal [21; 22]. Moreover, in this last era, many organisms are experiencing new and rapid modifications of their environments due to climate change and anthropogenic disturbances, such as habitat fragmentation and the introduction of non-native species [23]. Changing climatic conditions can alter the optimum phenotype in an ancestral range, as well as lead populations to move into new areas and/or expand their ranges. Extreme environmental conditions may reduce or eliminate the morphological plasticity that can accompany speciation [24, 25]. Thus, more disturbance in the landscape can cause habitats to move from older heterogeneity settings to new configurations of environments. As a result, the best niche breadth for species may change [26].

In summary, phylogenetic reconstructions require both native and endemic taxa, as these data are essential to understand the taxa's complete evolutionary processes. In fact, studying observed evolutionary changes and biodiversity patterns is crucial for understanding the speciation process of species and effectively conserving unique biodiversity hotspots [27]. As a result, the increase of worldwide destruction and disturbance of natural ecosystems is thought to be responsible for the species catastrophic extinctions [28, 29]. Therefore, the primary challenge in preserving global biodiversity and habitats is to prevent habitat loss, which often involves estimating species richness and endemism [30].

The reasons to be focus on Africa

Africa encompasses a particularly rich array of flora and fauna that are fascinating to study for their evolutionary history and current biogeography. The distribution and evolution of organisms worldwide heavily depend on the biodiversity of Africa [33, 34]. The remarkable biodiversity found in this country includes many different habitats, ranging from luxuriant rainforest to arid desert, which are populated by unique species well adapted to any specific environmental conditions [35, 36]. Various factors contribute to the dynamic evolution process of Africa,

including its geographic isolation, climatic fluctuations, interactions among the organisms. Africa has undergone significant climate changes over time, including arid periods and glaciation, which have impacted species distribution and adaptation [37, 38, 39]. Today, Africa exhibits a wide range of biological diversity and ecological adaptation, leading to the presence of many unique species and biodiversity hotspots [40]. As a result, human activities like habitat destruction, overexploitation of resources, pollution, climate change pose major risks to biodiversity. Furthermore, the distribution of taxa across continents was shaped thanks to the presence of a very typical land bridge between the Northern and Southern Hemispheres that has facilitated both vicariance and dispersal events [41, 42]. Notably, combining phylogenetic analyses with assessments of endemism and extinction risk can help pinpoint priority areas for effective conservation efforts [43, 44]. In fact, numerous studies on the historical climate changes in Africa and the genetic adaptations of its species can provide insights into the resilience of lineages and their survival strategies for future environmental challenges [45].

In summary, comprehending the evolutionary processes in Africa is vital for conservation initiatives to reduce biodiversity loss and maintain ecosystem health also anywhere else [46].

Why put attention on African Myrtaceae

Reconstructing the taxa phylogenetic tree is a common way to explore the evolutionary relationships within a monophyletic group (clade) [47]. In order to enhance this goal, it has been emphasized in several publications that integrating phylogenetic data from both native and endemic taxa into the data matrix is crucial. This approach allows for a more comprehensive analysis of the data table, elucidating the evolutionary history of the studied group. Furthermore, historical processes like vicariance events, dispersal events and adaptive radiations within the same group can be deduced [48, 49, 50]. As a result, a precise phylogenetic reconstruction of African Myrtaceae can enhance our understanding of the family's evolution and geographical distribution. Reports frequently mention that specific lineages of

Myrtaceae exhibit a higher degree of endemism compared to other African plant species [51, 58]. Many more recent reports on this continent noted that angiosperm phylogenetic diversity is lower in Africa than in South America [72, 73]. Therefore, it is crucial to identify areas at higher risk of habitat loss or fragmentation, as these factors can lead to a decline in distinct genetic diversity. Myrtaceae is considered an old family [52, 53, 54] with many taxa in it, over 5500 species. The family is divided into two subfamilies: Psiloxylodeae, which is the older group and has species that are only found on this continent [55, 56]: because Myrtaceae has some species that are naturally in Africa and a few that were brought there by humans. Daru and his collaborators have localised areas of dense endemism in the Indo-Australian Archipelago, assessing the evolutionary processes that have shaped plant diversity in this biodiversity hotspot [57]. Similarly, Razafimandimbison with other researchers did a study that showed different patterns of diversification and historical biogeographies for the Myrtaceae endemic genera in the Mascarene Islands. Their research revealed the significant influence of geological events and environmental factors on the evolution of various species within the Myrtaceae family [58].

In conclusion, by analysing information on native and endemic taxa of African Myrtaceae, it is possible to have a more profound understanding of the main processes shaping plant evolution and biodiversity in Africa and individualise the conservation priorities for the same African flora [58, 59].

Case study *Eugenia* (Myrtaceae) in Africa

Eugenia (genus) is placed into the Myrteae tribe, which is ascribed to the Myrtaceae family [60, 56], mainly based in the southern hemisphere [61, 51, 56, 53]. Myrtaceae is divided into approximately 5,500 species, 144 genera and 17 tribes, mainly centred in East Asia and with mainly only the Myrteae tribe in South America [55, 62]. *Eugenia* as a genus is part of the hyperdiverse Myrteae tribe [63, 64, 65], known for its two main large genera: *Eugenia*, with about 1,200 species, and *Myrcia*, with approximately 751 species [65, 66].

Eugenia, as a genus, has a broad distribution and high diversity, primarily concentrated in South America. There are significant native and

endemic species in Africa, described in the last area, totalling approximately 160 species, including around 157 native and 21 endemic species [66]. There have been instances of morphological confusion between *Eugenia* and *Syzygium* species within the Myrtaceae [67, 52, 53, 68]. These genera present an interesting gradient but with opposite proportions. *Eugenia* has the highest number of species in South America, reducing towards East Asia, while the *Syzygium* hotspot is in East Asia, graduating towards the western hemisphere and arriving just till the African continent but not beyond (it does not arrive till South America). Several recent studies have concentrated on exploring the phylogenetic relationships within African *Eugenia*, specifically examining the diversity and endemic patterns in this genus [69, 70]. However, *Eugenia* often presents areas with high concentrations of endemic species, which are usually considered of particular concern for conservation efforts. The phylogenetic reconstructions are helpful for elucidating the phylogenetic relationships among species. They also provide useful information about how this diverse genus has changed over time. For example, telling the difference between native and endemic species could help to find places that need the most protection and places that might be in danger.

The paper conclusion remarked that combining phylogenetic reconstructions with consistent data distribution is extremely beneficial for underlining regions with high levels of endemism [71]. Moreover, these actions are important for prioritising different geographical areas for the protection and management of native and endemic species.

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