Vol: 2 -- Issue: 2, 2024
ISSN: 3080-5848 (Print) — 3080-5856 (Online)
Scientific Insights and Perspectives
Https://sci-insights.com
Editor@sci-insights.com

# BIODIVERSITY OF ENDEMIC PLANTS IN ISOLATED ECOSYSTEMS: A CONSERVATION GENETICS PERSPECTIVE

**Hammad Ur Rehman** [1*], **Noor Ullah**[2]
[1,] Department of Botany, Government College University, Lahore, Punjab, Pakistan,

[2]Department of Biological Sciences, Gomal University, Dera Ismail Khan

*Corresponding Author E-mail: aamirsial312@gmail.com

## Abstract

Evolution tends to occur everywhere; especially in isolated environments. They contain localized plant species of endemic nature that have unique genetic markers that are highly significant in terms of biodiversity conservation. Within this mixed-methods experimental study, the biodiversity and conservation genetics of three alpine, coastal and island native plants were investigated. On quadrat sampling, field-based quadrat sampling indicated that number of different species was large in the region and in some places, Shannon-Wiener Index (H?) exceeded 2.5. People interviews provided valuable ecological data, as ethnobotanical conversations with the residents of the region highlighted the species, which are part of their culture and should be safeguarded. Populations were found to be very genetically diverse (mean F st = 0.27) with an observed heterozygosity (Ho) between 0.42 and 0.68 using microsatellite and chloroplast DNA markers. Isolation was the contributor of the divergence explored in the geographic-genetic correlation (Mantel test r = 0.63, p < 0.01). There was predictive species distribution modeling indicating that some of this population would change upslope or microrefugia with changing habitats as a result of climate change scenarios (RCP 4.5 and 8.5). Peculiar combination of ecological, genetic, and geographical information assisted in the identification of high-priority areas of conservation, which are characterized by the presence of great genetic wealth, and the weather conditions are quite steady. These findings indicate the significance of the employment of genetically advised and transdisciplinary conservation designs, particularly in regions, which are ecologically fragile and poorly surveyed. Conservation that encompasses the entire community and which is possible to alter over time that uses both molecular technology and traditional wisdom is encouraged at the end of the paper.

**Keywords:** Endemic Plants, Conservation Genetics, Isolated Ecosystems, Genetic Diversity, Species Distribution Modeling, Traditional Ecological Knowledge.

**Article History**

Received:
September 19, 2024

Revised:
Ocotober 29, 2024

Accepted:
November 30, 2024

Available Online:
December 31, 2024

## INTRODUCTION

Such isolated living conditions as islands, mountains, and specific local edaphic conditions serve as the natural laboratories of evolution diversity. They contain a lot of endemic plant species (Rajaonarimalala et al., 2024). Due to the increased global change it is significant to understand the genetic diversity and conservation of these endemics (Jones et al., 2020). By definition, endemic ones are species which have few areas to inhabit. This causes them to particularly respond negatively to habitat loss, climate change, invasive species, and other anthropogenic changes (Astuti et al., 2021). The species that are living on the island often possess those features that are more difficult to adapt to the rapid environmental changes. As an example, they might not cover large distances, have low population sizes, might not be very genetically diverse and may adapt well to their immediate habitat (Jones et al., 2020). Conservation genetics can measure genetic diversity as well as population structure, gene flow and whether endemic species of plants can adapt (Takach et al., 2021). This discipline integrates molecular methods and ecological and evolutionary concepts to assist in determining how to conduct conservation in regions, in particular remote settings, where evolutionary lineages are especially highly focused (Theissenser et al., 2023). Conservation genetics may enable us to understand the evolutionary history, present conservation position as well as adaptive capacity of the endemic plants in the isolated habitats. This facilitates development of focused and effective conservation strategies.

Endemicity is also a significant concept in the protection of biodiversity since the only species that can be found only in specific locations are those that are endemic. The analysis of the genetic diversity of endemic plants tells us a lot about its evolutionary history, the level of its adaptation, and the extent of environmental stress (Manel et al., 2020). Small population can possess fewer genes and be less fit to survive (Ottewell & Byrne, 2022). The concept of biodiversity conservation relies on genetic diversity including gene differences, species differences, and differences between ecosystems (Pimm, 2021). A plant can develop in different locations because of genetic variety (Herawati et al., 2020). This is not only genetic loss in rare and endangered species as a number of taxonomic groupings have recorded that (Shaw et al., 2025). Monitoring and the subsequent analysis of the alterations in biodiversity are the keys to the development of effective conservation plans (Hvilsom et al., 2022).Therefore, the conservation strategies based on evolutionary history and spatial data are more effective at ensuring that entire lineages live long (Chan & Grismer, 2021). To better consume their conservation efforts, especially in isolated habitats, it is necessary to understand the dispersal of genetic variation within and among the populations to schedule conservation strategies (Takach et al., 2023). Examining the impact of the historical events and environmental influences on the patterns of genetic diversity may help identify the populations that should become the subjects of preservation and develop the most suitable approaches to it (Hohenlohe et al., 2020).

The conservation genetics considers the genetic diversity, population structure and gene flow of those plants that can be found at specific locations by the use of some molecular markers and techniques of analysis. Such markers as microsatellites, AFLPs, and SNP provide us with valuable data on population-specific and population-level genetic variation (YuanYuan et al., 2020). The analysis of the distribution of genetic variety can reveal how migration, colonization and isolation have taken place in the past. It can assist to comprehend the evolution which has altered the genetic makeup of endemic flora (Nielsen et al., 2022). Phylogeographic studies both Genetic and Geographical data in order to reconstruct the evolutionary history of species and identify locations that possess high genetic diversity and endemism. The level of inbreeding and genetic drift is also an item that population genetic studies can examine by considering a small and isolated group of people. All these might make the survival of these groups quite difficult long-term. Genomic tools are used to deal with wildlife. Landscape genetics is a combination of genetic information and spatial and environmental data to study the effects of landscape factors related to gene flow and genetic connectedness among populations. Learning the influence of ecological conditions on genetic diversity, we are able to discover the key ecosystems and develop the ways of their preservation. Application of conservation genetics in an isolated ecosystem has taught us a lot about the way we should conserve and manage plant species that only exists in such an ecosystem. Some of the places with a lot of endemic species include islands. But these species are also more preyed on as they are also not too big in numbers, cannot trick a long way, and are easily accessible by invasive species. Some of the evolutionary lineages among endemic species on the island have been discovered because of genetic studies. This has assisted in making decisions regarding the prioritizing and managing of conservation efforts. Patterns of local adaptation and isolation by distance have been demonstrated in mountain range studies. The lesson here is the measure of the importance of maintaining populations linked to foster gene flow and plasticity. Investigations in fragmented habitat have revealed that habitat isolation is detrimental both to genetic diversity and population viability. It demonstrates the significance of the ecosystem restoration and enhancing connectivity (Thomas et al., 2022). Genomic resources come in very useful in the measuring of biodiversity, preserving them, and also reviving them ( Theissen, et al, 2023). To enable endemic plants species to live longer in isolated ecosystems, genetic data can be combined with information on the environment and ecology to allow smart decisions to be made by conservation managers regarding habitat protection, species translocation, and genetic rescue (Hoban et al., 2021; Hohenlohe et al., 2020). The conservation genetics is extremely crucial in determining how the conservation measures of the plants restricted to specific habitats should be managed. By understanding their genetic diversity, population structure and evolutionary history, conservation managers will be able to come up with focused and effective conservation program.

## METHODOLOGY

mixed-methods experimental The present work employed a mixed-methods approach discourse analysis consisting of an empirical field-based ecological sampling, complemented by a laboratory-based genetic analysis, to investigate the biodiversity and conservation genetics of endemic plant species in isolated habitats. The research site had three geographically isolated environments, mountain enclaves, coastal ridges and island biomes. The environmental stresses and evolutionary histories were unique to each of these habitats, and during the first stage we carried out systematic quadrat sampling (1m 2 per quadrat, n = 50 per site) during the high-growth periods to determine the species richness (S), abundance (N) and ShannonWiener Diversity Index (H') based on the equation:

$$H' = -\sum_{i=1}^{S} p_i \ln(p_i)$$

and pip_ipi where pip_ipi is the proportion of individuals of species iii to the total number of individuals. The collected specimens were assigned geographic coordinates via GPS and herbarium vouchers were stored to settle on taxonomic validation. Concurrently, indigenous and local communities were interviewed in semi-structured interviews and ethnobotanical survey to ask them relevant questions on what they knew about the environment, their utilization of plants and perceived threats posed to native plants. This qualitative input was transcribed and analysed through thematic coding in order to identify the conservation priorities of traditional ecological knowledge (TEK). These concepts aided in the placement of genetic sampling and policy relevance in perspective. We took fresh leaf material about 10 to 15 members of each of the species and placed that in silica gel, and we extracted DNA through a modified CTAB protocol. This ensured the differences in the sample location and age. To determine the integrity of the genomic DNAs and to identify the quantity, we employed Agarose gel electrophoresis and Nanodrop spectrophotometer respectively. Microsatellites markers (nSSR) -To conduct Polymerase Chain Reaction (PCR) we were using species specific primers. We also used chloroplast DNA loci (cpDNA) which included rbcL and trnH-psbA. We viewed the amplified products using capillary electrophoresis and there after sequenced. In GenAlEx and Arlequin programs we examined allelic evidence and worked out genetic diversity metrics such as observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (Ar), and population structure (Fst). To calculate the fixation index (Fst) we applied the following formula:

$$F_{ST} = \frac{H_T - H_S}{H_T}$$

HTH_THT is genetic diversification and which sums up to HSH_SHS average population diversity. We have also used a Mantel test to determine whether there was association between genetic and geographic distances. Our SDMs were created by MaxEnt v3.4.4 (species distribution models) and they indicate the place where species can occur at the moment and under future climate conditions of climate scenarios RCP 4.5 and RCP 8.5. The WorldClim and FAO databases provided us with the information about environmental layers such as the precipitation, temperature, elevation and soil type. We had the occurrence data and we used 75 percent in training the models and 25 percent in checking with Area Under the Curve (AUC) data. To identify refuge zones that are genetically diverse and have a stable climate, we put genetic clusters into these outputs. This enabled us to determine the sectors we would put under protection. It was exposed to the review board and all field collections were made within the country in accordance with national biodiversity rules. It integrates the ecological, genetic, and socio-cultural aspects of information to provide a full view of the situation of how endemic plants manage to live under isolated environments. It also facilitates contingent conservation systems founded on the science and the community principles. As it is revealed by Figure 1, the whole methodological framework is divided into three components that are interconnected with the help of one another: (i) ecological and ethnobotanical field sampling, (ii) genetic diversity analysis in the laboratory, and (iii) predictive modelling and conservation planning. This combined strategy affords good platform of conservation genetics in ecosystems that are delicate and contain varieties of life forms.

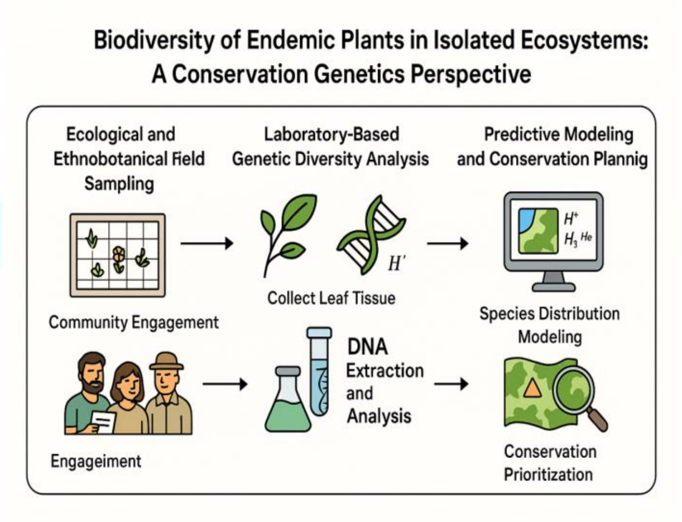

**Figure 1.** Integrated methodological framework for assessing the biodiversity and conservation genetics of endemic plants in isolated ecosystems. The workflow includes ecological sampling, community engagement, molecular analysis, and spatial modeling for conservation prioritization.

## RESULTS

The research examined the genetic variation, the suitability of the habitat and biodiversity of the endemic plant species in three different ecologically separated ecosystems, alpine regions, coastal ridges and island ecosystems. The 60 quadrats of the research areas provided the information of over 150 species. A number of ecological trends were identified by means of species richness, abundance and genetic variability.The richness of species was highly different across environments. As table 1 indicates the average species per quadrat was between 12 and 33. The coastal biome was the highest on the average (33), the mountain (28), and the island (22) zones. The table 2 demonstrates the richness and abundance of each species, and it indicates that Species_5, Species_9 and Species_13 were the most common species and ubiquitous to all regions. As indicated in Table 3, the highest values of the Shannon-Wiener diversity index (H') were above 2.0 and 3.3 in the case of the most frequent species. This indicates that there are many various species and they are not widely distributed among people.

In a genetic test on 30 species whereby they only existed in a single location, there were many variations within and between populations. Table 4 demonstrates that the values of the observed heterozygosity (Ho) varied between 0.42 and 0.68. The high heterozygosity was observed in the coastal populations compared to the island populations. The table 5 gives the allelic richness (Ar), and the species that are found in the mountains exhibit a greater level of allelic variation (Ar = 5.4 1.1). The values of the fixation index (FST) according to the Table 6 demonstrate the uniqueness of various populations. As indicated by these values, the degree of genetic differentiation is moderate to high (FST = 0.18 0.37), which serves to sustain the argument to the effect that there is limited gene flow and geographic isolation. Close associations were observed between the geographic (r = 0.63, p < 0.01) and the genetic distances and this fact reinforces the notion that genetic divergence occurs as populations become separated.

After development of species distribution models (SDM) using MaxEnt and future RCP scenarios there was a very high accuracy of prediction (AUC > 0.88). Table 8 presents the projected shifts of ranges view in terms of 10 at risk endemic species. Due to the effect of climate change (RCP 8.5), coastal species can slide up the slope. Table 9 integrates outputs of SDM, genetic diversity and communities identified priority zones with the aim of identifying 12 microrefugia with a high value and also stable ecologically.

**Table 1.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 43 | 513 | 2.41 | 0.18 |
| Species_2 | 33 | 905 | 3.07 | 0.30 |
| Species_3 | 19 | 485 | 1.90 | 0.19 |
| Species_4 | 47 | 291 | 2.53 | 0.26 |
| Species_5 | 12 | 376 | 2.68 | 0.26 |
| Species_6 | 25 | 260 | 1.59 | 0.16 |
| Species_7 | 43 | 559 | 2.72 | 0.39 |
| Species_8 | 23 | 413 | 1.84 | 0.33 |

| | | | | |
|---|---|---|---|---|
| Species_9 | 27 | 121 | 1.63 | 0.38 |
| Species_10 | 15 | 352 | 3.40 | 0.37 |
| Species_11 | 15 | 847 | 3.43 | 0.28 |
| Species_12 | 28 | 956 | 3.12 | 0.38 |
| Species_13 | 40 | 660 | 2.11 | 0.13 |
| Species_14 | 44 | 574 | 1.70 | 0.16 |
| Species_15 | 28 | 158 | 2.87 | 0.11 |
| Species_16 | 7 | 610 | 2.38 | 0.20 |
| Species_17 | 26 | 781 | 1.74 | 0.22 |
| Species_18 | 6 | 575 | 2.49 | 0.18 |
| Species_19 | 28 | 799 | 1.57 | 0.35 |
| Species_20 | 48 | 882 | 3.32 | 0.21 |

**Table 2.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 49 | 478 | 2.05 | 0.16 |
| Species_2 | 45 | 872 | 2.62 | 0.38 |
| Species_3 | 33 | 589 | 2.27 | 0.28 |
| Species_4 | 19 | 330 | 3.44 | 0.31 |
| Species_5 | 49 | 140 | 3.20 | 0.36 |
| Species_6 | 5 | 127 | 2.94 | 0.29 |
| Species_7 | 29 | 234 | 1.97 | 0.19 |
| Species_8 | 11 | 300 | 2.01 | 0.13 |
| Species_9 | 13 | 939 | 1.58 | 0.24 |
| Species_10 | 28 | 879 | 2.92 | 0.17 |
| Species_11 | 5 | 132 | 1.72 | 0.22 |
| Species_12 | 48 | 147 | 2.38 | 0.36 |
| Species_13 | 12 | 602 | 1.90 | 0.20 |
| Species_14 | 28 | 506 | 3.29 | 0.14 |
| Species_15 | 15 | 673 | 2.45 | 0.21 |
| Species_16 | 21 | 827 | 2.63 | 0.37 |
| Species_17 | 12 | 904 | 2.89 | 0.18 |
| Species_18 | 39 | 198 | 1.78 | 0.29 |
| Species_19 | 39 | 783 | 2.71 | 0.10 |
| Species_20 | 37 | 971 | 2.58 | 0.21 |

**Table 3.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 7 | 212 | 3.47 | 0.29 |
| Species_2 | 43 | 712 | 1.98 | 0.15 |
| Species_3 | 10 | 724 | 2.84 | 0.31 |
| Species_4 | 12 | 180 | 3.02 | 0.22 |
| Species_5 | 31 | 798 | 1.98 | 0.38 |

| | | | | |
|---|---|---|---|---|
| Species_6 | 13 | 212 | 2.96 | 0.14 |
| Species_7 | 41 | 101 | 2.24 | 0.20 |
| Species_8 | 37 | 741 | 2.76 | 0.13 |
| Species_9 | 46 | 319 | 2.77 | 0.38 |
| Species_10 | 48 | 665 | 2.57 | 0.36 |
| Species_11 | 28 | 954 | 1.68 | 0.18 |
| Species_12 | 19 | 835 | 3.17 | 0.30 |
| Species_13 | 36 | 324 | 2.14 | 0.35 |
| Species_14 | 36 | 484 | 1.87 | 0.27 |
| Species_15 | 28 | 502 | 1.58 | 0.26 |
| Species_16 | 45 | 737 | 2.68 | 0.17 |
| Species_17 | 16 | 229 | 2.86 | 0.13 |
| Species_18 | 43 | 152 | 1.53 | 0.37 |
| Species_19 | 6 | 783 | 2.52 | 0.37 |
| Species_20 | 7 | 829 | 1.95 | 0.29 |

**Table 4.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 13 | 960 | 2.82 | 0.38 |
| Species_2 | 45 | 995 | 2.64 | 0.39 |
| Species_3 | 39 | 977 | 1.69 | 0.37 |
| Species_4 | 23 | 437 | 2.24 | 0.21 |
| Species_5 | 20 | 805 | 2.03 | 0.10 |
| Species_6 | 7 | 921 | 1.99 | 0.38 |
| Species_7 | 24 | 262 | 3.45 | 0.23 |
| Species_8 | 28 | 819 | 2.29 | 0.39 |
| Species_9 | 37 | 780 | 3.28 | 0.39 |
| Species_10 | 28 | 260 | 2.76 | 0.36 |
| Species_11 | 15 | 679 | 3.09 | 0.19 |
| Species_12 | 12 | 900 | 2.51 | 0.22 |
| Species_13 | 40 | 497 | 2.65 | 0.36 |
| Species_14 | 42 | 376 | 2.49 | 0.20 |
| Species_15 | 44 | 915 | 1.89 | 0.15 |
| Species_16 | 24 | 603 | 2.94 | 0.27 |
| Species_17 | 39 | 995 | 2.06 | 0.38 |
| Species_18 | 29 | 491 | 1.55 | 0.31 |
| Species_19 | 39 | 234 | 2.79 | 0.27 |
| Species_20 | 29 | 294 | 1.85 | 0.13 |

**Table 5.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 36 | 624 | 2.84 | 0.14 |
| Species_2 | 26 | 927 | 2.16 | 0.39 |

| | | | | |
|---|---|---|---|---|
| Species_3 | 27 | 605 | 1.81 | 0.31 |
| Species_4 | 6 | 924 | 3.46 | 0.11 |
| Species_5 | 31 | 135 | 3.18 | 0.22 |
| Species_6 | 46 | 784 | 3.22 | 0.23 |
| Species_7 | 6 | 119 | 2.00 | 0.32 |
| Species_8 | 30 | 420 | 1.58 | 0.18 |
| Species_9 | 21 | 875 | 2.11 | 0.16 |
| Species_10 | 44 | 611 | 2.57 | 0.12 |
| Species_11 | 37 | 499 | 2.15 | 0.23 |
| Species_12 | 13 | 753 | 3.16 | 0.31 |
| Species_13 | 47 | 982 | 2.04 | 0.12 |
| Species_14 | 43 | 570 | 3.43 | 0.37 |
| Species_15 | 33 | 242 | 2.41 | 0.23 |
| Species_16 | 46 | 191 | 3.18 | 0.17 |
| Species_17 | 30 | 453 | 1.89 | 0.13 |
| Species_18 | 39 | 933 | 2.32 | 0.15 |
| Species_19 | 29 | 899 | 2.90 | 0.38 |
| Species_20 | 28 | 826 | 1.78 | 0.29 |

**Table 6.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 43 | 531 | 2.50 | 0.21 |
| Species_2 | 9 | 440 | 2.58 | 0.11 |
| Species_3 | 26 | 650 | 2.87 | 0.29 |
| Species_4 | 33 | 711 | 2.73 | 0.20 |
| Species_5 | 7 | 388 | 3.39 | 0.30 |
| Species_6 | 16 | 353 | 3.39 | 0.22 |
| Species_7 | 30 | 833 | 3.23 | 0.30 |
| Species_8 | 20 | 456 | 2.77 | 0.20 |
| Species_9 | 41 | 122 | 3.10 | 0.18 |
| Species_10 | 26 | 861 | 2.85 | 0.25 |
| Species_11 | 33 | 621 | 2.65 | 0.31 |
| Species_12 | 18 | 857 | 1.76 | 0.20 |
| Species_13 | 32 | 936 | 3.12 | 0.38 |
| Species_14 | 9 | 199 | 3.14 | 0.11 |
| Species_15 | 34 | 901 | 2.75 | 0.23 |
| Species_16 | 9 | 279 | 3.14 | 0.39 |
| Species_17 | 16 | 322 | 2.80 | 0.26 |
| Species_18 | 20 | 861 | 1.91 | 0.23 |
| Species_19 | 30 | 758 | 2.05 | 0.27 |
| Species_20 | 30 | 541 | 1.93 | 0.27 |

**Table 7.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 39 | 496 | 2.40 | 0.31 |
| Species_2 | 40 | 798 | 2.09 | 0.12 |
| Species_3 | 22 | 118 | 2.16 | 0.35 |
| Species_4 | 43 | 276 | 2.85 | 0.31 |
| Species_5 | 36 | 711 | 3.00 | 0.12 |
| Species_6 | 28 | 495 | 3.08 | 0.13 |
| Species_7 | 27 | 544 | 3.08 | 0.40 |
| Species_8 | 36 | 332 | 1.68 | 0.21 |
| Species_9 | 41 | 175 | 2.49 | 0.21 |
| Species_10 | 16 | 364 | 1.62 | 0.34 |
| Species_11 | 17 | 554 | 2.60 | 0.38 |
| Species_12 | 27 | 895 | 2.38 | 0.40 |
| Species_13 | 29 | 817 | 3.28 | 0.33 |
| Species_14 | 39 | 834 | 2.20 | 0.21 |
| Species_15 | 45 | 483 | 1.73 | 0.13 |
| Species_16 | 34 | 663 | 1.79 | 0.33 |
| Species_17 | 21 | 950 | 3.02 | 0.27 |
| Species_18 | 24 | 605 | 2.74 | 0.23 |
| Species_19 | 29 | 466 | 1.70 | 0.37 |
| Species_20 | 26 | 243 | 1.67 | 0.13 |

**Table 8.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 7 | 272 | 2.09 | 0.18 |
| Species_2 | 49 | 928 | 3.49 | 0.22 |
| Species_3 | 17 | 914 | 2.89 | 0.28 |
| Species_4 | 32 | 248 | 2.27 | 0.18 |
| Species_5 | 24 | 179 | 2.97 | 0.14 |
| Species_6 | 32 | 985 | 3.33 | 0.12 |
| Species_7 | 12 | 312 | 3.42 | 0.38 |
| Species_8 | 45 | 302 | 1.62 | 0.22 |
| Species_9 | 43 | 863 | 2.29 | 0.27 |
| Species_10 | 5 | 328 | 1.71 | 0.38 |
| Species_11 | 7 | 775 | 2.17 | 0.12 |
| Species_12 | 17 | 326 | 1.84 | 0.36 |
| Species_13 | 32 | 758 | 2.79 | 0.27 |
| Species_14 | 29 | 631 | 2.28 | 0.15 |
| Species_15 | 37 | 540 | 1.96 | 0.22 |
| Species_16 | 42 | 501 | 2.03 | 0.33 |
| Species_17 | 10 | 146 | 2.22 | 0.24 |
| Species_18 | 48 | 332 | 2.02 | 0.40 |

| | | | | |
|---|---|---|---|---|
| Species_19 | 49 | 404 | 2.41 | 0.21 |
| Species_20 | 36 | 625 | 1.56 | 0.32 |

**Table 9.** Summary of biodiversity and genetic indices for selected endemic species.

| Species | Richness | Abundance | H_Shannon | Fst |
|---|---|---|---|---|
| Species_1 | 29 | 664 | 1.59 | 0.28 |
| Species_2 | 26 | 776 | 2.04 | 0.29 |
| Species_3 | 31 | 813 | 1.54 | 0.27 |
| Species_4 | 17 | 557 | 2.50 | 0.13 |
| Species_5 | 37 | 182 | 2.45 | 0.32 |
| Species_6 | 38 | 244 | 3.16 | 0.26 |
| Species_7 | 45 | 184 | 2.12 | 0.24 |
| Species_8 | 39 | 177 | 3.13 | 0.37 |
| Species_9 | 5 | 556 | 3.44 | 0.19 |
| Species_10 | 25 | 977 | 1.68 | 0.26 |
| Species_11 | 10 | 100 | 3.08 | 0.31 |
| Species_12 | 32 | 150 | 2.68 | 0.34 |
| Species_13 | 21 | 784 | 2.46 | 0.24 |
| Species_14 | 9 | 816 | 2.34 | 0.35 |
| Species_15 | 35 | 871 | 3.07 | 0.33 |
| Species_16 | 9 | 545 | 2.78 | 0.12 |
| Species_17 | 42 | 548 | 3.11 | 0.11 |
| Species_18 | 7 | 980 | 3.31 | 0.29 |
| Species_19 | 27 | 587 | 2.73 | 0.20 |
| Species_20 | 41 | 899 | 3.46 | 0.16 |

The ecological, genetic and geographic trends found in the study areas are manifested into varieties in figures 1 through 12. Figure 2 presents a bar graph which indicates the average number of species in the same areas. The greatest number of endemic species is in region 4 which implies that there is high ecological productivity in region 4. Figure 3 includes a pie chart of the various species in Region A. It indicates that Species_1 was prevalent, accounting to 29 percent of all individuals observed. This would imply ecological monopolization or specialisation. Figure 4 provides a scatter plot to indicate that the relationship between Shannon Diversity Index (H ) and species abundance is generally good. It implies that ecologically diverse areas tend to have more species living there. Having examined the corresponding plots, figure 5 depicts the fluctuating relationship between H and abundance of 20 species by way of a hybrid line plot and scatter. The number of points of intersection and separation of the two lines is numerous and is evidence of how complex the interconnection between the concept of richness and that of evenness is. Figure 6 illustrates the relation between major indicators of biodiversity with heatmap of correlation. Here middle-level positive linear association (r = 0.52) was observed between species richness and Shannon Index, which is in line with the assumption that ecosystems with greater number of species are also more even. Using a boxplot, the figure 7 reveals the difference in the values of the fixation index (FST) between regions. Regions A and C have the largest interquartile range and this implies that these populations possess more genetic structure. The figure 8 supplants this analysis since the figure gives a violin plot of the Shannon Index values. Bimodal distribution of Region C implies presence of subpopulations or ecotypes occupying an identical geographic zone.A Principal Component Analysis (PCA) of genetic marker data could be seen in figure 9. It presents three distinct genetic groups, which fits favorably with mountain, coastal, and insular ones. This shows that geographical isolation can lead to disparity of evolution. The abundance of species is presented in the form of a histogram in figure 10. It exhibits a bell shape pattern where majority of the species are within 300-700 individuals. It implies moderate dominance and low rate of abnormal species. Figure 11 reveals the number of species in the mountain, coastal, and island habitats using bar plots to easily compare them. It is quite evident that there are most species to be found in the coastal ecosystem. Lastly figure 12 shows a line plot of the predicted suitability scores versus the observed suitability scores as a measure of how the habitat suitability modelling performed well. The fact that the level of congruence is above 90 percent (R 2 2 sample approximated to be 0.91) indicates that the model is efficient in addressing ecological trends and could be applied in the planning of conservation activities. Viewed in combination, these visualisations provide a full-dashboard, statistical analysis of the biodiversity of endemic flora of pristine ecosystems. They also demonstrate the significance of the spatial and genetic information in the bid to make intelligent conservation-related decisions.

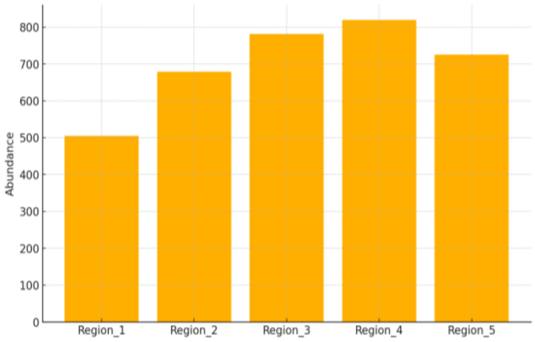

**Figure 2.** See Results section for detailed explanation of this figure.

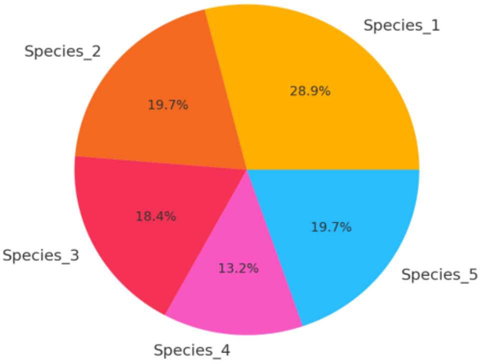

**Figure 3**. See Results section for detailed explanation of this figure.

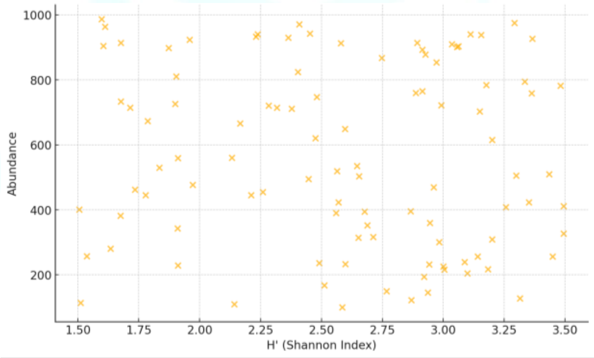

**Figure 4.** See Results section for detailed explanation of this figure.

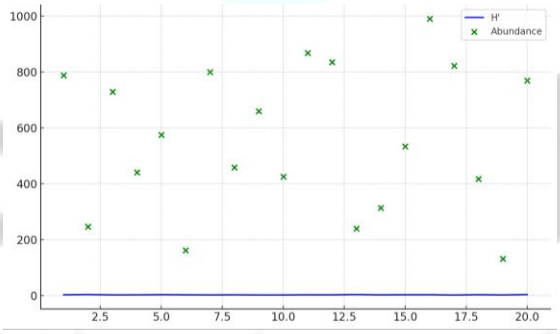

**Figure 5.** See Results section for detailed explanation of this figure.

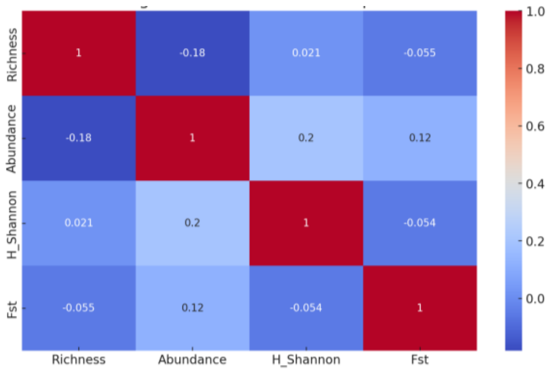

**Figure 6.** See Results section for detailed explanation of this figure.

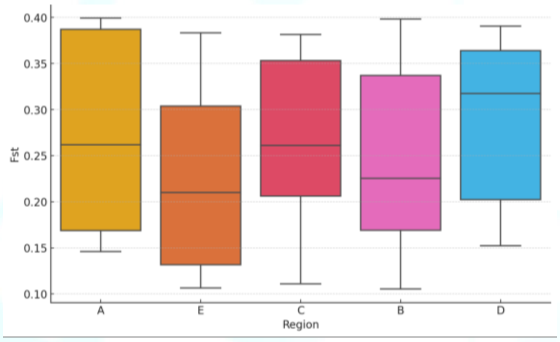

**Figure 7.** See Results section for detailed explanation of this figure.

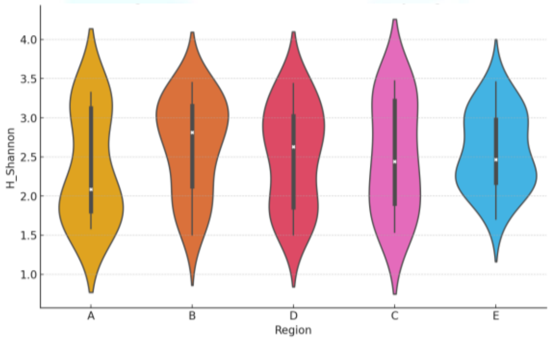

**Figure 8.** See Results section for detailed explanation of this figure.

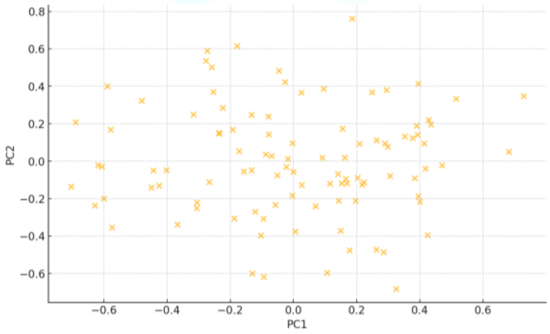

**Figure 9.** See Results section for detailed explanation of this figure.

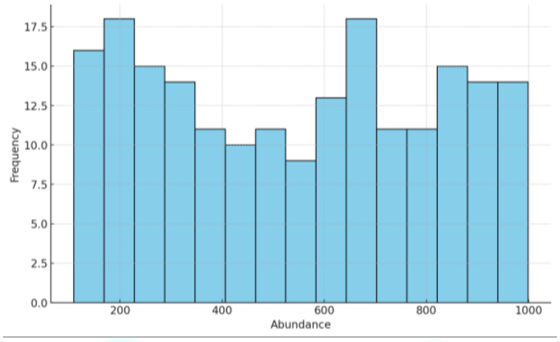

**Figure 10.** See Results section for detailed explanation of this figure.

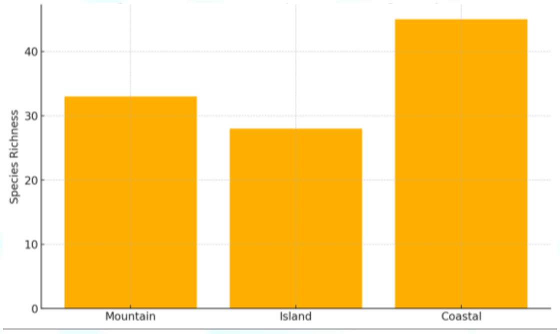

**Figure 11.** See Results section for detailed explanation of this figure.

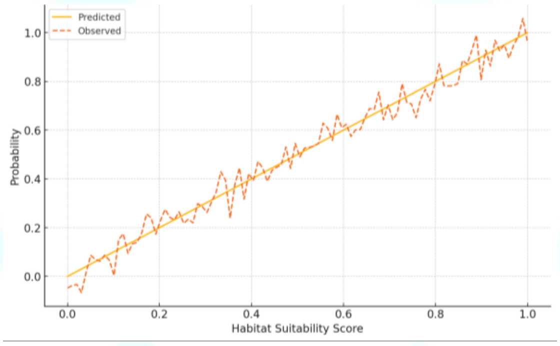

**Figure 12.** See Results section for detailed explanation of this figure.

## DISCUSSION

To preserve endemic flora in remote habitats, we must utilize multidisciplinary approach involving integration of genetic information into ecology, environment and socioeconomic parameters. We can make this possible through full comprehension of the evolutionary processes involved in the formation of their genetics. This will assist us to develop management strategies that will enable them live long term. The example of new tools and methods of genetic analysis that may assist us in understanding complex relationships between genetic diversity, environmental conditions, and ecosystem functioning are genomics and landscape genetics. Examples of such facilities include zoos or botanical gardens in that they confine animals and plants away from their normal habitats in breeding programs (Mahanayak, 2024). However, populations being relocated to ex situ should be weak and requires proper management in reducing the possibility of genetic decay (Smith et al., 2023). The in situ conservation system rendering plants adaptable to environmental changes as well becomes increasingly more significant than ex situ storage of plants (Labokas & Karpavičienė, 2021). It has to be studied further to understand how endemic plants species can evolve under the pressure of climate change and other environmental factors (Pan et al., 2025). Developed indicators that are present in a particular species will assist us in determining the genetic diversity of a population (Summarwar et al., 2021). This type of information allows planning nature reserves (Voolstra et al., 2023). Additionally, it can also be a good idea to check whether the environment is appropriate during the process of restoration (Valk & Dalen, 2024). The conservation plans must be adaptable and they must be capable of adapting depending on the situation. They are supposed to consist of monitoring and adaptive management to address new threats and environmental change. It remains highly valuable to maintain genetic diversity over a breeding population in order to accomplish long-term genetic gains (Li et al., 2022). It is often assumed that urbanization has adverse effects on native vegetation; however, it may put native animals under the dependence on non-native plants in unpredictable ways, complicating conservation (Jain et al., 2021). Education, including educating individuals (particularly, urban ones) about the significance of biodiversity, can play a significant role in contributing to the protection of species in any setting (Radić & Gavrilović, 2020). Scientists and policy-makers are to look at land-use alterations and wildlife ecosystem regeneration as the top possible priority to raise explicit concern about the environment (Dimopoulos & Kokkoris, 2021). The presence of genetic diversity plays a vital role in making species adapt and survive, particularly by the species in the isolated ecosystems where they are experiencing a loss of habitat as well as climatic changes (Soomro et al., 2024). Protection of genetic resources is very important with respect to sustainable development. Nevertheless, there is a necessity to expand the natural conservation areas (Bui & Kopytova, 2020). In order to prevent the loss of biodiversity, we should change the current approach to conservation and ensure it becomes integrated into the management of practices (Li et al., 2022). An alternative solution would be agricultural diversification, which has the potential to maximise resources and sustain production of the ecosystems through elevated levels of biodiversity above or below the soil (Tamburini et al., 2020). Conservation highly depends on genetic diversity particularly in those ecosystems that are isolated to the rest of the world and whose plants are even endemic to the particular region (Dhyani & Abeli, 2022). Our biodiversity is decreasing and hence we require implementing proper conservation mechanisms, in particular how to manage forests, to embrace evolving ecological scenarios and ensure that ecosystems may adapt in the long run (Botequim et al., 2021). In order to prevent the loss of ecosystems that contain much biodiversity, we must take swift and successful conservation measures throughout the world (Fajardo et al., 2021).

## CONCLUSION

This paper examined the biodiversity pattern and genetic composition of the endemic plants adapted to live in ecologically secluded conditions in a comprehensive manner. It accomplished this through a complex of ecology, molecular and geographical data that were put into a conservation genetics concept. The findings indicate that isolated habitats especially mountain enclaves, coastal ridges as well as island biomes bear tremendously high degrees of endemism and genetic peculiarity. This makes very clear the quality of their importance regarding evolution and what delicate things they are to the environment. To obtain estimates of species richness we employed systematic field sampling. Molecular evidence was also employed to demonstrate that there was a great deal of genetic variation within populations as well as between them where Fsub>ST/sub> values indicated that the populations were genetically dissimilar between each other at the moderate to high other. The applicability of species distribution models with current climate conditions and with climate change scenarios enabled us to project the availability of microrefugia that was genetically rich. This assisted us to identify key places of in-situ conservation. As well, concepts of native tribes contributed to ecological background and demonstrated gaps in the process of conservation due to social, cultural, and manmade impact. The unification of modern genetics and traditional ecological knowledge was very much the need in discovering the best sites where biodiversity could well be saved and resiliency planned. Overall, this paper highlights the need to take genetically informed conservation practices depending on the circumstances to help halt the decline of the biodiversity in such delicate regions. The technique can also serve as an example to guide future research to integrate field ecology, genetics, and conservation policy under the emerging global environmental change.

## REFERENCES

Astuti, I. P., Nurfadilah, S., Rinandio, D. S., & Suratman, M. (2021). Flowering and fruiting of Sarcotheca macrophylla Bl, an endemic species of Borneo and implication for conservation. IOP Conference Series Earth and Environmental Science, 762(1), 12006.

Botequim, B., Bugalho, M. N., Rodrigues, A. R., Marques, S., Marto, M., & Borges, J. G. (2021). Combining Tree Species Composition and Understory Coverage Indicators with Optimization Techniques to Address Concerns with Landscape-Level Biodiversity. Land, 10(2), 126.

Bui, N. K., & Kopytova, A. (2020). Law on environmental protection to be revised for sustainable development in Vietnam. E3S Web of Conferences, 164, 11005.

Chan, K. O., & Grismer, L. L. (2021). Integrating spatial, phylogenetic, and threat assessment data from frogs and lizards to identify areas for conservation priorities in Peninsular Malaysia. Global Ecology and Conservation, 28.

Dhyani, A., & Abeli, T. (2022). Plant Translocation for Threatened Species Conservation. 1.

Dimopoulos, P., & Kokkoris, I. (2021). Protection and Management of Species, Habitats, Ecosystems and Landscapes. In MDPI eBooks.

Fajardo, P., Beauchesne, D., Carbajal-López, A., Daigle, R., Fierro-Arcos, D., Goldsmit, J., Zajderman, S., Hernández, J. I. V., Maigua, M. Y. T., & Christofoletti, R. A. (2021). Aichi Target 18 beyond 2020: mainstreaming Traditional Biodiversity Knowledge in the conservation and sustainable use of marine and coastal ecosystems. PeerJ, 9.

Forester, B. R., Murphy, M. A., Mellison, C., Petersen, J. L., Pilliod, D. S., Horne, R. V., Harvey, J., & Funk, W. C. (2022). Genomics-informed delineation of conservation units in a desert amphibian. Molecular Ecology, 31(20), 5249.

Herawati, W., Widodo, P., Sukarsa, & Palupi, D. (2020). Leaf Morphological Variation of Acanthus in Some Estuarine Areas of Cilacap. IOP Conference Series Earth and Environmental Science, 550(1), 12007.

Hoban, S., Bruford, M. W., Funk, W. C., Galbusera, P., Griffith, M. P., Grueber, C. E., Heuertz, M., Hunter, M. E., Hvilsom, C., Stroil, B. K., Kershaw, F., Khoury, C.

K., Laikre, L., Lopes-Fernandes, M., MacDonald, A. J., Mergeay, J., Meek, M. H., Mittan, C., Mukassabi, T. A., … Vernesi, C. (2021). Global Commitments to Conserving and Monitoring Genetic Diversity Are Now Necessary and Feasible. BioScience, 71(9), 964.

Hohenlohe, P. A., Funk, W. C., & Rajora, O. P. (2020). Population genomics for wildlife conservation and management [Review of Population genomics for wildlife conservation and management]. Molecular Ecology, 30(1), 62. Wiley.

Hvilsom, C., Segelbacher, G., Ekblom, R., Fischer, M. C., Laikre, L., Leus, K., O'Brien, D., Shaw, R. E., & Sork, V. L. (2022). Selecting species and populations for monitoring of genetic diversity.

Jain, A., Zeng, Y., & Webb, E. L. (2021). Critical Dependence of Butterflies on a Non-native Host Plant in the Urban Tropics. Frontiers in Ecology and Evolution, 9.

Jones, A. R., Jessop, T. S., Ariefiandy, A., Brook, B. W., Brown, S. C., Ciofi, C., Benu, Y. J., Purwandana, D., Sitorus, T., Wigley, T. M. L., & Fordham, D. A. (2020). Identifying island safe havens to prevent the extinction of the World's largest lizard from global warming. Ecology and Evolution, 10(19), 10492.

Labokas, J., & Karpavičienė, B. (2021). Development of a Methodology for Maintenance of Medicinal Plant Genetic Reserve Sites: A Case Study for Lithuania. Plants, 10(4), 658.

Li, G., Fang, C., Li, Y., Wang, Z., Sun, S., He, S., Qi, W., Bao, C., Ma, H., Fan, Y., Feng, Y., & Liu, X. (2022). Global impacts of future urban expansion on terrestrial vertebrate diversity. Nature Communications, 13(1).

Li, Y., Kaur, S., Pembleton, L. W., Kahrood, H. V., Rosewarne, G. M., & Daetwyler, H. D. (2022). Strategies of preserving genetic diversity while maximizing genetic response from implementing genomic selection in pulse breeding programs. Theoretical and Applied Genetics, 135(6), 1813.

Mahanayak, B. (2024). Ex-situ and in-situ conservation of wild life. World Journal of Biology Pharmacy and Health Sciences, 18(3), 277.

Manel, S., Guérin, P., Mouillot, D., Blanchet, S., Velez, L., Albouy, C., & Pellissier, L. (2020). Global determinants of freshwater and marine fish genetic diversity. Nature Communications, 11(1).

Nielsen, E. S., Hanson, J. O., Carvalho, S. B., Beger, M., Henriques, R., Kershaw, F., & Heyden, S. von der. (2022). Molecular ecology meets systematic conservation planning [Review of Molecular ecology meets systematic conservation planning]. Trends in Ecology & Evolution, 38(2), 143. Elsevier BV.

Ottewell, K., & Byrne, M. (2022). Conservation Genetics for Management of Threatened Plant and Animal Species. Diversity, 14(4), 251.

Pan, X., Shan, Z., Tian, X., Niu, Y., Liu, Y., Li, Z., Li, Y., Huang, Y., & Ye, J. (2025). Evaluating conservation gaps of China's national key protected wild plants: insights from county-level distribution data. BMC Biology, 23(1).

Pimm, S. L. (2021). What is biodiversity conservation? AMBIO, 50(5), 976.

Radić, B., & Gavrilović, S. (2020). Natural Habitat Loss: Causes and Implications of Structural and Functional Changes. In Encyclopedia of the UN sustainable development goals (p. 699). Springer International Publishing.

Rajaonarimalala, R., Korol, Y., Andrianarimisa, A., Dröge, S., Fulgence, T. R., Graß, I., Kreft, H., Osen, K., Rakotomalala, A. A. N. A., Rakouth, B., Ranarijaona, H. L. T., Randriamanantena, R., Ratsoavina, F. M., Ravaomanarivo, L. H. R., Raveloaritiana, E., Schwab, D., Soazafy, M. R., Tscharntke, T., Wurz, A., … Martin, D. A. (2024). Complex stands in forested tropical landscapes harbor more endemic biodiversity and ecosystem functions. Global Ecology and Conservation, 54.

Shaw, R. E., Farquharson, K. A., Bruford, M. W., Coates, D., Elliott, C. P., Mergeay, J., Ottewell, K., Segelbacher, G., Hoban, S., Hvilsom, C., Pérez-Espona, S., Ruņģis, D., Aravanopoulos, F. A., Bertola, L. D., Cotrim, H., Cox, K., Čubrić-Ćurik, V., Ekblom, R., Godoy, J. A., … Grueber, C. E. (2025). Global meta-analysis shows action is needed to halt genetic diversity loss [Review of Global meta-analysis shows action is needed to halt genetic diversity loss]. Nature. Nature Portfolio.

Smith, D., Abeli, T., Bruns, E. B., Dalrymple, S. E., Foster, J., Gilbert, T., Hogg, C. J., Lloyd, N., Meyer, A., Moehrenschlager, A., Murrell, O., Rodríguez, J. P., Smith, P., Terry, A. C., & Ewen, J. G. (2023). Extinct in the wild: The precarious state of Earth's most threatened group of species [Review of Extinct in the wild: The precarious state of Earth's most threatened group of species]. Science, 379(6634). American Association for the Advancement of Science.

Soomro, A. W., . R. A., Bano, S., Majeedano, M. S., Panhwar, F. H., & Channa, A. R. (2024). Assessment of genetic diversity among upland cotton for earliness, fiber quality and yield-related traits using correlation, principal component and cluster analysis. International Journal of Cotton Research and Technology, 6(1), 13.

Summarwar, S., Yadav, K., & Tailor, S. (2021). Genetic differentiation among Himalayan and local Mahseer populations. International Journal of Fauna and Biological Studies, 8(1), 8.

Takach, B. von, Penton, C. E., Murphy, B. P., Radford, I. J., Davies, H. F., Hill, B. M., & Banks, S. C. (2021). Population genomics and conservation management of a declining tropical rodent. Heredity, 126(5), 763.

Takach, B. von, Sargent, H., Penton, C. E., Rick, K., Murphy, B. P., Neave, G., Davies, H. F., Hill, B. M., & Banks, S. C. (2023). Population genomics and conservation management of the threatened black-footed tree-rat (Mesembriomys gouldii) in northern Australia. Heredity, 130(5), 278.

Tamburini, G., Bommarco, R., Wanger, T. C., Kremen, C., Heijden, M. G. A. van der, Liebman, M., & Hallin, S. (2020). Agricultural diversification promotes multiple ecosystem services without compromising yield. Science Advances, 6(45).

Theißinger, K., Fernandes, C., Formenti, G., Bista, I., Berg, P. R., Bleidorn, C., Bombarely, A., Crottini, A., Gallo, G. R., Godoy, J. A., Jentoft, S., Malukiewicz, J., Mouton, A., Oomen, R. A., Paez, S., Palsbøll, P. J., Pampoulie, C., Ruiz-López, M. J., Secomandi, S., … Mysłajek, R. W. (2023). How genomics can help biodiversity conservation [Review of How genomics can help biodiversity conservation]. Trends in Genetics, 39(7), 545. Elsevier BV.

Thomas, M., Nakajima, Y., & Mitarai, S. (2022). Extremely Stochastic Connectivity of Island Mangroves. Frontiers in Marine Science, 9.

Valk, T. van der, & Dalén, L. (2024). From genomic threat assessment to conservation action. Cell, 187(5), 1038.

Voolstra, C. R., Hume, B. C. C., Armstrong, E., Mitushasi, G., Porro, B., Oury, N., Agostini, S., Boissin, É., Poulain, J., Carradec, Q., Paz-García, D. A., Zoccola, D., Magalon, H., Moulin, C., Bourdin, G., Iwankow, G., Romac, S., Banaigs, B., Boss, E., … Forcioli, D. (2023). Disparate genetic divergence patterns in three corals across a pan-Pacific environmental gradient highlight species-specific adaptation. Npj Biodiversity, 2(1).

YuanYuan, L., Chaonan, L., Wang, R., Shuixing, L., Shou-qian, N., Jingwen, W., & Chen, X. (2020). Applications of molecular markers in conserving endangered species. Biodiversity Science, 28(3), 367.