bol.cient.mus.hist.nat. 29(1), enero-junio, 2025. 129-144. ISSN: 0123-3068 (Impreso) ISSN: 2462-8190 (En línea)

BOLETÍN CIENTÍFICO
CENTRO DE MUSEOS
MUSEO DE HISTORIA NATURAL

Genetic diversity of butterflies and its perspectives as key information for defining conservation strategies in the high-mountain ecosystems of Colombia

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Abstract

Colombia stands out as one of the most biologically diverse countries in the world. However, this natural wealth is threatened due to the continuous transformation of its ecosystems, driven largely by human activities. High-mountain ecosystems, known as "paramos", are among the priority biomes for conservation in the country. These environments harbor high levels of endemism and beta diversity and play a critical role in the capture, regulation, and provision of water resources. Population parameters derived from genetic analysis have become a fundamental tool for characterizing the structure, variability, and connectivity of natural populations. Insects such as butterflies have been used as a reference for the state of an ecosystem since butterfly population parameters can be extrapolated to the rest of the local biota. This information is key for identifying priority conservation areas and designing effective management strategies. In this context, diurnal butterflies emerge as valuable bioindicators: their response to environmental changes and genetic diversity allows inferences about the health and resilience of paramo ecosystems. This article presents key perspectives on the relevance of genetic diversity as a useful input in defining conservation strategies in Colombian "paramos". By applying genetic analysis to focal butterfly species, the aim is to strengthen decision-making, prioritize vulnerable populations, support supplementation programs, guide assisted migration efforts, and ultimately contribute to the formulation of long-term conservation policies.

Keywords: Genetic analysis, biodiversity, conservation, diurnal butterflies, Papilionoidea.

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*FR: 2-II-2025. FA: 10-V-2025.

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CÓMO CITAR:
Hernán-Pérez, J., Parrales-Ramírez, D. A., Rocha-Gil, Z. E., Fonseca-Guerra, I. R., Pedraza-Jiménez, Y., Fagua, G. (2025). Genetic diversity of butterflies and its perspectives as key information for defining conservation strategies in the high-mountain ecosystems of Colombia. *Bol. Cient. Mus. Hist. Nat. Univ. Caldas, 29*(1), 161-179. https://doiorg/10.17151/bccm.2025.29.1.7

Diversidad genética de mariposas y sus perspectivas como información clave para la definición de estrategias de conservación en los ecosistemas de alta montaña de Colombia

Resumen

Colombia se destaca como uno de los países con mayor diversidad biológica del mundo; sin embargo, esta riqueza natural se encuentra amenazada debido a la transformación continua de sus ecosistemas, impulsada en gran medida por actividades antrópicas. Entre los biomas prioritarios para la conservación en el país se encuentran los ecosistemas de alta montaña, conocidos como páramos. Estos ambientes albergan altos niveles de endemismo y diversidad beta, además de cumplir un papel crítico en la captura, regulación y provisión del recurso hídrico. Los parámetros poblacionales derivados de análisis genéticos se han convertido en una herramienta fundamental para caracterizar la estructura, variabilidad y conectividad de las poblaciones naturales. Insectos como las mariposas se han utilizado como referencia del estado de un ecosistema, ya que sus parámetros poblacionales pueden extrapolarse al resto de la biota del lugar. Esta información resulta clave para identificar áreas prioritarias de conservación y diseñar estrategias efectivas de manejo. En este contexto, las mariposas diurnas emergen como valiosos bioindicadores: su respuesta frente a los cambios ambientales y su diversidad genética permiten realizar inferencias sobre la salud y resiliencia de los ecosistemas de páramo. Este artículo presenta perspectivas clave sobre la relevancia de la diversidad genética como insumo útil en la definición de estrategias de conservación en los páramos colombianos. A través del análisis genético de especies focales de mariposas, se busca fortalecer la toma de decisiones, priorizar poblaciones vulnerables, apoyar programas de suplementación, orientar esfuerzos de migración asistida y, en última instancia, contribuir a la formulación de políticas de conservación a largo plazo.

Palabras clave: análisis genético, biodiversidad, conservación, mariposas diurnas, Papilionoidea.

Introduction: An overview of biodiversity and high-Andean ecosystems in Colombia

Colombian high-Andean ecosystems are among the most biologically rich environments on the planet. However, intense anthropogenic pressures driven by economic growth and market demands has altered their ecological and functional processes, causing its progressive degradation (Pérez et al., 2019; Ramírez-Restrepo & Halffter, 2013). Since the Industrial Revolution, the trajectory of environmental deterioration has eroded the benefits provided by ecosystem services, essential for human well-being and environmental sustainability, thereby threatening the survival of numerous species (Armenteras et al., 2003; Lemes et al., 2015).

The establishment of protected areas has emerged globally as a central strategy to safeguard ecosystems and natural resources threatened by human activity (Pérez et al., 2019; Woodcock et al., 2013). These strategies materialize in the designation of territories with specific limits and use dynamics which help to contain habitat transformation and promote biodiversity conservation (Albright & Crow, 2019; Freitas et al., 2009; Henao-Díaz et al., 2019). Therefore, the creation of protected areas represents a significant approach to the valuation and maintenance of the environment and existing natural resources (Gurrutxaga & Lozano, 2006; Quiceno-Urbina et al., 2016). Hence, ecosystem conservation is vital, not only to maintain biodiversity but also to preserve the ecological functions it performs, such as water regulation and carbon reserves (Parra-Romero & Estupiñán, 2023; Vasseur & Andrade, 2024).

In this context, conservation genetics emerges as a particularly relevant tool that allows for the application of genetic theories and techniques to minimize species extinction risks and preserve their genetic diversity (Smith et al., 2009; Virgilio et al., 2010). The loss of genetic variability is a central issue in conservation genetics since small populations in fragmented areas may suffer from inbreeding depression, which leads to a loss of heterozygosity, genetic diversity, and adaptability (D'Ercole et al., 2021; Noriega et al., 2018). While each biological group has traits that indicate certain phenomena or variables of interest, a combination of characteristics favors the selection of specific groups as references applicable to the rest of the local biota. These organisms should have a well-established taxonomy, be closely associated with other taxa, resources, or environmental features, demonstrate rapid responses to habitat condition changes, be feasible for sampling in a practical and cost-effective way, and be potentially more suitable for diagnostic and biomonitoring events (Brown et al., 2018; Melo et al., 2019; Santos et al., 2016). Since insects constitute most of the world's biodiversity, it is essential to identify representative groups that reflect the diversity of these organisms (Montejo-Kovacevich et al., 2022; Pyrcz et al., 2016). Several studies have that diurnal butterflies can be considered effective indicators of environmental changes, reinforcing their use in monitoring even subtle alterations in their habitats (Fagua, 1996; Labadessa et al., 2021; Mahecha-Jiménez et al., 2011; Pérez et al., 2017).

In high-mountain ecosystems, diurnal butterflies significantly contribute to biodiversity and biomass, fulfilling key functions such as pollination, herbivory, and trophic support for other levels of the food chain (Marín et al., 2009; Pérez et al., 2017; Ribeiro et al., 2012). In particular, species of the subtribe Pronophilina, belonging to the subfamily Satyrinae (Nymphalidae), have a long evolutionary history in Colombian "paramos" (Adams & Bernard, 1997; Álvarez-Hincapié et al., 2017; Pyrcz et al., 2016). Genera such as *Pedaliodes, Lymanopoda,* and *Manerebia* have been established as suitable models for understanding community responses to environmental variability, making them ideal candidates for bioindication studies of evolutionary processes in the face of climate change scenarios (Dan et al., 2021; Mahecha-Jiménez et al., 2021; Marín et al., 2009; Pyrcz et al., 2016).

Colombian "paramos" stand out for their water regulation capacity: their hydromorphic soils store large volumes of water, controlling water flows through watersheds (Benavides-Martínez et al., 2007; Forero-Gómez et al., 2020; Gil-Leguizamón et al., 2020). Furthermore, they constitute unique habitats that host endemic species, creating spaces for genetic isolation (Quiceno-Urbina et al., 2016) and providing essential environmental services for human well-being (Flantua et al., 2019; Gil-Leguizamón et al., 2021).

Despite their importance, "paramos" often represent biodiversity refuges in isolated and poorly studied fragments (Olaya-Angarita et al., 2019). Understanding the distribution and dynamics of biodiversity in these areas is key to making informed conservation decisions (Henao-Díaz et al., 2019). In a megadiverse country like Colombia, the lack of knowledge about the biology of certain species hinders their effective conservation (Avellaneda-Torres et al., 2015; Ramírez-Restrepo et al., 2007).

Given the impossibility of protecting all natural areas, it is essential to establish conservation priorities, considering vulnerability, species composition, connectivity, population flow, matrix resilience, as well as local ecological and evolutionary processes (Casas-Pinilla et al., 2017; Pyrcz et al., 2016). Although scattered information exists to prioritize paramo protection, it has not been systematized or standardized, which makes its use difficult (Cadena et al., 2007; Pérez et al., 2017). In this context, it is vital to generate and organize data to strengthen debate, improve decision-making, and ensure adequate management of these strategic ecosystems.

Methodology

This literature review was conducted with the aim of analyzing the role of genetic diversity in butterflies as a key tool for the formulation of conservation strategies in high-mountain ecosystems in Colombia, particularly the "paramos". To this end, a systematic search strategy was implemented in the international scientific databases Scopus and Web of Science, both recognized for their rigorous indexing of high-impact academic publications. Combinations of keywords such as genetic diversity, butterflies, conservation, paramos, Colombia, population structure, and bioindicators were used, applying Boolean operators and filters by subject area (biology, ecology, genetics), document type (research articles and reviews), and publication date (last 20 years).

After defining the bibliographic corpus, a critical and systematic reading of the selected documents was carried out, prioritizing studies focused on genetic analyses of diurnal butterflies and their usefulness as bioindicators in high-mountain contexts. The information was organized based on key methodological approaches, focal species, findings related to population structure, genetic connectivity, and conservation applications. This methodology allowed the construction of a rigorous and updated state-of-the-art that supports the analysis of the implications of genetic diversity for territorial planning, the identification of vulnerable populations, and the formulation of long-term conservation policies in Colombian "paramos".

Implementation of conservation actions in Colombian paramo ecosystems

Colombian paramo ecosystems represent 50% of the total global extent of these ecosystems. Due to their complex functioning as high-mountain ecosystems, they have been affected by geomorphological and climatic processes that generate events of isolation and population reconnection. As a result, paramo ecosystems harbor a high level of endemism and beta diversity (Avellaneda-Torres et al., 2015; Gil-Leguizamón et al., 2020; Olaya-Angarita et al., 2019), in addition to being an important source of water catchment and regulation (Pérez et al., 2023). High mountain ecosystems are particularly vulnerable to climate change, which poses significant risks to endemic species with restricted distribution areas that have already suffered habitat loss and displacement. The climatic conditions of the Andes are unique as rainfall patterns create a mosaic of habitats that, while sustaining biodiversity, make high-altitude species more susceptible to local extinctions (Dirnböck et al., 2011). Despite strategic efforts to protect them, these natural environments continue to face intense anthropogenic pressures that endanger the maintenance of biodiversity as well as the water economy of the country (Jiménez & González, 2017; Pérez et al., 2023, 2024; Quiceno-Urbina et al., 2016; Vergara-Buitrago et al., 2018).

In fact, implementing conservation actions and minimizing the effects of environmental degradation is a need for Colombian "paramos" to ensure the availability of natural resources necessary for sustainable development, as recommended by various environmental regulations. In particular, the Ministry of Environment and Sustainable Development requires the creation of Environmental Management Plans to guarantee the right to an ecologically balanced environment (Pérez et al., 2017; Sarmiento et al., 2017), considering that anthropometric pressures, particularly related to agricultural expansion and urbanization, further aggravate the challenges faced by high Andean ecosystems. Habitat fragmentation due to land use changes has been shown to alter ecological processes and reduce genetic diversity within populations, which is critical for species resilience (Rodríguez et al., 2019). This urgency is especially pronounced in the high-Andean areas of the department of Boyacá, where few studies have focused on conservation genetics, hindering the understanding of ecological and evolutionary processes that support ecosystem functions (Gil-Leguizamón et al., 2020). Key species such as the Andean bear (*Tremarctos ornatus*) or the Andean tapir (*Tapirus pinchaque*) are particularly affected by habitat fragmentation, which limits their ability to move between suitable habitats, thus threatening their survival (Cepeda-Duque et al., 2024; Rodríguez et al., 2019). The application of conservation biology tools, in particulary the genetic analysis of insects, has allowed researchers to generate hypotheses about genetic variability and its relationship to environmental changes, providing crucial information for the design of landscape-based conservation strategies. These advances could become a cornerstone for the comprehensive and adaptive management of Colombian "paramos" (Freitas et al., 2009; Prado et al., 2017). In addition, the current human footprint in these areas has been mapped to identify the regions where conservation efforts are most needed (Correa-Ayram et al., 2020).

The state of Colombian mountain ranges and their biological characteristics

The Andes, considered the most diverse mountain range in the world, hosts approximately one-sixth of the known biota, despite occupying only 4% of the surface of the Earth (Armenteras et al., 2003). This region constitutes an important reservoir of neotropical diversity, acting as a biogeographical region shaped by glaciation processes, where environmental conditions converge to influence the adaptation of exclusive biota (Flantua et al., 2019; Gil-Leguizamón et al., 2020). The remarkable biodiversity of the Colombian Andes and the unique biological conditions of its mountain ranges have made the country a global biodiversity hotspot (Saavedra-Ramírez et al., 2018). In this context, the three mountain ranges of Colombia constitute unique ecogeographical units with remarkable levels of diversity and endemism. For example, frogs have levels of endemism up to 84% (Jiménez & González, 2017). High levels of endemism in the Colombian Andes can be attributed to various factors, such as geological history, climate changes and habitat isolation due to topographic barriers (Muñoz-Valencia et al., 2021). Considering that altitude plays a fundamental role in shaping biodiversity patterns, as species richness tend to peak at medium altitudes and decrease at both low and high altitudes between the Andean Mountain systems, the paramo stands out as an ecosystem of high biological, ecological, and economic value, hosting biodiversity at genetic, species, and ecosystem levels, and exhibiting high levels of endemism. Furthermore, it provides essential ecosystem services, including carbon dioxide capture, nutrient storage, and water supply (Méndez-Polo, 2019). Despite its importance, the paramo faces severe threats, such as deforestation, intensive grazing, expansion of crops such as potatoes, and mining, all driven by changes in native vegetation cover (Armenteras et al., 2003; Balvanera, 2012; Newbold et al., 2015).

The species that inhabit the high-Andean ecosystems are not only threatened by anthropogenic activities but also have high vulnerability to global warming. This phenomenon, exacerbated by the current overexploitation of ecosystems, could lead to mass extinctions due to its scale and widespread effects, impacting ecosystems to varying degrees (Echeverría et al., 2016; Pérez et al., 2017; Pyrcz & Garlacz, 2012). Today, the estimated effects of global warming on high-Andean ecosystems are well-recognized. These include desertification, fragmentation, a reduction of the paramo area to approximately one-quarter of its current size, the disappearance of the superparamo ecosystem, and differential changes in precipitation and temperature that could significantly affect resident biota (Arellano & Rangel, 2008). These effects should be analyzed on a case-by-case basis depending on the area affected. For example, the Sierra Nevada de Santa Marta is recognized as an important center of evolution of endemic species, presenting young and old lineages of flora and fauna (González-Orozco, 2023). In addition, the Andean uplift has facilitated the diversification of numerous species, particularly in response to climate change and habitat fragmentation (Sanín et al., 2024). Likewise, phenomena such as the replacement of specialist species with generalist ones have been observed (Marín et al., 2009; Pérez et al., 2017).

Biodiversity studies for the creation and conservation of protected areas

Conservation biology, as a fundamental multidisciplinary science for both scientific inquiry and sustainable development, relies on precise data from ecology, physiology, biogeography, systematics, and genetics (Kim et al., 2021; Noriega et al., 2018; Zhang et al., 2010). Conservation genetics emerges as a particularly significant area for assessing the degree of population isolation following habitat fragmentation and the extinction risks associated with genetic phenomena such as drift, diversity los and the harmful effects of inbreeding (Dan et al., 2021). Identifying taxonomic value to conservation policies, defining management units among at-risk populations, and implementing short-term conservation measures are essential aspects of this field (Arellano & Rangel, 2008; Woodcock et al., 2013).

In Colombia, efforts to conserve biodiversity have materialized through the creation of the National System of Protected Areas, the primary strategy in the country to safeguard its biological diversity (De Palma et al., 2016; Echeverría et al., 2016; Méndez-Polo, 2019). This system includes public protected areas such as National Natural Parks, Protective Forest Reserves, Regional Natural Parks, Integrated Management Districts, Soil Conservation Districts, and Recreation Areas, as well as private protected areas integrated into the Civil Society network of Nature Reserves. These private initiatives are led by individuals and organizations that dedicate their lands to conservation (Gil-Leguizamón et al., 2021; Pérez et al., 2017). The strategic expansion of protected areas is essential, as it allows for the efficient use of limited conservation resources while addressing the urgent need to protect diverse ecosystems and species diversity (Sarmiento et al., 2017).

The definition of areas of high conservation value has been based primarily on data from well-studied biological groups such as mammals, plants, and birds. A notable example is the Important Bird Areas (IBA) program, which demonstrates how biological information can accurately guide the identification and delineation of priority areas (Avellaneda-Torres et al., 2015; Bell et al., 2022; De Palma et al., 2016;

Ribeiro et al., 2012). Research indicates that the establishment of new protected areas should be based on the distribution of threatened species and current biodiversity hotspots (Flantua et al., 2019; Peluso et al., 2023).

The selection of one or a few indicator species can optimize the identification of protected areas and the formulation of conservation strategies. These species act as "umbrella" or "surrogate" species, focusing conservation efforts and resources while facilitating indirect assessments of the impact of human activities on biodiversity. This approach provides essential insights into population dynamics under scenarios of habitat transformation, promoting more effective actions to safeguard biodiversity (Labadessa et al., 2021; Noriega et al., 2018; Pérez et al., 2019).

Another obstacle to biodiversity preservation in protected areas is climate change. Expanding the extent of these habitats and improving their connectivity is essential to facilitate species migration and adaptation in response to changing climate conditions (Benavides-Martínez et al., 2007). Research has shown that while these areas can buffer habitat loss and fragmentation, they may not be sufficient to protect species from this phenomenon (Berteaux et al., 2018; Pérez et al., 2019). In this sense, participatory monitoring has emerged as a useful technique for collecting data on biodiversity, which enriches the knowledge necessary for the effective management of these protected areas (Mandeville et al., 2023).

Ecological relationships of butterflies with the natural environment

Diurnal butterflies are widely recognized as biological indicators of overall biodiversity and potential ecological changes within ecosystems (Crone & Schultz, 2022; Fagua, 1996; Mahecha-Jiménez et al., 2011). Their sensitivity to environmental changes and habitat fragmentation allows them to respond quickly and directly to environmental impacts (Adams, 1986; Marín et al., 2009; Pyrcz & Garlacz, 2012). With a high richness and abundance of species, butterflies are relatively easy to observe, assess, and identify in the field (Ramírez-Restrepo & Halffter, 2013). Their strong interactions with their environments and sensitivity to environmental changes make them excellent indicators of environmental quality and the integrity of natural landscapes (Lemes et al., 2015; Rangel-Acosta & Martínez-Hernández, 2017).

Diurnal butterflies participate in numerous ecological interactions within communities, such as mutualistic pollination and herbivorous predation (Casas-Pinilla et al., 2017; Pérez et al., 2017). They are also used as models in research on population ecology and behavior, natural selection, genetics, and fundamental processes such as feeding, parasitism, competition, predation, camouflage, and mimicry (Sun et al., 2021). Protected habitats such as riparian forests host a greater diversity of butterflies compared to disturbed or degraded areas (Pérez et al., 2019). One of the main ecological relationships of these insects is their dependence on specific habitats that provide them with food and shelter, among others (Hailay & Getu, 2023).

Incorporating genetic approaches into the study of these ecological interactions provides new opportunities to understand population dynamics and the ability of butterflies to respond to long-term environmental changes (Pérez et al., 2019). Genetic analyses can detect barriers to gene flow, estimate connectivity between habitat patches, and quantify intrapopulation genetic diversity parameters that help identify populations at higher risk and prioritize conservation actions (Limeira et al., 2019; Sun et al., 2021).

A comprehensive understanding of the ecological relationships of butterflies with their environment, combined with conservation genetics tools, provides a more solid foundation for formulating effective management and protection strategies for the Colombian high-mountain ecosystems (Forero-Gómez et al., 2020; Gil-Leguizamón et al., 2021). In addition, the role of butterflies as pollinators and their different contributions to ecosystem services allow for the interconnection of different species within ecosystems. Therefore, the conservation of these populations is crucial both for maintaining their own diversity and for preserving the ecological functions they support (Rushayati et al., 2024).

Genetic diversity and population structure

Biological diversity encompasses all forms of life, including their genetic variations at the species, races, and population levels, each with unique attributes (Cognato & Sperling, 2000; Prado et al., 2017). Biodiversity loss, driven by human activities, has accelerated the extinction of an unknown number of species and reduced the size of many populations, placing them at risk (Freitas et al., 2009; Leinster & Cobbold, 2012). From the perspective of conservation genetics, this problem becomes critical as the continuous loss of biodiversity restricts the evolutionary capacity of populations to adapt to changing environments, making it difficult for them to be resilient in the long term (Smith et al., 2009).

In this context, genetic variability, defined as the variety of alleles and genotypes present in populations, constitutes the fundamental raw material for evolutionary adaptation. Natural selection acts on this diversity, favoring the most suitable genotypes for environmental conditions. Reduced variability limits evolutionary potential, thus resulting in negative consequences for population persistence and stability. Understanding how these genetic resources are distributed and which environmental or species-specific factors influence this distribution is essential for designing effective conservation strategies, especially in unique and fragile environments such as high-altitude ecosystems (D'Ercole et al., 2021; Sun et al., 2021). Population genetic structure refers to how genetic variability is distributed between and within hierarchical subdivisions of a species. The study of population structuring is based on the distribution of genotypic and allelic frequencies under the influence of four evolutionary forces: natural selection, genetic drift, mutation, and recombination (Dan et al., 2021; Lanfear et al., 2012). Other events, such as migration, inbreeding, and effective population size, also affect genetic structure (Campbell et al., 2022).

Structurally, genetic variation can manifest between geographically distinct populations, within local groups of individuals, or even within progeny groups. It is defined as the non-random distribution of alleles and genotypes (Echeverría et al., 2016; Marín et al., 2009; Shi et al., 2015). Genetic structure can be demographic, referring to the spatial distribution of individuals, which varies by species and is determined primarily by reproductive systems and dispersal patterns. Temporal genetic structure refers to the subdivision of genetic diversity across generations, such as between parents and offspring, developmental stages, or even between generations contained in seed or germplasm databases (Ahola et al., 2014; Gil-Leguizamón et al., 2020; Woodcock et al., 2013).

The importance of this genetic structure is exemplified by the study on Colombian coconut germplasm conducted by Muñoz-Perez et al. (2002). Using genome-wide diversity analysis to infer population structure and linkage disequilibrium, the researchers demonstrated that there is a marked genetic break between accessions from the Atlantic and the Pacific coasts, highlighting the need for targeted conservation efforts to maintain genetic diversity within these two distinct populations.

Similarly, in insect vectors, understanding the genetic structure is crucial for managing animal and human diseases they can transmit. In *Rhipicephalus sanguineus* (a tick species), genetic characterization in different regions of Colombia revealed high haplotype diversity but low nucleotide diversity, a pattern indicative of historical population expansions followed by bottlenecks, which could have implications for disease transmission dynamics (Páez-Triana et al., 2021). Therefore, a crucial aspect of using genetic diversity information in decision making is the identification of key populations that contribute to overall genetic variation.

Gene flow as a homogenizing agent of natural populations

Gene flow encompasses all mechanisms that result in the transfer of alleles between populations and can occur both intraspecifically and interspecifically. It refers to the proportion of new immigrant genes introduced into a population through individual or gamete movement (D'Ercole et al., 2021; Papasotiropoulos et al., 2013). This fundamental microevolutionary force can determine the potential for genetic differentiation between populations and local adaptation, as well as influence the geographic spread of new adaptations (Schaefer & Renner, 2008; Sun et al., 2021). Reduced or absent gene flow may lead to population divergence and differentiation over time, ultimately resulting in speciation (Kim et al., 2021).

Regardless of the mechanism, gene flow determines the degree of genetic differentiation in local populations (Tan et al., 2021). Gene flow can hinder evolution by reducing adaptation to local conditions or promote it by spreading new genes and combinations across the geographic distribution area of a species (Campbell et al., 2022; Chang et al., 2014). When natural selection drives and maintains ecological divergence between species, gene flow can affect the genome in variable ways. Genomic regions subjected to divergent selection or influenced by genetic drift may exhibit significant differentiation, even when the gene flow homogenizes the rest of the genome (Dincă et al., 2021).

Several studies have shown that gene flow can mitigate the consequences of urbanization and agricultural growth, which are of concern in Colombia due to their potential to cause habitat fragmentation. For example, the study on urban pigeons (Columba livia) by Pardo-Perez et al. (2024) revealed a moderate genetic divergence due to high levels of gene flow between populations, indicating that substantial genetic exchange can mitigate the impacts of local adaptation and genetic drift (Pardo-Pérez et al., 2024).

In Colombia, where conservation efforts can focus on facilitating gene flow between fragmented populations to prevent inbreeding depression and promote genetic diversity, the concept of genetic rescue is applied, which emphasizes the potential benefits of introducing gene flow in small and inbred populations to improve their fitness and evolutionary potential (Frankham, 2015).

Geographic barriers, such as the Andes, lead to reduced gene flow and increase genetic differentiation between populations, as observed in malaria vectors of Colombia, *Anopheles albimanus* and *Anopheles nuneztovari*. This suggests that while such flow can homogenize populations, geographical characteristics may also hinder it, leading to distinct genetic structures (Altamiranda-Saavedra et al., 2023). In addition, factors such as pollen and seed dispersal are crucial for genetic exchange between populations. In *Passiflora edulis*, for example, gene flow, essential for the genetic health of populations, is enhanced by cross-pollination facilitated by long-distance flying pollinators (Martínez et al., 2020). The extent of gene flow depends largely on two intrinsic biological traits of organisms: reproductive modes and individual mobility. Highly mobile species can spread across vast distances, resulting in more genetically homogeneous populations (D'Ercole et al., 2021; Traut et al., 2023). Conversely species with lower mobility exhibit a genetic structuring on a larger scale (Dan et al., 2021; Sun et al., 2021). Sex-dependent dispersal, where one sex disperses while the other remains faithful to its home territory or social group, can influence the distribution of genes on sex chromosomes or matrilineally inherited genomes, such as mitochondrial DNA (Azrizal-Wahid et al., 2021). Reproductive behavior also affects gene flow. For example, philopatry, where individuals return to their birthplace to reproduce can severely limit gene flow, leading to population differentiation. Preferential mating may similarly increase spatial structure in low-mobility species (Azrizal-Wahid et al., 2021; Sheffield et al., 2009; Traut et al., 2023). Ecological factors affecting gene flow vary both intraspecifically and interspecifically, including dietary specialization, phenological asynchrony between populations, habitat persistence, population longevity, and environmental factors such as physical surroundings, spatial habitat structure, and geographic distance (Tan et al., 2021; Wilson, 1997). Understanding individual movement within a species is critical for studying the relationship between gene flow, habitat spatial structure, and landscape connectivity (Dan et al., 2021; Noriega et al., 2018; Smith et al., 2012). Landscape connectivity, as defined by landscape ecologists, refers to the degree to which the structure of a landscape facilitates or impedes species movement (Fagua, 1996; Pérez et al., 2019; Pyrcz et al., 2016). A well-connected landscape allows organisms to move easily between habitat patches over time. Since landscapes consist of diverse fragments with varying physical attributes, connectivity is an attribute both of a landscape as a whole and the specific fragment (Casas-Pinilla et al., 2017).

By understanding the complex interactions between gene flow, evolutionary forces, species biological traits, and landscape connectivity, it is possible to delineate more effective conservation strategies (Cadena et al., 2007; Casas-Pinilla et al., 2017; Nates-Parra et al., 2008). These strategies seek to maintain or restore ecological corridors to facilitate individual movement, preserving genetic diversity, resilience, and the adaptive potential of populations in high-altitude environments where environmental conditions and habitat fragmentation pose unique challenges (Gurrutxaga & Lozano, 2006; Mahecha-Jiménez et al., 2011).

Genetic diversity as a decision-making model

Genetic diversity serves as a key tool for conservation decision-making by providing indicators of connectivity, isolation, and population resilience. Two methodological approaches have been developed to specifically evaluate gene flow: direct and indirect estimates (Azrizal-Wahid et al., 2021; Kim et al., 2014). Direct techniques, such as mark-recapture (MR), allow the observation and quantification of the actual movement of individuals between habitat patches, generating empirical evidence of intra- and interpopulation movement (Liu et al., 2020). In well-studied species such as the butterfly *Mellicta ambigua* Ménétriès, 1859 (Lepidoptera: Nymphalidae), or in agricultural pests, these data have improved the understanding of dispersal patterns. However, direct methodologies have significant limitations: they require a substantial number of marked individuals, prolonged sampling efforts over time and space, and do not directly measure gene flow but rather individual movement. These challenges are exacerbated at larger scales and with multiple populations, increasing costs and logistical complexity (Campbell et al., 2022; Lanfear et al., 2017; Shi et al., 2015).

In contrast, indirect estimates of gene flow, based on genetic markers and molecular tools, more efficiently reflect evolutionary history and contemporary connectivity at large spatial scales (Azrizal-Wahid et al., 2021; Lanfear et al., 2012). Techniques such as genomic sequencing, genotyping-by-sequencing, and other genetic analysis methods have improved the understanding of how landscape structure influences the distribution of genetic variants. These methods illustrate patterns of gene flow between populations and reveal conservation units at broader scales (Ahola et al., 2014; Timmermans et al., 2014). In the case of insects, integrating molecular data into multi-population or metapopulation demographic models makes it possible to assess the impact of habitat fragmentation on population dynamics. These models incorporate migration, colonization, and local extinction within a realistic spatial and temporal framework (Dan et al., 2021; Lanfear et al., 2012; Smith et al., 2012).

Landscape fragmentation, along with its degree of connectivity and patch isolation, affects genetic diversity by reducing it and increasing the long-term risk of extinction (Balvanera, 2012; Möhlenhoff et al., 2001). Understanding how habitat spatial structure alters the genetic organization of populations is crucial to refine population genetics theories and predict the effects of anthropogenic transformations on the genetic integrity of species (Cameron, 2014; Kim et al., 2014).

In highly sensitive environments such as high-mountain ecosystems, genetic information is critical in identifying conservation priorities. It guides ecological restoration efforts and the development of biological corridors to strengthen genetic resilience and ensure long-term population viability (Labadessa et al., 2021; Pérez et al., 2019; Smith et al., 2012).

In *Passiflora edulis* allelic richness has been shown to serve as a measure of genetic diversity, which is vital for selecting populations for conservation. Genetic assessments in decision-making related to conservation policies can identify populations that possess unique genetic traits necessary for adaptation to changing environmental conditions (Ocampo et al., 2017).

In captive jaguars (*Panthera onca*), a genetic characterization reflected the potential of these populations as genetic reservoirs due to their high variability, reflecting their potential to revitalize wild populations that may be experiencing low diversity and genetic bottlenecks. This highlights the role of captive breeding programs in conservation strategies, particularly for species facing habitat loss and fragmentation (Gonzalez et al., 2017). Therefore, the role of genetic diversity should be a standard in conservation planning, as it should consider the genetic health of captive and wild populations to improve their overall viability and ensure that they maintain the variability necessary for adaptation by incorporating genetic determinants, which is especially crucial in the face of global climate change and continued environmental degradation.

Conclusions

The identification and protection of priority conservation areas in paramo ecosystems represents a crucial step toward mitigating fragmentation and degradation while fostering a culture of protection for these high Andean environments in Colombia. Strengthening the legal framework, whether through the creation of new constitutional provisions or the reform of Law 1930 of 2018 ("Paramos Law") in conjunction with the guidelines issued by the Regional Autonomous Corporations, is imperative to ensure the survival of the rich biodiversity associated with these systems.

Integrating conservation and development policies is essential to safeguarding the natural resources present in the "paramos". The creation of specific funds to finance research projects, academic programs aimed at assessing the state of these ecosystems, and the implementation of educational strategies to restore degraded areas, protect water sources, and consolidate existing protected areas could make a tangible difference in preserving these environments.

The most critical component in genetic diversity studies lies in intrapopulation variability. This is largely due to the significant gene flow between populations and the reproductive characteristics of species, particularly their allogamous nature and individual diversification. Numerous scientific studies have shown that cytoplasmic markers reveal limited variability within populations derived from maternal transmission patterns and the low mutation rate of this genome, making these markers less practical for genetic studies.

The development of research projects using molecular tools and analysis remains a vital evolutionary force affecting populations in the different ecosystems of the Earth. Its maintenance undoubtedly depends on the preservation of priority conservation areas. The effectiveness of *in situ* biodiversity conservation strategies for insect populations in megadiverse countries like Colombia can be effectively demonstrated.

The inclusion of genetic diversity in conservation planning enables effective strategies for ecosystem sustainability by facilitating the adaptation of conservation efforts to climate change and habitat fragmentation. The studies included in this review show the need to incorporate molecular and population genetic assessments in the selection of conservation priorities, mitigating genetic bottlenecks and maintaining the evolutionary potential of high mountain ecosystems. In the Colombian High

Andean regions, the identification of key genetic reservoirs makes it possible to prioritize conservation actions, facilitating the connectivity of habitats and the resilience of species to environmental change.

In the future, the promotion and consolidation of research projects that integrate genetic, ecological, and territorial approaches will be essential to strengthen conservation strategies in strategic ecosystems such as the Andean "paramos". These projects contribute to deepening knowledge of biodiversity from a scientific and contextualized perspective that responds to the biological and sociocultural particularities of each territory. Furthermore, they foster the development of local and regional capacities for environmental management, as well as the training of researchers committed to the sustainability of high-mountain ecosystems.

Additionally, the continuity of these initiatives supports the creation of interdisciplinary and interinstitutional networks that contribute to the formulation of evidence-based public policies. These projects provide the basis for designing monitoring, restoration, and environmental education models that can be replicated in other high-biodiversity contexts, particularly in regions facing similar pressures. Eventually, their development represents a commitment to ecological resilience, scientific sovereignty, and shared responsibility among academia, communities, and institutions for the conservation of the natural heritage of Colombia.

Acknowledgments

The authors of this work would like to express their gratitude to the higher education institutions that supported the development of this manuscript. The also would like to thank the reviewers for their valuable comments and they would also like to express their gratitude to Vicerrectoría de Investigaciones (UPJ), project ID 08141. The first author of this work dedicates this paper to the memory of his grandfather, Luis Rafael Pérez Español, whose life example continues to inspire his academic path.

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