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PERSPECTIVE

Landscape genetics in plants: challenges and insights from the XX International Botanical Congress

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Abstract

Context Plant landscape genetics is a rapidly developing discipline that examines how habitat loss and fragmentation due to anthropogenic pressures shape plant genetic diversity, gene flow, and potential adaptation. Despite its potential, many aspects remain underexplored, limiting its effective incorporation into conservation planning.

Objectives This study aims to identify current trends, challenges, and practical opportunities for applying landscape genetics in plant conservation, framed within the Madrid Declaration (XX International Botanical Congress, IBC, in Madrid, July 2024).

Methods Insights were gathered from presentations and discussions held during the symposium "Across Land and Water: Understanding Plant Gene Flow at a Landscape Scale" (XX IBC), targeted literature review, and interviews with conservation practitioners.

Results Findings highlight major gaps in bryophyte genetics and vector ecology. Methodological challenges include accounting for life history traits and time-lags. Landscape genetics and genomics have rarely been applied in conservation planning. Effective communication between scientists and stakeholders, increased public awareness, and user-friendly tools are crucial for translating genetic research into conservation action.

Conclusions Addressing methodological challenges and fostering interdisciplinary collaboration will increase the field's impact. Improved knowledge exchange can strengthen conservation planning, promote genetic diversity, and ecosystem resilience in human-modified landscapes.

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Introduction

Anthropogenic habitat destruction and climate change are significant drivers of biodiversity loss worldwide (Fischer and Lindenmayer 2007; Haddad et al. 2015). Plants, due to their sessile nature and reliance on both biotic and abiotic vectors for dispersal, are particularly vulnerable to these environmental changes (Auffret et al. 2017). Habitat loss and fragmentation reduce population size and disrupt the connectivity between native habitats (Leimu et al. 2010; Delnevo et al. 2021; Pinto et al. 2023), leading to the erosion of genetic diversity within increasingly small and isolated plant populations (Aavik et al. 2017; González et al. 2020). This erosion is primarily driven by restricted gene flow, increased inbreeding, and genetic drift (Templeton et al. 1990; Young et al. 1996), which may ultimately limit the capacity of populations to adapt to shifting selection pressures (Chung et al. 2023). Moreover, climate change introduces significant stressors by altering temperature and precipitation patterns, often pushing many plant species to exceed their tolerance limits (Thuiller et al. 2005; Jump and Peñuelas 2005; Rennenberg et al. 2009). Unlike mobile organisms, plants face significant challenges in migrating to more favourable environments, resulting in a mismatch between their current range and future climatic conditions (Corlett and Westcott 2013). The speed of change of selection pressures makes many plant populations highly susceptible to local extinction. This risk is greatest in fragmented landscapes where potential migration routes are limited, hindering connectivity between isolated populations and their ability to colonise new sites (Saltré et al. 2015). In addition, many plants rely on mutualistic relationships for fertilisation (e.g. via animal-pollinators) and nutrient acquisition (e.g. via mycorrhizal fungi), both important factors for population survival. Therefore, future plant population success depends not only on how plants respond to climate change but also on the response of multiple interacting organisms (Kolanowska et al. 2022; Kolanowska 2023). Landscape genetics and genomics explicitly incorporate the spatial context in which plant populations thrive, considering their interactions with biotic and abiotic factors, as well as the structure and dynamics of the landscape to understand gene flow and adaptation (Manel et al. 2003).

To tackle the urgent plant biodiversity crisis, scientists and practitioners from across the globe gathered at the XX International Botanical Congress in Madrid in July 2024, advocating for action through ten strategic initiatives presented in the Madrid Declaration (Gostel et al. 2024). These initiatives highlight the critical importance of scientific collaboration and transdisciplinary approaches in plant research, engaging a diverse range of participants, including plant scientists, botanical institutions, governments, conservation practitioners, indigenous and rural communities, the private sector, and civil society. Within this framework, we recognise that plant research would greatly benefit from adopting the comprehensive approach outlined in landscape genetics and genomics.

Integrating landscape genetics and genomics more broadly into plant research allows for the assessment of spatial, demographic, and adaptive processes in plant populations over both short and long-term scales. Such an approach enables the identification of genetic variation, the evaluation of population viability, and the monitoring of adaptive responses to environmental changes, ultimately guiding more effective restoration strategies that enhance plant resilience, facilitate habitat recovery, and promote biodiversity. Crucially, fostering effective communication between scientists, practitioners, local communities, and governments is necessary to translate increasingly complex research findings into actionable public policies, ensuring that ecosystem restoration efforts are both scientifically informed and broadly supported by all stakeholders involved. These topics were presented and discussed in the symposium titled “Across Land and Water: Understanding Plant Gene Flow at a Landscape Scale” at the XX International Botanical Congress. Rather than providing an exhaustive review of plant landscape genetics, already covered by Holderegger et al. (2010) and Cruzan and Hendrickson (2020), our work builds on the symposium’s talks and conversations to emphasize how landscape genetics and genomics can contribute to addressing the plant biodiversity crisis and support implementing the key initiatives of the Madrid Declaration.

Definition and scope

Within the literature the terms *Landscape Genetics* and *Landscape Genomics* are widely used (eg. DiLeo and Wagner 2016; Aitken et al. 2024). In its strictest sense, the former covers gene flow studies based on long-established genetic methods and the latter those that incorporate modern Next Generation Sequencing (NGS) data. However, they are often used interchangeably. It would be correct to utilise the overarching term *Landscape Genetics and Genomics*, yet, for simplicity, and given the need for practitioners to communicate with stakeholders, politicians, and other members of the public, allied to the wide understanding of the term 'genetics', *Landscape Genetics* is used hereafter in this manuscript.

Landscape Genetics of plants is the understanding of the patterns of neutral and adaptive genetic variation in the context of topography, anthropogenic factors, the environment, and their biotic and abiotic interactions (Auffret et al. 2017). It includes vascular plants and bryophytes. While the focus is typically upon terrestrial species, it also incorporates riparian, riverine, and coastal species, given that freshwater and marine plants are also influenced by geographic and anthropogenic habitats (Ngeve et al. 2017; Arjona et al. 2020; Żukowska and Lewandowski 2025).

Gene flow as the fundamental concept of landscape genetics

Selection, drift, and stochastic processes reduce the levels of genetic variation within a population. This is offset by the source of evolutionary novelty; gene flow, mutation, hybridisation, and introgression. Given that mutation, hybridisation, and introgression are rare, gene flow is therefore the primary source of variation within populations. Without this exchange of genetic material, the population gene pool may become impoverished, resulting in disadvantageous aspects such as greater inbreeding (Frankham et al. 2019), fixation of deleterious alleles (Andrews 2010), and a reduction in overall genetic diversity (Hoffmann et al. 2020). This in turn, reduces a population's ability to respond to selection with a corresponding rise in extinction risk (Ralls et al. 2017).

Plants are sessile hence, gene flow between populations is via pollen movement and dispersal of propagules. They also rely upon propagule dispersal for the colonisation of new areas. This is a key aspect of responding to climate change. These propagules may be haploid or diploid and take the form of seeds, spores, or vegetative material (Ravigné et al. 2006; Mau et al. 2021). They may be allied to complex and varied dispersal vectors. Plants which rely upon animal vectors are also influenced by the interaction of the environment on their vectors. In addition to these vectors, propagule dispersal is strongly influenced by geography, life history, and ecology of plants (Croteau 2010). These factors can interact, influencing the genetic structure and evolutionary potential of the species (Linhart 2014) (see Fig. 1).

Pollen movement may be mediated via wind (anemophily) or by animals (zoophily) (Butcher et al. 2020). These may be generalist or specialist interactions, influenced by geographical and biological factors. For instance, *Plantago* may be both wind- and animal-pollinated (ambophily), utilising additional dispersal mechanisms to increase seed production (Abrahamczyk et al. 2020). More specialist species, such as those in the Orchidaceae, typically experience pollen limitation, in which its utilisation of pollen dispersal vectors is restricted (Ackerman et al. 2023), resulting in specialist pollinator relationships or autogamy being prioritised (Vitt et al. 2023; Ackerman et al. 2023).

Understanding pollen dispersal distances is a fundamental aspect of gene flow in plants. The small size of pollen makes the study of the dispersal itself difficult and time-consuming, as is tracking wind or insects to understand vector movement. Utilising genetics to assess pollen dispersal is significantly easier, hence the incorporation of such methods into gene flow studies. Pollen dispersal distances are variable; *Pulsatilla alpina* has a mean pollen dispersal distance of 3.16 m (Chen and Pannell 2024), whereas *Euterpe edulis* may spread its pollen as far as > 20 km (Santos et al. 2018). It is generally considered that species utilising zoophily via large-bodied animals have greater pollen dispersal distances (Butcher et al. 2020), than anemophilic species (Chen and Pannell 2024).

Seed dispersal distance is the second key component of understanding gene flow in seed plants. The main dispersal vectors are anemochory (wind), hydrochory (water), and zoochory (animal), encompassing endo (internal) and ecto-zoochory

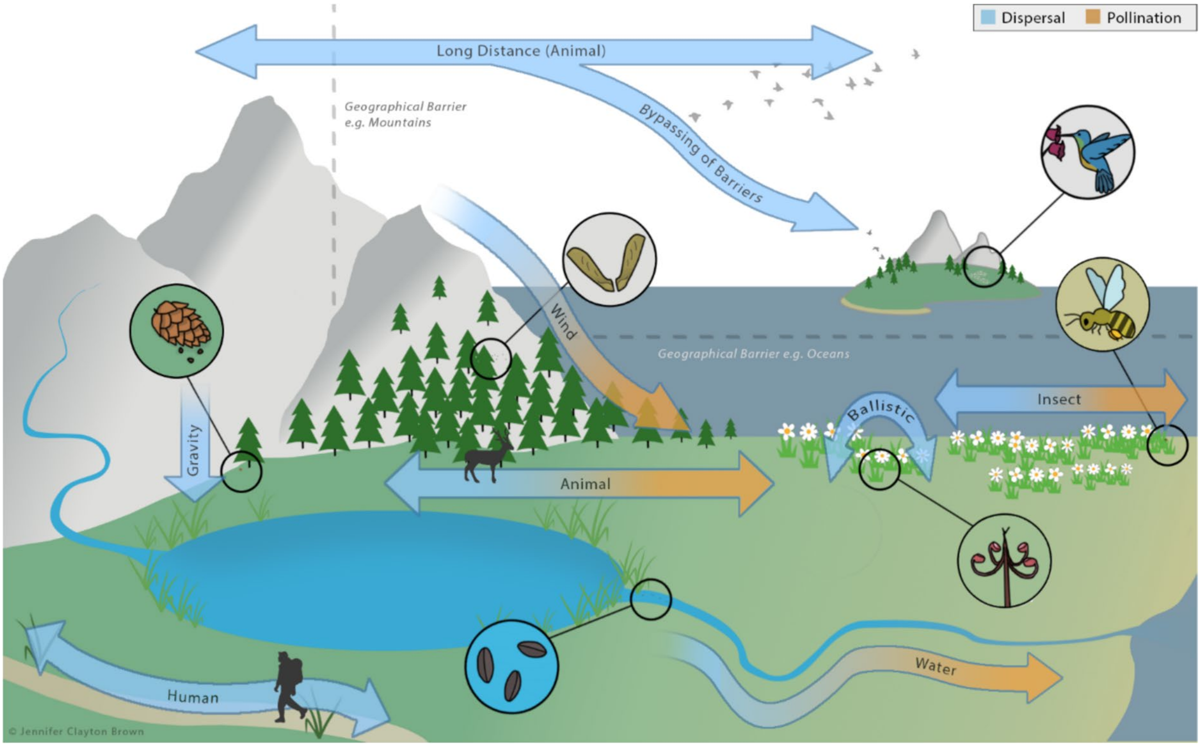


Fig. 1 Illustration of seed dispersal and pollination mechanisms in a heterogeneous landscape. The figure depicts natural dispersal modes including gravity, wind, water and animals, as well as anthropogenic influences (blue arrows). Genetic exchange also occurs through pollination, mediated by insects, animals, wind, and water (orange arrows). Geographic barriers, such as mountains and oceans, can restrict connectivity, although long-distance dispersers, like birds, may help overcome these obstacles. Both seed dispersal and pollination are key drivers of gene flow, shaping genetic structure and evolutionary potential—central themes in landscape genetics

(external), with anthropochory (human) taking an increased role in dispersal (Auffret 2011; Hodkinson & Thompson 1997; Lososová et al. 2023).

Data on seed dispersal is still lacking for most species despite its importance (Lososová et al. 2023; Vittoz & Engler 2007). The development of the seed disperser effectiveness (SDE) framework, however, has significantly advanced our understanding by better capturing the complexities of this mechanism and a deeper appreciation for its ecological importance (Schupp 1993; Schupp et al. 2010; van Leeuwen et al. 2022). Subsequent reviews of seed dispersal literature have resulted in dispersal distance datasets (Chen et al. 2019), with the European flora well represented (Lososová et al. 2023; Vittoz & Engler 2007). These reviews show that most seeds have very localised dispersal without the mediation of animal vectors (Johnson & Harder 2023; Lososová et al. 2023).

Many plants are capable of clonal reproduction, in which the cost of sexual reproduction is mitigated by rapid production via vegetative propagules (Eckert 2001; Barrett 2015; Yang and Kim 2016) such as leaves, stems, roots, rhizomes, and stolons (Sádlo et al. 2018). These propagules become detached from the maternal plant and are subsequently dispersed. They may ultimately colonise a new area (Stöcklin and Winkler 2004; Thomson et al. 2015). Clonal propagules may be dispersed via allochory systems such as anemochory, hydrochory, zoochory, and anthropochory, and may be spread across a range of geographical distances (Fahrig et al. 1994; Winkler and Fischer 2002; Berković et al. 2014; García et al. 2016). Asexual reproduction may be particularly important in extreme environments where sexual recruitment is often restricted, such as saltmarsh habitats (Barrett 2015). Therefore, knowledge of the relative proportions of asexual and sexual reproduction (outcrossing and inbreeding) is critical to understanding geographic patterns of diversity. It is also important to determine if any self-fertilisation or inbreeding is a consequence of fragmentation or an intrinsic feature of the species.

Bryophytes do not produce pollen or seeds. Instead, they rely upon specialised diaspores for dispersal, and their interplay with the wider environment is largely unknown. Moreover, the haploid dominated life cycle of bryophytes plus the utilisation of wind dispersal means that bryophyte patterns of gene flow are likely to be distinctive when compared with the broad agents of dispersal in vascular plants.

The general evidence is that small spore size (27–32 µm in *Sphagnum;* Sundberg 2013) ensures wide dispersal with very little genetic structuring at a landscape scale (Muñoz et al. 2004; Sundberg 2013). However, many bryophytes never produce spores (Wyatt 1994). Dispersal is then reliant upon asexual reproduction whether that be clonal (without meiotic divisions) or intragametophytic selfing, implying more distinct genetic structuring. This is largely supported in the few experimental studies documented, but there are exceptions (Wyatt 1992; Patiño and Vanderpoorten 2018). This lack of knowledge of the landscape genetic structure of bryophytes, despite the group representing a significant proportion of plant diversity, is a significant omission.

Landscape genetics approaches

Depending on the study question, landscape genetics of plants utilises a wide variety of approaches. Studies invariably incorporate a genetic component and a geographic aspect, and frequently an additional approach. This may be distribution modelling, morphology, phylogeny, life history aspects, or other approaches to aid interpretation of the context of the geospatial genetic information (Cruzan and Hendrickson 2020).

The genetic component measures genetic diversity, gene flow, or adaptation. Gene flow and dispersal have long been of interest to biologists. These were initially investigated by experimental and observational methods, for instance Darwin's experiments on the duration that seeds maintained buoyancy in seawater (Darwin 1859; Costa 2017) through to experiments utilising the radioactively labelled pollen and sticky traps (Colwell 1951) or direct observation of ant mediated seed dispersal distances (Handel and Beattie 1990). Likewise, adaptation was typically measured by reciprocal transplant experiments such as those of Clausen et al. (1939, 1940) across the Californian climate zone.

The development of molecular methods, initially protein variation via allozymes, latterly DNA variation, has allowed more sophisticated approaches to be adopted. To assess genetic diversity and gene flow, most landscape genetic studies have traditionally utilised neutral genetic markers (not under natural selection), such as microsatellites. These have enabled insights into the species and population biology and are frequently interpreted in the light of dispersal routes (eg. Sullivan et al. 2019; Quail et al. 2023). However, genetic techniques have advanced significantly in recent years. Modern methods, such as the detection of variability at single-nucleotide polymorphism (SNP) markers through next-generation sequencing approaches, now enable researchers to examine genetic diversity across a much larger number of loci, allowing for a deeper exploration of adaptive genetic diversity (Rellstab et al. 2015). Despite these molecular advancements, careful attention to sampling design is crucial, as poor design or biased datasets can lead to misleading conclusions about gene flow and adaptation. Furthermore, the specific limitations of each marker type should also be considered when designing a study (Allendorf 2017).

As adaptive and neutral loci are subject to different processes, they are often not correlated (Chung et al. 2023). Importantly, the effects of landscape features on gene flow are typically studied using neutral markers, while the selective pressures of environmental factors are more closely associated with adaptive genetic diversity (Holderegger et al. 2010; Cruzan and Hendrickson 2020; Chung et al. 2023). Therefore, both components should be considered for a comprehensive understanding of biodiversity at the genetic level. In the studies presented at landscape genetics symposium in IBC, both types of markers were used depending on the study question. It shows that despite the clear shift of conservation genetics into the genomics era over the past decade (Ouborg et al. 2010; Wright et al. 2020; Heuertz et al. 2023), microsatellites continue to be useful for answering questions about the role of landscape characteristics, habitat connectivity, gene flow, and genetic drift on shaping the structure of plant populations. Nevertheless, it needs to be kept in mind that patterns assessed at neutral genetic loci, such as microsatellites, cannot be directly used for predicting population fitness or adaptability, which is an important key question in conservation applications.

Symposium talks addressing the adaptation of plant populations to changing conditions used SNPs. These markers may be both neutral or adaptive, so it must be determined if a SNP is neutral or adaptive in a particular situation. This is typically done by screening thousands of loci and identifying those potentially adaptive (Balkenhol et al. 2015). Two common methods for detecting putatively adaptive markers are (1) the outlier approach, which looks at the allele frequencies (frequencies of gene variants) of thousands of loci and compares the frequencies to those assumed under neutral expectations, and (2) genome–environment association (GEA) analysis, which links allele frequencies to environmental factors (Balkenhol et al. 2015). Most landscape genetic studies exploring adaptive signatures in plants have focused on climate as the environmental variables of interest, while other factors like soil nutrients and light conditions, though also highly significant resources for plants, are often overlooked due to the difficulty of obtaining fine-scale data (Cortés et al. 2018; Lasky et al. 2023; Dauphin et al. 2023). The symposium talk on the genetic diversity of a grassland specialist, *Primula veris,* in fragmented semi-natural grasslands addressed this gap by discriminating neutral loci from putatively adaptive SNPs showing a relationship to soil and light variables (Reinula et al. 2024, Reinula et al., unpublished). This study showed a contrasting response of adaptive and neutral genetic diversity to habitat fragmentation, with adaptive genetic diversity being higher in connected grassland systems and lower in fragmented grasslands, while the reverse trend occurred for neutral genetic diversity. This finding clearly shows that caution is needed when using diversity assessed at neutral loci as a proxy for adaptive potential of plants.

As the ultimate aim of landscape genetics of plants is to understand genetic variation in the context of topography, land use, and other factors relevant to long-term population sustainability, DNA approaches are combined with other methods. These include conducting common garden experiments to validate the relevance of putatively adaptive loci (Johnson et al. 2022), utilising species distribution models, resistance analysis, and metabolomics. Alongside these approaches is a recognition of the importance of life history characteristics of the species under study. Along with the advancement of genetic techniques, the availability and complexity of landscape and environmental data have also increased (e.g. LiDAR data). This brings additional opportunities, but also challenges for data analysis, and makes collaboration with different scientific fields even more important.

The symposium talks demonstrated the usefulness of different tools to assess the relative role of landscape quality around and between study populations on the genetic diversity and gene flow, respectively. Assessment of the proportion of different landscape elements in both node- and link-based approaches (DiLeo and Wagner 2016; Reinula et al. 2021; Sarmiento et al., submitted, Figs. 2, 3) to disentangle the effect of these elements on genetic structure was applied in several studies. These approaches have been criticised for missing likely gene flow routes (Balkenhol et al. 2015). Alternative approaches, such as the assessment of least-cost paths or resistance surfaces have also been utilised. Assigning resistance values can be subjective, though recent methods like ResistanceGA reduce this bias (Peterman 2018). Studies presented at the symposium revealed no consensus on the best method for studying landscape effects on gene flow. Using different methods on the same dataset allow for testing distinct hypotheses and may yield different outcomes. Furthermore, the response of gene flow to different landscape elements when applying distinct tools can depend on the measure of gene flow, but also on landscape context, suggesting that caution is needed when interpreting the results based on only one approach, genetic measure, or landscape setting (Balkenhol et al. 2015; Epps and Keyghobadi 2015; Reinula et al. 2024).

From the various approaches presented in the symposium, there is no fixed set of research methods in landscape genetics. This reflects the nascent nature of the subject and the rapid evolution of molecular tools and computational capacities, alongside the increasing availability of environmental information (Dauphin et al. 2023). This is a strength and reflects the adaptability of the subject. Additional methods will doubtless be added in the future. At the same time, it is crucial to consider species-specific biology both

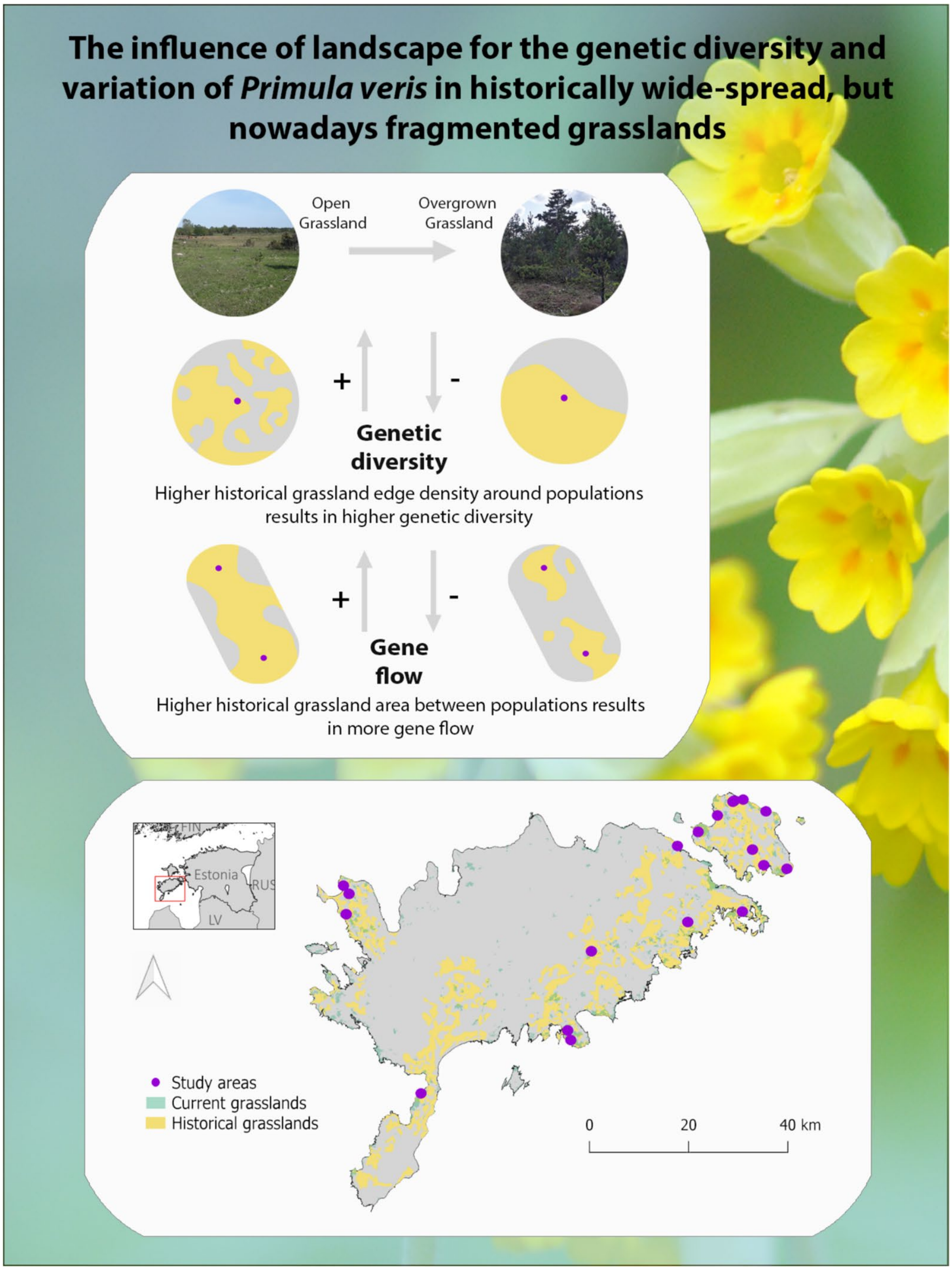
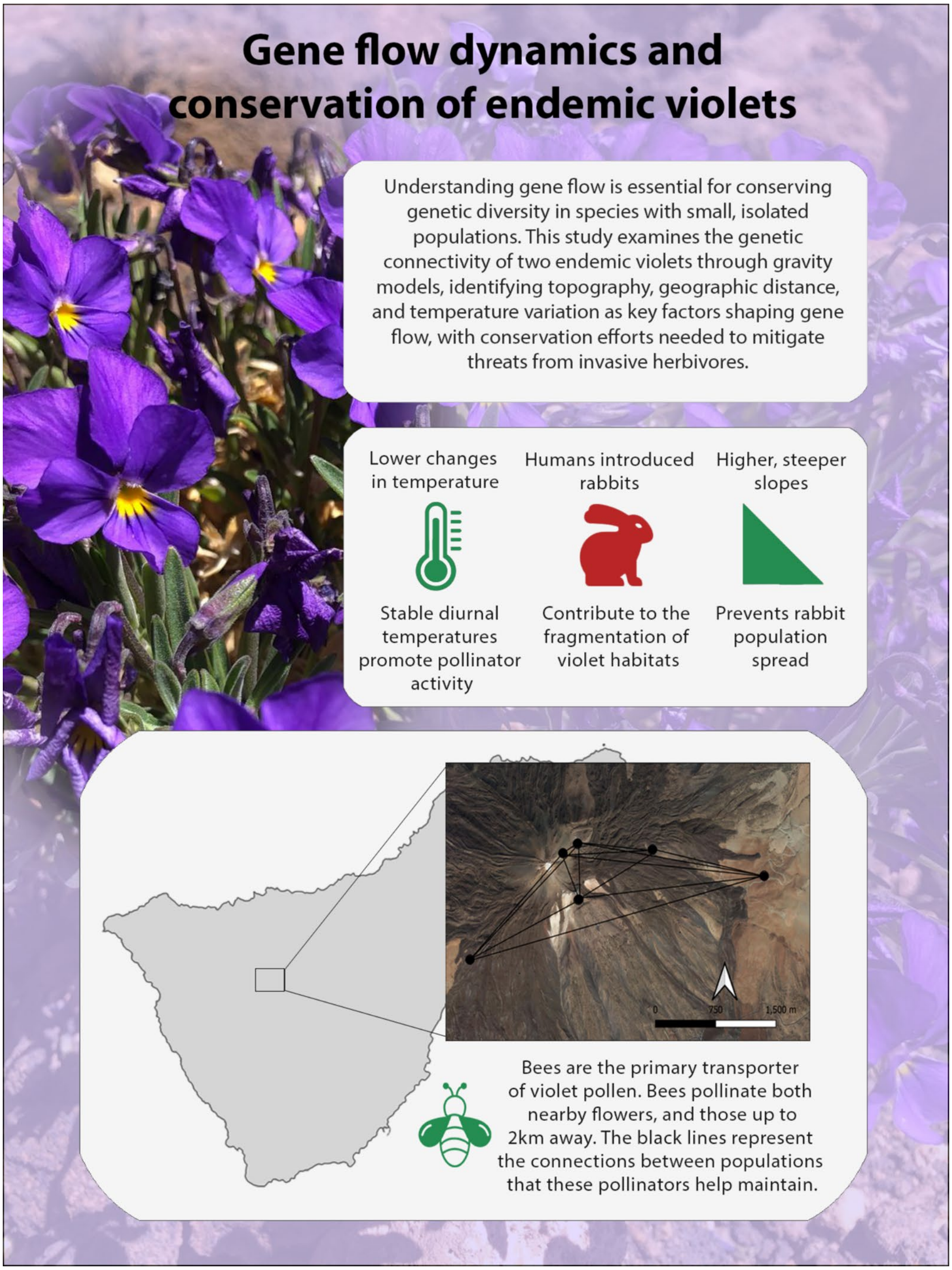


Fig. 2 An infographic summarizing key landscape factors influencing the genetic diversity and gene flow of a characteristic grassland species (*Primula veris*) populations in the semi-natural grasslands of Western Estonia (Reinula et al. 2021). The map shows the location of the populations along with the historical (yellow) and current (green) area of grasslands highlighting the drastic loss and fragmentation of these grasslands. This infographic is an example of how to make complex genetic and conservation results more accessible to a broader audience (e.g. conservation practitioners, policy-makers, municipality)



Gene flow dynamics and conservation of endemic violets

Understanding gene flow is essential for conserving genetic diversity in species with small, isolated populations. This study examines the genetic connectivity of two endemic violets through gravity models, identifying topography, geographic distance, and temperature variation as key factors shaping gene flow, with conservation efforts needed to mitigate threats from invasive herbivores.

Lower changes in temperature	Humans introduced rabbits	Higher, steeper slopes
Stable diurnal temperatures promote pollinator activity	Contribute to the fragmentation of violet habitats	Prevents rabbit population spread

Bees are the primary transporter of violet pollen. Bees pollinate both nearby flowers, and those up to 2km away. The black lines represent the connections between populations that these pollinators help maintain.

Fig. 3 Infographic summarizing key factors influencing gene flow in endemic violets of Tenerife (*Viola cheiranthifolia*), using a landscape genetics approach, based on Sarmiento Cabello et al., (submitted). Green elements indicate factors that enhance gene flow, while red elements highlight resistance to gene flow. The map below illustrates genetic connectivity between populations, with black lines representing pollination-mediated gene flow. This example of an infographic is designed to make complex genetic, and conservation results accessible to a broader audience. *Background photo:* © Jose Luis Martín Esquivel when designing the studies as well as interpreting the results. In particular, given that seed and plant longevity influence genetic diversity, the incorporation of such demographic characteristics would be a necessary addition to the field. Seeds typically remain viable for long periods, some enduring for years (El-Maarouf-Bouteau and Bailly 2022) while many plants, especially trees, but also many perennial grassland plants are long-lived (Ehrlén et al. 2002). Thus, practitioners need to be confident that patterns of connectivity reflect the current habitat condition situation rather than being a signature of historical patterns of gene flow (time-lag effects).

Landscape genetics and conservation policies

Despite decades of scientific advancement and international agreements, genetic diversity remained marginalized in practical conservation policy until very recently. Key international agreements aimed at protecting biodiversity, for instance the Rio convention (1992) and Paris Convention (2016) did not explicitly consider the conservation of genetic diversity. Consequently, it has been absent from core agreements on biodiversity protection, such as the Convention of Biological Diversity (CBD); and the Habitats Directive of the European Union (EU). Only with the Kunming-Montreal Global Biodiversity Framework (GBF; CBD/COP/DEC/15/4, CBD/COP/DEC/15/5), agreement in 2022, was policy implemented to address the loss of genetic diversity in both model and non-model wild species. Effective population sizes (Ne) below 500 and the loss of genetically distinct populations are the key indicators standardising the measurement of genetic diversity loss (Laikre et al. 2020; Hoban et al. 2020). Although their effectiveness remains debated (Teixeira and Huber 2021), these indicators have been adopted in the GBF (CBD 2022a, 2022b), thus requiring parties of the CBD to report progress over the next decade (Hoban et al. 2024; Mastretta-Yanes et al. 2024). The next crucial step is to establish a well-thought-out and robust consensus on how to assess Ne and genetic distinctiveness between populations in practice to effectively inform conservation (Fedorca et al. 2024). Also in this process, landscape genetics can provide valuable insights, such as delineating population boundaries in different landscape settings.

The EU has very recently adopted the Nature Restoration Law (NRL 2024), setting ambitious goals for the conservation and restoration of biodiversity for the near future. EU Member States are required to define areas where intensification of land use and other anthropogenic factors have led to insufficient connectivity and impoverished diversity of habitats to prioritise national-level restoration planning (NRL 2024). Although, the restoration of landscape-scale diversity and connectivity of habitats encompasses an important aim of NRL, it does not include the need to enhance gene flow and genetic diversity, thus neglecting the understanding that the species diversity and related ecosystem functions can be protected and supported through maintaining genetic variability (O'Brien et al. 2025).

Despite the lack of formal legislation specifying genetic diversity at a landscape scale, some national and local governments have developed initiatives to support biodiversity conservation and the sustainable use of genetic resources. In Spain, for example, the Strategic Plan for Natural Heritage, Biodiversity and Plant Conservation (RD 1057/2022) focuses on the sustainable use and preservation of plant genetic resources, highlighting the role of biodiversity preservation initiatives in this effort. At a regional level, the Smart Specialisation Strategy (UE 2021/1058) in the Canary Islands recognises the region's biological and geographical diversity as one of its most valuable assets, advocating for its protection to promote green growth and sustainability.

Within the UK the Lawton report (2010), commissioned by the government, called for 'more, bigger and joined up' nature reserves. The 'joined up' aspect is underpinned by habitat connectivity, and by inference, genetic connectivity. This has led to schemes by various NGOs to enhance such connectivity. Indeed, habitat connectivity analysis has become an integral part of many modern conservation strategies (Crooks and Sanjayan 2006), offering a better understanding of how landscape and habitat features influence species responses (Baguette et al. 2013; González et al. 2017; Resasco 2019; Hendrickson and Cruzan 2024). Landscape genetic studies have helped to bring insight into the complex relationships between landscape characteristics and the structuring of genetic variation in plants, as demonstrated by earlier studies

(Damschen et al. 2008, 2019) and broadened by the talks in the symposium.

Landscape genetics can directly support the fulfilment and assessment of the goals of the Kunming-Montreal agreement as well as EU NRL, alongside other regional and national action plans in several crucial ways. Firstly, landscape genetics addresses habitat fragmentation by identifying connectivity corridors within fragmented landscapes and by understanding landscape elements critical for enhancing and maintaining landscape-scale connectedness between plant populations (Reinula et al. 2021, 2024; See Fig. 2). Secondly, it can identify areas of high genetic diversity and adaptive potential, substantial for helping ecosystems adapt to environmental changes. Finally, landscape genetics informs land-use planning by identifying genetic refugia and areas with significant evolutionary potential that should be prioritised for conservation efforts of threatened plant species (Aavik et al. 2017).

One major advantage of landscape genetics is the availability of existing environmental data, the potential of which has been underused until recently (Dauphin et al. 2023). Vast background information reduces the need for new data collection and accelerates research. Typically, it is only the genetic data that is absent. Additionally, similar landscape features often affect multiple species in the same way, allowing for broader predictions when species are grouped by their dispersal mechanisms or life history traits– an approach which could be particularly beneficial for planning and monitoring EU NRL (Rico et al. 2014). Lastly, landscape genetics enhances conservation communication by providing clear, actionable insights into how specific landscape features influence gene flow, i.e. the patterns of functional connectivity, which may not be mirrored in the spatial diversity and arrangement of habitats (Auffret et al. 2017). This knowledge enables more precise land-use planning, such as creating buffer zones that enhance connectivity while preserving local adaptations.

Besides addressing the effective management of rare or threatened plant species, landscape genetics, by identifying patterns of structural and functional connectivity, supports the development of more targeted, cost-effective, and practical management strategies against invasive species. For example, studies have shown a link between human population density and genetic differentiation in invasive plant populations movement (Alvarado-Serrano et al. 2018; Arredondo et al. 2018), emphasising the significant role of human activity in shaping population connectivity and driving species (Fig. 1). These results are critical for informing management strategies, as they help identify high-risk areas influenced by human activity, enabling more focused and effective prevention and control efforts.

Implementation challenges of landscape genetics in conservation

Conservation efforts prioritise several key goals: conducting successful restoration initiatives, overcoming obstacles that threaten species survival in their habitats, and addressing climate change impacts. To gain insights into these priorities, we interviewed conservationists of two National Parks in the Canary Islands, where genetic research has been a cornerstone of conservation strategies (Sosa et al. 2010; Sosa Henríquez 2021). In these parks, directors emphasised the importance of carefully selecting replanting sites, examining the genetic diversity of plant communities, and overcoming germination challenges. They also noted the difficulties posed by invasive herbivores, which hinder replanting efforts and complicate climate mitigation plans. Additionally, they highlighted the need to improve public understanding and support for conservation work.

Landscape genetics can provide valuable tools for addressing these conservation priorities. For example, it can identify optimal replanting zones by analysing genetic connectivity and corridors (Manel et al. 2003; Rico et al. 2023). It can also examine whether invasive herbivores disrupt gene flow (Sarmiento Cabello et al., submitted), as well as assessing herbivore dispersal patterns (Frantz et al. 2012; Berkman et al. 2018). Furthermore, landscape genetics allows researchers to assess habitat connectivity under projected climate scenarios, offering guidance for long-term conservation planning (Sork et al. 2010; Johnson et al. 2017). By working closely with conservation practitioners, landscape genetics has the potential to make significant contributions to conservation success.

Despite its potential, there are significant challenges in implementing landscape conservation measures informed by genetic data. Although landscape genetic concepts (such as gene flow) are often easy to understand, practical difficulties arise from differences in priorities between researchers and government bodies (Keller et al. 2015). Researchers provide essential, science-based guidance, yet decision-making bodies may not always act on these recommendations. This can result from limited public interest, funding constraints, or the need to balance conservation with established human activities that communities value, such as recreational practices or traditional land use. These competing priorities can sometimes lead policymakers to make compromises that do not fully align with scientific advice.

Increasing public awareness of landscape genetics could help bridge these gaps, as public support can shape policies favouring science-driven conservation. A straightforward and powerful strategy for enhancing public engagement is to share research findings visually through maps, websites, infographics (eg. Figures 2, 3), and territory planning tools. These need to be engaging, accessible, and communicate complex genetic and environmental data effectively (Manel et al. 2003; Pedregal et al. 2015). Furthermore, emerging tools now integrate landscape genetics within single platforms, some with user-friendly interfaces that eliminate the need for coding skills (Chambers et al. 2023; Sunny et al. 2025), which facilitates the use of these analyses into conservation planning. By making research more accessible and engaging, public awareness and education efforts can help build a foundation for policies that align with long-term, science-based conservation goals, ultimately ensuring that landscape genetics can be more widely and effectively applied in conservation practices (see Figs. 2, 3).

To effectively address challenges related to communicating the potential of landscape genetics for conservation, the research community should also turn more attention to diminishing internal barriers that hinder the broader implementation of these tools. First, although landscape genetics has advanced rapidly—driven by progress in genomic tools and its relatively recent emergence—its theoretical foundations and conceptual framework remain fragmented and lack sufficient integration. This conceptual ambiguity weakens the coherence of the field and hampers efforts to build a shared understanding. Second, the absence of consolidated frameworks, combined with rapidly evolving methodologies, makes it difficult to establish a solid educational foundation for formally teaching landscape genetics in academic programs. We believe that addressing these academic gaps is essential to strengthening the discipline and fostering stronger links between research and practical conservation.

Concluding remarks

Plant landscape genetics is a developing discipline enabled by developments in DNA analysis, mapping, and computational power. It aims to understand the extent and apportionment of genetic diversity, the connectivity of sessile photosynthetic organisms across an increasingly fragmented and urbanised landscape in a time of rapidly shifting environmental pressures. Hence, it is key to understanding plant species mobility. This understanding can then be incorporated into conservation policy such that we maximise the opportunity to have a resilient interconnected planet that maintains biodiversity.

As such landscape genetics should underpin wider public and political conservation action. This raises the demand of its practitioners to communicate their findings to stakeholders, whether they be conservation practitioners, politicians or the general public.

The challenges to this are multiple, though not insurmountable. Significant amongst these challenges is the requirement for landscape genetics scientists to communicate to the intelligent layperson, conservationist and politician the concept, findings and implications of the discipline in an accessible and easily understood format.

The XX International Botanical Congress in 2024 set out the Madrid Declaration detailing ten points for action for a sustainable future (Gostel et al., 2024). “Across Land and Water: Understanding Plant Gene Flow at a Landscape Scale” symposium was a significant part of that Congress and the subject is implicitly relevant to the majority of the ten points. We have selected three points to which it is particularly relevant (Box 1); It plays a major role in conservation (Point 6), and this information enables society to make evidence-based decisions (Point 7), using communication strategies suggested in this work. Finally, nature-based solutions (Point 8), which

Box 1 The Madrid Declaration and Landscape Genetics

The Madrid Declaration written at the XX International Botanical Congress listed ten points to ensure a sustainable planet. The three points listed below are those most underpinned by Landscape Genetics

6. Plant Diversity is Central to Ecosystem Protection and Restoration: Participants call for conservation and restoration strategies that prioritize plant diversity while protecting the functioning of ecosystems and landscapes
7. Policy Based on Sound Knowledge About Plants: Participants call for evidence-based decision-making with improved integration of botanical knowledge into sustainable long-term policy decisions
8. Harnessing Nature-Based Solutions: Participants call for the increased recognition and implementation of diverse nature-based solutions that maximize species diversity, increase resilience to climate change, enhance plant conservation, and encourage sustainable management and ecosystem restoration

will give us a resilient and biodiverse planet are underpinned by landscape genetic knowledge.

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Author contribution All authors contributed equally to this work. All authors presented work at the 'Across Land and Water' symposium at the XX IBC meeting in Madrid in 2024. TA, YR and PA organised the symposium. All stages of the article writing have been discussed throughout by all authors, all authors contributed to the text and the final document has been agreed by all authors. JCB drew the figures with agreement on content and style from all authors but particularly from those whose work it represents, TA, IR and SSC. The final edit was undertaken by PA. The response to reviewers was undertaken by all and co-ordinated by SSC.

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Declarations

Conflict of interest The authors declare no competing interests.

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