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REVIEW

Population genetics for insect conservation and control

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Abstract

Insects are essential not only for ecosystem functioning and food security but also comprise some of the world's most destructive invasive species. Therefore, both insect declines and invasions raise major conservation concerns globally and call for respective conservation or mitigation measures. However, studies of insects are hampered by intrinsic biological features of these organisms, which include extreme population fluctuations, a huge diversity of ecological strategies, and common cryptic species. Population genetics provides a large toolkit to adequately accommodate those features, thereby enabling researchers to inform and monitor the efficacy of conservation and mitigation programs. Here, we provide an overview of the molecular and analytical methods that are relevant to insect conservation or mitigation and highlight the challenges involved in their implementation. We detail how and why temporal changes in genetic diversity, population structure and migration, and the genetic basis of adaptation should be taken into account to inform insect management programs. Finally, we review the barriers to the broad adoption of population genetics in insect research and provide guidelines to facilitate the use of these methods by stakeholders. Overall, this review provides theoretical and practical guidelines for implementing population genetics in both insect conservation and control.

KEYWORDS
Conservation of biodiversity, Entomology, Genomics, Invasive species, Molecular Ecology

1 | INTRODUCTION

Insects comprise the most diverse class of the animal kingdom (Stork et al., 2015). These species are key components of natural ecosystem functioning and human food security by providing a wide range of services ranging from pollination, natural pest control, and soil fertilization (Basset & Lamarre, 2019; Straub et al., 2015). However, insect diversity is crumbling in many regions globally (Powney et al., 2019; Wagner, 2020). Although we currently ignore the conservation statuses of most insects, alarming reports suggest an ongoing global mass extinction (Hallmann et al., 2017; Sánchez-Bayo & Wyckhuys, 2019). In sharp contrast, some insects constitute the worst invasive species, causing massive ecological and economic damages globally (Bradshaw et al., 2016; Vaes-Petignat & Nentwig, 2014), as well as increasing public health hazards (Cuthbert et al., 2023).

To adequately solve the challenges associated with both insect declines and invasions, it is mandatory to understand the ecological and evolutionary processes involved (Pyšek & Richardson, 2010). Effective conservation or mitigation strategies rely on sound understanding of population diversity and dynamics (Perry et al., 1997), for example, the resilience or invasiveness potential of populations is often directly linked to their levels of genetic diversity (Chaturvedi et al., 2021; Ochocki & Miller, 2017). Therefore, population genetics is highly informative to guide conservation practitioners (Allendorf et al., 2013). However, at present, this discipline is not sufficiently applied for entomology. Here, we provide guidelines for scientists and stakeholders aiming at using population genetics for the conservation or the mitigation of insects.

2 | CHALLENGES IN INSECT PROTECTION AND CONTROL

In contrast to other organisms for which conservation genetics is established, this field is not well developed for insects. This can possibly be explained by insects' intrinsic features (such as their inconspicuous nature), rendering them particularly challenging to study (Luke et al., 2023).

First, visually tracking and identifying insects can be far more complex than or other animals (Samways et al., 2010). Due to the large number of cryptic species, correctly recognizing target insect species is challenging, even in common and well-studied systems. Because traditionally trained entomologists are becoming scarcer, this challenge is likely to grow in the next years (Drew, 2011). Therefore, most studies on insect conservation have grouped multiple insect taxa under the same umbrella and drawn general conclusions based on field observations (Simmons et al., 2019). Consequently, novel extinction or invasion events may remain hidden.

In parallel, the migration patterns of insects are often poorly understood (Kral-O'Brien & Harmon, 2021). Because a single insect population can comprise both migratory and non-migratory individuals (Yadav et al., 2019), correctly apprehending the movements of individuals in space and time is challenging (Menz et al., 2019). This aspect is of the utmost importance when designing conservation plans to protect their habitats. The ecological preferences of target insect species should also be carefully considered when planning conservation study designs. While some species may be highly conspicuous, others remain difficult to observe and/or capture, leading to potential differences in the attractiveness of the traps used to conduct population censuses, thereby biasing estimates (Didham et al., 2020).

Insects are also known for their general propensity to be r-strategists (i.e., displaying high levels of reproduction) and to undergo extreme population fluctuations across space and time (Hassell et al., 1991). This creates a need to study populations over large spatio-temporal scales and questions the precision of surveys based on single snapshot censuses, that is, those that do not sufficiently take into consideration these fluctuations.

In addition to this, insects use very diverse mating systems that can vary not only between but also within species and populations. They display extreme differences in mating levels, ranging from zero (i.e., asexual reproduction) to up to ∼100 mates (Boomsma & Ratnieks, 1996). A prominent example of this is the polyphenism displayed by aphids, in which asexual and sexual reproduction can be found in the same population (Le Trionnaire et al., 2008). Such fluctuating mating systems can significantly complicate assessments of population dynamics and conservation statuses, as not all individuals of a population contribute to mating similarly.

3 | POPULATION GENETICS TO GUIDE INSECT CONSERVATION AND CONTROL

Population genetics comprise diverse tools to diagnose health statuses and understand the dynamics of populations (Figure 1). Traditional population genetic approaches are sufficient for a large number of goals in conservation genetics (Hauser et al., 2021), for example, estimating parameters such as effective population size, levels of gene flow, and inbreeding. This can be used to determine aspects of demographic history such as genetic structure, population bottlenecks, and introgression between species. In parallel, the use of genomics, in which thousands of loci or whole genomes can be analyzed simultaneously, can add additional precision to these analyses, such as the accurate dating of population splits and the precise characterization of hybridization events (Webster et al., 2023). Genomics also enables analyses that go beyond the basic measures of genetic variation and allows identifying the genes involved in evolutionary processes. For example, genomic analyses can pinpoint the molecular bases of adaptations to environments and define locally adapted subpopulations. With information on the genetic basis of local adaptation, it becomes possible to predict the degree of maladaptation that a population will face under future environmental changes (Waldvogel et al., 2020) or the mechanisms allowing invasive species to spread in new environments (Parvizi et al., 2023).

To study genetic variation with next-generation sequencing data, a reference genome assembly is helpful. This may lead to the overrepresentation of studies on species with available genomes, or further complicate studies

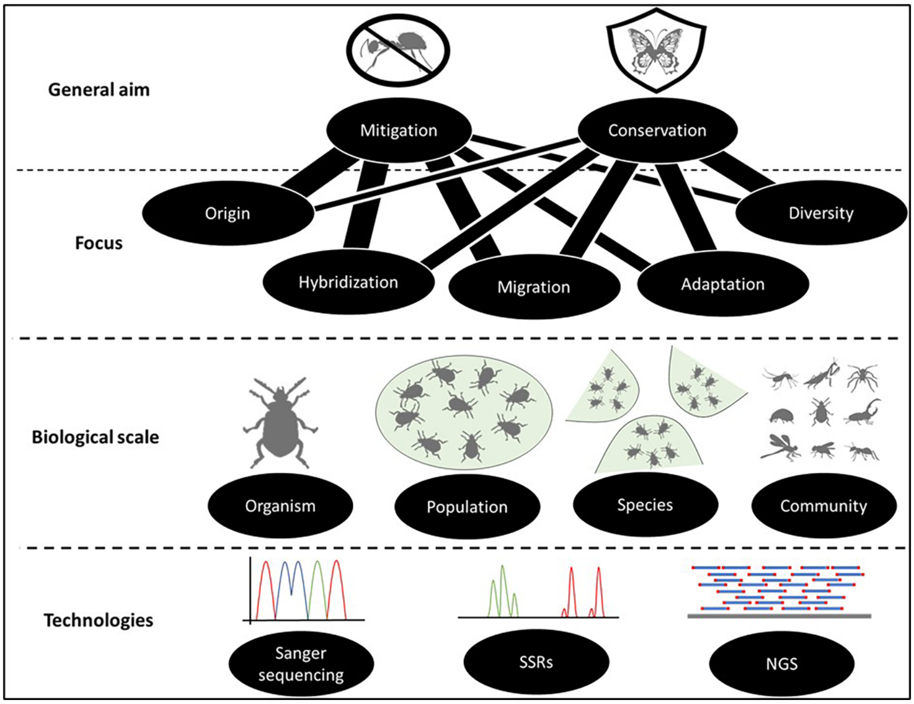

FIGURE 1 Overview of genetics and genomics for the mitigation or conservation of insects. The main items involved when designing a research study are displayed. General aim, focus, biological scale, and technologies are shown. The thickness of the black lines represents the relative importance of the items for mitigation and conservation, respectively. For instance, using genetic data to assess the population of origin can be of significant interest to mitigate an invasive species, while this information might not be as relevant when aiming to conserve a population. Once the focus is determined, the aim should be to select the relevant biological scale for the question to be answered. The choice of level directly derives from the research objectives and will determine the subsequent methods to be used. Finally, once the biological scale is determined, the choice of the relevant technologies can be made. NGS, next-generation sequencing; SSRs, simple sequence repeats.

on less common organisms due to the need for de novo assembly steps. However, several initiatives such as the i5k Earth BioGenome Project (Robinson et al., 2011), the European Reference Genome Atlas (Mazzoni et al., 2023), and the Darwin Tree of Life (Blaxter, 2022), aim at producing tens of thousands of insect genomes in the coming years and will facilitate the use of nonmodel biological organisms. It is therefore likely that high-throughput technologies will become more standard, even when traditional population genetics with only a few loci would be sufficient.

Both traditional and novel molecular tools are very useful to inform conservation and mitigation strategies. For instance, molecular tools can help defining Evolutionarily Significant Units (ESUs), which can be defined as "populations exhibiting discontinuous genetic divergence patterns, geographic isolation, and significant genetic distance" (Dizon et al., 1992). ESUs have been widely adopted in conservation genetics as such units are considered pertinent entities to measure and monitor diversity (Casacci et al., 2014). However, population genetics is not limited to defining ESU and can provide a wide diversity of insights into insect populations dynamics and dispersal. In the next paragraphs, we detail how traditional and recent population genetics approaches can help in answering questions related to the status and dynamics of insect populations to enhance the accuracy of conservation and mitigation strategies.

4 | ASSESSING GENETIC DIVERSITY

A general consensus in ecology is that genetic diversity fosters the resilience of communities, species, and populations by buffering the impact of stressors (Oliver et al., 2015). Surveying populations using solely morphological analyses may be unsuitable for predicting conservation statuses or invasive potentials. Assessing the genetic diversity of insect populations is, therefore, central to understanding the health and viability of populations and to guiding conservation or mitigation decisions (Box 1).

BOX 1 Genetic diversity to drive conservation policies

The rate of ongoing insect losses urgently calls for adequate conservation measures. Since finite supplies can be used for insect protection, this implies careful maximization of the resources available. In this regard, the determination of optimal conservation units is a central step (Casacci et al., 2014). To do so, analyses of genetic diversity can be used, but the categorization of genetic data into such units can be complex (Coates et al., 2018). Although this issue remains problematic in protecting a single target species, conservation strategies generally aim at restoring and protecting habitats in order to preserve communities (Possingham et al., 2015). When it comes to choosing which habitats to preserve and which to abandon, we argue that priority should be given to those hosting the insect communities harboring the most genetically diverse populations. Indeed, diverse populations are generally more resilient and more likely to cope with future challenges (Maebe et al., 2021). In parallel, genetic diversity estimates are critical to understanding if and how invasive insects will prosper in their new range (Parvizi et al., 2023).

4.1 | Estimating species diversity

Molecular analyses allow quantifying genetic diversity at different levels, from communities to individuals. A level that is often used in conservation is the species level, for example, to compare diversity between communities. However, boundaries between species are not always easy to define. Although genetics can help in this tremendously, finding clear genetic cutoff between species is difficult and necessitate in-depth studies. Consequently, this information is only available for a restricted number of species, including pests threatening public health (e.g., malaria-vectoring mosquitoes from the *Anopheles gambiae* species complex, Neafsey et al., 2010) or the global economy (e.g., *Bactrocera dorsalis* fruit flies, San Jose et al., 2023).

Conventional methods to assess species diversity are analyses of the taxonomic richness or abundance through field collections and morphological identification. These techniques are highly dependent on the biology of the species studied and on the availability of experts for the target organisms. However, such experts have become scarce due to a shift in interest in the research community (Drew, 2011). Additionally, the insect class comprises a multitude of cryptic species (Bickford et al., 2007), making the identification of species using morphology impossible. Indeed, distinguishing cryptic taxa is, by definition, not possible with morphology alone and must rely on molecular techniques. Identifying the presence of cryptic species is of the utmost importance in conservation. Cryptic species living in sympatric conditions generally display distinct ecological traits, meaning that conservation measures can have very different outcomes on two seemingly identical species (Friberg et al., 2013). Additionally, the use of incorrectly identified species may create involuntary introductions (Morais & Reichard, 2018) and result in biological invasions and/or unwanted introgressions (Williams et al., 2012).

DNA barcoding is routinely used in modern taxonomy (Orr et al., 2020). The individual barcoding by Sanger sequencing of a short gene portion (usually a portion of the mitochondrial Cytochrome Oxidase I gene, or *CoxI*) can be easily performed and quickly analyzed but may become costly and time consuming when large sample sizes are to be analyzed. In contrast, DNA barcoding based on next-generation sequencing (NGS) can be used to identify species from bulk samples (Morinière et al., 2016), thereby allowing the characterization of communities. Likewise, sequencing environmental DNA (eDNA) can be used to analyze species diversity without the need for species-specific sampling design (e.g., using malaise traps), making the collection of data and categorization of species communities easier (Thomsen & Sigsgaard, 2019). Notably, assaying insect species diversity from eDNA will be vastly aided by initiatives to massively sequence the full genomes of insects (e.g., Robinson et al., 2011).

4.2 | Quantifying population-level diversity

Direct estimates of the number of organisms in insect populations can provide information about the distribution of species and allow the measuring of census population sizes (Nc). However, such estimates require great resources, and obtaining accurate data is severely hampered by many of the intrinsic traits of insects, such as large population fluctuations. Furthermore, such surveys may be inadequate to decide whether populations need protection, as estimates of abundance or richness alone do not allow assessing the reproductive potential of individuals, the past and/or the ongoing dynamics of target populations, and the adaptive potential and viability of insect populations (Hoffmann et al., 2017).

Genetic analyses can help overcoming the limitations of traditional insect monitoring approaches (i.e., surveys). For instance, levels of genetic variation can be used to estimate effective population size (Ne) (Wright, 1931). In contrast to Nc, which focuses on the number of individuals in a population, Ne reflects the impact of genetic drift on the composition of populations, which can be used to assess the level of genetic variability in a population (Charlesworth, 2009). Populations with Ne < 500 are commonly considered to be vulnerable to extinction in the long term and in need of protection (Allendorf et al., 2013; Franklin, 1980). However, the calculation and the interpretation of these estimates is complex. The measures of Ne derived from the levels of genetic variation, based on measures such as Watterson's theta (Watterson, 1975), reflect both long-term population size over evolutionary timescales, recent population fluctuations due to anthropogenic effects, and intrinsic biological features. The relative importance of these effects may be difficult to ascertain.

Across multiple species of vertebrates, it is well known that those threatened tend to have lower levels of variation (Genereux et al., 2020). However, it has also been shown that the life history and ecological traits of an organism are important determinants of their Ne (Romiguier et al., 2014), and species that are highly ecologically specialized may have intrinsically low Ne, not reflective of recent declines. The interpretation of Ne is, therefore, problematic and the differences in Ne between species are not necessarily informative of their conservation status (Díez-del-Molino et al., 2018). Estimates of Ne are often discordant with Nc; this can inform us about the health of a population. It has been suggested that populations of conservation concern have vastly lower Nc than predicted by their Ne, indicating that population bottlenecks do not have an immediate effect on Ne (Peart et al., 2020).

The use of traditional population genetics can provide valuable information about genetic diversity levels and the distribution of this genetic variation within populations simply from assaying the levels of sequence variation at a subset of neutral loci. More recently, a large number of approaches relying on population genomic data can allow inferring the entire temporal continuum of Ne (Nadachowska-Brzyska et al., 2022). Such methods provide a window into the demographic changes that occurred in the evolutionary history of a species and how they have been affected by past population fluctuations. For example, the Pairwise Sequentially Markovian Coalescent method and related methods estimate variation in time to the most recent common ancestor along the genome (Mather et al., 2020), which allows past fluctuations in Ne to be inferred in detail. This can also be achieved by modeling the allele frequency spectrum using approaches such as ∂a∂i (Gutenkunst et al., 2009). Furthermore, recent demography can be inferred from the genome-wide patterns of linkage disequilibrium or the distribution of blocks of identity-by-descent along the genome (Browning & Browning, 2015; Nadachowska-Brzyska et al., 2022; Santiago et al., 2020).

Whole-genome sequence data can also be used to directly measure the levels of harmful genetic variation in populations that can result from inbreeding or the accumulation of deleterious variation. Inbreeding leads to runs of homozygosity, in which harmful recessive mutations can be exposed. Runs of homozygosity can be directly detected in sequence data. Several approaches are available to estimate the proportion of harmful genetic variants in a population (Kumar et al., 2009). For instance, the effect of genetic variants can be predicted from the levels of sequence conservation in noncoding regions or by computationally predicting the effects of amino acid changes (Bertorelle et al., 2022). Using these methods, it is possible to determine whether populations have suffered the deleterious effects of population declines and to assess the need for and feasibility of specific measures to restore their level of diversity, for example, using genetic rescue (Frankham, 2015). These methods have also been used to investigate the genomic signals of population decline leading to the extinction of the Xerces Blue butterfly, *Glaucopsyche xerces* (De-Dios et al., 2023). Screening for such signals might be very useful to detect and prevent future extinctions. Additionally, gathering data on the diversity of invasive insect populations can allow estimating their origin and predict their adaptability potential in their new habitats (Tay & Gordon, 2019). Indeed, genetic diversity might promote successful colonization of new habitats, as was suggested for the black locust gall midge, *Obolodiplosis robiniae* (Yao et al., 2020).

5 | ESTIMATES OF MIGRATION

Tracking the movement of individuals through gene flow analyses can allow understanding how to protect habitats that are relevant for populations, for example, through inferring the optimal geographical scales to be preserved (Manel et al., 2003). In contrast, studying migration allows estimating the origin and dispersion patterns of invasive populations (Idrissou et al., 2019). Although it is possible for larger organisms, direct tracking of the movement of insects is often challenging and costly (e.g., the use of radar to track invasive hornets, Maggiora et al., 2019). Consequently, there is currently a considerable lack of understanding of the seasonal migration patterns of many insects (Satterfield et al., 2020). Yet the assessment of the individual movements and boundaries between populations is possible through analyses of genetic structure. In addition to providing information on the migration of individuals, these analyses can allow the assessment of the environmental factors representing barriers to gene flow.

Identifying the origin, distribution, and movement of species is particularly relevant in the context of biological invasions. Insect introductions have been strongly enhanced by anthropogenic activities in the last century and are expected to continue expanding in the short and medium terms (Bertelsmeier et al., 2017). Identifying the routes of introductions and further spread of invasive species is key to adopting and applying strategies to mitigate the damages caused and to understand the factors driving unwanted introductions. For example, the spread of small hive beetles, *Aethina tumida*, has recently been linked to global beeswax export patterns (Idrissou et al., 2019), showing the need for stricter regulations of the commerce of this good.

Although barcoding may help in identifying the sources of introductions, tracking the dispersion of invasive species with these tools is limited due to bottleneck events restricting the genetic diversity, resulting in a lack of variability for the analyses. Using population genetic studies with markers displaying higher resolution (e.g., microsatellites) can allow for overcoming these issues. Because of their higher mutation rates, these markers are more adapted for categorizing the strength of bottlenecks (Yang et al., 2012) and differentiating between single versus multiple introductions through, for example, analyses of population structure (Pritchard et al., 2000). The use of genomics in this context can provide very detailed information about gene flow at the population and individual levels and help in understanding local adaptation patterns (see next part).

6 | ADAPTATIONS

Conservation strategies are often directed at habitats, not specifically to species or populations (see Box 1). Understanding the adaptation of organisms to their habitats is key to designing pertinent conservation strategies (Hällfors et al., 2016). Moreover, predicting how species and populations will change in response to environmental conditions is fundamental to better understand their resilience and to design applicable conservation measures. To do this, NGS studies are particularly appropriate, as they can precisely reveal which genomic regions are involved in adaptations (Christmas et al., 2019). Comparing different populations facing similar environmental conditions also allows the researcher to pinpoint the general molecular mechanisms responsible for the status of organisms in their habitats (Adrion et al., 2015).

A particularly exciting prospect in this field is the ability to predict the population response to environmental changes based on the genomic variation correlated with these responses. There is much evidence for genetic variation in climate responses in nature, beginning with the classic observations that the frequencies of chromosomal inversions in *Drosophila* fruit flies vary along latitudinal clines (Adrion et al., 2015). For example, the analysis of genomic variation in a species of coral showed that the degree of bleaching expected due to warming oceans is dependent on local genotypes at specific loci (Fuller et al., 2020). Furthermore, new statistical approaches have been developed to use variation at these loci to predict genomic vulnerability (also called genetic offset), which is the difference between existing allele frequencies in a population and those predicted to be most adaptive in a local environment (Fitzpatrick & Keller, 2015).

7 | GENETIC MONITORING

Monitoring genetic changes through time allows assessing the evolution of populations and their dynamics, which are essential for the estimation of conservation statuses (Hansen et al., 2012). Analyzing the continuity in lineages and changes in genetic variation is particularly useful to protect the genetic pool of native species or to evaluate the risk associated with the spread of invasive species, for example, by studying genetic introgression. Although hybridization might be used to rescue endangered populations by increasing genetic diversity (Frankham, 2015), the anthropogenic movement of species can lead to increased instances of undesired and potentially detrimental hybridization (Larson et al., 2019). It is generally believed that hybridization can drive taxa to extinction through the production of nonviable or nonreproductive offspring. Although there is some knowledge about the detrimental impact of such introductions, for example, of social bees (Byatt et al., 2016) and invasive mosquitoes (Gomes et al., 2012), the extent and consequences of this phenomenon in other insects is currently not known due to a lack of studies.

Population genetics analyses can provide accurate measures of the extent of hybridization in insects. This can be useful to detect events of genetic introgression or to measure the success of targeted gene flow strategies. In addition, NGS methods can be used to study the molecular patterns of introgression and how these are involved

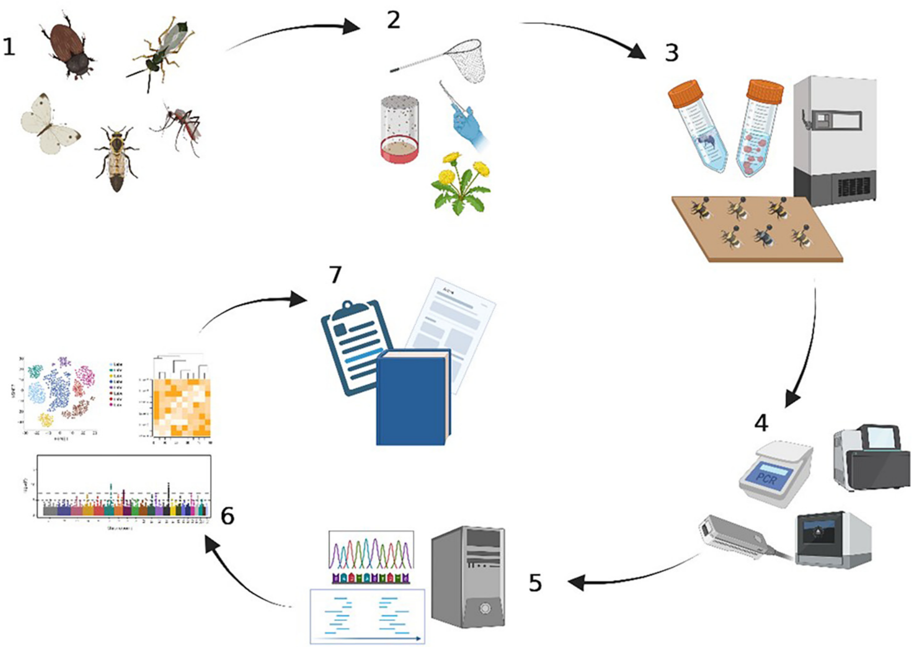

FIGURE 2 Step by step guide to population genetics for insect conservation of mitigation. The main steps involved to conduct a research study about insect conservation or mitigation. The decision-making process involves the choice of (1) target model species; (2) collection methods; (3) adequate sample storage; (4) preprocessing and sequencing of sample; (5) bioinformatic analyses; (6) result visualization; (7) dissemination and exploitation of results. Figure made with Biorender.

in successful outbreeding events (Anderson et al., 2018). This can, in turn, help in understanding the molecular mechanisms behind species and population boundaries (Twyford & Ennos, 2011). Furthermore, this will enable the estimation of the efficacy of conservation measures, that is, whether population size has actually increased or not.

Genetic monitoring can also help in understanding the molecular mechanisms behind local adaptation in invasive and native species. Recent advances in paleogenetics (i.e., the study of ancient DNA) have allowed deeper insights into the evolution of species. Recently developed methods to extract and sequence ancient DNA allow for the comparison of changes in the genome between historical and current samples to analyze changes in population sizes and adaptation to novel stressors. In recent years, a growing number of studies have used insect museum specimens to investigate the temporal patterns of molecular evolution over longer time scales (e.g., Gauthier et al., 2020; Parejo et al., 2020).

8 | ADOPTING GENETICS FOR INSECT CONSERVATION AND MITIGATION

Designing strategies to protect or mitigate insects is challenging due to a number of factors (see Section 2). Here, we provide some general guidelines to help scientists and stakeholders to design projects involving molecular tools to protect or control insect populations and identify some barriers to their successful adoption.

Acquiring pertinent data to inform conservation or mitigation strategies is a lengthy task with multiple steps and obstacles (Figure 2). First, the collection of individuals can prove particularly challenging in the field. Studying endangered insect populations requires the development of nonlethal methods, which may be more trivial when using field assessment (e.g., capture–recapture) compared with molecular work (e.g., DNA extraction). The recent improvements of DNA isolation kits, nonlethal sampling, and eDNA analyses offer a growing number of options to overcome this obstacle. Once the samples are collected, appropriate measures to preserve the biological material for later use should be implemented, thereby allowing researchers to further process specimens in the near or distant future. Efforts to compare and standardize methods are underway (e.g., Evans et al., 2013), and an increasing number of studies comparing storage, extraction, and library preparation methods in a growing diversity of insects are being conducted (e.g., Ballare et al., 2019).

In addition, the comparatively greater infrastructural and financial resources needed to use molecular tools compared with morphological analyses are clearly a significant obstacle to their adoption. However, the increasing outsourcing options and the sizable decrease in costs over the last decades render molecular tools more accessible. Additionally, recent advances, such as the development of portable sequencing technologies, have drastically changed how genomics can be implemented (Watsa et al., 2020). Yet once data are acquired, their analysis can represent another barrier.Although some sequencing companies offer bioinformatics assistance, these remain costly and, thus, cannot be broadly used. Here, the development of accessible and user-friendly analysis pipelines, as well as the training of bioinformaticians for insect conservation purposes, is urgently needed to guide and assist unfamiliar scientists and stakeholders. Some notable efforts are underway (e.g., Hoban et al., 2022) and will hopefully drive the research community to move in this direction.

The availability of molecular resources to compare and interpret results (e.g., the availability of high quality and annotated genomes) may also limit the extent of possible analyses and constrain studies to the most studied organisms. However, diverse projects aim at filing these knowledge gaps in the short and medium term (Robinson et al., 2011) and will greatly facilitate the use of genetics and genomics tools, even in nonmodel species.

Finally, as genomes are being produced exponentially, storage capacity is becoming increasingly challenging. Given the impact of data storage issues, research on this topic is quickly advancing and exciting progress has been made in the past years, including the molecular digital storage of data using DNA (Ceze et al., 2019). While this may solve the issues of capacity, it is also essential to optimize and homogenize the information provided about the origin and processing of the data to guarantee that pipelines can be rerun, repeated, reproduced, reused, and replicated (Benureau & Rougier, 2018). The development of tools to help in guiding the acquisition and storage of such meta-data, such as workflow engines used for human genomics (Tanjo et al., 2021), is urgent.

9 | CONCLUSIONS

Given the key role of insects in food security and ecosystem functioning and their impact on the world's economy and public health, genetic studies should be included routinely in field surveys. While population genetics studies are inarguably demanding in terms of finances and work efforts, many aspects relevant to conservation or mitigation can only be addressed using molecular tools. Taking into account molecular estimates, in addition to traditional field surveys, will lead to more holistic and efficient insect conservation strategies. Population genetics do not rely on knowledge on specific taxa but rather on general skills and methods that can be used over a diverse range of species, it seems molecular analyses for insect conservation and mitigation have a very promising future. Yet given the tremendous diversity of insects and the finite resources to study them, it seems more realistic to perform baseline molecular studies on selected indicator species reflecting the range of insect life histories and functional roles in given habitats.

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ALB and PN conceived and designed the manuscript and contributed to writing of the paper; MTW contributed to writing of the paper.

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All authors disclose any potential sources of conflict of interest.

DATA AVAILABILITY STATEMENT

None.

PERMISSION TO REPRODUCE MATERIALS FROM OTHER SOURCES

Figure 2 was made with Biorender, as stated in the legend.

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