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Population Structure and Genetic Adaptation of Domestic and Wild Ducks Across Different Climatic Regions

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Abstract Having a perception of how domestic and wild ducks (Anas genus) adapt to climatic zones is extremely significant to evolutionary biology as well as conservation of species. In the present work, the study examines systematically the population structure and genetic adaptation of ducks common in tropical, temperate, and cold regions. By integrating mitochondrial and nuclear DNA data, we reconstructed phylogenetic relationships, estimated the times of lineage divergence, and compared genetic lineage diversity in domestic duck breeds and their wild relatives. The findings revealed clear genetic structuring across populations from different geographic regions, which reflects previous domestication events as well as ongoing gene flow. In addition, we identified genomic signatures of environmental adaptation, which comprised functional genes known to play roles in thermoregulation, metabolism, and immune response. Ecological niche modeling and spatial analysis based on GIS also evidenced that the genetic differentiation patterns are influenced by geographical discontinuity and climatic heterogeneity. The study bears witness to the evolutionary flexibility of ducks and establishes the value of molecular ecology for biodiversity conservation and adaptive management, and offers a scientific basis for the sustainable use and conservation of waterfowl resources under global climate change.

Keywords Population structure; Genetic adaptation; Ducks (Anas genus); Phylogeography; Climate-driven evolution

1 Introduction

Anas ducks are typical waterbirds with broad range variation in aquatic habitats, ranging from freshwater marshes and lakes to beaches. They are typical of their active migratory pattern, sexual dimorphism, and adaptive feeding, for example, dabbling. Mallard (*Anas platyrhynchos*) is particularly regarded as the ancestor of the majority of domesticated ducks. Genomic studies in recent decades have illustrated immense genetic diversity among *Anas* species and populations. Whole-genome resequencing and SNP-based methods revealed extensive genetic differentiation between domestic and wild ducks, as well as among populations of wild ducks from various climatic regions (Wolc et al., 2024). They highlight the evolutionary potential and conservation value of genetic diversity in ducks, especially under continued environmental stress and domestication bottlenecks.

Ducks play a significant ecological role in wetland ecosystems by being involved in nutrient cycling, seed dispersal, and management of aquatic plants and invertebrates. They help maintain the health and richness of wetlands that are widely recognized as significant habitats for numerous species. Ducks are economically important as a source of meat, eggs, and feathers in much of Asia and elsewhere, especially in Asia where rice-duck farming systems are common (Veeramani et al., 2021). Not only are ducks a source of agricultural products, but with enhanced pest control, natural fertilization of the soil, and reduced chemical input usage, they enhance sustainable agriculture. Understanding the ecological functions and economic importance of ducks constitutes a strong rationale for conserving both wild and domestic stocks as well as for studying their adaptability to diverse habitats (De et al., 2021; Adeola et al., 2022).

Population composition and genetic adaptation in ducks are relevant to examine to determine how the bird developed over varied environments and is going to respond to impending climatic change. Population composition reflects previous dispersal, isolation, and gene flow, while genetic adaptation suggests selective pressures on survival- and reproduction-based traits. Molecular ecology combines genetic data with environmental and spatial data to expose evolutionary pressures at genome and landscape scales. The aim of this study is to examine differential genetic structure and adaptive traits of domesticated and wild duck populations in various climatic zones, employing the presently available molecular tools including genome-wide SNP analysis, ecological niche modeling, and phylogeographic reconstruction. These results can be utilized to guide conservation programs, inform breeding schemes, and refine the understanding of bird response to environmental change.

2 Phylogeny and Lineage Evolution of Domestic and Wild Ducks

2.1 Taxonomic history and phylogenetic controversies of ducks

The classification of ducks, especially in the genus *Anas*, has been confusing regarding which immediate wild relatives of domesticated ducks. The mallard (*Anas platyrhynchos*) and Chinese spot-billed duck (*A. zonorhyncha*) were historically proposed as primary ancestors. However, new genomic studies report broad introgression and deduces the real wild ancestor of the domestic duck to be potentially an as-yet-undefined or unsampled population, rather than was believed previously and despite present phylogenetic divergence (Guo et al., 2020; Feng et al., 2020; Zhang et al., 2023).

2.2 Phylogenetic relationships revealed by molecular data

Molecular investigations, including whole-genome resequencing and mitochondrial DNA sequencing, have clarified domestic-wild duck relationships. Chinese domestic duck breeds are mostly discovered to carry mallard and spot-billed duck haplotypes, indicating both species' contributions to domestic lineages (Zhang et al., 2023). Phylogenetic network analysis and networks never reveal a deep divergence between wild ducks and domestic ducks with signatures of hybridization events and gene flow, particularly among Chinese spot-billed ducks and domestic ducks (Feng et al., 2020; Guo et al., 2020; Feng et al., 2021; Pal et al., 2022; Zhang et al., 2023) (Figure 1).

2.3 Methods for phylogenetic tree construction and lineage divergence time estimation

Researchers employ a suite of molecular and computational methods of duck phylogeny reconstruction. Maximum-likelihood (ML) phylogenies and median-joining (MJ) networks are the preferred mitochondrial DNA data (Zhang et al., 2023). Population and demographic inferences may be achieved by resequencing the complete genome, including divergence time estimation using coalescent-based and molecular clock methods. These methods have shown that domestic ducks descended from mallards and spot-billed ducks hundreds of thousands of years ago, prior to the supposed period of domestication (Guo et al., 2020; Feng et al., 2020; Liu et al., 2020; Pal et al., 2022).

2.4 Evolutionary trends in wild duck lineages and domestication events of domestic ducks

Genetic research indicates that wild duck lineages split relatively extensively during the most recent glacial cycle and that mallards and spot-billed ducks speciated around 70 000 years ago (Liu et al., 2020). Domestic ducks are also believed to have diverged from their closest wild ancestors even earlier, with domestication then having had sophisticated selection trends for aspects such as egg and meat production, feather pigmentation, and domesticatability (Zhang et al., 2018; Feng et al., 2020; Liu et al., 2020; Zhu et al., 2021). Hybridization and introgression between wild and domestic animals have also contributed to the genetic landscape, resulting in phenotypic diversity among modern domestic ducks (Feng et al., 2020; Guo et al., 2020; Liu et al., 2020; Zhu et al., 2021).

3 Geographic Origin and Dispersal History of Ducks

3.1 Hypotheses on the origin of ducks and their biogeographical background

Anas genus and related groups of ducks are believed to have originated in Eurasia, with fossil and molecular evidence proposing widespread Eurasian distribution during the Miocene, followed by dispersal across other continents (Zelenkov et al., 2018). Phylogeographic study indicates that huge duck lineages, such as mallard-like ducks, spread across Oceania, broader Indonesia, and the Philippines over the last 1~2 million years, developing unique genetic lineages in island regions (Kaminski et al., 2024) (Figure 2). High dispersal capacity of ducks enabled them to have broad biogeographical distribution and complex evolutionary history (Zelenkov et al., 2018).

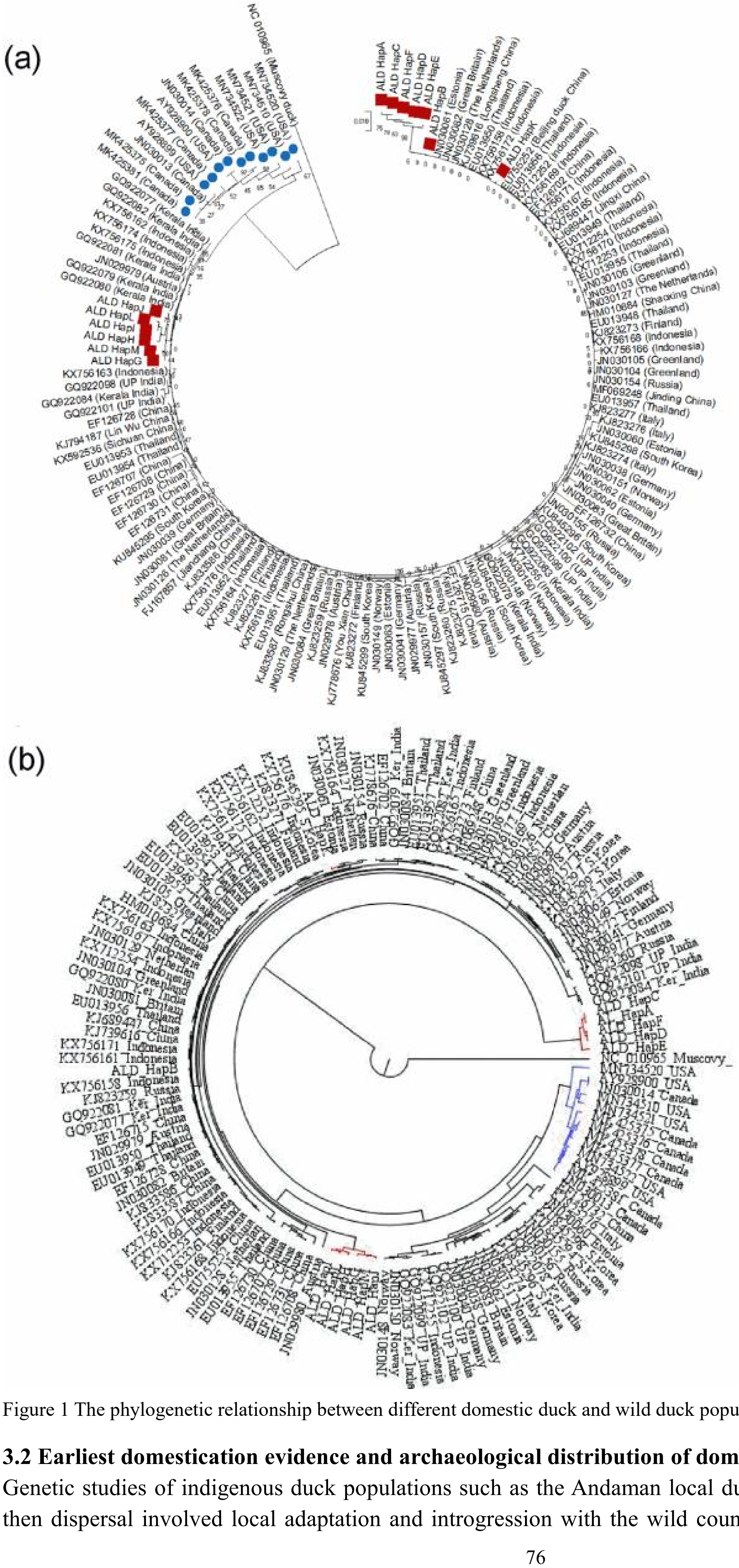

Figure 1 The phylogenetic relationship between different domestic duck and wild duck populations (Adopted from De et al., 2021)

3.2 Earliest domestication evidence and archaeological distribution of domestic ducks

Genetic studies of indigenous duck populations such as the Andaman local duck indicate that domestication and then dispersal involved local adaptation and introgression with the wild counterparts. Archaeological as well as genetic data indicate that domestic ducks also originated matrilineally through genetics within Eurasian mallards and were migrating and pouring into island nations like the Andaman and Nicobar Islands from southern India and Southeast Asia (De et al., 2021). The presence of rare genetic clusters in these countries implies more than a single process of domestication and dispersal.

3.3 Molecular clock estimates of domestication and divergence time windows

Estimates of molecular clocks based on whole-genome resequencing and ddRAD-seq data locate the split of mallard-like ducks from their closest relatives around 1~2 million years ago, followed by Holocene and Pleistocene radiations and divergences in populations (Jiang et al., 2021; Kaminski et al., 2024). Demographic analysis has shown that house ducks have undergone population bottlenecks since the last glacial maximum, and differentiation between large geographic populations is pre-human mediated domestication, suggesting complex demographic history subject to natural as well as anthropogenic pressures (Jiang et al., 2021).

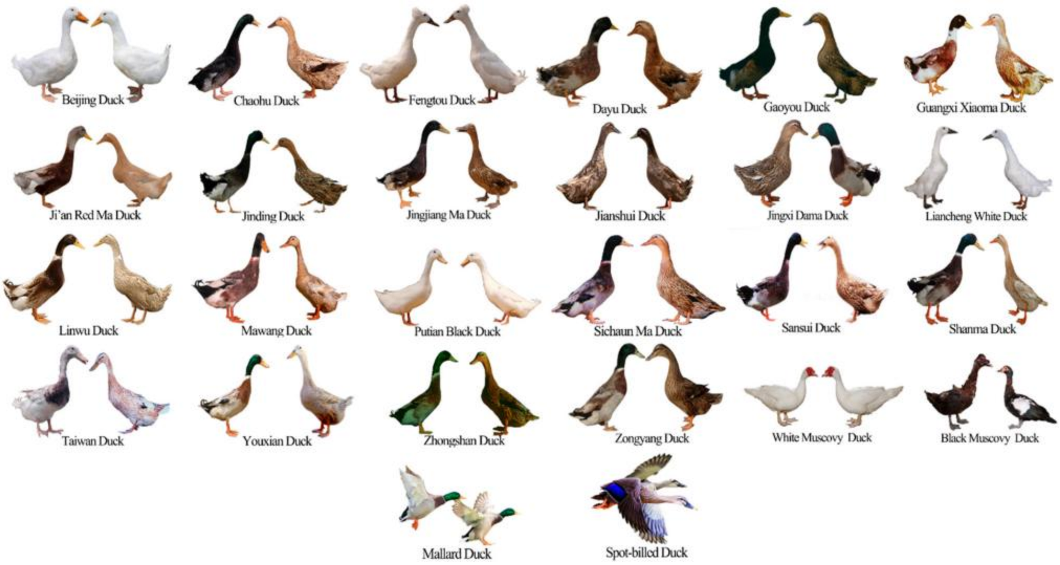

Figure 2 Images of 26 individual duck populations (Adopted from Zhang et al., 2023)

3.4 Environmental changes as drivers of duck migration and population formation

Environmental disturbances, for instance, glacials and climatic cycles, have been worldwide forces in causing duck migration, population bottlenecks, and novel population formation. The final glacial maximum, for instance, caused severe bottlenecks within Chinese domestic ducks, whereas postglacial periods facilitated stepwise colonization and secondary contact among lineages (Jiang et al., 2021; Scribner et al., 2024). Natural adaptation and adaptation of native environments, like that in the Andaman local duck case, have also influenced the genetic composition of duck populations and climate-change tolerance (De et al., 2021).

4 Distribution Patterns and Dispersal Pathways of Duck Populations in Different Climate Zones

4.1 Distribution characteristics and population connectivity of ducks in tropical, temperate, and frigid zones

Duck populations in varying climatic zones show intense variation in distribution and connectivity. Spot-billed Ducks and Mallards overwhelm the most species-rich species in temperate coastal wetlands in eastern China, with the greatest diversity and abundance on tidal flats (Han, 2024). Abundance and duck community structure vary significantly among habitats as a response to adaptation against environmental elements and resources in local habitats (Luo et al., 2024). In frigid habitats, i.e., Arctic and subarctic, long-tailed ducks breed in the northern breeding sites and move to temperate marine habitats for wintering, indicating high migratory connectivity between breeding and wintering sites (Karwinkel et al., 2020). These patterns indicate the ecological flexibility and broad climatic tolerance of duck species.

4.2 Historical dispersal and phylogeographic patterns of domestic duck breeds across climate regions

Genomic analysis indicates that Asian domestic duck populations are geographically divided into Southeast/South Asian, wild, and local Chinese. Historical demographic reconstructions indicate that Southeast/South Asian and Chinese domestic ducks experienced strong population bottlenecks, particularly during domestication and the last glacial maximum. Despite such bottlenecks, there has been widespread and enduring gene flow among neighboring populations, especially between Guangxi (China) and Southeast/South Asia, that has shaped the current genetic structure of domestic ducks in climatic regions (Jiang et al., 2021). Phylogeographic studies of wild ducks, such as the Harlequin Duck, also show that early colonization from glacial refugia and contact events subsequently have encouraged regional and continental-scale genetic differentiation (Scribner et al., 2024).

4.3 Influence of hydrology and habitat changes on dispersal and isolation

Hydrological regimes and habitat dynamics are the principal reasons for duck dispersal and population fragmentation. Seasonal and inter-annual timescale changes in water level, food and habitat structure affect ducks' abundance and mobility. For example, the body shape and mass of Chinese coastal wetland ducks are based on the coverage and connectivity of wetland habitats and tidal flats that also determine their seed dispersal role (Luo et al., 2024). In the Baltic Sea, water quality and water nutrient levels regulated through processes such as runoff fertilizer have direct effects on long-tailed duck population and overwintering success (Rintala et al., 2022).

4.4 Dual Impacts of anthropogenic interference and natural barriers on population structure

The organization of duck populations is shaped by human-induced and natural influences (e.g., climate change, land cover change, hunting) and natural barriers (e.g., ocean basins, geographic distance). Historical records throughout North America suggest that the ranges of ducks have adapted to changing climate and land cover and show species- and subpopulation-specific autumn and winter northward or southward migration (Verheijen et al., 2023; 2024). Within the subarctic and Arctic, climate change and human activity threaten significant habitats, encouraging elevation in isolation and modifying migration corridors (Karwinkel et al., 2020). Genetic analysis confirms vicariance during the past and recent gene flow are accountable for spatial patterns of duck genes as natural and human-made structures jointly condition differentiation and connectivity (Jiang et al., 2021; Scribner et al., 2024).

5 Adaptive Evolutionary Mechanisms of Ducks in Different Ecological Zones

5.1 Morphological and physiological adaptations under habitat variation

Ducks illustrate typical skeleton and physiological specializations to ecological niches. Mallards possess dense and heavy bones adapted for generalized locomotion and utilization of diversified environments, while Green-Winged Teals possess less dense and lighter bones adapted to enable speed in flight in shallow wetland environments. Tufted Ducks, being deep-divers, illustrate heavy and rigid bones adapted to underwater searching (Osiak-Wicha et al., 2024). Duck species that inhabit high altitudes possess physiological specializations towards hypoxia, including structure and function adaptations of hemoglobin to enable the transport of oxygen in hypoxic environments (Graham and McCracken, 2019).

5.2 Genomic-level adaptive differences and functional gene analysis

Genomic research establishes adaptive evolution in ducks to involve regulatory and structural genetic innovations. Convergent evolution of high-altitude ducks is observed in hypoxia-inducible factor (HIF) pathway gene EGLN1 and EPAS1, consistent with vertebrate high-altitude adaptation (Graham and McCracken, 2019). Positive selection in tissue repair, immune response, and anti-tumorous activity is observed in the Chinese crested duck, reflecting life's gene compensation and gene stability preservation mechanisms. TAS2R40 harbors a causative crest character mutation in this breed (Chang et al., 2023).

5.3 Evolutionary trends in ecological niche differentiation and behavioral adaptation

Phenotypic and behavioral divergence to ecological niche filling causes adaptive radiation in dabbling ducks. Variation in bill shape creates variation in foraging efficiency and prey preference that results in niche partitioning of sympatric species. Aggression and mate preference are other behavioral characters that are involved in ecological speciation and maintenance of species boundaries. Ecological pressures and sexual selection contribute to cause reproductive isolation and phenotypic divergence (Brown et al., 2022).

5.4 Balance between gene flow and local adaptation among populations

The evolution of ducks is shaped by dynamic interaction between gene flow and local adaptation. While gene flow can contribute new genetic variation and retard divergence at neutral sites, strong local selection for hypoxia tolerance or immunity, for instance, can maintain adaptive differentiation even under some gene flow (Graham and McCracken, 2019; Lavretsky et al., 2021). In other cases, gene flow then and now has resulted in hybrid speciation and adaptive transfer of alleles between species, such as in the case of sea ducks (Lavretsky et al., 2021). Natural barriers and ecological specialisation are commonly the constraints to gene flow, resulting in marked population structure and evolutionary independence (Peters et al., 2016; Lavretsky et al., 2021).

6 Applications of Phylogeny-Based Ecological Models and Methods

6.1 Population geographic modeling integrating genetic and distribution data

Combination of phylogenetics with environment and geospatial data makes the geographic models of the population more precise. Adding phylogeny to models enhances ecological parameter prediction, such as species presence, by the addition of evolutionary relations and environment simultaneously. Addition of phylogenetic topology in logistic models, for example, enhances the prediction of species distribution and ecological response over non-phylogenetic models, illustrating why evolutionary context is crucial to the structure of the population (Morales-Castilla et al., 2017; Godoy et al., 2018).

6.2 Joint application of phylogeny and gis-based spatial analysis

The combination of phylogenetic frameworks and spatial modeling using GIS allows for more powerful species distribution modeling. It leverages both the evolutionary past and the spatial co-presence of closely related species, improving model fit and predictive power, especially for data-poor species. The addition of phylogeny as a substitute for lacking trait data into spatial models has the potential to disentangle contemporary and historical determinants of species distributions and reconcile differences between modern and historical biodiversity patterns (Morales-Castilla et al., 2017; Li et al., 2020).

6.3 Ecological niche modeling (enm) and paleoclimate simulation for supporting adaptive evolution studies

Ecological niche models (ENMs) are increasingly being applied in phylogeographic analysis to model past and future environment tolerances and species' potential range at current and past climates. ENMs reveal profound insights into the effect that climate change through time had upon evolutionary adaptation and genetic diversity. Advances in using ENM output in genetics enable researchers to test hypotheses about the power of the environment in eliciting evolutionary change, in addition to predicting adaptive hot spots or susceptibility hot spots (Wang and Chen, 2024).

6.4 Application prospects of models in duck conservation and genetic resource management

Phylogeny-based ecological models have great potential for duck conservation and genetic resource conservation. By integrating evolutionary history, trait data, and location, these models have the potential to advise knowledge on how to conserve genetic diversity, manage population, and predict response to environmental change. They also provide a system for ranking conservation priorities, e.g., unique evolutionary lineages or climate- or habitat-threatened populations, to enable more effective and targeted management action (Li et al., 2020; Lemos-Costa et al., 2023; Lemos-Costa et al., 2024).

7 Concluding Remarks

Here, we conduct an integrative study of population structure and adaptation genetics among domesticated and wild ducks (*Anas* genus) across different climatic regions. On the basis of whole-genome resequencing data, we found extreme genetic divergence among wild species and domestic breeds. Domestic ducks exhibited recognizable genetic clusters, which reflected their corresponding breeding history and selection pressures. This was not found in wild ducks. Conversely, genetic structure was more gradational across wild duck populations, owing to natural dispersal and gene flow. We also identified genomic regions with selection for environmental adaptation, such as genes that regulate thermoregulation, metabolism, and immunity. The findings illustrate the complex interaction between domestication, natural selection, and environmental pressures on duck population genetic structure.

Despite the advancement of genomic technologies, there are still some areas of duck population genetics research. One critical area is that wild duck populations are underrepresented in genomics, and this impacts our understanding of their genetic diversity and evolutionary history. Second, it is still challenging to separate signals of natural selection from those of genetic drift, particularly in recently demographically sampled populations. Technical limitations such as assembly errors and sequencing errors can also be a cause of instability in genomic analysis. Moreover, the merging of genomic data with ecological and environmental information includes complex analytical methods, which are under development.

Subsequent studies will have to embrace an interdisciplinary platform that unifies genomics, ecology, and the environment in order to understand duck population dynamics in fine detail. Landscape genetics integration may shed light on the effects of spatial barriers and environmental gradients on gene flow as well as adaptation. Ecological niche modeling and genomic data can also provide us with predictions about how duck populations are likely to react to climate change. There needs to be collaborative effort between ecologists, conservationists, and geneticists to develop efficient tools for ensuring genetic diversity and conserving domestic and wild duck populations as sustainable against environmental hazards.

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Conflict of Interest Disclosure
The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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