Genetic Responses to Climate Change in Montane Birds Across Asian-Pacific Mountain Systems

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Abstract. Climate change profoundly alters montane ecosystem stability, driving upslope habitat compression, population fragmentation and elevated extinction risks for specialized mountain bird species. Montane avifauna are highly susceptible to climatic fluctuation due to narrow elevational niches and topographically limited dispersal ability. This narrative paper systematically synthesizes recent genomic and ecological evidence across Asian-Pacific mountain systems to clarify how climate change shapes population connectivity, genetic diversity, local adaptation, and genomic vulnerability of montane birds. Existing studies demonstrate that historical climatic cycles and persistent geographic barriers jointly structure contemporary genetic differentiation, while intraspecific populations exhibit highly variable genomic offset, genetic load and climate resilience. Gene flow and interspecific introgression can partially mitigate climate-driven genetic degradation, yet such beneficial effects are context-dependent and spatially heterogeneous. Current research suffers from unbalanced geographic sampling and insufficient real-time genomic evidence for modern warming. This paper summarizes core genetic response mechanisms and key research gaps, providing targeted genomic insights for future adaptive conservation and evolutionary prediction of montane bird biodiversity.

Keywords: Climate change, montane birds, genetic diversity, population connectivity, genomic vulnerability.

1. Introduction

Climate change is a growing threat to biodiversity, particularly in mountain ecosystems. Rising temperatures and changes in precipitation can alter habitat suitability, species distributions, and population persistence. Mountain species may be especially sensitive because suitable climatic conditions often occur within relatively narrow elevational ranges. As temperatures increase, these conditions can move toward higher elevations, leaving less available habitat for species that already live near mountain summits. Recent research has shown that tropical and high-elevation mountain species may be particularly vulnerable to continued warming [1].

Montane birds provide a useful group for studying these effects because many species are closely associated with particular elevations, forest habitats, temperature ranges, and precipitation conditions. When suitable habitats move or become fragmented, populations may become more isolated from one another. This can affect not only where birds occur but also how much gene flow takes place among populations. Research combining genomic offset and ecological niche modelling has shown that populations of the same species can respond differently to future climatic conditions [2]. Population differentiation is also influenced by mountain barriers, elevational distribution, and historical gene flow [3].

Genetic variation is important because it provides the basis for populations to respond to environmental change. Populations with greater genetic diversity may have more variation available for selection, while small and isolated populations may lose genetic variation through genetic drift. Reduced connectivity can also increase differentiation among populations. In the New Guinean mountain bird *Amblyornis macgregoriae*, geographically separated populations showed clear genetic structure, limited gene flow, and differences in predicted climate vulnerability [4]. Studies of other New Guinean montane birds also show that historical climatic changes altered habitat connectivity, although strong geographic barriers continued to maintain genetic differentiation [5].

Recent studies from Southeast Asia and nearby mountain systems show similar patterns. Research on Indo-Pacific montane birds suggests that geographic origin and dispersal history have influenced how populations formed across different mountain systems [6]. Population genomic research on five montane bird species in Vietnam found that Pleistocene climatic cycles repeatedly changed connectivity among mountain forests and contributed to long-term population differentiation [7]. In Sundaland, historical palaeoriver systems have also left clear signals in the present population structure of forest birds [8]. More recent work in Taiwan has shown that some low-elevation populations have lower genetic diversity and higher genetic load, while greater gene flow may reduce these differences [9]. Hybridization may also introduce additional climate-related genetic variation into some mountainous bird populations [10].

This paper discusses how climate-related habitat change affects population connectivity, genetic diversity and differentiation, genomic vulnerability, and adaptive potential in montane birds. Particular attention is given to Southeast Asia and comparable Asian-Pacific mountain systems, where complex geography and high levels of biodiversity make these processes especially important.

2. Genetic Responses of Montane Birds to Climate Change

2.1. Climate-Driven Habitat Change and Population Connectivity

Climate change is an important driver of montane bird distributions and population connectivity because it can alter habitat suitability and connections among populations (Fig. 1). Because many montane species are restricted to cool, high-elevation environments, climatic shifts can move suitable habitat upslope, reduce its extent, and increase fragmentation. These effects are especially pronounced in mountain systems, where valleys, lowland forests, and ocean barriers can isolate populations and create sky-island patterns [1, 3].

Historical climatic fluctuations show that changes in climate can either increase or reduce connectivity. In New Guinea, Quaternary climate cycles repeatedly changed the distribution of montane habitat occupied by the blue-grey robin, *Peneothello cyanus*. Cooler conditions during glacial periods may have increased habitat continuity in parts of the central highlands, but strong genetic differentiation remained among populations. This suggests that topography and limited dispersal continued to restrict gene flow even when habitats became more connected [5].

Similar patterns have been found in mainland Southeast Asia. Several montane bird populations in Vietnam experienced repeated changes in connectivity during Pleistocene climatic cycles. Cooler periods allowed montane forests to extend farther downslope, while warmer periods increased isolation among mountain populations. These changes contributed to the present genetic structure of populations in northern and south-central Vietnam [7].

The wider Indo-Pacific region also shows that connectivity depends on geographic history and dispersal ability. Montane bird populations can form through movement between separate mountain systems or through elevational shifts from surrounding areas, and these different histories can lead to different patterns of population connection [6]. In Sundaland, present genetic relationships among *Mixornis* tit-babblers still reflect palaeoriver systems that existed when the Sunda Shelf was more continuously exposed [8].

Together, these findings show that climate change affects montane birds not only by shifting suitable habitat, but also by changing the degree of connection among populations. Reduced connectivity can restrict gene flow and increase isolation, while greater habitat continuity may increase opportunities for dispersal. The final effect, however, depends on topography, landscape history, habitat specialization, and dispersal ability [3].

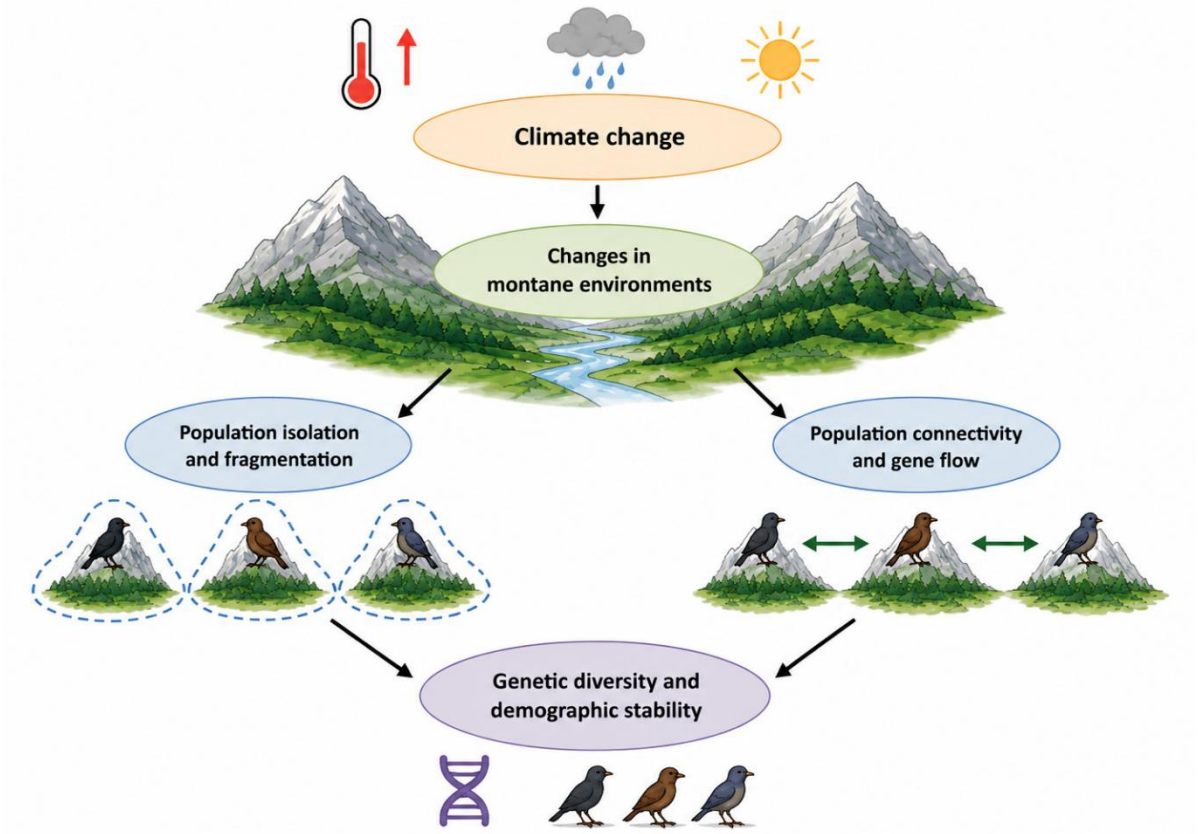


Fig. 1 Effects of climate change on population connectivity, genetic diversity and demographic stability in montane birds. (Picture credit: Original)

2.2. Genetic Diversity and Population Differentiation

Genetic diversity and population differentiation in montane birds are closely related to habitat isolation, population size, gene flow, and mountain geography (Fig. 2). When populations remain separated for long periods, restricted gene flow can increase genetic differentiation. Small and isolated populations may also lose genetic variation more easily through genetic drift.

In New Guinea, *Amblyornis macgregoriae* showed clear population structure, with six geographically separated populations grouped into three major genetic clusters and limited gene flow among populations [4]. Long-term isolation among mountain regions contributed to genetic divergence, while repeated expansion and contraction of montane habitat also influenced population size and genetic structure [4].

A similar pattern has been found in *Peneothello cyanus*. Three major lineages were associated with different montane regions in New Guinea. Although cooler climatic periods may have increased connectivity among some populations, strong regional differentiation remained, indicating that both historical climate and present-day geography contributed to population structure [5].

Montane birds in Vietnam also show clear differentiation between northern and south-central populations. Some populations from the Central Highlands had lower genetic variation than northern populations, particularly where regional population sizes were smaller. Long-term isolation and demographic history can therefore influence both genetic diversity within populations and differentiation among populations [7].

Across the broader Indo-Pacific region, stronger geographic barriers are generally associated with greater population differentiation, although some gene flow can still occur across these barriers [3]. Historical landscape structure can also remain visible in present genetic patterns. In Sundaland, population structure in *Mixornis* tit-babblers follows palaeoriver systems that existed when the Sunda Shelf was exposed, showing that current geographic distance alone does not fully explain genetic relationships [8].

Genetic vulnerability can also differ between elevations. In Taiwan, low-elevation populations of two songbird species on the eastern side of the Central Mountains had lower genetic diversity and higher genetic load. On the western side, stronger gene flow between low- and high-elevation populations was associated with smaller differences in genetic load [9].

These results show that climate-related genetic vulnerability is not limited to high-elevation populations. High-elevation populations may face habitat contraction, while low-elevation populations can also be affected by fragmentation, disturbance, and reduced connectivity. Changes in population size and gene flow therefore play an important role in shaping both genetic diversity and population differentiation.

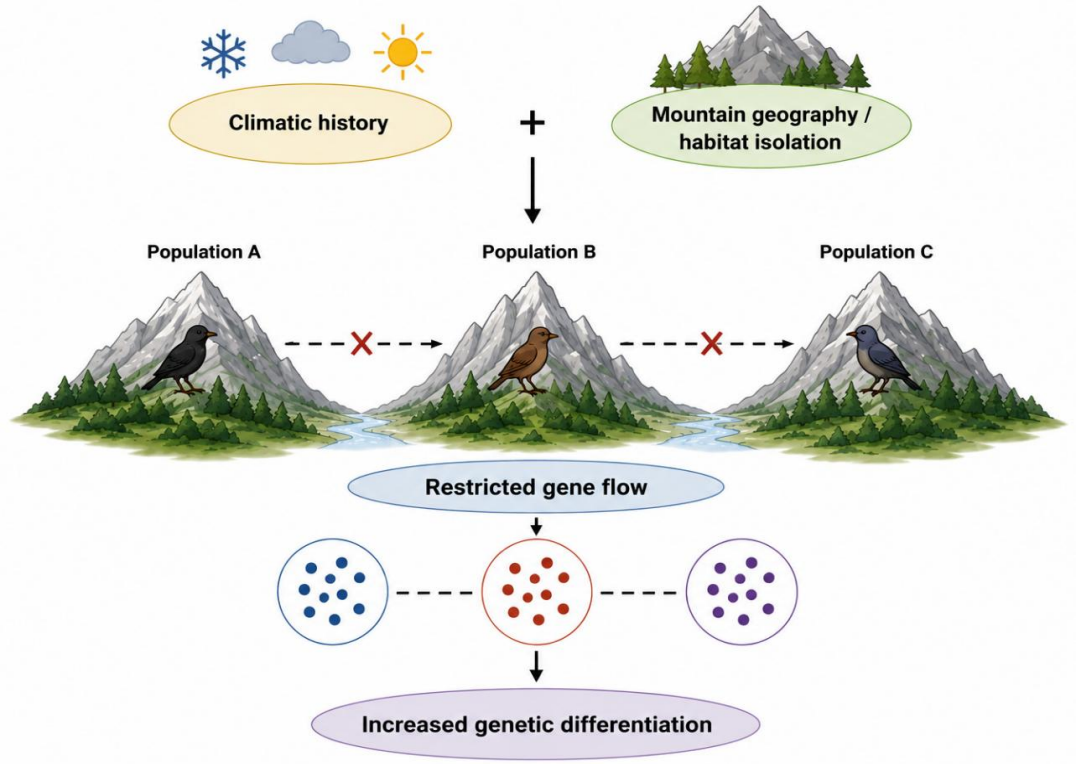


Fig. 2 Effects of climatic history and geographic isolation on gene flow and genetic differentiation in montane bird populations. (Picture credit: Original)

2.3. Genetic Diversity and Population Differentiation

Genomic studies provide more detailed information on how montane bird populations may respond to changing climatic conditions (Fig. 3). In addition to population structure and genetic diversity, genomic data can reveal local adaptation, genetic load, genomic offset, and differences in vulnerability among populations. In *Amblyornis macgregoriae*, genomic variation among populations was associated with climatic factors including annual precipitation, seasonal temperature variation, and differences between daytime and nighttime temperatures [4]. When current genomic patterns were compared with projected future climatic conditions, populations near the Strickland Gorge showed particularly high genomic offset. This indicates that populations within the same species can differ considerably in their expected response to future climate change [4].

Genomic offset can also provide information that is not always consistent with projected changes in habitat suitability. Comparisons between genomic offset and ecological niche modelling show that a population may retain apparently suitable habitat while still having a relatively large mismatch between its present genomic composition and future climatic conditions [2]. Distributional change alone may therefore not fully represent climate vulnerability. Local adaptation adds another complication. Populations living under different climatic conditions may develop genetic differences associated with their local environments. These differences can be useful under current conditions, but rapid climatic change may make existing genetic variation less suitable for future environments.

Genetic load may further influence population vulnerability. Some low-elevation populations in Taiwan had both lower genetic diversity and higher genetic load, while populations with stronger gene flow across elevations showed smaller differences [9]. Gene flow may therefore help maintain genetic variation, although its effects can differ among populations that are already adapted to different local environments [3, 4]. Overall, genomic evidence shows that populations of the same species can differ in genetic diversity, local adaptation, genetic load, and projected genomic offset. These differences may lead to very different levels of vulnerability under future climatic conditions [2, 4, 9].

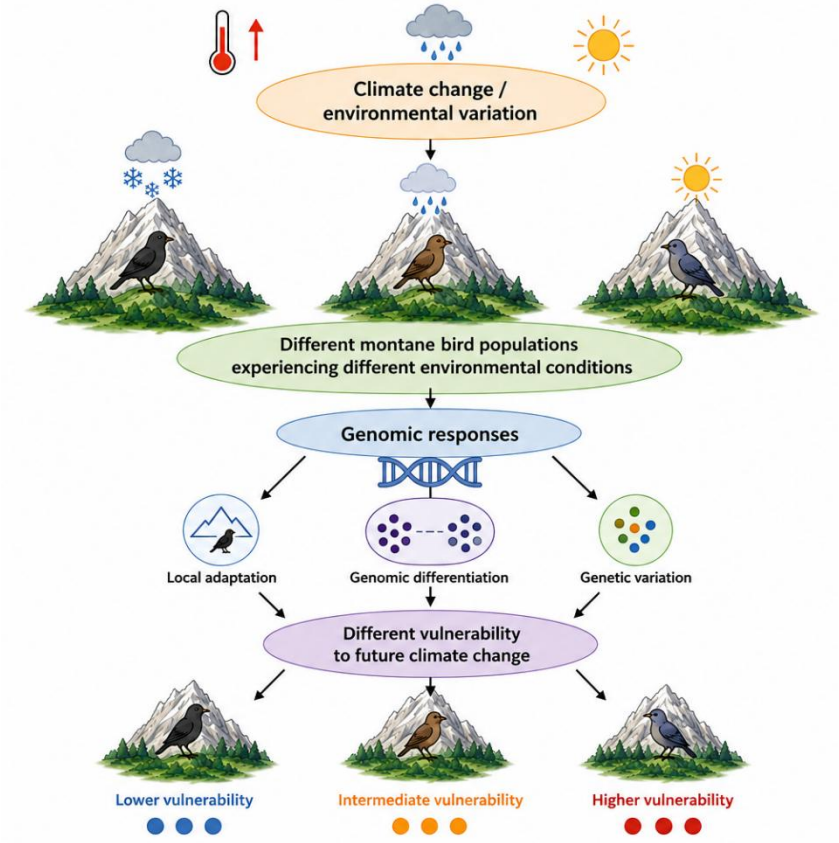


Fig. 3 Genomic responses and climate vulnerability among montane bird populations. (Picture credit: Original)

2.4. Adaptive Potential, Gene Flow and Hybridization

Adaptive potential depends on the capacity of populations to respond to environmental change through existing genetic variation, gene flow, and local adaptation (Fig. 4). This capacity can vary among populations depending on genetic diversity, population size, environmental specialization, and connectivity. Different populations of *Amblyornis macgregoriae* show local adaptation as well as substantial differences in projected genomic vulnerability [4]. Some low-elevation populations in Taiwan also have reduced genetic diversity and increased genetic load, which may indicate lower adaptive potential. In contrast, stronger gene flow between elevations may help maintain genetic variation [9]. Historical connectivity may also influence the capacity of montane birds to respond to environmental change. Repeated climatic cycles changed the degree of connection among montane forests in Vietnam, while long-term isolation in New Guinea contributed to strong population differentiation [4, 5, 7].

Gene flow may provide additional genetic variation when populations become isolated. Hybridization can have a similar effect in some cases. In mountainous fulvettas, introgressed climate-associated genetic variants were found in hybrid populations, which also showed lower projected climate vulnerability than non-hybrid populations [10]. This suggests that gene exchange between closely related populations or species may sometimes contribute to adaptive potential.

However, the effects of hybridization and gene flow are unlikely to be the same in every population. Their importance depends on the genetic variants involved and the environmental conditions under which populations live. Adaptive potential therefore reflects interactions among genetic diversity, local adaptation, gene flow, population size, habitat connectivity, and environmental change.

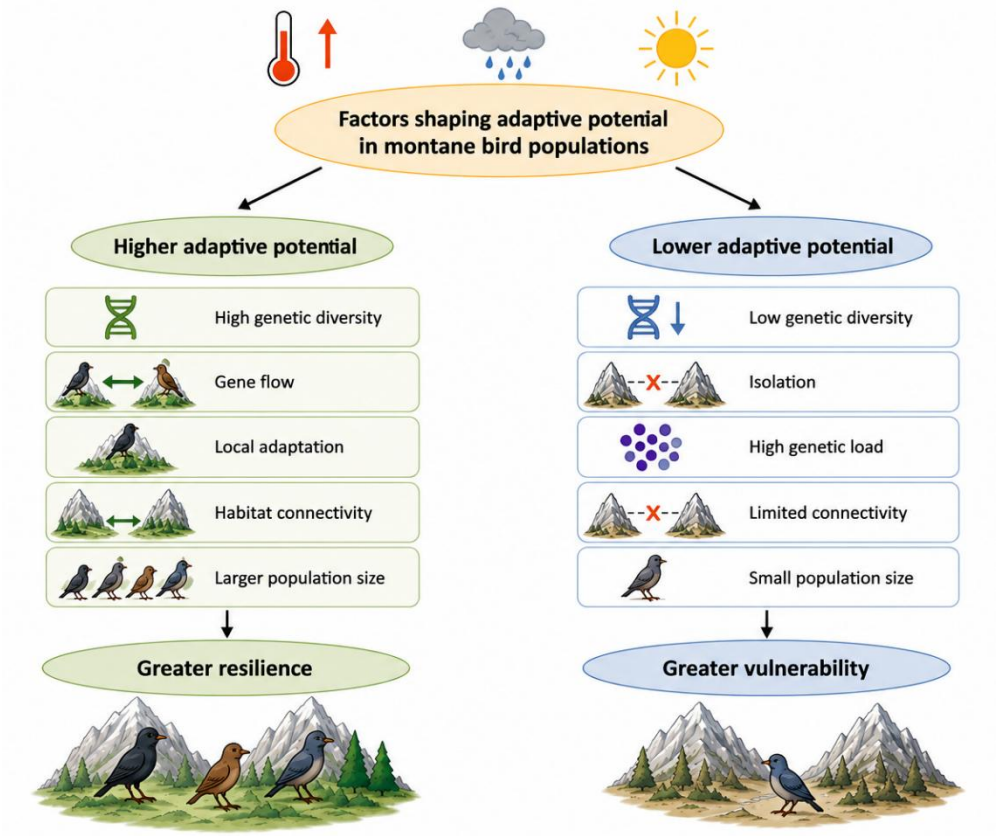


Fig. 4 Factors influencing adaptive potential in montane bird populations. (Picture credit: Original)

2.5. Conservation Implications for Climate-Vulnerable Montane Birds

Genetic diversity and population connectivity are important when considering the vulnerability of montane birds to climate change. Changes in geographic distribution are often easier to observe, but genetic changes may occur before major population declines become obvious. Reduced gene flow, lower genetic diversity, and increased genetic load can gradually increase the vulnerability of isolated populations.

Strong genetic differentiation has been found among populations occupying separate mountain regions in New Guinea [4, 5]. These populations may contain genetic variation that is not well represented elsewhere, meaning that the loss of one isolated population could also result in the loss of unique genetic diversity.

Maintaining connectivity across elevational and geographic gradients may help reduce some of these risks. In Taiwan, stronger gene flow between low- and high-elevation populations was associated with smaller differences in genetic load [9]. Continuous habitat across elevational gradients may therefore help populations remain connected as climatic conditions shift.

At the same time, connectivity should not be considered independently from local adaptation. Some isolated populations may contain genetic variation associated with particular environmental conditions. Conservation planning therefore needs to consider both population connectivity and existing genetic differentiation.

Hybrid zones may also contain climate-related genetic variation. Introgression has been associated with lower projected climate vulnerability in some mountainous bird populations, although it is not yet clear whether the same pattern occurs widely across species [10].

Genetic diversity, gene flow, local adaptation, genetic load, and genomic offset can help identify populations that may be at greater risk even when changes in distribution or population size are not yet obvious (Fig. 5) [2, 4, 9].

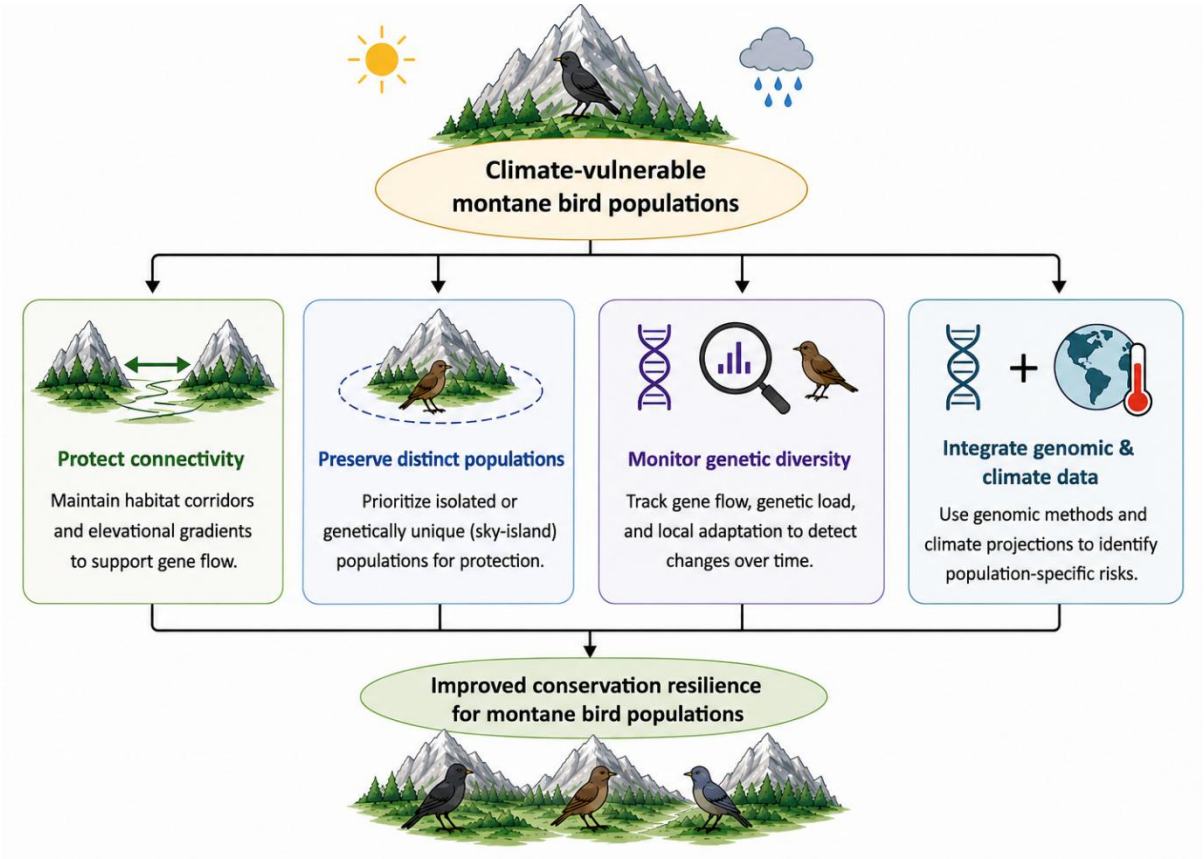


Fig. 5 Conservation actions for climate-vulnerable montane bird populations. (Picture credit: Original)

2.6. Genetic Diversity and Population Differentiation

Although recent studies provide valuable insights into the genetic and genomic responses of montane birds to climatic and environmental change, several important knowledge gaps remain. One major limitation is that much of the available evidence still concerns historical climatic change rather than direct genetic responses to contemporary warming. Pleistocene climatic cycles provide useful information about how changes in habitat distribution and connectivity shaped present population structure, but these historical responses may not fully represent the effects of current rapid warming [5, 7].

Geographic coverage is also uneven. Recent research provides useful information from New Guinea, Vietnam, Taiwan, Sundaland, and several Indo-Pacific island systems [4-9]. However, many mountain regions in mainland Southeast Asia, Borneo, Sumatra, Java, Sulawesi, and the Philippines remain poorly studied. More regional sampling is needed to determine whether patterns found in relatively well-studied mountain systems also occur elsewhere.

Taxonomic coverage remains limited as well. Montane bird species differ in dispersal ability, habitat specialization, population size, and elevational range. These differences may influence how strongly geographic barriers and habitat change affect gene flow. Studying a wider range of species would help identify which characteristics are associated with greater genetic vulnerability.

Long-term monitoring is another important gap. Genetic changes may occur gradually and can be difficult to detect from samples collected at a single point in time. Repeated sampling of the same populations could reveal changes in genetic diversity, effective population size, allele frequencies, and gene flow as climatic conditions continue to change.

Further research is particularly needed on adaptive potential and genomic vulnerability. Current evidence is still insufficient to determine whether montane bird populations possess enough genetic variation to respond to projected climatic conditions. Future studies could examine genomic offset, genotype-environment relationships, local adaptation, genetic load, effective population size, inbreeding, and contemporary gene flow under alternative climate scenarios. These approaches may help distinguish populations that are already genetically vulnerable from those that may become increasingly mismatched with future environmental conditions, as well as populations that retain sufficient variation or connectivity to support adaptation. Greater attention should also be given to both low- and high-elevation populations because vulnerability may arise through different mechanisms across elevational gradients.

Future research should expand geographic and taxonomic sampling across Southeast Asia and make greater use of genome-wide approaches. Long-term monitoring and comparative analyses across elevations, habitats, and degrees of isolation would help clarify how genetic responses develop over time. Integrating genomic information with ecological data and future climate projections could also improve understanding of how montane bird populations respond to rapid environmental change and help identify populations that may be especially vulnerable.

3. Conclusion

This paper systematically summarizes the multi-dimensional genetic and genomic responses of Asian-Pacific montane birds to ongoing climate change. Historical climatic oscillations and complex mountain topography collectively shape the contemporary population genetic structure of montane avifauna, driving widespread genetic differentiation and heterogeneous population connectivity. Intraspecific bird populations exhibit distinct genomic vulnerability, with divergent genomic offset and genetic load decoupled from conventional habitat suitability evaluation. Cross-elevation gene flow and interspecific hybridization can effectively supplement adaptive genetic variation and alleviate climate-induced genetic degradation, yet their conservation benefits are spatially and taxonomically inconsistent. Unlike traditional perceptions, low-elevation montane populations face equivalent genetic risks and adaptive constraints as high-altitude populations. Current research is restricted by imbalanced regional sampling, limited species coverage, and insufficient real-time genomic evidence for modern climate warming. This paper integrates ecological and genomic perspectives to clarify core evolutionary mechanisms of montane bird climate adaptation, providing reliable theoretical support and practical guidance for precision conservation of mountain biodiversity under global change. Future expanded comparative genomic research will fill existing research gaps and improve the accuracy of climate vulnerability prediction for montane avian communities.

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