

## Genomics of Adaptation in Birds and Adaptive Variants

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### DESCRIPTION

The majority of nuclear markers and Sanger-sequenced mitochondrial genes were used in the study of avian evolutionary genetics until a little more than ten years ago. Since then, whole genome databases with high-quality species-specific annotated reference genomes have replaced these methods [1]. The capacity to amplify and sequence homologous markers across species that diverged from those for whom the genetic resources had been produced using polymerase chain reaction had placed restrictions on the field. Now, the ability to obtain sizable genomic datasets from species without existing genomic resources, combined with specific characteristics of avian genomes (such as relatively small and conserved genome sizes or the low density of transposable elements), has enabled researchers to take advantage of the main benefits of studying evolution through avian systems [2-4].

These benefits result from a long history of ornithological research, which has led to a thorough understanding of the taxonomy and phylogenetic relationships between birds, diverse within-species phenotypic variation, a clear understanding of range limits, and extensive sampling efforts using genetic materials preserved in natural history collections. As a result, our understanding of the genomics of avian adaptations has rapidly increased because to the availability of avian genomic resources including re-sequencing datasets and progressively high quality annotated reference genomes. Here, we examine the molecular mechanisms behind those changes, spanning studies utilising various kinds of genomic data (e.g., transcriptomics, reduced-representation genomic techniques, or whole-genome re-sequencing) [5].

### Genomics of adaptive variants

Genome-wide traits, some of which are unique to avian genomes, predictably make adaptation easier. Hence, the genomic architecture—the underlying genetic foundation for a trait—can have an impact on how that trait evolves. A gene's placement inside a chromosome might affect its neighbours by defining the degree of linkage to surrounding genes. For instance, the precise chromosome on which a gene is located will

determine its inheritance pattern (through variation in recombination rate). By definition, non-synonymous mutations result in phenotypic variation. The total selection benefit of such alterations would, however, probably rely on how the mutation affects the many functions of that gene in pleiotropic genes, which have several impacts [6].

With the exception of a minor pseudo-autosomal area, the ZW sex chromosome system in birds has heterogametic (ZW) females. The W sex chromosome is largely non-recombining. In birds, the Z chromosome evolves more quickly than the autosomes (also known as the "fast-Z effect") due to a variety of factors, such as a wider range of circumstances under which a mutation can become more frequent (for instance, recessive mutations are subject to selection in females), a slightly higher mutation rate, and increased genetic drift (due to its effective population size being one-third that of an autosome). As a result, in many taxa, the Z chromosome exhibits more differentiation than autosomes, and it may be contributing disproportionately to the diversification and adaptation of birds [7,8].

### Genomics of adaption birds

**Plumage coloration:** Birds generally use melanins and carotenoids among other pigment molecules to colour their feathers (which produce a range of yellow, orange, and red colors). In contrast to *Peromyscus* mice or peppered moths, where colour variation has been clearly connected to fitness and survival, colouring research in birds has also been seen through the prism of sexual selection. Studies on the melanin variation in the following species: *Sporophila* seedeaters, *Monarcha flycatchers*, *Lonchura munias*, *Motacilla wagtails*, and parulid warblers 16 have all pointed to shared targets of selection, most notably asip and, to a lesser extent. In some instances, individual variants have been connected to changes in the colour or pigment concentration of particular body patches. Coloration differences are assumed to be mediated by both coding and probably regulatory alterations [9].

**Elevational and altitudinal adaptation:** It has long been of interest to understand how birds have evolved to survive at high elevations and fly at high altitudes, but doing so in the wild is

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logistically difficult. Study on bar-headed geese (*Anser indicus*), which migrate over the Himalayas, has been documented at elevations of 6,000 metres, where the partial pressure of oxygen is greatly reduced, and is an example of the molecular and physiological adaptations in this area. Early studies revealed that these geese naturally had higher haemoglobin O<sub>2</sub> affinity, but they also have mitochondria placed towards the cell membrane, possibly as adaptations to increase the efficiency of oxygen transport [10].

## CONCLUSION

By concentrating on the technical components of studying avian genomes and talking about the existential threat given to biodiversity by habitat alteration and climate change, we conclude by turning to what we think to be significant hurdles to this subject. The more successful approach for confirming the relationship between gene connections and adaptive characteristics in birds has been transcriptomics, and it is likely to remain so in the near future.

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