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Global Population Genomics of Chickens and Their Adaptation to Diverse Environments

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Abstract Chickens (*Gallus gallus domesticus*) represent one of the most widely domesticated and distributed livestock species globally, offering a unique model for exploring population genomics and adaptive evolution. In this study, we investigated the global genomic diversity and environmental adaptation of chickens by analyzing whole-genome resequencing data and single nucleotide polymorphism (SNP) arrays across diverse geographic populations. We characterized regional genomic structures, examined the impact of artificial selection, and highlighted the role of indigenous breeds in shaping genetic landscapes. Specific adaptation signatures were identified in populations exposed to high altitudes, extreme temperatures, and pathogen pressures, revealing key loci associated with physiological resilience and immune function. Methodologically, we employed population structure analyses, phylogenetic reconstruction, selection scans, and functional annotation to uncover evolutionary trajectories. A focused case study on East African chickens demonstrated context-specific adaptations driven by unique environmental and cultural factors. Our findings underscore the underrepresentation of certain populations in genomic surveys and emphasize the importance of integrating genomics with ecological and phenotypic data. This study not only advances our understanding of chicken evolution and adaptation but also provides genomic insights that can inform sustainable breeding, conservation efforts, and global food security strategies.

Keywords Chicken population genomics; Genetic diversity; Environmental adaptation; Selection scans; Sustainable breeding

1 Introduction

Chickens are one of the most common poultry in the world and have been domesticated by humans for a long time. The chickens we can see now have many different shapes and characteristics, and they can survive in various environments, such as plateaus, tropical and arid areas. These characteristics are mainly due to the combined effect of natural selection and artificial selection, which slowly adapted chickens to different places (Shi et al., 2022; Zhang et al., 2024; Hu et al., 2025). Chickens spread to all parts of the world with human migration, bred in different places, and gradually formed a variety of mixed types and different evolutionary characteristics. These changes not only explain how chickens were brought to the world step by step, but also reflect how they adapt to different ecological environments (Tian et al., 2020; Dementieva et al., 2024).

How can chickens survive well in various environments? In fact, the answer is hidden in their genes. However, this is not something that one or two chickens can tell us. To see it, we have to start with the genes of the entire group. Studies have shown that whether it is natural selection or the "intentional arrangement" of human breeding, it will slowly leave traces on the genes of chickens. These changes are sometimes to adapt to the climate, sometimes to cope with hunger, and sometimes to avoid the attack of viruses (Li et al., 2019; Gheyas et al., 2020; Bai et al., 2024). Of course, this kind of research is not just as simple as understanding evolution. It can really help the breeding industry a lot, especially now that the weather is becoming more and more unpredictable. How to improve the resistance of chickens and stabilize meat and egg production depends on these genetic discoveries (Fleming et al., 2016; Fleming et al., 2017).

This study mainly summarizes the latest research results on chicken genes around the world. The focus is on the genetic diversity and population structure of chickens, and how they adapt to various environments. We especially introduce some important information found by whole genome analysis, such as which genes and pathways are related to adaptability. We will also introduce how these research results can be used in breeding and protecting chickens. We collated data from different regions, hoping to gain a clearer understanding of how chickens adapt to different living environments through their genes, and to provide some ideas for improving the adaptability and production capacity of chickens in the future.

2 Global Patterns of Chicken Genetic Diversity

2.1 Regional genomic variation and structure

Chickens around the world have rich genetic diversity and a relatively complex population structure. These changes are the result of natural environmental selection on the one hand, and are also related to human breeding selection on the other. Scientists have conducted whole-genome analysis of chickens from China, Africa, Europe and Asia, and found that there are obvious genetic differences between chicken breeds in different regions. Chickens in many places have their own unique genetic changes, which are closely related to the environment in which they live (Hu et al., 2025). For example, in chickens adapted to high altitudes, droughts, tropical or cold regions, researchers have found genes related to energy metabolism, ion channels, and stress responses (Shi et al., 2022). After analyzing a large amount of SNP data, people have also found that chicken breeds on different continents have a complex genetic history of mixing and differentiation (Dementieva et al., 2024).

2.2 Influence of human-mediated selection

In fact, many of the genetic changes in chickens are man-made. In order to make chickens more in line with human requirements, such as growing faster, laying more eggs, and having beautiful feather colors, or even just to cater to the market's preference for skin color, people have long begun to select and breed from generation to generation. The genes in some areas, especially the gene loci related to traits, and even the sex chromosomes, clearly show the "traces" of these selections (Li et al., 2019). However, not all chicken selections are for economic benefits. Some chicken breeds are actually preserved to adapt to the local environment. For example, tropical chickens are more heat-resistant, while northern chickens are more cold-resistant. However, this kind of artificial selection also has side effects, especially in large-scale commercial breeding. In order to maintain the desired characteristics, the genetic diversity of many breeds has been compressed a lot, sometimes even to the point of inbreeding. In contrast, this situation is less common in local chicken breeds (Fleming et al., 2017; Bai et al., 2024).

2.3 Contributions of indigenous and local breeds

Local and indigenous chicken breeds are critical in maintaining genetic diversity. They have evolved over a long period of time in complex local environments, so they have strong adaptability, such as being able to withstand high temperatures, drought, and certain diseases (Zhang et al., 2024). Genomic studies of chickens in Africa, Asia and other places have found that these local breeds often contain special genes related to stress response, immune function and metabolic capacity. These genes are rare in commercial chickens (Fleming et al., 2016). These genetic characteristics make local chickens particularly valuable in sustainable farming. If we have to face the challenges brought by climate change in the future, these breeds may play a big role in breeding (Gheyas et al., 2020).

3 Genomic Signatures of Environmental Adaptation

3.1 High-altitude adaptation

Chickens living on the plateau, such as Tibetan chickens, have some special genes that help them adapt to the thin air at high altitudes. Studies have found that some of the parts of these chickens' genes related to calcium signals have changed, which may be related to their ability to cope with hypoxia (Wang et al., 2015). In addition, local chickens in Africa have similar situations. Some areas in their genomes have been found to be related to high altitude stress, such as hypoxia and susceptibility to blood clots. This shows that whether chickens can adapt to the plateau has a lot to do with some specific genes (Gheyas et al., 2020).

3.2 Heat and cold stress tolerance

Chickens in tropical and cold regions also have their own genetic adaptability. Some genes of chickens living in the tropics, such as *TSHR*, *HSF1* and *SLC33A1*, have undergone significant changes, which may help them better regulate body temperature and metabolism (Figure 1) (Rachman et al., 2024). For chickens living in cold places, genes such as *NDUFS4* are considered to be critical for their survival in low temperatures (Shi et al., 2022). These adaptations usually do not rely on many genes, but on a few key genes (Gheyas et al., 2021). Other studies have found that some chickens from the tropics may improve their heat tolerance through "epigenetic regulation", that is, not only the genes themselves have changed, but also the way the genes are expressed will be affected.

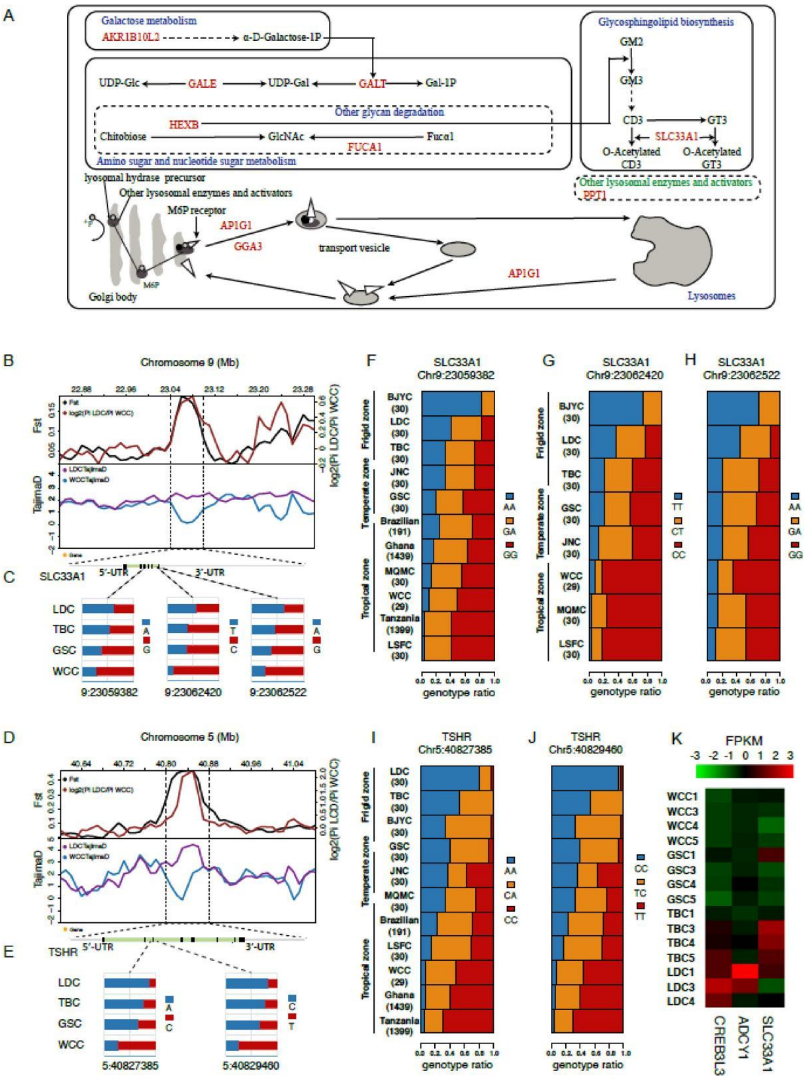

Figure 1 Analysis of the signatures of positive selection in the genome of chicken breeds and the adaptions to tropical Environments (Adopted from Shi et al., 2022)

Image caption: (A) Schematic mechanisms of signaling pathways for genetic adaptions to tropical environments in chicken; The names of the KEGG pathways are shown in blue; The candidate genes positively selected in the two methods of FST and θ_π ratio tests are shown in red; Dotted arrows indicate an indirect effect; (B) (D) log2 (θ_π ratios), FST value and Tajima's D values around the *SLC33A1* locus, TSHR locus, respectively. The black and red line represent FST and log2 (θ_π ratios) values, respectively. The blue and purple lines represent the WCC, LDC Tajima's D values, respectively. (C) (E) Allele frequencies of two and three SNPs within the *SLC33A1*, *TSHR* gene across the four breeds, respectively; The red alleles are consistent with reference genome, and the blue alleles represent mutant alleles; (F)(G)(H) Genotype frequencies of three SNPs within the *SLC33A1* gene were determined in our 119 individuals and chickens from Tanzania, Ghana, and Brazil using the Affymetrix 600 k SNP database, as well as in four Chinese breeds with PCR; For the abbreviations of the breeds, see supplementary table S16 and Supplementary Material online; (I)(J) Genotype frequencies of two SNPs within the *TSHR* gene were determined in our 119 individuals and chickens from Tanzania, Ghana, and Brazilian using the Affymetrix 600 k SNP database, as well as in four Chinese breeds with PCR; For the abbreviations of the breeds, see supplementary table S16 and Supplementary Material online; (E) Gene expression of *SLC33A1*, and the gene expression of the TSHR downstream genes, including *ADCY1* and *CREB3L3* in chicken liver of four breeds based on RNA-seq analysis; The FPKM (fragments per kilobase of transcript per million mapped reads) value is used to measure the expression level (Adopted from Shi et al., 2022)

3.3 Disease resistance and immunity

Scientists have also found genes related to immunity and disease resistance, especially in chickens that live in harsh conditions. In chickens living in tropical deserts, some genes, such as *TLR7* and *ZC3HAV1*, can inhibit the replication of viruses, which means that they can better cope with diseases that both humans and animals may get (Tian et al., 2020). Genes related to immune response, antioxidants, and anti-inflammation have also been found in some native chickens in Africa and Asia. These genes may make them more resistant to local pathogens and environmental stresses (Fleming et al., 2016; Xie et al., 2024). These studies show that the immune genes of chickens are very important (Li et al., 2024). It is precisely because of these genetic adaptations that chickens can survive in many different and even harsh environments and maintain a certain level of production capacity.

4 Methodologies in Population Genomic Studies

4.1 Whole genome resequencing and SNP arrays

To study the chicken genome, some efficient technologies are generally used, such as whole genome sequencing (WGS) and SNP chips. WGS can scan the entire genome and find a large number of SNPs (small genetic variations) in different chicken populations, including some new variations that have not been discovered before (Li et al., 2017). SNP chips such as Illumina 60K are more cost-effective and suitable for large-scale analysis, which can help us understand the genetic diversity, population structure and relationship between breeds of chickens (Dementieva et al., 2024). There is also a method called GBS (genotyping by sequencing), such as CornellGBS, which is low-cost and efficient. It is particularly suitable for studies with a large number of samples and can quickly find many SNPs (Pértille et al., 2016). If we use multiple reference samples to "complete" some unmeasured sites, we can also make the results more accurate, especially for better identification of some relatively rare genetic variants (Ye et al., 2019).

4.2 Population structure and phylogenetic analyses

Sometimes it's hard to tell how chickens are related just by looking at their appearance, after all, some differences are natural, while others are artificially selected. To figure out where these chickens came from and how close they are to each other, researchers will first do some data analysis. For example, they will use some tools to look at the composition and ancestral clues of different chicken groups, such as principal component analysis (PCA) and ADMIXTURE clustering, which are actually quite commonly used. Of course, it doesn't mean that you can draw a conclusion at a glance. Scientists will also analyze the genetic data of many chickens together, especially using genetic markers such as SNPs to draw a phylogenetic tree similar to a "family tree", so that you can see which chicken breeds are from the same branch and which ones have gradually evolved later (Yan et al., 2024). Although the method sounds a bit technical, the purpose is actually very direct, which is to figure out how chickens have gradually become so diverse. These analyses sometimes reveal things that don't seem obvious. For example, some chickens look similar, but they have actually been separated genetically for a long time; while some chickens with big differences may have common ancestors. Behind this, there are both natural evolutionary factors and human breeding selection (Rosenberg et al., 2001). Therefore, these tools and maps are not just for academic research, they also help us understand a larger and more complex story.

4.3 Selection scans and functional annotation

To understand how chickens adapt to the environment, we need to find out which gene regions are selected naturally or artificially. Researchers use methods such as iHS, XP-EHH, FST and Pi, which can help us find genes or gene regions related to environmental adaptation (Chen et al., 2011). After finding these candidate genes, we need to further look at what they do specifically. At this time, we will use some annotation tools, such as GO and KEGG pathway analysis, to determine whether these genes are related to the growth, body shape or environmental adaptability of chickens (Bello et al., 2023). Sometimes, we will combine different methods to more accurately find truly useful gene markers and gain a deeper understanding of the genetic mechanism of chicken adaptation (Liang and Xuan, 2024).

5 Case Study: Chickens in East Africa

5.1 Unique environmental and cultural context

In East Africa, most chickens are raised by rural families, usually in free-range, low-input conditions. These chickens face many challenges, such as heat, drought, hunger, and frequent diseases (Fleming et al., 2016). Despite the harsh environment, these chickens are important to family life. They not only provide food but also bring in some income. In many rural families, the task of caring for the chickens is often the responsibility of women (Mujyambere et al., 2021). East African chickens did not come from just one place. In the past, Asian chickens were brought to East Africa many times, some by sea and some by land. These chickens later mixed with local chickens, forming a relatively rich genetic background. Judging from their genes, the maternal origins of these chickens are very complex, reflecting ancient trade and cultural exchanges (Mwacharo et al., 2011).

5.2 Key genomic findings

By studying genes, scientists have found that local chickens in East Africa are not only genetically diverse, but also have many characteristics that adapt to the local environment (Figure 2) (Morris et al., 2024). Researchers used high-density SNP chips and whole genome sequencing to find that these chickens have many traces of mixing local breeds and foreign chickens. In addition, some of their genes are related to fat metabolism, immune system and stress response. Some genes selected by nature or artificially can help these chickens adapt to high altitudes. For example, some genes are involved in angiogenesis and oxygen carrying capacity, and some genes are related to disease resistance and anti-oxidative stress (Elbeltagy et al., 2019). Through mitochondrial and autosomal analysis, several different gene groups were also found, indicating that East Africa may be an important intersection for the spread and adaptation of chickens (Mwacharo et al., 2013).

Feathered shank chicken Frizzled feathered chicken Normal feathered chicken

Rump-less chicken Crest-headed chicken Naked neck chicken

Figure 2 Unique attributes of indigenous chicken (Adopted from Pius et al., 2021)

5.3 Implications for conservation and breeding

The local chickens of East Africa are actually quite special, not only because they are highly adaptable, but also because they are rich in genetic diversity. Although many places are promoting high-yield commercial chickens, these local breeds are more resilient in the face of climate change and various new diseases (Gheyas et al., 2022).

However, things are not without risks. Once they are randomly hybridized with foreign breeds, the original disease-resistant genes may be gradually diluted, and even some of the ability to adapt to the local environment may be lost (Pius et al., 2021). Some people may ask, should we protect these local chickens and prevent them from being improved? In fact, there is no need to go to extremes. Some scientists now propose that we can first find out which genes are related to disease resistance or environmental adaptation, and then do selective breeding on this basis (Banos et al., 2020). In this way, not only can the egg production or growth rate of chickens be increased, but the good genes in them will not be lost. So, in the final analysis, it is not about completely protecting the original state, nor is it about pursuing high yields only, but about finding the difficult but important balance between "improvement" and "preservation". If the poultry industry in East Africa wants to go further, it must consider this point.

6 Challenges and Future Perspectives

6.1 Underrepresentation of certain populations

Speaking of which, we have done a lot of research on the chicken genome, but in fact, chickens from many places have not been carefully examined. Some local chickens in Africa, South America, and Asia are often absent from large-scale genetic data. You will find that researchers are more willing to focus on commercial chickens or well-known breeds, and data collection mainly revolves around these (Dementieva et al., 2024). This brings about an embarrassing situation: the global chicken genetic map looks quite rich, but it is actually biased. What's worse is that many genetic resources that we don't know about have been ignored. Think about it, some chickens may be naturally adaptable or have other good genes, but because no one has studied them, their advantages have not been discovered, and there is no talk of using them in breeding or protection (Guo et al., 2021).

6.2 Integrating genomics with phenotypic and ecological data

Although we can now collect a lot of genetic information, such as using whole genome resequencing and SNP chip technology to find mutations, it is still difficult to link this data with the chicken's traits and living environment. Many studies do not record the specific environment in which the chickens live, how they are managed, and detailed data on their traits (Li et al., 2017; Menchetti et al., 2024). Without this information, it is difficult to see which characteristics a gene is related to. In order to more accurately identify the genetic reasons for chickens' adaptation to the environment, and to better use genetic information for breeding in different breeding systems, we need to establish a model that can take genes, traits, and ecological environment into consideration (Zhang et al., 2017).

6.3 Ethical and policy considerations

Genetic technology is developing rapidly, and it has also brought many new problems. For example, some breeding methods may bring bad mutations or make the population smaller and smaller, which will affect the health of chickens. To avoid these problems, we need to develop more reasonable breeding methods that can increase production without damaging the genetic health of chickens (Wang et al., 2021). Another issue is resource fairness. Some people are worried that the genes of local chickens are taken by big companies without getting the due return. Some people are also worried about the impact of genomic technology on small farmers and traditional farming methods. In the future, we need to establish some international norms and policies to ensure that genetic resources can be used reasonably and long-term, and at the same time, everyone can share the benefits of these resources fairly. There is still a lot to do in chicken genome research, such as expanding the sampling range, strengthening data integration in different fields, and solving ethical and policy issues. Only in this way can these genetic resources be used safely, effectively and fairly.

7 Concluding Remarks

Through global genome research, scientists have found that chickens have rich genetic diversity, and chicken breeds in different regions also have complex genetic structures. These diversities are affected by both natural selection and artificial breeding. Now many genes related to plateau, high temperature, low temperature, drought and other environments have been found. These genes are mainly related to energy metabolism, immune system and stress response. There are many special adaptive genes in local chicken breeds in Africa and Asia. The genes of these chickens are often mixed together, which on the one hand shows that there were many routes for the spread of chickens in ancient times, and on the other hand, it also shows that these chickens have been under the pressure of natural and artificial selection for a long time.

Sometimes, when facing high temperatures, diseases or other environmental changes, local chickens actually perform more stably than some breeds in breeding farms. Why? In the final analysis, it is the genes that have been left by long-term natural selection that play a role. The diversity and adaptability of these genes, to put it bluntly, is our trump card to deal with the uncertain environment in the future. However, many people have not yet realized its true value. Population genomics research can help us find these "useful genes" and then use them in breeding to make chickens more adaptable to different breeding conditions. But things are not that simple. The data we have is not comprehensive enough, especially for local chickens in remote areas, which have been studied too little. Although some genes have been found, the relationship between them and the actual performance and living environment of chickens is still vague, like a few pieces of a puzzle are missing.

In addition, there is another issue that cannot be avoided - ethics and policy. Not everyone can use these genes casually. This involves issues of resource sharing and fair distribution, which are especially sensitive for small farmers. In other words, in addition to scientific research, there must be rules. Now talking about sustainable breeding, food security, and increased income for farmers sounds like big talk, but in the final analysis, it still depends on concrete actions to support it. What's next? Sampling more extensively, recording ecological information more carefully, and advancing breeding programs more responsibly. These are not easy things to do, but if we want to have a proactive role in a future with increasingly problematic agriculture and the environment, we have no choice.

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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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