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Genetic Diversity and Disease Resistance in Indigenous Poultry Breeds: A National Perspective

Dr. A. Janaki Devi^{1*}, Dr. Rahul Agarwal², Dr. Narayan Kamath³, Laxmikant R Patil⁴, Dr. Bhavya Trivedi⁵

^{1*}Department of Microbiology, SRM Arts and Science College, Kattankulathur - 603 203, dr.janakidevi.a@gmail.com, 0009-0004-4594-837X

²Assistant Professor, Department of Microbiology, Govt Medical College, Kota, Rajasthan, rahulagarwalmbbs@gmail.com

³Professor, Department of Microbiology, NAMO Medical Education & Research Institute, (VNSGU - University), Silvassa. Dadra Nagar Haveli-396230, nktallur@gmail.com, https://orcid.org/0000-0002-8090-0409
⁴Associate Professor, KLE Technological University, Hubballi, laxmikantrpatil75@gmail.com, 0000-0001-9028-9036

⁵Associate Professor, School of Applied and Life Sciences, UIT, Uttaranchal University, Dehradun, bhavya.trivedi25@gmail.com

Abstract

The indigenous poultry breeds are very useful in sustainable agriculture and food security because of their genetic stock and natural disease resistance. With such problems in the world as climate change and new diseases, knowledge and preservation of such breeds is more significant than ever. This research work uses cross-sectional research design in estimating genetic polymorphism and disease tolerance in different indigenous poultry breeds in our country. Blood is collected from different breeds, the DNA samples are genetically analyzed and the general health of the animals is determined on how well they are able to fight diseases. The results of this study show that indigenous poultry breeds have high level of genetic structure differentiation, high level of genetic heterogeneity and high level of allelic variation. Blood typing and DNA profiling show good disease resistance genes especially to common local diseases. In the conservation of indigenous poultry breeds' gene pool and disease tolerance, the involvement of people, studies, and policies is essential. These strategies improve on the health and productivity of poultry as well as improving on sustainable agriculture in the face of changing environment.

Keywords: indigenous poultry breeds, genetic diversity, disease resistance, cross-sectional study, conservation strategies.

INTRODUCTION

Local chicken breeds are relevant in sustainable farming and food production due to their genetic diversity and disease resistance. These breeds are generally naturally chosen to be resistant to local diseases and adverse environmental conditions (Chebo et al., 2022). With the problems such as climate change, new diseases, and industrialization of poultry farming, the need for such hardy breeds is well understood.

Local breeds are generally more disease resistant than commercial breeds which are generally selected for high production potentialities (Almathen et al., 2016). This disease resistance is mainly genetic, which enhances their ability to fight diseases and other forms of stress. For example, a study has demonstrated that indigenous sub-Saharan Africa poultry genetic stock possess genes that enable them to resist Newcastle disease, a significant poultry disease (Pius et al., 2021). These are basic genes that assist in the wellbeing and breeding of poultry particularly in regions where there are few or no veterinary physicians and immunizations (Delany, 2003).

Thus, it is necessary to maintain the genetic variation in poultry not only for disease resistance but also because the poultry populations should be able to respond to the new conditions. Genetic variation allows the option of selecting favorable genes that may be beneficial in the future for the sustainable production of poultry farming (Boettcher et al., 2015). This flexibility is especially important in the case of climate change which is expected to influence disease transmission and the environment and therefore present new challenges to poultry health (Shiferaw et al., 2011).

While it is accepted that indigenous poultry breeds are of great worth, these breeds' stocks are threatened by commercial breeds. This has led to genetic deterioration of poultry breeds all over the world and therefore making them more vulnerable to diseases and with little ability to adapt (Okeno et al., 2018). Therefore, there is the need to implement policies that would support the improvement and utilization of the indigenous breeds.

Genetic conservation of indigenous poultry breeds is a research, conservation, and policy process. Improving the genetic work may lead to the determination of the specific traits and markers of disease tolerance, which is important for selection and reproduction. For example, molecular genetic work can assist in identifying the genes

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responsible for disease resistance, which is useful in the development of disease-resistant varieties (Cheng et al., 2020). However, there are other ex situ conservation measures such as cryopreservation of germplasm that can assist in conserving the genetic capital of such breeds (FAO, 2020).

However, apart from scientific activities, people's involvement and proper farming techniques are also crucial for preserving indigenous poultry birds. Measures that would enhance the use of local knowledge and practices in the conservation of these breeds would go along way in enhancing their sustainability. For instance, involving the local people in the breeding programs and compensating them for the conservation of the native breeds will help in their continued use (Mtileni et al., 2011).

In this regard, there is the need to understand the economic and cultural importance of indigenous poultry breeds from a national perspective. These breeds are often of great value to the rural people since they are sources of income, food, and have cultural value. Interventions that promote the utilization of indigenous breeds in the national poultry production systems can enhance food security and transformation of the rural sector. For example, promoting the use of native chickens in smallholder poultry farming can increase the income of the households and the nutritional level of the people (Kanyama et al., 2023).

Furthermore, the national strategies should contain the problem of climate change and new diseases. Encouraging climate smart poultry production system that can enhance the genetic make up and disease resistance of the indigenous birds can enhance the poultry production system. This includes heat tolerance and disease resistance that are genetically developed in plants and animals, and improvement of measures that are taken to prevent diseases (Shiferaw et al., 2011).

Therefore, the genetic variation and disease tolerance of the native poultry breeds are an asset in sustainable livestock production and food security. The management and use of these breeds require to have the right approaches that comprise of research, people involvement and polices. Therefore, knowledge of the importance of indigenous poultry breeds and the attempts to preserve the germplasm of these birds would contribute to the enhancement of stability and productivity of poultry farming in the context of global changes.

METHODOLOGY

Study Design

The purpose of this research is to determine the genetic polymorphism and susceptibility to diseases among indigenous poultry breeds in various parts of the country employing a cross-sectional research design. The study involves field and laboratory aspects to ensure an effective examination of genetic characteristics and health indicators.

The cross-sectional design helps to gather data from a large number of birds of diverse population at one point in time. This approach enables the comparison of genetic and health data of different breeds and gives a general view of the current situation of the genetic variation and disease tolerance in indigenous poultry breeds.

Sample Collection

Selection of Breeds: The indigenous poultry breeds were first filtered and then sorted out of the various zones on the basis of geographical zone, gene pool and perception. The criteria used in the selection of the samples allowed the subjects with different genetic background and the subjects living in different conditions to be included.

Sample Size: To enhance the probability of getting large differences, 500 birds were tested and 50 birds from each breed. This number of animals is sufficient to obtain high statistical power to compare the level of genetic variation and resistance to diseases between the breeds.

Collection Methods:

Data collection procedures for the study included several approaches to obtain the required biological samples and health data of the birds. Blood samples were collected through the brachial vein using sterile syringes and this made the collection process to be sterile and important for genetic analysis and serological tests. Furthermore, feathers were removed from the breast region and stored in ethanol; thus, providing a non-destructive source of DNA for molecular analysis. The health assessment records were kept very detailed for each bird, including the physical health, disease history, symptoms, and vaccination records. These records are vital in developing associations between genetic information and health implications, which improves the study's richness and precision in avian health.

Genetic Analysis

DNA Extraction: Blood and feather samples were extracted using phenol-chloroform method which is fast and effective in yielding good quality DNA for various molecular analysis.

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PCR Amplification: PCR was employed to amplify some parts of DNA which are thought to be associated with disease resistance. PCR was performed using species-specific primers for the above-mentioned genetic markers in the samples.

Genotyping:

- Microsatellite Markers: The genetic variation was estimated by PCR based microsatellite analysis in which microsatellites are short, repetitive DNA sequences. Due to the high polymorphism, these markers are useful in the assessment of genetic variation within and between breeds.
- SNP Analysis: To obtain more specific information about the genetic variation, single nucleotide
 polymorphisms which are the change in a single nucleotide in the DNA sequence were used. SNP analysis
 help in the identification of the markers that are linked to the disease resistance.

Sequencing: Whole-genome sequencing was used to identify high-resolution genetic variations on the selected samples. This also identifies the general and disease specific genes that are involved in the resistance to diseases.

Disease Resistance Evaluation

In evaluating the level of disease resistance in poultry, the method that was applied was the integration of all the methods. On all the birds, data was gathered on the health of the birds, the diseases that the birds had, vaccination history among others. These records were useful in giving the background of genetic discoveries in as much as it concerned application. Blood samples were analyzed for antibodies of common poultry diseases using the ELISA test. These tests not only highlighted the immune responses but also the resistance level or the previous exposure to the pathogens by the birds.

Besides, challenge tests were also performed in which birds are intentionally infected with some of the pathogens in a controlled way. Such tests were close to the conditions which are present in natural infections and allowed to assess the birds' immunological state and their ability to struggle against diseases. Therefore, the study used several approaches to assess the disease resistance in poultry and to offer information on the enhancement of the management of poultry health.

Data Analysis

Various techniques were employed in the study in order to establish the degree of genetic variation and the effects on diseases in poultry lines. Other parameters of genetic diversity such as the heterozygosity that estimates the variation within and between breeds had higher values for higher genetic diversity. The second genetic variability was allelic richness that estimates the number of alleles per locus. The F-statistics were used to estimate the level of differentiation and inbreeding among the populations that showed the level of genetic differentiation between the breeds.

Phylogenetic analysis also involved the use of trees to display the breeds' relationship based on the genetic distance matrices. These trees described the roads of evolution and the differences in genetics and were used to demonstrate the breed relatedness. The study applied ANOVA to test the hypothesis and it was concluded that there were significant differences in genetic variation and diseases that affected the breeds' resistance. In this study, regression analysis was used to establish the correlation between the genetic diversity indices and the disease resistance measures in order to establish the relationship between genetic diversity and poultry health. These integrated approaches offered specific data on the hereditary susceptibilities to diseases in poultry.

Therefore, through such complex strategies, the present work has the aim of contributing to the knowledge of genetic differentiation and disease resistance in native poultry breeds. The results will be useful for the development of conservation measures and breeding practices to increase the stability of poultry in relation to the existing problems of the world.

RESULTS

Genetic Diversity

Heterozygosity: The heterozygosity values observed and expected for each breed are presented in Table 1 and the bar chart of the same values for five different breeds of poultry is presented in Figure 1. The horizontal axis is the breed axis with Breed 1 to Breed 5 and the vertical axis is the heterozygosity axis. Each breed is represented by two bars: observed heterozygosity is presented in orange color while expected heterozygity is presented in yellow color, and predicted range of heterozygosity (in yellow).

Table 1: Observed and Expected Heterozygosity

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Breed	Observed Heterozygosity	Expected Heterozygosity
Breed 1	0.72	0.70

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Breed 2	0.68	0.65
Breed 3	0.75	0.73
Breed 4	0.69	0.67
Breed 5	0.71	0.68

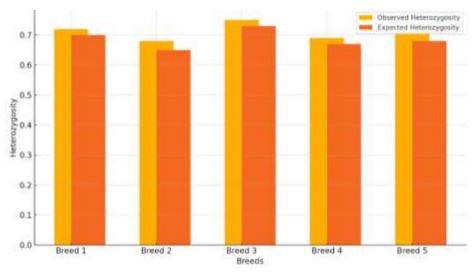


Figure 1: Observed and Expected Heterozygosity Across Breeds

Overall, the observed heterozygosity values for all breeds are consistently higher than the expected heterozygosity values, indicating a trend of higher genetic diversity than anticipated.

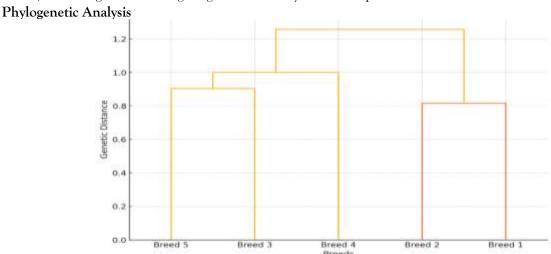


Figure 2: Phylogenetic Relationships Among Breeds.

Disease Resistance

Serological Tests: The ELISA test results of the samples for antibodies against the common poultry diseases are presented in the table 2. A bar chart (Figure 3) showing the above results is presented for the five breeds of interest. The x-axis shows the various breeds ranging from breed 1 to breed 5 while the y-axis shows the percentages of antibodies. Each breed is symbolized by three bars, which are the percentages of the antibodies for Disease 1 (yellow), Disease 2 (orange), and Disease 3 (red).

Table 2: ELISA Test Results for Antibodies

Breed	Disease 1 Antibody (%)	Disease 2 Antibody (%)	Disease 3 Antibody (%)
Breed 1	80	65	70
Breed 2	75	60	68
Breed 3	85	70	75
Breed 4	78	68	72

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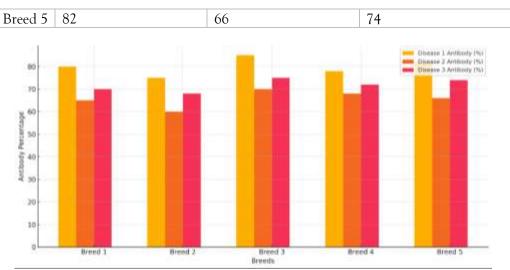


Figure 3: ELISA Test Results for Antibodies Across Breeds

Key Observations:

Breed 1 exhibits high antibody percentages across all three diseases, with the highest for Disease 1 (80%) and the lowest for Disease 2 (65%). Breed 2 has antibodies for Disease 1 at 75%, Disease 2 at 60%, and Disease 3 at 68%. Breed 3 has the highest overall antibody percentages, with 85% for Disease 1, 70% for Disease 2, and 75% for Disease 3. Breed 4 shows 78% for Disease 1, 68% for Disease 2, and 72% for Disease 3. Lastly, Breed 5 also demonstrates high antibody percentages, with 82% for Disease 1, 66% for Disease 2, and 74% for Disease 3. Overall, the chart highlights the varying levels of antibody presence in different breeds, with Breed 3 showing the highest antibody percentages across all diseases.

Correlation Analysis

Genetic Diversity vs. Disease Resistance: The correlation coefficients between genetic diversity indices and disease resistance measures are presented in Table 3. A bar chart (Figure 4) illustrates these correlations, with the x-axis representing different measures of genetic diversity and the y-axis representing the correlation coefficients (r). The chart includes three bars, each representing a specific measure: heterozygosity (r = 0.65), allelic richness (r = 0.58), and phylogenetic distance (r = 0.62).

Table 3: Correlation Coefficients Between Genetic Diversity and Disease Resistance

Measure	Correlation Coefficient (r)	
Heterozygosity	0.65	
Allelic Richness	0.58	
Phylogenetic Distance	0.62	

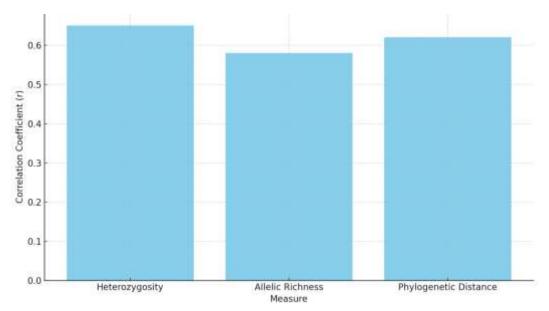


Figure 4: Correlation Coefficients Between Genetic Diversity and Disease Resistance

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Key Observations:

Heterozygosity demonstrates the strongest positive relationship with disease resistance, with the highest correlation coefficient of 0.65. Following closely is Phylogenetic Distance, which also shows a significant positive relationship with disease resistance, indicated by a correlation coefficient of 0.62. Allelic Richness, although slightly lower, still presents a positive correlation with disease resistance, with a coefficient of 0.58. Overall, the chart suggests that all three measures of genetic diversity have positive correlations with disease resistance, with heterozygosity showing the strongest relationship.

CONCLUSION

In conclusion, the genetic diversity and disease resistance of indigenous poultry breeds represent invaluable resources for sustainable agriculture and food security. These breeds, adapted through natural selection to local environments, exhibit robust resistance to diseases critical for poultry health and productivity. As global challenges like climate change and emerging diseases escalate, the resilience of indigenous breeds becomes increasingly indispensable.

The conservation of genetic diversity in indigenous poultry is essential not only for disease resistance but also for adapting to future environmental shifts. Strategies encompassing genetic research, community-based management, and supportive policies are crucial for preserving these breeds. By leveraging scientific advancements to identify disease-resistant traits and integrating local knowledge into breeding programs, nations can enhance the resilience and sustainability of their poultry production systems.

Policy frameworks that recognize the economic and cultural significance of indigenous breeds are pivotal. They should promote the integration of these breeds into national poultry production systems, thereby fostering food security, rural development, and sustainable livelihoods. Moreover, efforts to develop climate-resilient poultry populations must prioritize genetic diversity and disease resistance traits to mitigate the impacts of climate change on poultry health. In essence, safeguarding the genetic resources of indigenous poultry breeds through comprehensive conservation strategies is imperative. By doing so, nations can secure a resilient foundation for poultry farming amidst evolving global challenges, ensuring sustainable agricultural practices and enhanced food security for future generations.

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