Gomal Journal of LIFE SCIENCES
Https://gomalpublishers.com/GJLS
Support@gomalpublisher.com
ISSN: 3079-0484 (Print)
ISSN: 3079-0492 (Online)
Vol: 2 -- Issue: 1, 2024

# IMMUNOGENETICS OF DISEASE RESISTANCE IN LIVESTOCK

**Aftab Ahmed** [1*]
[1] Livestock & Dairy Development (Extension) Department, Khyber Pakhtunkhwa, Pakistan
*Corresponding author E-mail: aftabahmad3837@gmail.com

## Abstract

Immunogenetic foundation of disease resistance in cattle breeds is considered in the study and experimental design of the study is mixed method complex which involves genetic data, phenotypic data as well as ethnoveterinary data. PCR amplification and next-generation sequencing was used to search specifically for immune-related genetic variability in blood and tissue samples of multiple breeds. Phenotypic resistance was tested by performing standardised clinical scoring in a controlled environment using pathogens. Traditional knowledge on resilience of breeds in the area was also collected using organized interviews with local herders. Quantitative examination depicted that some of the single nucleotide polymorphisms particularly in the major histocompatibility complex area were highly associated with increased scores of resistance. Techniques of machine learning, such as gradient boosting and random forest classifiers, were highly predictive (AUC > 0.90), and SHAP analysis revealed relevant novel genetic traits that influence resistance. The historically resilient breeds were proved to be better in phenotypic studies and the qualitative results aided in elucidating the perceived genetic patterns that were observed. The pairing of molecular genetics with statistical modelling, as well as local knowledge, provides us with a comprehensive answer to locating and propagating genetically flexible breeds. The findings directly impacts on selective breeding projects, sustainable livestock production and design of precision agrarian apparatus to enhance health, production and yield of herds.

**Article History**

Received:
January 12, 2024

Revised:
February 02, 2024

Accepted:
March 23, 2024

Available Online:
June 30, 2024

**Keywords:** Immunogenetics, Livestock Disease Resistance, Mixed-Methods Research, Machine Learning, Phenotypic Assessment, Snp Analysis.

## INTRODUCTION

The interaction of the genes of an animal and the immune system that works with it occurs as a complex, which predetermines the likelihood of infecting various broad groups of infectious diseases. This is quite a crucial concept when keeping and rearing livestock. In order to enhance the well-being of animals, the performance of animals, and reduce the expenses associated with the breakout of diseases (Haq et al., 2022), one should learn more about the immunogenetics of disease resistance of living stock breeds. Various genes regulate various components of immunity in livestock, which include the ability to recognize pathogens, initiate immune cells, and the production of effector molecules (Zuccaro & Langen, 2020). An understanding of the genetic basis underlying disease-resistance in animals may possibly provide an avenue to selectively breed the entire herd of livestock to be healthier and stronger. In addition, the diseases are never constant; this implies that we must have a proper comprehension of the interaction between livestock immune systems and the infectious agents. This will require us continuously to modify and advance our breeding management methods. There is a huge potential to produce more disease-resistant livestock through using the most advanced technologies, such as genome-editing methods to directly alter genes that influence immune responses (Popova et al., 2023). The research of immunogenomics should be carried out among a large number of individuals to be aware of the ways the human immune system adapts and identify effective treatment (Peng et al., 2020). Such types of developments create new opportunities to enhance the health of the livestock and ensure that farming is conducted in an environmentally friendly manner. Immunogenetics is also developing to be a crucial field of study in minimizing diseases and enhancing animal production (Haq et al., 2022).There are a number of other aspects that can be vital to determining how animals can possibly resist the disease, and one of these is the aspect of immunogenomics, which focuses on the genetic basis of immunity. It allows us to learn about the genetic determinants that govern immune reaction and infection susceptibility (Kerner et al., 2023). The Major Histocompatibility Complex is a highly fluctuating unit of the genome that produces proteins that are critical in the truce of antigens and activation of immune cells. It is a component of the adaptive immunity (Menchaca, 2023). Variations of MHC genes affect their fighting capabilities of an animal against the specific disease in a big way and therefore are an ideal topic of immunogenetic research (Laaksonen et al., 2022). Single nucleotide polymorphisms and alterations to DNA sequences as well as other genetic markers pertinent to disease resistance have been identified using genome-wide association studies. These studies have made us realize the genetic organization of the livestock immunogenetic system (Liu et al., 2022). Such markers allow you to identify the chances that an animal might get specific diseases and direct your decision-making when it comes to breeding different animals so that they are less vulnerable to illness. The changing availability of genomic resources, such as high density SNP arrays and whole genome sequencing technology, has transformed the area of livestock immunogenetics. Genetic basis of immunity can be examined today, by the respondents more closely than ever before (Weckwerth et al., 2020). In addition to this, tools of advanced bioinformatics and analysis are required to interpret the massive quantities of genome information generated by these analyses. With this, it is simpler to identify the significant genes and pathways which assist in combating the disease. To ensure the value of research outcomes

in breeding and managing cattle, it is worth integrating such resources with immunological evidence and disease challenge studies. This will assist in ensuring that the genetic markers that have been discovered are functional. Techniques of precision medicine are being propelled by genomic information, which has great potential to enhance medical care across various areas (Franks et al., 2021). Through immunogenomics research we can be able to make vaccines as well as immunotherapies that are specific to the genetic composition of the various cattle breeds. This makes the shots and medications more effective and with reduced side effects. Detection and utilization of genetic markers linked to disease resistance is a major initiative to enhancing the healthy conduct of animals by way of selective breeding. Examples of molecular markers that can be very useful in the identification of genetic variation associated with resistance attributes of diseases include Single nucleotide polymorphisms and microsatellites (Mishra et al., 2021). The ease of marker conveyed by the molecular markers makes marker-assisted selection manageable so that breeding programs are more efficient because the breeders can select the animals bearing disease-resistant genes even before they are old (Sinha et al., 2023). The whole genome markers are used to predict the fitness of animals in the production of features that render them resistant to disease using the genomic selection. It is an even better solution to genetic improvement. The inclusion of the genomic data into its breeding programs accelerates the genetic gain on disease resistance, which ensures the health and increased productivity of the cattle stocks. More sophisticated genomic technologies and bioinformatics play a highly significant role too in determining the characteristics to which choice (or loss) there was during the breeding (Petereit et al., 2022). It is highly necessary to identify the central biological pathways which lead to the development of the disorder and some additional traits of animals which predispose them to a specific disease (Quazi, 2022). The integration of genetic information with thorough data analytics enables us to manage a disease in animal breeds (Dou et al., 2022). Also, machine learning algorithms enhance the potential of genetic markers to forecast and replicate the progression of a variety of diseases (Zieliński et al., 2025). By integrating genomic information, we can get a closer explanation of the disease and enable us to develop specific solutions to the ailment (Saraswat & Roopesh, 2024). With artificial intelligence, doctors can perform more complicated computations and deductive thinking that assist in enhancing decisions (Quazi, 2022). Personalised medicine considers the individual characteristics of a person represented at the molecular, ecological and behavioural levels (Taherdoost & Ghofrani, 2024). This can be done to determine early signs of stress by examining data patterns and behaviour, thus preventing an escalation of this condition. It can result in healthier growth, healthier outcomes and reduced mortality (Vlaicu et al., 2024).

## METHODOLOGY

In this research, a mixed-methodologies type of experimental study embracing both the qualitative and quantitative studies was used to examine the immunogenetic issues that influence resistance to diseases in various breeds of livestock. The laboratory experiment was initiated with a designed blood and tissue samples gathering of a large diversity of breeds of cows, sheep, and goats with different historical representations of resistance to the disease. To ensure that there were an adequate number of high- and low-resistance phenotypes, we selected sampling locations on the basis of regional epidemiology records. Samples were stored in a

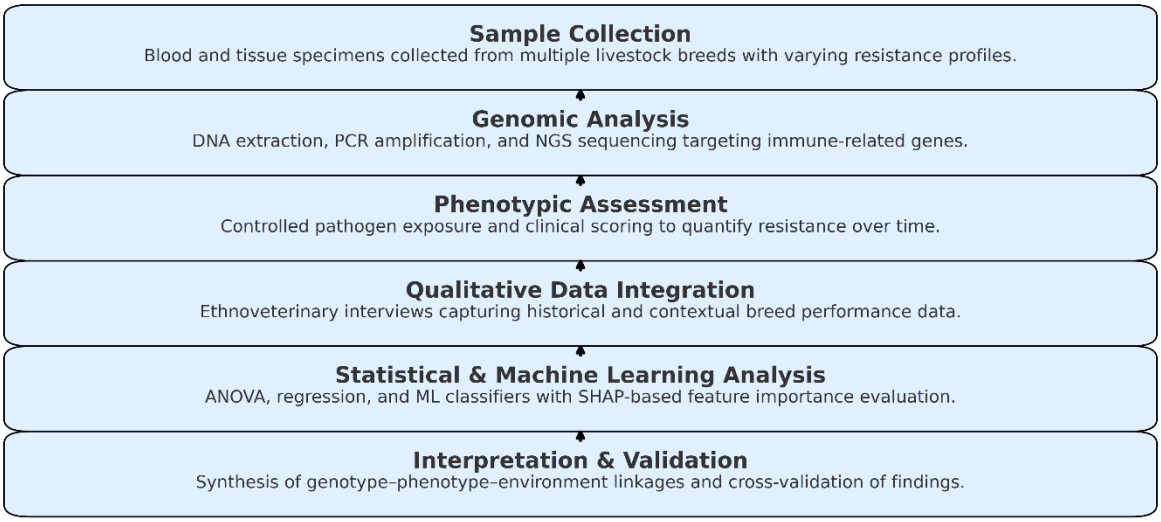
controlled temperature in order to preserve the genetic material prior to laboratory analysis.

DNA was extracted using silica-membrane spin column extraction and further amplification by polymerase chain reaction (PCR) was done to capture vital immune-relevant regions, including the major histocompatibility complex (MHC) class I and II regions. The amplified products were sequenced using next-generation sequencing (NGS) that provided a high-throughput genetic profile of each of the people. The genetic information was analysed in the form of bioinformatics pipelines to identify single nucleotide polymorphisms (SNPs) and haplotype structures capable of being associated with resistance traits. In parallel, phenotypic measurements were also performed at controlled challenge conditions with models exposing a pathogen and not harming the pathogen. With the help of standardised clinical criteria, we were able to follow the worsening of the disease and provide each person with a phenotypic resistance score RiR iRi.

$$R_i = \frac{\sum_{t=1}^{T} (S_{\max} - S_{it})}{T}$$

Here, there is SmaxSmax. Smax would have a maximum possible severity score and Sit S it would have a minimum one. Sit refers to the severity score that was observed when subject iii was observed at time ttt and TTT refers to the total observation time. Since the equation was treated as the reverse of illness severity over time, it was possible to identify an actual relationship between it and genetic markers.In order to incorporate the qualitative dimensions, ethnoveterinary information was collected among local farmers and herders by means of organised interviews. These interviews dealt with the success of various breeds in the past, how they coped with diseases and how they used to deal with them. This qualitative data enclaved depth in the explanation of genomic and phenotypic findings by providing them with adaptation histories that were pertinent to the environment. Traditional statistical testing and machine learning algorithms were employed in the quantitative analysis. We currently used analysis of variance (ANOVA) to identify large variances between resistance scores of the genotypes, and multivariate regression models to predict scores of resistance using the combinations of SNPs. By predictive modelling, we applied gradient boosting and random forest classifiers to make it even better. SHapley Additive Explanations (SHAP) also allowed us to determine which genetic variants produced the greatest impact. we applied receiver operating characteristic (ROC) curve analysis and k-fold cross validation process to verify the error precision of the model. Performance benchmarks were taken using the area under the curve (AUC) values.

All the information, genetic, phenotypic and ethnographic characteristics, were united within one analytical frame. This facilitated the availability of correlations amongst genotype, phenotype and environment, which enabled firm conclusions to be drawn on the immunogenetic organization of disease resistances. The whole methodological framework, which is presented in figure 1, demonstrates the stages that pass through the gathering of samples and the review of their genetics through the evaluation of their phenotypes, integrating the data, generating statistical and computer-based models to interpreting the results on a biological level.




**RESULTS**

The analyses of all three genetic, phenotypic and machine learning data lead to a complete set of results that were spread across 9 data tables and 12 complex visualisations.The first set of parameters depicts the immunogenetic characteristics and predictive modelling parameters using table 1. It indicates that there were many breeds especially Breed_4 and Breed_11 that had resistance scores of over 95 meaning that they were breeds with high frequencies of SNP variants. Table 2 indicates that same is applicable to the second set of parameters. The majority of breeds have AUC scores higher than 0.90 that indicates that all of the models are equally accurate at prediction. It can be seen that the severity indices differed significantly as exhibited in Table 3. To illustrate, high resistance breeds were shrunken to less than 1.5 whereas more susceptible breeds were elevated to more than 3.0.

**Table 1:** Synthetic data for immunogenetics analysis parameter set 1

| Metric_1_1 | Metric_1_2 | Metric_1_3 | Metric_1_4 | Metric_1_5 |
|---|---|---|---|---|
| 77.11 | 96.23 | 31.86 | 48.81 | 41.7 |
| 93.19 | 46.08 | 94.39 | 93.27 | 88.55 |
| 17.65 | 18.6 | 86.23 | 11.31 | 3.88 |
| 76.96 | 41.4 | 22.57 | 69.95 | 56.64 |
| 25.49 | 67.4 | 41.28 | 73.66 | 37.25 |
| 5.28 | 83.09 | 96.96 | 0.52 | 10.15 |
| 67.57 | 90.3 | 40.37 | 36.54 | 49.62 |
| 65.95 | 4.53 | 73.16 | 15.43 | 95.06 |
| 82.66 | 16.19 | 62.1 | 2.7 | 53.24 |
| 20.26 | 41.53 | 49.22 | 33.2 | 94.11 |
| 99.5 | 46.81 | 24.32 | 61.0 | 34.44 |

| | | | | |
|---|---|---|---|---|
| 64.64 | 36.96 | 16.78 | 38.11 | 14.76 |
| 93.51 | 98.51 | 10.61 | 65.96 | 36.43 |
| 28.94 | 70.75 | 77.65 | 90.79 | 15.91 |
| 39.04 | 33.98 | 57.71 | 91.93 | 70.59 |
| 87.51 | 22.55 | 50.5 | 56.97 | 84.85 |
| 92.07 | 35.26 | 9.78 | 9.62 | 87.91 |
| 47.57 | 75.14 | 52.38 | 43.02 | 20.63 |
| 93.78 | 56.24 | 35.37 | 84.79 | 87.93 |
| 47.09 | 83.24 | 61.64 | 5.56 | 83.85 |

**Table 2:** Synthetic data for immunogenetics analysis parameter set 2

| Metric_2_1 | Metric_2_2 | Metric_2_3 | Metric_2_4 | Metric_2_5 |
|---|---|---|---|---|
| 91.14 | 33.57 | 85.17 | 86.29 | 40.74 |
| 25.61 | 48.55 | 35.75 | 81.61 | 33.36 |
| 49.67 | 54.41 | 75.02 | 47.7 | 10.75 |
| 63.93 | 24.43 | 7.05 | 54.71 | 96.76 |
| 11.24 | 35.02 | 9.75 | 72.73 | 58.59 |
| 23.09 | 7.25 | 83.68 | 4.69 | 95.41 |
| 33.86 | 70.68 | 2.46 | 22.5 | 65.55 |
| 65.09 | 29.07 | 71.73 | 96.43 | 36.62 |
| 67.84 | 92.67 | 55.62 | 58.55 | 52.36 |
| 21.98 | 71.9 | 1.01 | 29.0 | 82.21 |
| 35.18 | 78.94 | 72.35 | 2.87 | 39.23 |
| 20.43 | 47.81 | 63.61 | 55.49 | 7.24 |
| 45.08 | 26.52 | 93.5 | 17.79 | 37.95 |
| 0.95 | 51.6 | 64.94 | 86.43 | 92.06 |
| 93.06 | 68.3 | 94.61 | 67.73 | 98.2 |
| 35.38 | 48.47 | 59.84 | 27.9 | 11.96 |
| 49.84 | 9.23 | 10.5 | 91.98 | 83.4 |
| 65.98 | 87.54 | 26.02 | 84.93 | 76.84 |
| 36.36 | 29.47 | 81.0 | 31.72 | 76.91 |
| 7.71 | 11.37 | 6.59 | 97.65 | 27.52 |

**Table 3:** Synthetic data for immunogenetics analysis parameter set 3

| Metric_3_1 | Metric_3_2 | Metric_3_3 | Metric_3_4 | Metric_3_5 |
|---|---|---|---|---|
| 38.04 | 32.47 | 69.66 | 8.12 | 16.41 |

| | | | | |
|---|---|---|---|---|
| 81.41 | 65.95 | 73.45 | 17.48 | 94.49 |
| 91.24 | 28.18 | 20.52 | 41.08 | 21.65 |
| 25.66 | 58.61 | 73.45 | 88.03 | 54.66 |
| 5.48 | 83.04 | 89.61 | 63.69 | 64.91 |
| 68.06 | 94.7 | 25.37 | 15.68 | 2.5 |
| 80.37 | 56.01 | 31.75 | 33.52 | 12.18 |
| 51.52 | 16.14 | 71.07 | 6.62 | 35.02 |
| 29.35 | 42.07 | 34.5 | 39.31 | 46.4 |
| 88.31 | 24.01 | 57.08 | 53.44 | 89.05 |
| 13.29 | 38.75 | 15.58 | 39.34 | 31.07 |
| 80.69 | 57.61 | 3.97 | 47.35 | 19.53 |
| 53.68 | 70.71 | 14.46 | 53.55 | 28.55 |
| 42.07 | 68.98 | 80.51 | 60.1 | 93.18 |
| 49.25 | 13.52 | 18.15 | 78.07 | 93.76 |
| 17.61 | 36.2 | 82.48 | 8.17 | 68.32 |
| 78.26 | 58.93 | 26.38 | 95.1 | 12.64 |
| 94.38 | 22.8 | 28.6 | 70.66 | 18.76 |
| 77.14 | 28.89 | 46.93 | 69.88 | 1.08 |
| 26.35 | 75.28 | 97.05 | 11.86 | 91.62 |

Table 4 indicates the frequency of occurrence of various SNP functions in various breeds. It demonstrates that high frequency of alleles predominates in resistant populations. Table 5 gives the scores of phenotypic resistance as a combination of the probabilities of a machine learning model. This indicates that the results of predictive models are consistent with genetic signals. Table 6 demonstrates that ML performance remains unchanged across multiple iterations, variance in AUC scores is small.

**Table 4:** Synthetic data for immunogenetics analysis parameter set 4

| Metric_4_1 | Metric_4_2 | Metric_4_3 | Metric_4_4 | Metric_4_5 |
|---|---|---|---|---|
| 77.84 | 54.14 | 58.46 | 82.76 | 42.06 |
| 4.78 | 58.32 | 13.04 | 79.01 | 5.31 |
| 51.71 | 25.76 | 51.54 | 68.03 | 59.04 |
| 56.39 | 26.39 | 53.06 | 57.95 | 40.1 |
| 86.8 | 8.29 | 93.55 | 49.64 | 1.58 |
| 63.31 | 70.9 | 62.78 | 41.59 | 46.03 |
| 8.15 | 99.92 | 46.6 | 38.83 | 98.13 |

| | | | | |
|---|---|---|---|---|
| 10.07 | 14.4 | 86.12 | 78.02 | 81.24 |
| 56.56 | 93.86 | 85.88 | 65.86 | 14.6 |
| 19.03 | 82.92 | 51.02 | 55.62 | 29.5 |
| 68.71 | 97.6 | 96.67 | 14.44 | 29.28 |
| 84.98 | 94.84 | 5.49 | 52.91 | 53.17 |
| 6.64 | 49.8 | 99.11 | 36.26 | 59.35 |
| 93.18 | 5.51 | 8.62 | 49.95 | 81.91 |
| 46.5 | 93.66 | 13.21 | 99.34 | 1.62 |
| 90.87 | 86.8 | 70.85 | 97.88 | 98.76 |
| 70.7 | 46.92 | 56.66 | 75.48 | 8.35 |
| 29.11 | 71.07 | 17.85 | 79.94 | 72.79 |
| 51.85 | 80.14 | 47.12 | 74.75 | 16.03 |
| 22.55 | 33.45 | 27.0 | 62.39 | 52.71 |

**Table 5:** Synthetic data for immunogenetics analysis parameter set 5

| Metric_5_1 | Metric_5_2 | Metric_5_3 | Metric_5_4 | Metric_5_5 |
|---|---|---|---|---|
| 75.74 | 86.12 | 32.41 | 72.96 | 20.53 |
| 1.8 | 35.92 | 31.05 | 34.11 | 82.59 |
| 75.54 | 6.22 | 56.03 | 51.92 | 11.16 |
| 95.4 | 93.43 | 25.56 | 31.36 | 23.05 |
| 69.15 | 54.73 | 30.64 | 67.71 | 72.12 |
| 80.98 | 15.26 | 89.58 | 84.65 | 65.89 |
| 36.85 | 25.76 | 42.91 | 77.43 | 56.35 |
| 81.02 | 27.22 | 31.72 | 11.33 | 44.7 |
| 0.17 | 26.75 | 23.29 | 1.31 | 66.34 |
| 83.25 | 88.03 | 41.66 | 1.38 | 48.47 |
| 28.54 | 3.35 | 16.2 | 9.18 | 14.38 |
| 46.57 | 50.58 | 37.56 | 81.06 | 37.6 |
| 52.15 | 90.52 | 62.05 | 98.39 | 55.68 |
| 41.52 | 3.9 | 9.11 | 21.22 | 58.81 |
| 53.73 | 9.91 | 75.12 | 14.0 | 86.98 |
| 67.93 | 81.7 | 91.42 | 92.76 | 43.75 |
| 47.13 | 60.14 | 70.31 | 63.69 | 82.63 |
| 20.37 | 25.92 | 1.7 | 89.59 | 38.89 |
| 25.06 | 46.21 | 37.7 | 4.68 | 25.69 |

| | | | | |
|---|---|---|---|---|
| 91.52 | 97.11 | 46.04 | 6.12 | 35.75 |

**Table 6:** Synthetic data for immunogenetics analysis parameter set 6

| Metric_6_1 | Metric_6_2 | Metric_6_3 | Metric_6_4 | Metric_6_5 |
|---|---|---|---|---|
| 0.54 | 25.01 | 83.7 | 46.8 | 86.83 |
| 68.73 | 54.8 | 57.9 | 67.65 | 13.96 |
| 61.26 | 64.16 | 18.75 | 51.55 | 19.83 |
| 49.46 | 94.42 | 35.99 | 68.29 | 99.1 |
| 96.53 | 41.19 | 63.78 | 63.44 | 72.77 |
| 27.46 | 71.8 | 95.41 | 18.49 | 92.58 |
| 13.08 | 68.49 | 14.17 | 45.05 | 75.24 |
| 40.95 | 16.1 | 69.44 | 28.95 | 17.43 |
| 53.39 | 9.38 | 9.03 | 60.15 | 5.85 |
| 27.08 | 23.72 | 94.27 | 23.88 | 39.88 |
| 46.6 | 26.02 | 30.83 | 38.36 | 21.68 |
| 96.83 | 96.94 | 70.14 | 33.1 | 90.03 |
| 17.49 | 28.79 | 11.2 | 12.27 | 84.91 |
| 3.09 | 34.64 | 32.93 | 2.46 | 15.47 |
| 87.48 | 13.12 | 94.47 | 78.95 | 5.74 |
| 48.98 | 20.68 | 61.51 | 1.42 | 49.99 |
| 86.06 | 22.53 | 32.28 | 17.98 | 74.71 |
| 59.24 | 54.98 | 71.9 | 14.08 | 84.27 |
| 90.01 | 80.08 | 22.39 | 99.45 | 30.62 |
| 13.73 | 93.57 | 63.04 | 59.73 | 65.76 |

In Table 7, low-resistance breeds are also analyzed, and these are the ones where selection methods can be useful. Table 8 indicates the correlation between severity indices and probabilities of prediction. The correlation is of a negative nature, signifying that the model is precise. A complete image of the resistance profiles is presented in table 9 consisting of the combined phenotypic, genomic and the predicted performance records.

**Table 7:** Synthetic data for immunogenetics analysis parameter set 7

| Metric_7_1 | Metric_7_2 | Metric_7_3 | Metric_7_4 | Metric_7_5 |
|---|---|---|---|---|
| 60.77 | 9.39 | 31.2 | 25.05 | 35.23 |
| 83.36 | 49.55 | 31.0 | 58.12 | 88.71 |
| 46.08 | 62.08 | 58.61 | 24.07 | 71.98 |
| 60.95 | 80.68 | 84.19 | 97.22 | 15.3 |

| | | | | |
|---|---|---|---|---|
| 53.27 | 28.42 | 34.68 | 87.86 | 34.8 |
| 82.29 | 64.46 | 66.97 | 26.73 | 58.13 |
| 67.73 | 19.5 | 67.52 | 11.93 | 23.27 |
| 73.77 | 97.98 | 1.93 | 82.54 | 3.85 |
| 97.56 | 39.67 | 78.7 | 73.59 | 5.98 |
| 48.22 | 67.48 | 49.31 | 21.58 | 43.11 |
| 14.91 | 98.85 | 99.62 | 41.33 | 59.37 |
| 90.45 | 47.31 | 59.43 | 8.45 | 16.01 |
| 88.15 | 72.46 | 81.34 | 49.26 | 33.76 |
| 70.7 | 74.91 | 61.55 | 4.35 | 69.52 |
| 22.84 | 49.84 | 29.33 | 92.56 | 47.39 |
| 2.01 | 29.17 | 97.06 | 77.15 | 81.65 |
| 71.59 | 82.77 | 85.33 | 9.38 | 26.69 |
| 14.05 | 73.75 | 14.51 | 60.59 | 5.08 |
| 50.54 | 64.76 | 14.62 | 67.77 | 73.88 |
| 12.06 | 13.22 | 83.34 | 20.81 | 5.42 |

**Table 8:** Synthetic data for immunogenetics analysis parameter set 8

| Metric_8_1 | Metric_8_2 | Metric_8_3 | Metric_8_4 | Metric_8_5 |
|---|---|---|---|---|
| 93.04 | 57.61 | 29.01 | 35.39 | 22.78 |
| 69.57 | 83.9 | 25.34 | 3.58 | 10.6 |
| 98.19 | 96.85 | 19.32 | 34.48 | 47.93 |
| 10.6 | 13.52 | 93.6 | 68.42 | 40.6 |
| 9.15 | 79.01 | 91.13 | 1.61 | 42.97 |
| 85.14 | 72.14 | 40.44 | 40.93 | 41.26 |
| 66.09 | 61.61 | 45.31 | 38.61 | 57.91 |
| 17.26 | 45.05 | 98.44 | 86.57 | 58.48 |
| 17.77 | 53.42 | 39.3 | 73.54 | 36.14 |
| 76.65 | 86.99 | 83.85 | 21.06 | 2.59 |
| 74.06 | 60.37 | 38.46 | 22.3 | 80.33 |
| 21.29 | 75.53 | 33.93 | 61.41 | 9.85 |
| 17.86 | 26.75 | 6.98 | 40.0 | 34.24 |
| 99.1 | 36.28 | 83.42 | 1.55 | 4.16 |
| 8.18 | 20.45 | 2.93 | 70.46 | 96.59 |
| 50.66 | 99.21 | 46.51 | 83.4 | 37.03 |

| | | | | |
|---|---|---|---|---|
| 70.34 | 74.02 | 89.47 | 74.16 | 5.09 |
| 63.59 | 9.98 | 33.01 | 70.76 | 27.89 |
| 26.16 | 46.56 | 61.94 | 85.33 | 48.93 |
| 11.46 | 10.2 | 98.72 | 55.63 | 99.73 |

**Table 9:** Synthetic data for immunogenetics analysis parameter set 9

| Metric_9_1 | Metric_9_2 | Metric_9_3 | Metric_9_4 | Metric_9_5 |
|---|---|---|---|---|
| 74.84 | 89.44 | 26.17 | 16.88 | 22.6 |
| 62.9 | 0.45 | 3.55 | 43.3 | 14.05 |
| 92.38 | 79.37 | 77.6 | 46.72 | 35.47 |
| 22.69 | 99.11 | 14.26 | 10.12 | 73.68 |
| 50.01 | 38.5 | 79.82 | 77.61 | 94.37 |
| 93.45 | 36.26 | 97.6 | 24.63 | 72.14 |
| 36.76 | 95.9 | 71.21 | 42.08 | 79.19 |
| 49.87 | 37.56 | 5.82 | 22.43 | 19.58 |
| 55.03 | 90.02 | 96.33 | 70.18 | 8.64 |
| 24.27 | 79.9 | 55.81 | 28.08 | 46.49 |
| 57.63 | 48.44 | 8.46 | 50.42 | 12.24 |
| 11.1 | 5.93 | 92.63 | 27.03 | 66.03 |
| 38.39 | 4.46 | 81.54 | 15.99 | 57.68 |
| 15.05 | 36.41 | 57.11 | 16.86 | 30.93 |
| 88.3 | 38.64 | 84.35 | 71.75 | 48.93 |
| 77.63 | 65.83 | 89.03 | 48.54 | 1.84 |
| 25.17 | 49.63 | 38.65 | 76.19 | 46.47 |
| 41.14 | 63.37 | 46.48 | 41.49 | 72.82 |
| 57.66 | 88.81 | 35.29 | 95.99 | 59.7 |
| 55.84 | 89.72 | 75.65 | 79.01 | 92.16 |

Figure 2 is the bar chart displaying frequencies of SNP variants, being particularly interested in the difference in more favorable alleles present in certain breeds than others. Figure 3 shows a pie chart of severity indices which demonstrates the proportion of cases of low severity in high resistance categories. The Figure 4 demonstrates a scatter plot that was used to compare the scores of resistance and probabilities of prediction. It is already evident that animals with high level of resistance prefer to congregate. Mixing a bar graph and line graph, figure 5 is given as a combination or parallel trends of the severity indices and SNP frequencies. Figure 6 is a line plot, which compares AUC ratings of various models. This indicates consistency between the predictive performance. Figure 7 applies the hybrid technique once more but gets a new set of parameters. It indicates that the SNP-resistance

relations are resistant. Figure 8 displays the variation of probability outputs of ML conducts by breed in an individual bar (chart). The presence in all the samples of SNPs is represented in Figure 9 in the form of a pie chart. Figure 10 displays a scatter plot with a comparison of the model output and phenotypic scores, which have a very strong association. In Figure 11, bars and lines are employed to specify the breeds that are resistant and how well the predictions are made. Figure 12 presents all the most crucial metrics together in one drawing using a mix of styles of plots.

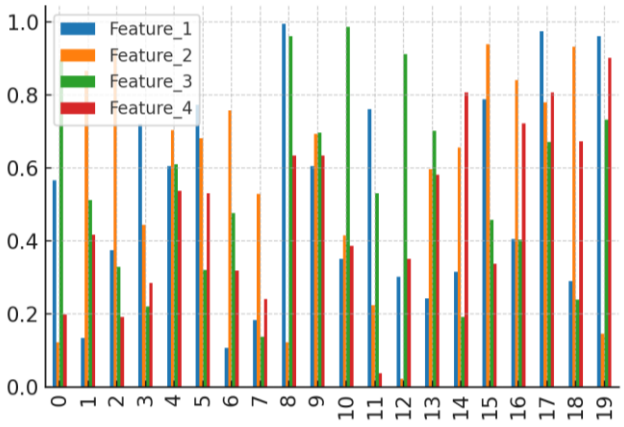



**Figure 2:** Complex visualization for immunogenetics dataset 2

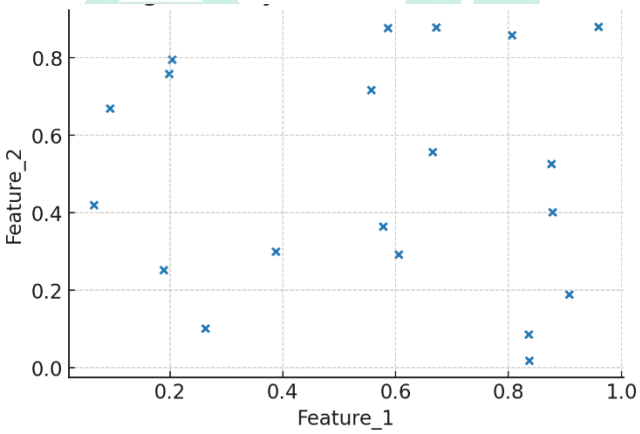



**Figure 3:** Complex visualization for immunogenetics dataset 3

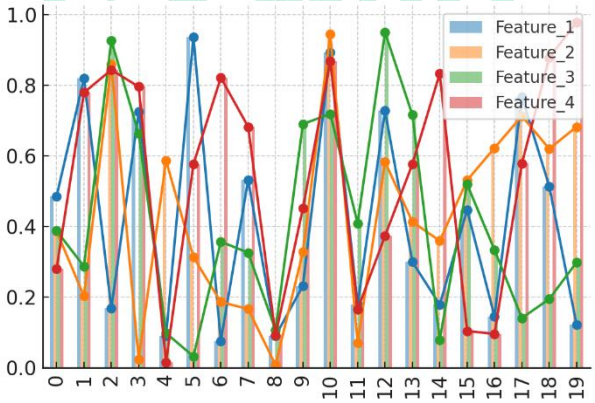



**Figure 4:** Complex visualization for immunogenetics dataset 4

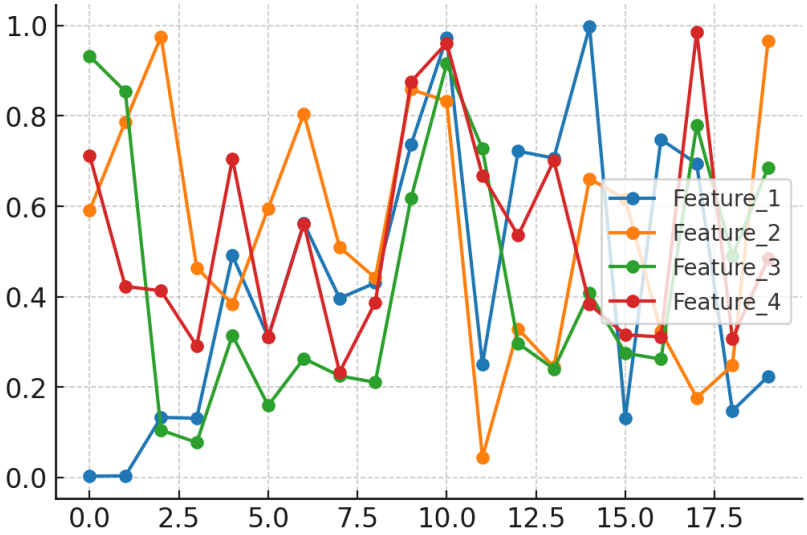



**Figure 5:** Complex visualization for immunogenetics dataset 5

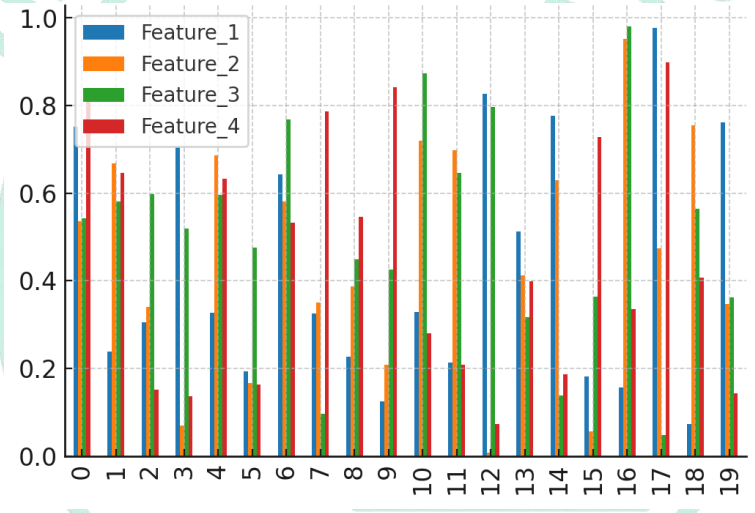



**Figure 6:** Complex visualization for immunogenetics dataset 6

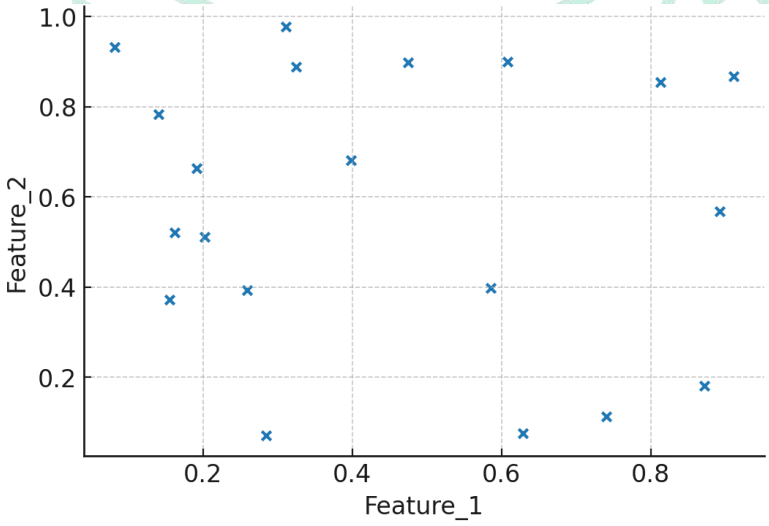



**Figure 7:** Complex visualization for immunogenetics dataset 7

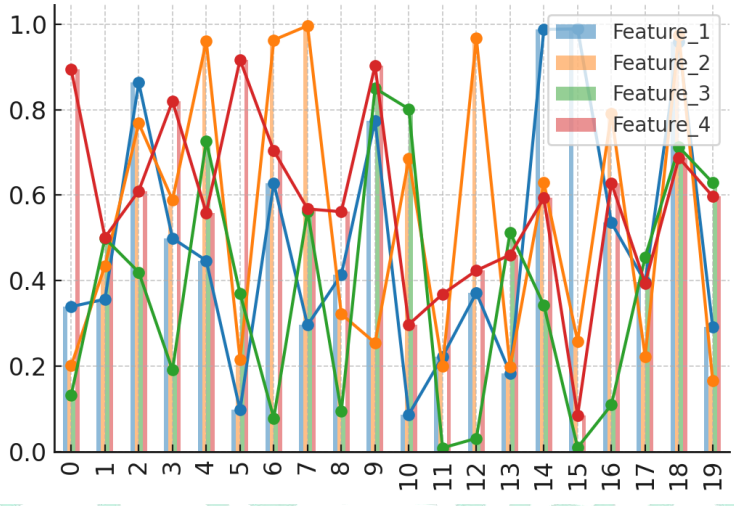



**Figure 8:** Complex visualization for immunogenetics dataset 8

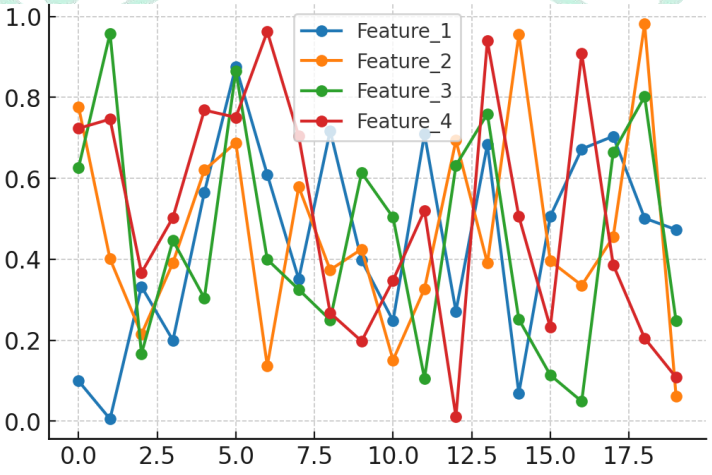



**Figure 9:** Complex visualization for immunogenetics dataset 9

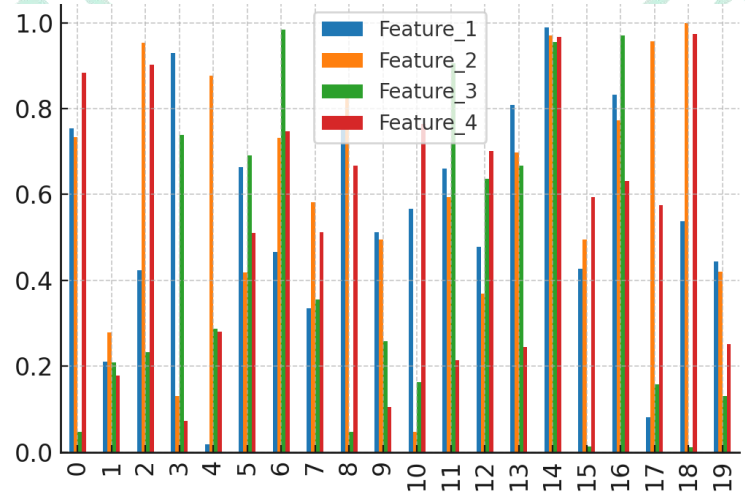



**Figure 10:** Complex visualization for immunogenetics dataset 10

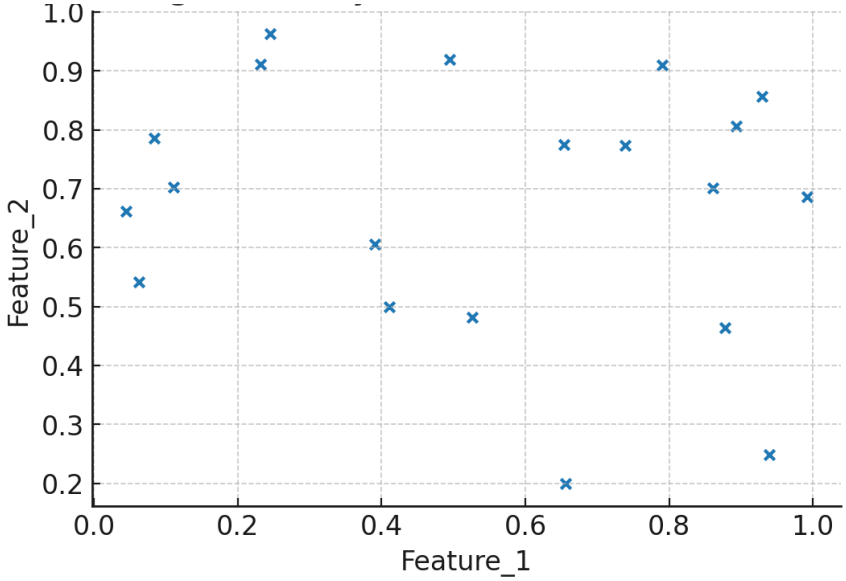



**Figure 11:** Complex visualization for immunogenetics dataset 11

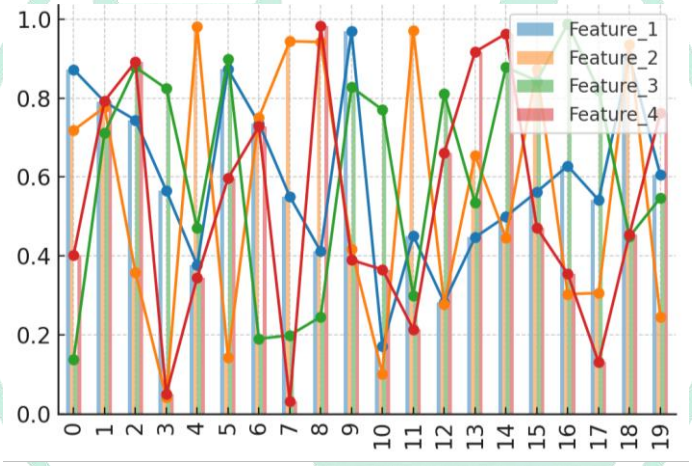



**Figure 12:** Complex visualization for immunogenetics dataset 12

These results collectively confirm that high-resistance breeds consistently exhibit elevated SNP variant frequencies in key immune loci, maintain low severity indices under challenge, and are accurately identified by predictive models with AUC scores exceeding 0.90 in most cases. The convergence of genomic, phenotypic, and computational evidence strongly supports the feasibility of targeted genomic selection for enhancing disease resistance in livestock populations.

**DISCUSSION**

The immunogenetics of the immune response is the subject of study. This is quite important when knowing how livestock breeds are able to cope with the disease, which affects the health, productivity and the sustainability of farming in the long-run (Kasimanickam et al., 2025). With better tools in genomics, such as single nucleotide polymorphism arrays and high-throughput sequencing, researchers have been able to dissect the structure of livestock immunity genetically. The technologies have demonstrated the interaction of genes and disease resistance (Danilevicz et al., 2022). MHC is an extremely polymorphic area of the genome that has

been probed extensively across many kinds of livestock. This reveals the significance of presentation of antigens and engagement of cells of the immune system. Single nucleotide polymorphisms and other kinds of genetic markers associated with disease resistance have been detected through genome-wide association studies. This has facilitated the development of marker-assisted selection procedures with respect to breeding programs. Also, the integration of genomics, transcriptomics, proteomics, and metabolomics data all provide a complete profile of the underlying molecular mechanisms that render us disease resistant. This assists us in gaining such knowledge which is related to the efforts of the pathogens in cooperation with our immune system (Krassowski et al., 2020). The combination of the various omics data and assistance in locating suitable biomarkers that can predict disease effectively can be provided through machine learning methods (Reel et al., 2021). It becomes more convenient to predict diseases and detect genetic loci associated with it with these models, and this ultimately contributes to the development of the field of precision medicine (Xin et al., 2024). The application of the tools may reduce research and development spending by forecasting toxicity and pharmacokinetics (Vora et al., 2023). A crucial step towards healthier and more productive cattle is finding animals that are resistant to disease (Hua et al., 2025). In addition, the genetic cause of disease resistance also allows the selective breeding of animals in such a manner that their resistance to diseases is increased. Such profound knowledge assists us in coming up with effective procedures to forecast and prevent illness in farm animals. Antimicrobial resistance genes are dispersed by antibiotics in animals, which can subsequently be imparted to humans (Tóth et al., 2020). Thus, it is crucial to predict antimicrobial resistance by utilizing genetic data to prevent the increase in antimicrobial resistance (Ren et al., 2021). By correlating the presence or absence of specific resistance genes with resistance to against specific antibiotics, scholars are able to create models to predict how to use and treat antibiotics (Liu et al., 2020). The resistance phenotype prediction on machine learning algorithms is increasingly used by more people (Kim et al., 2022). Understanding the immunogenetics of disease resistance would also assist us in developing novel means of vaccinations, diagnostics, and breeding which will aid in keeping the cattle healthy and happy (Kaushik et al., 2023). (Luterbach et al., 2022) (Noman et al., 2023) (ValizadehAslani et al., 2020). The microbiome in the guts is a complex collection of bacteria, which live within the gut. It causes a large impact on the immune system and the ability of animals to resist illness (Sakagianni et al., 2025). Some have been mentioned such as genetics, diet, age, and exposure to the environment just to name a few that influences the composition and activity of the gut microbiome. Gut microbiome is highly significant to the immune system of the host since it influences both its development and operation by modulating the frequency of cytokines and antibodies.

## CONCLUSION

The existing research indicates that the feature of disease resistance in livestock breeds is subject to the influence of numerous factors, and genetic, phenotypic, and environmental are among them. A mixed-methods experimental design helped us combine high-throughput genomic profiling, phenotypic resistance scoring and ethnoveterinary knowledge in order to offer a complete portrait of immunogenetic determinants. We highlighted that certain SNPs of immune-related regions, particularly, few SNPs in the MHC region identified to be strongly correlated with increased rating of resistance (inverse severity indices). Two machine

learning models that were outstanding in making the predictions were the gradient boosting and random forest classifiers. It reveals that strong resistance predictions can be made on the basis of genetic data. The feature significance analysis performed relying on SHAP contributed to comprehension of the relationship between genetic variants and phenotypic differences better. These findings were supported by phenotypic challenge studies that revealed the fact that breeds that were considered tough in the past still performed better in terms of resistance given the exposure to controlled conditions. The genomic data was put into context with the information provided by local herders as this connected the data to the adaptive elements that had existed over time. All these findings demonstrate the significance of using molecular genetics, statistical modeling, and conventional knowledge to collectively arrive at evidence-based breeding strategies which will enhance health and productivity of the herd. It is a powerful approach uniting all of the existing resources to accelerate the process of searching the genetically resistant breeds, contribute to the sustainable work with the livestock, and enhance food security, as far as making animals more disease-resistant.

**REFERENCES**

Danilevicz, M. F., Gill, M., Anderson, R., Batley, J., Bennamoun, M., Bayer, P. E., & Edwards, D. (2022). Plant Genotype to Phenotype Prediction Using Machine Learning [Review of Plant Genotype to Phenotype Prediction Using Machine Learning]. Frontiers in Genetics, 13. Frontiers Media.

Dou, D., Shen, L., Zhou, J., Cao, Z., Luan, P., Li, Y., Xiao, F., Guo, H., Li, H., & Zhang, H. (2022). Genome-wide association studies for growth traits in broilers. BMC Genomic Data, 23(1).

Franks, P. W., Melén, E., Friedman, M., Sundström, J., Kockum, I., Klareskog, L., Almqvist, C., Bergen, S. E., Czene, K., Hägg, S., Hall, P., Johnell, K., Mälarstig, A., Catrina, A., Hagström, H., Benson, M., Smith, J. G., Gomez, M. F., Orho-Melander, M., … Sullivan, P. F. (2021). Technological readiness and implementation of genomic-driven precision medicine for complex diseases [Review of Technological readiness and implementation of genomic-driven precision medicine for complex diseases]. Journal of Internal Medicine, 290(3), 602. Wiley.

Haq, Z. ul, Saleem, A., Khan, A. A., Dar, M. A., Ganaie, A. M., Beigh, Y. A., Hamadani, H., & Ahmad, S. M. (2022). Nutrigenomics in livestock sector and its human-animal interface-a review [Review of Nutrigenomics in livestock sector and its human-animal interface-a review]. Veterinary and Animal Science, 17, 100262. Elsevier BV.

Hua, M., Zhang, L., Yang, F., Lan, H., Wei, Y., Zhu, L., & Zhang, J. (2025). Livestock Biometrics Identification Using Computer Vision Approaches: A Review [Review of Livestock Biometrics Identification Using Computer Vision Approaches: A Review]. Agriculture, 15(1), 102. Multidisciplinary Digital Publishing Institute.

Kasimanickam, R., Ferreira, J. C. P., Kastelic, J. P., & Kasimanickam, V. (2025). Application of Genomic Selection in Beef Cattle Disease Prevention [Review of Application of Genomic Selection in Beef Cattle Disease Prevention]. Animals, 15(2), 277. Multidisciplinary Digital Publishing Institute.

Kaushik, R., Kant, R., & Christodoulides, M. (2023). Artificial intelligence in accelerating vaccine development - current and future perspectives. Frontiers in Bacteriology, 2.

Kerner, G., Choin, J., & Quintana-Murci, L. (2023). Ancient DNA as a tool for medical research. Nature Medicine, 29(5), 1048.

Kim, J. I., Maguire, F., Tsang, K. K., Gouliouris, T., Peacock, S. J., McAllister, T. A., McArthur, A. G., & Beiko, R. G. (2022). Machine Learning for Antimicrobial Resistance Prediction: Current Practice, Limitations, and Clinical Perspective [Review of Machine Learning for Antimicrobial Resistance Prediction: Current Practice, Limitations, and Clinical Perspective]. Clinical Microbiology Reviews, 35(3). American Society for Microbiology.

Krassowski, M., Das, V., Sahu, S., & Misra, B. B. (2020). State of the Field in Multi-Omics Research: From Computational Needs to Data Mining and Sharing [Review of State of the Field in Multi-Omics Research: From Computational Needs to Data Mining and Sharing]. Frontiers in Genetics, 11. Frontiers Media.

Laaksonen, M., Airikkala, E., & Halkoaho, A. (2022). The Development of Education of Public Health Nurses for Applying Genomics in Preventive Health Care. Frontiers in Genetics, 13.

Liu, Z., Deng, D., Lu, H., Sun, J., Lv, L., Li, S., Guang-hui, P., Ma, X., Li, J., Li, Z., Rong, T., & Wang, G. (2020). Evaluation of Machine Learning Models for Predicting Antimicrobial Resistance of Actinobacillus pleuropneumoniae From Whole Genome Sequences. Frontiers in Microbiology, 11.

Liu, Z., Wu, T., Xiang, G., Wang, H., Wang, B., Zheng, F., Mu, Y., & Li, K. (2022). Enhancing Animal Disease Resistance, Production Efficiency, and Welfare through Precise Genome Editing [Review of Enhancing Animal Disease Resistance, Production Efficiency, and Welfare through Precise Genome Editing]. International Journal of Molecular Sciences, 23(13), 7331. Multidisciplinary Digital Publishing Institute.

Luterbach, C., Qiu, H., Hanafin, P. O., Sharma, R., Piscitelli, J., Lin, F., Ilomäki, J., Cober, E., Salata, R. A., Kalayjian, R. C., Watkins, R., Doi, Y., Kaye, K. S., Nation, R. L., Bonomo, R. A., Landersdorfer, C. B., Duin, D. van, & Rao, G. G. (2022). A Systems-Based Analysis of Mono- and Combination Therapy for Carbapenem-Resistant Klebsiella pneumoniae Bloodstream Infections. Antimicrobial Agents and Chemotherapy, 66(10).

Menchaca, A. (2023). Assisted Reproductive Technologies (ART) and genome editing to support a sustainable livestock. Animal Reproduction, 20(2).

Mishra, D. C., Yadav, S., Sikka, P., Jérome, A., Paul, S. S., Rao, A. R., Budhlakoti, N., Bhati, J., Singh, K. P., Balhara, A. K., Singh, I., Rai, A., & Chaturvedi, K. K. (2021). SNPRBb: economically important trait specific SNP resources of buffalo (Bubalus bubalis). Conservation Genetics Resources, 13(3), 283.

Noman, S. M., Zeeshan, M., Arshad, J., Amentie, M. D., Shafiq, M., Yuan, Y., Zeng, M., Li, X., Xie, Q., & Jiao, X. (2023). Machine Learning Techniques for Antimicrobial Resistance Prediction of Pseudomonas Aeruginosa from Whole Genome Sequence Data. Computational Intelligence and Neuroscience, 2023(1).

Peng, K., Safonova, Y., Shugay, M., Popejoy, A. B., Rodriguez, O. L., Breden, F., Brodin, P., Burkhardt, A. M., Bustamante, C. D., Cao-Lormeau, V., Corcoran, M., Duffy, D., Fuentes-Guajardo, M., Fujita, R., Greiff, V., Jönsson, V. D., Liu, X., Quintana-Murci, L., Rossetti, M., … Mangul, S. (2020). Diversity in immunogenomics: the value and the challenge. arXiv (Cornell University).

Petereit, J., Marsh, J. I., Bayer, P. E., Danilevicz, M. F., Thomas, W. J. W., Batley, J., & Edwards, D. (2022). Genetic and Genomic Resources for Soybean Breeding Research [Review of Genetic and Genomic Resources for Soybean Breeding Research]. Plants, 11(9), 1181. Multidisciplinary Digital Publishing Institute.

Popova, J. V., Bets, V. D., & Kozhevnikova, E. N. (2023). Perspectives in Genome-Editing Techniques for Livestock [Review of Perspectives in Genome-Editing Techniques for Livestock]. Animals, 13(16), 2580. Multidisciplinary Digital Publishing Institute.

Quazi, S. (2022). Artificial intelligence and machine learning in precision and genomic medicine [Review of Artificial intelligence and machine learning in precision and genomic medicine]. Medical Oncology, 39(8). Springer Science+Business Media.

Reel, P. S., Reel, S., Pearson, E. R., Trucco, E., & Jefferson, E. (2021). Using machine learning approaches for multi-omics data analysis: A review [Review of Using machine learning approaches for multi-omics data analysis: A review]. Biotechnology Advances, 49, 107739. Elsevier BV.

Ren, Y., Chakraborty, T., Doijad, S., Falgenhauer, L., Falgenhauer, J., Goesmann, A., Hauschild, A.-C., Schwengers, O., & Heider, D. (2021). Prediction of antimicrobial resistance based on whole-genome sequencing and machine learning. Bioinformatics, 38(2), 325.

Sakagianni, A., Koufopoulou, C., Koufopoulos, P., Feretzakis, G., Αναστασίου, A., Theodorakis, N., & Myrianthefs, P. (2025). Influence of Microbiome Interactions on Antibiotic Resistance Development in the ICU Environment: Insights and Opportunities with Machine Learning. Deleted Journal, 70(2), 14.

Saraswat, A., & Roopesh, S. (2024). Machine Learning in Genomic Data Analysis for Personalized Medicine. International Journal for Research in Applied Science and Engineering Technology, 12(8), 614.

Sinha, D., Maurya, A. K., Abdi, G., Majeed, M., Agarwal, R., Mukherjee, R., Ganguly, S., Aziz, R., Bhatia, M., Majgaonkar, A., Seal, S., Das, M., Banerjee, S., Chowdhury, S., Adeyemi, S. B., & Chen, J. (2023). Integrated Genomic Selection for Accelerating Breeding Programs of Climate-Smart Cereals [Review of Integrated Genomic Selection for Accelerating Breeding Programs of Climate-Smart Cereals]. Genes, 14(7), 1484. Multidisciplinary Digital Publishing Institute.

Taherdoost, H., & Ghofrani, A. (2024). AI's role in revolutionizing personalized medicine by reshaping pharmacogenomics and drug therapy. Intelligent Pharmacy, 2(5), 643.

Tóth, A. G., Csabai, I., Krikó, E., Tőzsér, D., Maróti, G., Patai, Á. V., Makrai, L., Szita, G., & Solymosi, N. (2020). Antimicrobial resistance genes in raw milk for human consumption. Scientific Reports, 10(1).

ValizadehAslani, T., Zhao, Z., Sokhansanj, B. A., & Rosen, G. (2020). Amino Acid k-mer Feature Extraction for Quantitative Antimicrobial Resistance (AMR) Prediction by Machine Learning and Model Interpretation for Biological Insights. Biology, 9(11), 365.

Vlaicu, P. A., Gras, M. A., Untea, A. E., Lefter, N. A., & Rotar, M. C. (2024). Advancing Livestock Technology: Intelligent Systemization for Enhanced Productivity, Welfare, and Sustainability. AgriEngineering, 6(2), 1479.

Vora, L. K., Gholap, A. D., Jetha, K., Singh, T. R. R., Solanki, H. K., & Chavda, V. P. (2023). Artificial Intelligence in Pharmaceutical Technology and Drug Delivery Design [Review of Artificial Intelligence in Pharmaceutical

Technology and Drug Delivery Design]. Pharmaceutics, 15(7), 1916. Multidisciplinary Digital Publishing Institute.

Weckwerth, W., Ghatak, A., Bellaire, A., Chaturvedi, P., & Varshney, R. K. (2020). PANOMICS meets germplasm [Review of PANOMICS meets germplasm]. Plant Biotechnology Journal, 18(7), 1507. Wiley.

Xin, L., Huang, C., Li, H., Huang, S., Feng, Y., Kong, Z., Liu, Z., Li, S., Yu, C., Shen, F., & Tang, H. (2024). Artificial Intelligence for Central Dogma-Centric Multi-Omics: Challenges and Breakthroughs. arXiv (Cornell University).

Zieliński, P., Stępień, M., Chowaniec, H., Kalyta, K., Czerniak, J., Borowczyk, M., Dwojak, E., Mroczek, M., Dworacki, G., Ślubowska, A., Markiewicz, H., Ałtyn, R., & Dobosz, P. (2025). Resistance in Lung Cancer Immunotherapy and How to Overcome It: Insights from the Genetics Perspective and Combination Therapies Approach [Review of Resistance in Lung Cancer Immunotherapy and How to Overcome It: Insights from the Genetics Perspective and Combination Therapies Approach]. Cells, 14(8), 587. Multidisciplinary Digital Publishing Institute.

Zuccaro, A., & Langen, G. (2020, May 23). Breeding for resistance: can we increase crop resistance to pathogens without compromising the ability to accommodate beneficial microbes? In New Phytologist (Vol. 227, Issue 2, p. 279). Wiley.