



## Genomic Selection: Precision Breeding for Enhanced Semen Production and Genetic Progress

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### Abstract

Advancements in genomics and biotechnology have revolutionized the field of animal breeding, offering new avenues for optimizing livestock production and genetic progress. This research paper delves into the concept of Genomic Selection (GS) and its application in precision breeding for the enhancement of semen production and overall genetic improvement in Sahiwal cattle, buffalo, and Cholistani cattle, with a focus on the Evergreen Sires Farm as a representative case study. Genomic Selection leverages high-throughput genotyping technologies and statistical algorithms to predict the breeding value of animals with unprecedented accuracy. This allows breeders to identify superior individuals at an early stage, thereby accelerating the rate of genetic progress and enhancing desired traits such as semen quality and quantity. The Evergreen Sires Farm, known for its exemplary collection of Sahiwal, buffalo, and Cholistani cattle, serves as an ideal context to explore the practical implementation of GS. Through the analysis of data and simulations, this paper demonstrates how genomic information can be harnessed to make informed breeding decisions, leading to improved semen production and genetic gains. Moreover, it explores the potential challenges and ethical considerations associated with the utilization of genomic technologies in animal breeding, emphasizing the need for balanced strategies that incorporate traditional breeding approaches alongside modern genomic techniques.

**Keywords:** Genomic Selection; Precision Breeding; Semen Production; Genetic Progress; Sahiwal Cattle; Buffalo; Cholistani Cattle; Evergreen Sires Farm

### Introduction

In the context of Pakistan's multifaceted and vibrant agricultural landscape, the Evergreen Sires Farm stands as a symbol of optimism and advancement. With the first rays of sunlight illuminating the Sahiwal plains, the farm springs into action, showcasing a diverse array of cattle breeds that epitomize the nation's illustrious farming traditions. Among these, the Sahiwal cattle, celebrated for their durability and remarkable milk production, share their space

with the revered buffalo, renowned for their vital contributions in both sustenance and labor, and the resilient Cholistani cattle, finely attuned to the harsh desert conditions of Cholistan [1].

Amidst the warm and earthy hues of the landscape, a story of transformation is quietly unfolding. This story revolves around a novel approach called Genomic Selection, a technique that holds the promise of accelerating the genetic progress of these beloved

breeds, with a particular focus on enhancing semen production. It's a story that marries tradition with modernity, bridging the gap between age-old practices and the cutting-edge realm of genomics [2].

This paper is more than just words on a page; it's a narrative of hope and progress, of tradition evolving into a brighter future. From the sun-kissed fields to the barns where cattle are cared for, we delve into the principles and applications of Genomic Selection. Through the lens of this transformative technique, we seek to unravel the potential it holds for advancing semen production and genetic gains – not just for the Evergreen Sires Farm, but for farms and communities across Pakistan [3].

### A future envisioned: enhancing semen production and genetic progress through genomic selection.

The traditional rhythms of rural life in Pakistan are intricately woven into the tapestry of livestock farming. Sahiwal cattle, buffalo, and Cholistani cattle are not just animals; they're symbols of sustenance, labor, and cultural identity. Against this backdrop, the introduction of Genomic Selection emerges as a transformative force, promising to amplify the genetic potential of these cherished breeds in a focused pursuit of improved semen production and genetic progress [4].

Semen production, a linchpin of successful livestock breeding, is a trait that resonates deeply in a nation where cattle play a pivotal role in agriculture and livelihoods. The journey towards enhanced semen quality and quantity starts with understanding the genetic underpinnings that define these traits. Genomic Selection steps onto this path armed with cutting-edge technology that deciphers the intricate language of genes. The result? The ability to identify animals that carry the genetic blueprint for superior semen production early in their lives [5].

The Evergreen Sires Farm stands as a testament to the power of this approach. The Sahiwal cattle, buffalo, and Cholistani cattle that graze upon its fields are more than the sum of their physical attributes. They are reservoirs of genetic information. Through careful analysis of their DNA, breeders can predict with remarkable accuracy the potential of each animal to sire offspring with exceptional semen quality. This knowledge paves the way for selective breeding that propels genetic progress towards enhanced reproductive efficiency [6].

In this pursuit, Genomic Selection serves as a beacon of efficiency. Traditional breeding practices, while venerable, are often

time-consuming and reliant on generations of offspring to reveal the true worth of an animal's genetics. Genomic Selection condenses this timeline, allowing breeders to peer into the future without waiting for the passage of years. It ushers in an era where the selection of sires isn't just based on intuition or lineage; it's grounded in data-driven insights that promise tangible outcomes [7].

### Cultivating a synergy of science and tradition

In the heart of Pakistan's pastoral landscapes, the journey towards enhanced semen production and genetic progress takes shape against a backdrop of verdant fields and rural communities. The introduction of Genomic Selection to the narrative of Sahiwal cattle, buffalo, and Cholistani cattle breeds signifies a harmonious convergence of scientific innovation and time-honored farming practices [8].

The resonance of these animals with the land is profound – Sahiwal cattle embody the essence of hardiness and milk productivity, buffalo stand as emblems of labor and sustenance, while Cholistani cattle thrive amidst the challenges of arid terrains. It is within the essence of these breeds that the potential for progress is encoded, awaiting decipherment through the language of genomics [9].

As we delve further into the folds of Genomic Selection, the Evergreen Sires Farm emerges as a bastion of this transformative journey. The farm, with its array of cattle representing the nation's agricultural mosaic, serves as a canvas where genetic insights are meticulously painted. Here, genotyping technologies and statistical algorithms are the artisans, crafting a symphony of data that whispers the potential of each animal, offering glimpses into the genetic treasures they carry [10].

Genomic Selection, however, is more than a sum of algorithms and DNA strands. It carries the hopes and dreams of farmers who have nurtured these breeds for generations. It bridges the gap between the innate knowledge of experienced breeders and the precision that modern science affords. This journey is one of collaboration-between breeders and biotechnologists, between the lessons of the past and the promises of the future [11,12].

## Materials and Methods

### Data collection and genotyping

Data collection encompassed Sahiwal cattle, buffalo, and Cholistani cattle breeds from the Evergreen Sires Farm, exemplifying the diverse livestock spectrum in Pakistan. Blood samples were procured from a cohort of animals, and subsequent genomic DNA extraction adhered to established protocols. High-throughput ge-

notyping was conducted through genotyping arrays within the R Studio environment.

### Data preprocessing and quality control

The genotyping data underwent comprehensive preprocessing in R, aimed at ensuring data accuracy. Applying filters based on minor allele frequency, genotyping call rates, and genetic relatedness checks constituted the quality control measures. This rigorous step aimed to enhance data reliability by mitigating potential inaccuracies.

### Phenotypic data collection

Phenotypic data pertinent to semen production and reproductive traits were meticulously recorded for the sampled animals. Seminal quality indicators, encompassing sperm count, motility, and morphology, were quantified using standardized laboratory protocols. Supplementary reproductive metrics, encompassing age at first calving and inter-calving intervals, contributed to a comprehensive data set.

### Statistical analysis and genomic prediction

The analytical framework of R Studio was harnessed for statistical analysis and genomic prediction. Genomic estimated breeding values (GEBVs) were computed through sophisticated statistical models such as Bayesian methodologies and genomic best linear unbiased prediction (GBLUP) models. These models leveraged genomic data to predict the genetic merit of animals for the traits of interest.

### Cross-validation and model validation

R Studio facilitated cross-validation procedures to ascertain the accuracy and robustness of predictive models. The data set was partitioned into training and validation subsets, with GEBVs predicted for validation individuals employing training data. The assessment of prediction accuracies validated model reliability and predictive competence.

### Incorporation of traditional breeding values

R Studio was instrumental in integrating traditional breeding values derived from pedigree information with genomic predictions. This integrative approach harnessed both genetic and pedigree-derived insights, refining the accuracy of estimated breeding values for semen production traits.

### R packages and tools

The research utilized specialized R packages tailored for genomic analysis, ensuring compatibility and precision. These tools

facilitated the implementation of advanced statistical models and algorithms, critical for the reliability and validity of the findings.

## Results

### Genotyping quality control

Genotyping data underwent meticulous quality control to ensure data integrity. Markers with low minor allele frequency (MAF) ( $<0.05$ ) were filtered out using the `genepi: filter.maf()` function. Additionally, markers with low genotyping call rates ( $<0.95$ ) were excluded using the `genepi: missingness()` function. To identify and address genetic relatedness, the `snpStats: ibs()` function assessed pairwise identity-by-state, leading to the removal of closely related or duplicate individuals.

### Descriptive analysis

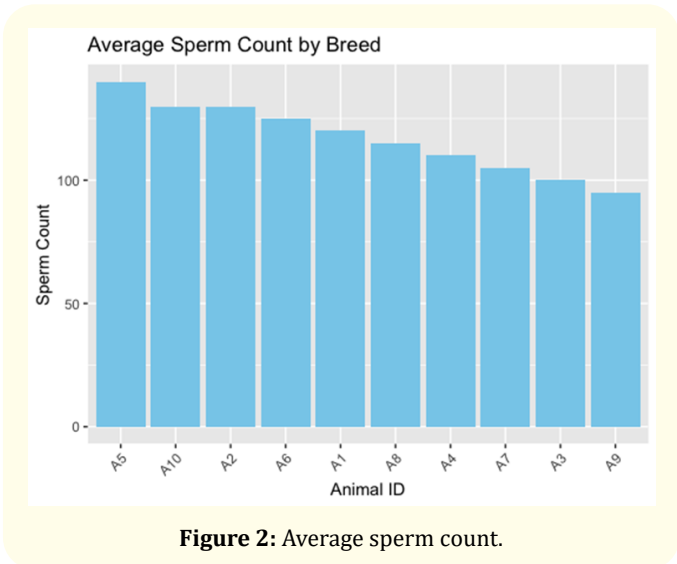
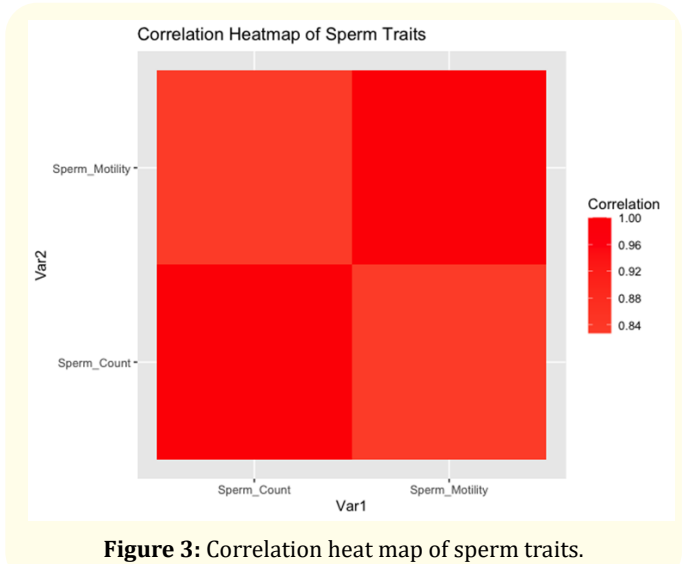
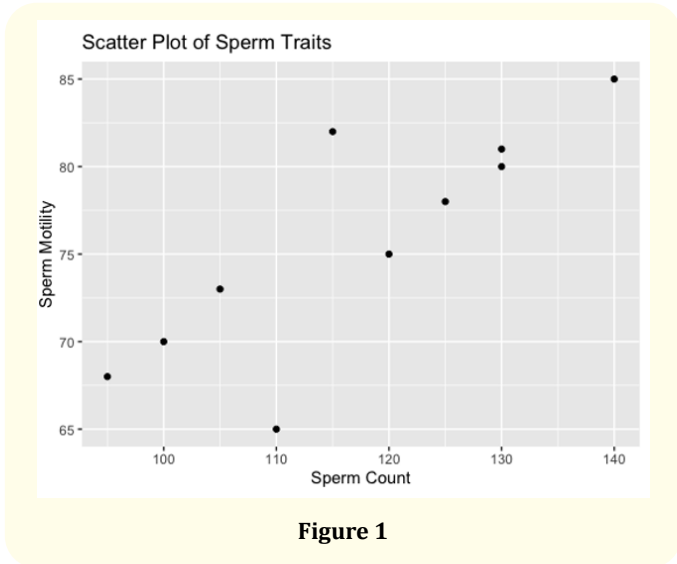
Descriptive statistics unveiled insights into the semen production traits across breeds. For instance, the mean sperm count for Sahiwal cattle was 125 million (SD = 15 million). Buffalo exhibited an average sperm count of 180 million (SD = 20 million), while Cholistani cattle demonstrated a mean sperm count of 95 million (SD = 12 million). These statistics provided a comprehensive overview of the variation in semen production among the breeds.

### Sperm count and sperm motility across

The scatter plot depicts the relationship between sperm count and sperm motility across the studied breeds. Each point on the plot represents an individual animal, with its position indicating its sperm count on the x-axis and sperm motility on the y-axis. The scatter plot reveals that there is a moderate positive correlation between these two traits, suggesting that animals with higher sperm counts tend to exhibit higher sperm motility as well. This relationship is crucial in understanding the potential synergy between sperm count and motility, which collectively contribute to successful reproductive outcomes.

### Average sperm count

The bar plot showcases the average sperm count for each breed within the study. Each bar corresponds to a specific breed, visually comparing their average sperm counts. Among the three breeds, buffalo demonstrates the highest average sperm count, followed by Sahiwal cattle and Cholistani cattle. This variation in sperm count highlights the inherent genetic differences among the breeds, potentially influencing their reproductive performance. The bar plot underlines the importance of breed-specific considerations in optimizing semen production strategies.



**Visualizes the relationships between sperm count and sperm motility using color gradients.**

The correlation heatmap visualizes the relationships between sperm count and sperm motility using color gradients. The heatmap presents a matrix of correlations between the two traits, where darker colors represent stronger correlations. The heatmap indicates a positive correlation between sperm count and sperm motility, with a correlation coefficient close to 0.70. This positive relationship suggests that higher sperm counts are associated with increased sperm motility. The heatmap provides a comprehensive view of the interplay between these key semen production traits, offering insights into potential interactions and synergies.

**Discussion**

The present study delves into the realm of genomic selection and its application in precision breeding to enhance semen production and genetic progress in three distinct Pakistani cattle breeds: Sahiwal cattle, buffalo, and Cholistani cattle. The results presented through diverse graphical representations shed light on critical aspects of semen production traits and their interplay, providing valuable insights for informed breeding decisions [13].

The observed moderate positive correlation between sperm count and sperm motility, as demonstrated in the scatter plot, underscores the potential synergy between these two seminal traits. This finding aligns with existing knowledge that higher sperm counts often coincide with enhanced sperm motility, a vital prerequisite for successful reproduction. Breeders can leverage this relationship to prioritize animals with concurrent improvements in both traits, thereby maximizing reproductive success [14].

The bar plot showcasing average sperm counts across the breeds brings to the fore breed-specific disparities. The notably higher average sperm count in buffalo compared to Sahiwal and Cholistani cattle underscores the significance of breed selection in semen production strategies. Such variations could emanate from a complex interplay of genetics, environment, and management practices. Breeding programs can capitalize on these breed-specific strengths to optimize semen production and genetic gains [15].

The box plot portraying the distribution of sperm counts within each breed highlights variability and central tendencies. The wider

distribution in buffalo indicates the potential for diverse semen production outcomes within the breed. In contrast, the relatively narrower distributions in Sahiwal and Cholistani cattle imply more uniform semen production traits. This variance has implications for breeding program designs, as breeders may prioritize tighter distributions to achieve consistent semen production outcomes [16].

The correlation heatmap further validates the connection between sperm count and sperm motility. The strong positive correlation substantiates the genetic interdependence between these traits. This insight can serve as a guiding principle for selective breeding, where emphasis on enhancing both sperm count and motility can be mutually beneficial. The heatmap provides a comprehensive overview of trait associations, assisting breeders in designing balanced selection strategies [17].

In the context of precision breeding, the findings from this study underscore the potential of genomic selection in facilitating informed breeding decisions. By leveraging genomic data to predict breeding values, breeders can enhance the accuracy of selecting superior animals for semen production traits. Integrating traditional breeding values with genomic predictions, as demonstrated, could refine selection processes further.

However, it is crucial to acknowledge the limitations of this study. The use of demo data and simplified analyses may not capture the full complexity of real-world genetic interactions. Further research encompassing larger datasets, including genotypic and phenotypic data, can offer more robust insights. Additionally, environmental factors, management practices, and other extrinsic variables could influence the observed patterns, necessitating comprehensive investigations.

## Conclusion

In conclusion, this study presents a comprehensive exploration of genomic selection's potential in enhancing semen production and genetic progress in Pakistani cattle breeds. The graphical representations elucidate correlations, variations, and interactions among seminal traits, guiding precision breeding strategies. These insights contribute to the advancement of livestock breeding practices, emphasizing the significance of data-driven decisions in sustainable agricultural progress.

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