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Heritability and Genetic Correlations of Semen Quality Traits in Indigenous Cattle Bulls of Rajasthan

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Abstract

The genetic evaluation of reproductive traits in indigenous cattle is essential for strengthening breeding programs in semi-arid regions. This study provides a detailed assessment of heritability and genetic correlations for semen quality traits: semen volume, sperm concentration, motility, total sperm count, and motile sperm count in four major indigenous breeds of Rajasthan (Gir, Rathi, Sahiwal, and Tharparkar). A large dataset comprising 40,539 ejaculations from 117 bulls was analysed using restricted maximum-likelihood (REML) procedures within a repeatability animal model, enabling the partitioning of phenotypic variance into genetic, permanent environmental, and residual components. Heritability estimates revealed moderate genetic control across most semen traits with motile sperm count and total sperm count showing the high estimates of heritability, underscoring their potential as reliable selection criteria. Genetic correlations among traits were consistently positive and significant, particularly between total sperm count and motile sperm count (0.84), suggesting that multi-trait selection can accelerate genetic gain. Breeding value estimation demonstrated substantial genetic variability within indigenous populations, with wide ranges observed for semen volume and other traits, indicating the presence of elite sires as well as individuals of lower genetic merit. Non-genetic influences such as age, season, and ejaculation order were also found to significantly affect semen quality, with peak performance observed in middle-aged bulls and during cooler months.

Major Findings: Moderate estimates of heritability were found for semen traits, supporting genetic selection. Significant genetic and phenotypic correlations among key semen traits were observed. Breeding values were estimated, revealing substantial variability among indigenous bulls.

Keywords: Artificial Insemination, Genetic Improvement, Heritability, Indigenous Cattle, Semen Traits

Abbreviations: BV: Breeding Value, FSB: Frozen Semen Bank, INAPH: Information Network for Animal Productivity & Health, REML: Restricted Maximum Likelihood, SSMS: Semen Station Management System

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1. Introduction

Genetic improvement of cattle populations remains a cornerstone of sustainable livestock production, particularly in regions where indigenous breeds are integral to rural economies and ecosystem services. Rajasthan, a semi-arid state in northwestern India, is home to diverse indigenous cattle breeds such as Gir, Rathi, Sahiwal, and Tharparkar, which have evolved under harsh climatic conditions. These breeds are valued for their heat tolerance, disease resistance, and adaptability to low-input systems, making them vital for dairy and draught power in resource-constrained environments. However, despite their resilience, indigenous breeds often lag behind exotic and crossbred populations in terms of reproductive efficiency and productivity, largely due to limited selection intensity and insufficient application of advanced breeding technologies.

Semen quality traits, including semen volume, sperm concentration, motility, total sperm count, and motile sperm count, are quantitative traits influenced by both genetic and environmental factors. These traits

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serve as proxies for male fertility and directly impact the success of Artificial Insemination (AI) programs, which are increasingly being adopted in India to accelerate genetic gain and conserve valuable germplasm. Recent studies have emphasised the importance of evaluating genetic parameters for semen traits in cattle and buffalo populations. For instance, research reported that both genetic and non-genetic factors significantly influence semen production traits in dairy bulls, highlighting the role of systematic data recording in improving the accuracy of genetic evaluations[1]. Similarly, research assessed seminal characteristics in indigenous and crossbred bulls, demonstrating breed-specific differences in semen quality that underscore the need for tailored breeding strategies[2]. Further, recent genetic evaluations using random regression models have shown that semen traits in indigenous bulls exhibit age-dependent variability, reinforcing the importance of longitudinal data for accurate parameter estimation[3].

Despite the recognised importance of indigenous cattle, there is a paucity of comprehensive studies assessing the genetic parameters of semen quality traits in these populations. Existing research has often focused on exotic and crossbred populations or has been constrained by limited sample sizes and methodological shortcomings[4,5]. The present study addresses this gap by providing a robust estimation of heritability and related genetic parameters for major semen traits in indigenous cattle bulls of Rajasthan, utilising large-scale, systematically collected data from a state-of-the-art frozen semen bank.

Semen quality traits in indigenous cattle bulls of Rajasthan exhibit moderate heritability and significant genetic correlations, thereby providing a strong basis for genetic improvement through systematic selection. This research utilises a large-scale dataset comprising over 40,000 ejaculations from indigenous bulls across multiple breeds, analysed using advanced Restricted Maximum Likelihood (REML) procedures within a repeatability animal model. By integrating genetic evaluation with the influence of non-genetic factors such as age, season, and collection protocols, this study provides the first robust, breed-specific estimates of heritability and genetic correlations for semen traits in Rajasthan's indigenous cattle. The findings not only fill a critical knowledge gap but also establish a framework for designing breeding programs that enhance reproductive efficiency, strengthen AI outcomes, and conserve native germplasm under semi-arid conditions.

2. Objective

Although semen quality traits have been widely studied in exotic and crossbred cattle populations, comprehensive genetic evaluations in indigenous breeds of Rajasthan remain limited. This has left a significant gap in understanding the heritability and genetic correlations of semen traits in native breeds that are uniquely adapted to semi-arid climates.

Therefore, the objective of this study is to estimate heritability, genetic correlations, and breeding values for key semen quality traits (semen volume, sperm concentration, motility, total sperm count, and motile sperm count) in indigenous cattle bulls of Rajasthan using large-scale, systematically recorded data and advanced REML models. By addressing this gap, the study aims to provide reliable genetic parameters that can guide sire selection, strengthen artificial insemination programs, and support the conservation and genetic improvement of indigenous cattle under challenging agro-climatic conditions.

3. Materials and Methods

3.1 General Appraisal of Data

The present investigation was conducted using records from breeding bulls maintained at the Frozen Semen Bank (FSB), Bassi, Jaipur, Rajasthan, India. The data were sourced from the Information Network for Animal Productivity and Health (INAPH), a digital platform supporting systematic data collection and management under the National Dairy Plan 1. The initial dataset comprised 60,347 records of ejaculations from 179 bulls sired by 68 sires, spanning six years (2017-2022). Bulls included in the analysis were those completing at least 18 months of age, reflecting the onset of reproductive maturity and relevance for semen evaluation. After data cleaning—removal of records lacking critical pedigree or phenotypic information, particularly missing birth dates (resulting in the exclusion of 13,832 ejaculations from 59 bulls)—the dataset was further refined to maintain consistency and minimise variability. Specifically, only bulls with complete records up to 81 months of age were included, yielding a final dataset of 40,539 ejaculations from 117 breeding bulls, representing 60 sires. This rigorous approach ensured the biological relevance and statistical robustness of the analysis.

3.2 Location of Experiment

The FSB Bassi is situated in a hot semi-arid subtropical region (26.80705°N, 76.12051°E), characterised by long, extremely hot summers (often exceeding 40°C), short mild winters (down to 5°C), and moderate monsoon rainfall (July-September), with the overall climate exerting significant influence on livestock management and reproductive performance. The facility employs controlled environments to mitigate the effects of ambient temperature and humidity on semen preservation and evaluation, a critical consideration in hot semi-arid regions where reproductive traits are particularly sensitive to environmental stressors.

3.3 Data Collection and Recording

Data collection was facilitated by the Semen Station Management System (SSMS), integrated with INAPH, enabling real-time recording of detailed phenotypic and pedigree information. Parameters recorded included:

Bull-specific data: Identification number, date of birth, dam and sire identification.

Collection-specific data: Date of ejaculation, ejaculation order, total volume (mL), sperm concentration (million/mL), sperm motility (%), number of sperm per ejaculation (million), and number of motile sperm count (million).

The data structure allowed for robust linkage between phenotypic records and genetic relationships, a prerequisite for accurate estimation of genetic parameters.

3.4 Semen Collection and Evaluation Protocols

Semen collection followed protocols defined by the Department of Animal Husbandry, Dairying, and Fisheries (DADF), emphasising individualised sexual preparation (including false mounts and restraint based on bull temperament), hygienic handling, and standardised intervals between collections (typically 30-60 min). Each collection session aimed for a minimum of two ejaculates per bull, with at least two sessions per week, targeting 90 collections and 180 ejaculates per bull annually. The actual number of collections per bull was adjusted based on individual capacity and health.

Semen volume was measured immediately after collection, and samples were processed under controlled temperature (34°C) using a laminar flow unit. Sperm concentration was determined using a Hamilton Microlab STAR automated liquid handling workstation and a Bovine Accucell digital photometer. Initial motility was assessed via phase-contrast microscopy equipped with digital imaging, and only samples exceeding 500 million/mL in sperm concentration were retained for further processing.

3.5 Classification of Data and Fixed Effects

The dataset was stratified according to several non-genetic factors to facilitate comprehensive statistical modelling:

Genetic group: Bulls were classified as indigenous (Gir, Rathi, Sahiwal, Tharparkar).

Season of ejaculation: Months were grouped into four seasons according to prevailing climatic conditions, with further division into bimestrial spans to capture intra-seasonal variability, reflecting the pronounced effects of seasonality in semi-arid climates[6].

Age of bull: Bulls up to 81 months were grouped into five age categories, with outliers outside the range of mean ± standard deviation (59.553 ± 22.159 months) excluded to maintain data consistency.

Period of ejaculation: Data from 2017 were excluded due to incomplete standardisation following the introduction of INAPH, resulting in the analysis of collections from 2018-2022.

Ejaculation order: Ejaculates were classified as first or second order, with the third and fourth orders consolidated due to small sample sizes.

3.6 Statistical Analysis

3.6.1 Estimation of Heritability and Breeding Values

Heritability (h^2) for semen traits (volume, sperm concentration, total sperm count, motile sperm count, motility) was estimated using a repeatability animal model, employing REML procedures as implemented in the WOMBAT software[7,8]. The statistical model included fixed effects (breed, season, period, parity) and random effects (sire), partitioning the observed phenotypic variance into additive genetic, permanent environmental, and residual components.

The general linear mixed model used for estimation was:

$$Y = Xb + Z_1u + Z_{2pe} + e$$

where:

Y = vector of phenotypic observations

X = design matrix for fixed effects

b = vector of fixed effects (season, period, parity)

Z_1 = design matrix for random genetic effects

u = vector of random genetic effects (individual bull)

Z_2 = design matrix for permanent environmental effects

pe = vector for permanent environmental effects

e = residual error vector

Breeding Values (BV) were estimated for each bull using BLUP (Best Linear Unbiased Prediction) derived from the fitted model, facilitating the ranking of bulls within genetic groups for each semen trait.

The general model used for breeding value estimation can be expressed as:

$$Y_{ij} - \mu + \sum \beta kXijk + Gi + PEi + eij$$

where,

Yij = observed semen trait for the j^{th} observation for the i^{th} individual

μ = intercept constant (baseline value of the trait) or standard notation for the overall population mean

βk = The coefficients associated with the predictor variables Xijk.

Xijk = k^{th} fixed effect of j^{th} observation of the i^{th} independent character or multiplier for the coefficient βk

Gi = Random genetic effect of the i^{th} individual.

PEi = Random Permanent Environmental effect of the i^{th} individual

eij = Residual error (unexplained variation).

3.6.2 Estimation of Genetic and Phenotypic Correlations

Genetic and phenotypic correlations among semen traits were estimated using multivariate REML procedures. Phenotypic correlations reflected the combined influence of genetic and environmental factors, while genetic correlations isolated the shared inheritance of traits, offering insights into the potential for indirect selection and correlated responses.

3.6.3 Data Analysis and Software

Data curation and initial analyses were conducted at the Rajasthan University of Veterinary and Animal Sciences (RAJUVAS), Bikaner, utilising SYSTAT 13 for descriptive statistics and data visualisation. Quantitative genetic analyses were performed using WOMBAT, which accommodates large datasets and complex pedigree structures.

4. Results

4.1 Descriptive Analysis and Data Structure

The refined dataset comprised 40,539 ejaculations from 117 indigenous cattle bulls, representing 60 sires. The bulls were distributed across the principal indigenous breeds of Rajasthan (Gir, Rathi, Sahiwal, Tharparkar), with each breed contributing a substantial number of records, ensuring breed-specific estimates possessed adequate statistical power.

The data displayed pronounced variation in semen traits across age groups, seasons, and ejaculation orders, underscoring the necessity of accounting for these effects in the genetic analysis. For instance, average semen volume and sperm concentration exhibited seasonal peaks corresponding to cooler months, aligning with previous findings on the influence of heat stress on reproductive performance in semi-arid climates[6].

4.2 Heritability Estimates

Heritability estimates for key semen traits are summarised in Table 1. These estimates indicate moderate heritability for all major semen traits, suggesting that a substantial proportion of the observed variation is attributable to additive genetic effects. Motile sperm count exhibited the highest heritability (0.626), followed closely by total sperm count (0.612). Motile sperm count showed high heritability, while sperm motility percentage exhibited low and uncertain heritability, consistent with literature emphasising the genetic control of sperm function and structure[4,5].

The partitioning of variance revealed that permanent environmental effects (*e.g.*, consistent management, housing, feeding) accounted for an additional significant portion of total variance, while residual variance captured unmeasured environmental effects and measurement error.

Table 1. Heritability estimates (h^2) for semen traits in indigenous cattle bulls of Rajasthan

Trait	h^2	SE(h^2)
Semen volume (mL)	0.129	0.046
Sperm concentration (million/mL)	0.104	0.002
Total sperm count (million)	0.612	0.297
Motile sperm count (million)	0.626	0.271
Sperm motility (%)	0.067	0.263

Table 2. Genetic (above diagonal) and phenotypic (below diagonal) correlations among semen traits

Trait	Volume	Concentration	Total Sperm	Motile Sperm	Motility
Volume	1	0.24 ± 0.12	0.82 ± 0.03***	0.52 ± 0.08***	-0.89 ± 0.30***
Concentration	0.14 ± 0.01***	1	0.57 ± 0.07***	0.79 ± 0.03***	-0.21 ± 0.19
Total Sperm	0.76 ± 0.00***	0.66 ± 0.00***	1	0.84 ± 0.02***	-0.82 ± 0.29***
Motile Sperm	0.13 ± 0.01***	0.95 ± 0.00***	0.63 ± 0.00***	1	-0.46 ± 0.23***
Motility	-0.64 ± 0.02***	0.09 ± 0.01***	-0.42 ± 0.02***	-0.01 ± 0.01	1

*p<0.10; **p<0.05; ***p<0.01

5. Genetic and Phenotypic Correlations

The correlation matrix presented in Table 2 illustrates both genetic (above diagonal) and phenotypic (below diagonal) relationships among key semen traits in Indigenous cattle. Genetically, semen volume shows a strong positive correlation with total sperm count (0.82 ± 0.03***) and motile sperm (0.52 ± 0.08***), while its association with sperm concentration is weaker (0.24 ± 0.12).

Notably, volume exhibits a strong negative genetic correlation with motility (-0.89 ± 0.30***), suggesting a potential trade-off between ejaculate volume and sperm movement efficiency. Phenotypically, volume is also positively correlated with total sperm (0.76 ± 0.00***) and motile sperm (0.13 ± 0.01***), but negatively with motility (-0.64 ± 0.02***), reinforcing this inverse relationship. Sperm concentration is positively correlated with motile sperm both genetically (0.79 ± 0.03***) and phenotypically (0.95 ± 0.00***), indicating that higher concentration tends to yield more motile sperm. However, its correlation with motility is inconsistent slightly negative genetically (-0.21 ± 0.19) and slightly positive phenotypically (0.09 ± 0.01***). Total sperm count shows strong positive genetic and phenotypic correlations with motile sperm (0.84 ± 0.02*** and 0.63 ± 0.00***, respectively), but a pronounced negative genetic correlation with motility (-0.82 ± 0.29***), suggesting that sperm output and motility may be governed by distinct physiological mechanisms. Motile sperm count is positively associated with other output traits but negatively correlated with motility both genetically (-0.46 ± 0.23***) and phenotypically (-0.01 ± 0.01), though the latter is negligible. Overall, sperm motility emerges as a trait largely independent of sperm quantity, with consistently negative or weak correlations, highlighting the need for balanced selection strategies that consider both sperm output and functional quality in breeding programs.

6. Breeding Value Estimation and Bull Ranking

Breeding Values (BV) for semen traits were estimated for all bulls and used to rank individuals within each genetic group. The range of standardised BV for semen volume in indigenous bulls was notably wide (-1.03 to 1.81 mL), reflecting considerable genetic diversity.

For example, the highest BV for semen volume was observed in bull GIR 0786 (1.81 mL), followed by SH 29 (0.79 mL). Conversely, the lowest BV was found in bull GIR 7176 (-1.03 mL) and SH 3565 (-0.79 mL). These results underscore the presence of superior and inferior genetic merit within the indigenous population, providing a basis for targeted selection and culling decisions[4].

Comparison with exotic and crossbred groups revealed narrower ranges of BV for semen volume (exotic: -0.13 to 0.09 mL; crossbred: -0.20 to 0.14 mL), consistent with more intensive selection and reduced genetic variability in these populations[9,10].

6.1 Influence of Non-Genetic Factors

Analysis of variance indicated significant effects of age, season, and period on semen traits. Semen quality parameters peaked in bulls aged 48-60 months and during the cooler months (October-February), reaffirming the need to control for these factors in genetic evaluations. The first ejaculation order generally yielded higher semen volume and motility, reflecting physiological recovery times.

7. Discussion

The present study demonstrates that semen quality traits in indigenous cattle bulls of Rajasthan are moderately

heritable, with motile sperm count and total sperm count showing the highest genetic control. These findings are consistent with earlier reports in buffalo and cattle populations, where reproductive traits were found to be influenced by additive genetic effects, thereby offering scope for genetic improvement through selection[4,5]. The moderate heritability estimates observed here indicate that while environmental factors play a role, genetic variance remains substantial enough to justify systematic sire selection programs.

The strong positive genetic correlations among semen output traits, particularly between total sperm count and motile sperm count, suggest that multi-trait selection can accelerate genetic gain. Similar correlations have been reported in Nellore cattle, where semen production traits were found to be genetically linked, reinforcing the feasibility of indirect selection strategies[11]. However, the negative correlations between semen motility and quantitative traits highlight a potential trade-off, indicating that selection focused solely on sperm output may compromise functional sperm quality. This antagonistic relationship has also been observed in studies on buffalo bulls, where higher sperm numbers did not always translate into improved motility or fertility outcomes[3].

Breeding value estimation revealed considerable genetic variability within indigenous populations, with wide ranges observed for semen volume and other traits. This variability underscores the presence of elite sires with superior reproductive potential, as well as individuals of lower merit, thereby providing a practical basis for targeted selection and culling decisions[4]. The broader genetic diversity observed in indigenous breeds compared to exotic populations aligns with findings from recent genomic studies, which emphasise the genetic diversity of native germplasm for reproductive improvement[12].

Non-genetic factors such as age, season, and ejaculation order were found to significantly influence semen traits, with peak performance observed in middle-aged bulls and during cooler months. These results corroborate earlier work showing that heat stress in semi-arid climates exerts deleterious effects on spermatogenesis and semen quality[6]. The importance of environmental management in conjunction with genetic evaluation is further supported by studies in Tamil Nadu, which demonstrated that semen production traits are strongly affected by both genetic and non-genetic influences[1]. Thus, while genetic selection can enhance reproductive efficiency, management interventions remain critical for optimising semen quality under challenging climatic conditions.

Taken together, the findings of this study establish that indigenous cattle of Rajasthan possess significant genetic potential for reproductive improvement. By integrating large-scale data recording systems, advanced statistical modelling, and controlled management practices, breeding programs can achieve meaningful genetic progress while conserving valuable native germplasm. This research fills a critical gap in the literature by providing robust, breed-specific estimates of heritability and genetic correlations for semen traits in indigenous cattle, which have been largely overlooked in previous studies. Future work incorporating genomic tools and evaluating gene-environment interactions will be essential to fully exploit this potential and ensure sustainable livestock productivity in semi-arid regions.

8. Conclusion

The present study clearly demonstrates that semen quality traits in indigenous cattle bulls of Rajasthan are moderately heritable, with motile sperm count and total sperm count showing the highest genetic control. These findings confirm that additive genetic effects play a significant role in determining reproductive performance, and that meaningful genetic progress can be achieved through systematic selection. The strong positive genetic correlations among semen output traits indicate that improvement in one trait, such as total sperm count, will yield favourable correlated responses in others, thereby simplifying multi-trait selection strategies.

Breeding value estimation revealed substantial genetic variability within indigenous populations, highlighting the presence of elite sires with superior reproductive potential as well as bulls of lower merit. This variability provides a practical basis for targeted sire selection, culling, and the design of structured breeding programs. At the same time, the influence of non-genetic factors such as age, season, and ejaculation order underscores the importance of integrating environmental management with genetic evaluation to optimise reproductive outcomes.

In conclusion, indigenous cattle of Rajasthan possess a robust genetic foundation for reproductive improvement. By leveraging advanced statistical models, robust data recording systems, and controlled management

practices, breeding programs can enhance semen quality traits, strengthen artificial insemination outcomes, and contribute to the long-term productivity and resilience of these native breeds in semi-arid environments.

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Author Contributions

R.T. and P.C. contributed equally to this work and R.T is corresponding author. M.G. conceptualised the study, led the data analysis, and coordinated manuscript preparation. R.T. and P.C. supervised the experimental design, managed project administration, and RT handled correspondence with the journal. M.G. performed the data conceptualisation and worked on data interpretation. All authors reviewed and approved the final manuscript.

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