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Genetic architecture of semen quality traits in breeding bulls

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Fertility is a key determinant of the economic sustainability and genetic progress of livestock production systems, particularly in breeding programs based on artificial insemination (AI). Among reproductive attributes, semen quality is one of the most critical factors influencing bull fertility and the overall success of AI programs. The use of high-quality semen from genetically superior bulls accelerates genetic improvement, enhances conception rates, and improves productivity across livestock populations. Semen quality traits, including ejaculate volume, sperm concentration, progressive motility, sperm viability, morphology, plasma membrane integrity, acrosome integrity and DNA integrity are complex quantitative traits controlled by multiple genes and substantially influenced by environmental and management factors such as age, nutrition, season, health status and housing conditions. Despite their economic importance, fertility and semen quality traits generally exhibit low to moderate heritability and are often expressed late in life, limiting the effectiveness of conventional phenotypic selection. Consequently, elucidating the genetic architecture of these traits is essential for the development of more efficient breeding strategies. Advances in genomic technologies have enabled the integration of dense genomic information into genetic evaluation, improving the accuracy of estimated breeding values, particularly for traits that are difficult, expensive, or sex-limited to measure. Genomic selection has therefore emerged as a powerful approach to accelerate annual genetic gain by reducing the generation interval and increasing selection accuracy.

Estimating genetic parameters, including additive genetic variance, heritability, and genetic correlations, provides fundamental insights into the inheritance and biological relationships among reproductive traits. Such information is indispensable for designing effective selection indices and optimizing breeding programs aimed at improving bull fertility and semen production. Furthermore, identifying the genetic factors governing semen quality traits will facilitate precision breeding and contribute to the sustainable enhancement of reproductive performance in livestock populations.

Genetic Components of fertility traits in bull

- **Polygenic inheritance:** Fertility traits are controlled by many genes, each contributing a small effect to the overall phenotype. These traits follow quantitative inheritance rather than simple Mendelian inheritance. The cumulative action of multiple loci determines overall semen quality.

- **Additive genetic effects:** A significant proportion of the genetic variation is additive, allowing improvement through selection across generations. Bulls with superior breeding values transmit favorable alleles to their offspring. Genomic estimated breeding values (GEBVs) improve selection accuracy.

- **Low to moderate heritability:** Most fertility traits have heritability ranging from **0.02 to 0.30**, indicating a strong influence of environmental factors.

- **Non-additive genetic effects:** Dominance and epistatic (gene–gene interaction) effects also contribute to reproductive performance but are generally less exploited in breeding programs.

- **Candidate genes:** Several genes involved in hormone synthesis, spermatogenesis, oogenesis, follicular development, embryonic development, and reproductive signaling influence fertility.

- **Quantitative Trait Loci (QTLs):** Numerous QTLs associated with semen quality, conception rate, age at puberty, and calving traits have been identified across the genome.

- **Sex-specific genetic expression:** Some fertility traits are expressed only in males (e.g., semen volume, sperm concentration, motility) or females (e.g., age at first calving, calving interval), making their genetic evaluation more challenging.

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- **Genotype × Environment (G×E) interaction:** The expression of genetic potential for fertility depends on environmental conditions such as nutrition, climate, disease status, and management.
- **Genetic correlations:** Fertility traits often exhibit favourable or unfavourable genetic correlations with production traits, requiring balanced selection to avoid deterioration in reproductive performance.
- **Functional genomic pathways:** Genes regulating the hypothalamic–pituitary–gonadal axis, steroid hormone biosynthesis, gametogenesis, fertilization, and early embryonic development play critical roles in fertility.
- **Epigenetic regulation:** DNA methylation, histone modifications, and non-coding RNAs influence gene expression and can affect sperm quality, embryo development, and fertility.
- **Genomic selection:** The use of genome-wide SNP markers improves the accuracy of breeding value estimation, especially for low-heritability and late-expressed fertility traits.
- **Whole-genome association studies (GWAS):** GWAS helps identify genomic regions and candidate genes associated with reproductive performance and semen quality traits.
- **Marker-assisted and precision breeding:** Molecular markers linked to favorable fertility alleles can be incorporated into breeding programs to accelerate genetic improvement.
- **Genetic diversity:** Maintaining adequate genetic variation is essential to sustain long-term improvement in fertility while minimizing the risks of inbreeding depression and reduced reproductive performance.

Importance of Evaluating Genetic Parameters of Bulls

The evaluation of genetic parameters in breeding bulls is fundamental to animal breeding programs because it helps quantify the genetic contribution to economically important traits, particularly fertility and semen quality. Accurate estimation of these parameters enables breeders to identify genetically superior bulls, improve selection efficiency, and accelerate genetic progress.

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Estimation of Heritability: Determines the proportion of phenotypic variation attributable to genetic factors. Identifies traits that can be effectively improved through selection.

Prediction of Genetic Gain: Facilitates estimation of the expected response to selection. Supports the design of breeding strategies for sustained genetic improvement.

Selection of Superior Breeding Bulls: Enables identification of bulls with high breeding values for fertility and semen quality traits. Improves the accuracy of sire selection for artificial insemination (AI) programs.

Understanding Genetic Correlations: Reveals relationships among semen quality, fertility, production, and health traits. Helps avoid unfavourable correlated responses during selection. **Development of Genomic Selection Programs**: Provides baseline parameters required for genomic prediction models. Enhances the accuracy of genomic estimated breeding values (GEBVs).

Optimization of Breeding Programs: Assists in developing balanced breeding objectives that include fertility alongside production traits. Improves long-term genetic improvement while maintaining genetic diversity.

Early Identification of Elite Bulls: Genomic information allows prediction of genetic merit before bulls reach reproductive maturity. Reduces the generation interval and increases annual genetic gain.

Improvement of Semen Quality: Identifies bulls genetically predisposed to superior semen volume, sperm concentration, motility, morphology, viability and freezability.

Improvement of Reproductive Efficiency: Selection based on favourable genetic parameters improves conception rates, pregnancy rates, and overall herd fertility. Reduces reproductive failures and economic losses.

Assessment of Environmental Influence: Separates genetic effects from environmental effects such as nutrition, season, age, heat stress, and management. Enables more accurate estimation of true genetic merit.

Conservation of Genetic Resources: Supports the maintenance of genetic diversity while selecting for desirable traits. Helps minimize inbreeding and preserve valuable germplasm.

Economic Benefits: Increases the efficiency of AI programs by producing semen from genetically superior bulls. Improves productivity, reproductive performance, and profitability of dairy and beef enterprises.

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