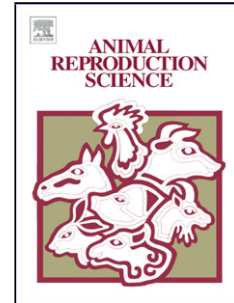


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Identification of Genomic Variants Causing Sperm Abnormalities and Reduced Male Fertility

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Highlights

Over 3,000 cattle have now been whole genome sequenced
More than 120 million bovine variants have been discovered
Variants with gene regulation or expression functions are almost completely unknown
Sequencing males divergent for fertility identifies candidate male fertility variants

ABSTRACT

Whole genome sequencing has identified millions of bovine genetic variants; however, there is currently little understanding about which variants affect male fertility. It is imperative that we begin to link detrimental genetic variants to sperm phenotypes via the analysis of semen samples and measurement of fertility for bulls with alternate genotypes. Artificial insemination (AI) bulls provide a useful model system because of extensive fertility records, measured as sire conception rates (SCR). Genetic variants with moderate to large effects on fertility can be identified by sequencing the genomes of fertile and subfertile or infertile sires identified with high or low SCR

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