Influence of microRNAs from Semen on Bovine Fertility

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Objective
The objective of this study was to compare the miRNAs within sperm cells of bulls considered to have high and low fertility.

Study Description
Bulls were selected and assigned to low and high fertility groups (n = 11 and n = 12, respectively) based on being a minimum of 6.5 sire conception rate units apart (average of 13,443 inseminations per sire). Straws of semen that had been collected on two different dates (mean of 5 months apart) were obtained from Select Sires. An equal number of straws from each collection date were pooled, and RNA was extracted separately for each bull. MicroRNAs were extracted and libraries were prepared using the Illumina TruSeq Small RNA preparation kit and sequenced on an Illumina MiSeq. Paired-end reads were merged with PEAR and adaptors were trimmed using Trimmomatic. Resulting reads were then mapped to the bovine genome and quantified using miRDeep2. Differential expression analysis was conducted using the DESeq2 package in R.

Take home points
MicroRNAs (miRNAs) are a family of small RNAs that play a key role in regulating gene expression by binding to complementary mRNA and altering translation. It has been reported that this alteration of specific RNAs plays a role in male fertility. Of the 516 miRNAs identified, 10 miRNAs were differentially expressed between bulls of high and low fertility ($P < 0.05$). These were bta-miR-9-5p, bta-miR-98, bta-miR-329a, bta-miR-142-5p, bta-miR-449a, bta-miR-126-5p, bta-miR-182, bta-miR-2284y, bta-miR-1839, and bta-miR-296-3p. PCR was performed to validate sequencing results on 3 miRNAs: miR-9-5p ($P = 0.76$), miR-2284 ($P = 0.05$), and miR-296-3p ($P = 0.01$). Micro-RNA-296-3p is regulated by neurofibromatosis 2, while miR-2284 and miR-9-5p have been identified in cells associated with immune response. These results support the idea that a small proportion of miRNAs may have a direct impact on fertility, possibly through early embryo development.

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