

## Discovery of a major gene for bovine ovulation rate

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Objectives of this research were to test the hypothesis of segregation of a major gene for bovine ovulation rate in a cattle family and to map the gene's location. Paternal half-sib females (n=88) were produced from a triplet-born bull, the son of a cow who had produced three sets of triplets over her lifetime. Daughters were born in 2008 (n=33) and 2009 (n=55) at University of Wisconsin farms. Females were evaluated for ovulation rate, genotyped and the resulting data used in a within-family linkage analysis. Heifers were evaluated for ovulation rate over an average of 4.1 estrous cycles between 12 and 17 months of age. Evaluation was performed by transrectal ultrasonography. The sire and all daughters were genotyped using a 3k BeadChip yielding genotypes for 2900 SNPs. Inheritance of alternative paternal haplotypes was deduced and used in linkage analysis. Average corpora lutea count per cycle was  $1.63 \pm 0.64$  with a range from 1.0 to 3.5. Evidence for a major gene was observed on bovine chromosome 10 ( $+1.02 \pm 0.083$  corpora lutea per cycle for carriers vs. non-carriers of the high ovulation rate allele,  $p < 1.1 \times 10^{-20}$ ). Major gene effect and chromosomal assignment were subsequently confirmed using 28 daughters born in 2010 ( $p < 5 \times 10^{-7}$ ). Medium density, 50k genotyping of the sire and daughters recombinant within the most significant region narrowed the location of the gene to a 2 megabase window. The region identified does not correspond to the location of any major genes for high ovulation rate previously identified in sheep.