

Applications of haplotypes in dairy farm management

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Haplotypes are now available for almost 100,000 dairy cows and heifers in the US. Genomic EBV values are accelerating the rate of genetic improvement in dairy cattle, but genomic information also is useful for making improved decisions on the farm. Mate selection strategies have usually been based on maximization of genetic progress subject to restrictions on inbreeding, and assuming the transmission of average rather than actual chromosomes, limiting selection gains. Genetic progress can be improved by simulating matings of all cows to a portfolio of potential mates and those which provide the desired outcomes selected. In the case of commercial cows, matings which minimize the variance of outcomes while conditioned on some average desired EBV should be selected. In the case of germplasm producers, the skewness parameter of distributions can be compared to identify matings with the greatest likelihood of producing offspring with superior EBV. This will increase the rate of genetic progress and reduce the number of animals culled for poor performance resulting from inferior genetics. Low-density SNP tests on dairy calves can be used to increase profitability by increasing the genetic value of the calves raised and used as replacements in the herd, increasing gains through the dams-of-cows pathway. Genotyping calves also can result in increased lifetime profitability. In a simulation study in which the top 90% of calves were retained based on parent average selected calves had EBV \$110 greater compared to all calves. When a low-density genomic test was used, \$14 per kept calf was gained, but the value of testing decreases as the proportion of calves kept increases. Haplotypes also have been used to identify novel recessives in the Brown Swiss, Holstein, and Jersey breeds, as well as to successfully fine-map the Weaver locus. Future uses of haplotypes include identification of animals resistant to common diseases and identifying those most likely to respond to nutritional and reproductive technologies.

Session 25**Poster 7****Candidate genes affecting twinning rate in Maremmana cattle**

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Twinning in cattle is a complex trait with multiple environmental and genetic influences. Ovulation rate has been worldwide recognized as the trait with the highest genetic correlation with twinning in mammals, and the genes controlling the ovulation rate have been the object of a number of studies. The transforming growth factor signaling pathway within the ovary is critical for the regulation of ovarian function, ovulation rate and fertility. In different species (sheep, human and mouse) mutation in three genes GDF9 (Growth Differentiation Factor 9), BMP15 (Bone Morphogenetic Protein 15), and BMPRI1B (Bone Morphogenetic Protein Receptor-1B), involved in this pathway, have been associated with either poly-ovulation or infertility. In a herd of 92 Maremmana cows, owned by the experimental farm of CRA-PCM, and deriving from a nucleus of 60 cows and 3 bulls, originally established in 1923, high frequency of twinning was registered along the years; the availability of calving records and genealogy registrations from 1923 allowed the reconstruction of the families where the twinning was more frequent. In a previous study Marchitelli *et al.* identified nine SNP in the GDF9, BMP15 and BMPRI1B genes. In the present study, all the cows of the experimental farm were genotyped at the detected SNP; allele and genotype frequencies, Hardy-Weinberg equilibrium were calculated, and haplotypes were inferred. We found that the cows with twin calvings had a different allele frequency, at the non-synonymous mutation (rs110553528) of the GDF9, than the cows with no twins. This missense mutation is located in the GDF9 pro-region, therefore it could affect the structure and the function of the GDF9 protein, that is implicated in a correct folliculogenesis. The allele differences in the cows of this trial allow to consider the rs110553528 mutation as a potential indicator of the ovulation rate.