

ABSTRACT #41

MATING PROGRAMS INCLUDING GENOMIC RELATIONSHIPS AND DOMINANCE EFFECTS

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Computer mating programs have helped breeders minimize pedigree inbreeding and avoid recessive defects by mating animals with parents that have fewer common ancestors. With genomic selection, breed associations, AI organizations, and on-farm software providers could use new programs to minimize genomic inbreeding by comparing genotypes of potential mates. A first task is to efficiently provide elements of the genomic relationship matrix from the central database to customers, such as by computing relationships between 1) only requested males and females via a web query, or 2) all genotyped females with only the marketed males (e.g., >160,000 females and >1,500 bulls for Holstein), because 3) relationships between all >230,000 genotyped animals for Holstein are difficult to store and transfer. Selection and mating programs were then tested in which 50 marketed bulls in each of breed (Jersey and Holstein) were selected for top genomic Lifetime Net Merit, top traditional Lifetime Net Merit, or randomly selected. The 500 youngest genotyped females in the largest herd were assigned mates of the same breed with limits of 10 females per bull and 1 bull per cow (for Brown Swiss, only 79 females and 8 bulls were included). Linear programming to maximize progeny values, a simple method based on sequential selection of least-related mates, and random mating were compared using either a genomic relationship matrix or pedigree relationship matrix as mates' inbreeding source and using additive effect only or additive plus dominance effect as mates' genetic value. Dominance effects for 45,187 markers and dominance variance were estimated and examined only for management group deviation of milk instead of lifetime net merit. Genomic relationships improved calf values and decreased calf inbreeding compared to pedigree relationships. Dominance variance was 3.7% and 4.1% of phenotypic variance for Jersey and Holstein breeds, respectively. Including dominance in a mating program increased the calf's predicted merit for milk by 52kg and 86kg for Jersey and Holstein when using the linear program, genomic relationships, and the top 50 bulls. Linear programming was always better than simple method and much better than random mating for all of the three breeds. Based on lifetime net merit, the best combination was selection on genomic breeding values and mate assignment by genomic relationships. The economic value of using genomic instead of using pedigree relationships is already >\$2 million per year for Holsteins when applied to all of the genotyped females, assuming that each provided 1 replacement every 2.5 yr, and will grow as more females are genotyped.