

Genomic Tools to Improve Progress and Preserve Variation for Future Generations

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Abstract

Use of genomic tools has greatly decreased generation intervals and increased genetic progress in dairy cattle, but faster selection cycles can also increase rates of inbreeding per unit of time. Average pedigree inbreeding of Holstein cows increased from 4.6% in 2000 to 5.6% in 2009 to 6.6% in 2015. The 0.17% per year recent rate of inbreeding is larger than in the previous decade but similar to the rate of 0.16% from 1985 to 2000. Recent rates from 2009 to 2015 were only 0.09% per year for Jersey and 0.13% for Brown Swiss cows. Breeders have reduced the effects of inbreeding depression in the short term by focusing on genomic rather than pedigree inbreeding in mating programs, avoiding carrier matings, selecting against lethal defects, or crossbreeding. Genomic relationships of > 1 million genotyped females with > 5,000 marketed males have been used in industry mating programs since 2014 and are updated monthly for new females. Haplotype or laboratory genotype tests for 22 recessive defects, red, and polled are provided for all genotyped animals. Pedigree breed composition has been provided since 2007 and genomic breed base representation since 2016, allowing breeders to examine ancestry of each animal even if pedigrees are incomplete or missing. Genomic evaluations on all-breed scale were computed but not released yet for 25 traits of 44,023 crossbreds including 20,367 with no official evaluation because of breed check edits. The new evaluations were for 1,822 Jersey x Holstein crossbreds with >40% of both breeds (F1 crosses), 7,237 Holstein backcrosses with >67% and <94% Holstein, 7,820 Jersey backcrosses, 388 Brown Swiss crosses, plus other mixtures. In the long term, selecting for rare favorable alleles within the same breed, introgressing new alleles from another breed, and gene editing or transgenic tools could help maintain or increase genetic variation. Many genomic tools are available to help breeders make progress and manage diversity in the current generation while preserving variation for future selection.

Keywords: inbreeding, crossbreeding, mating programs