

Using 90,113 Single Nucleotide Polymorphisms in Genomic Evaluation of Dairy Cattle

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Accuracy of genomic evaluation is expected to increase when more markers are used because of better tracking of causative genetic variants. However, Illumina BovineHD genotypes based on 777,962 single nucleotide polymorphisms (SNP) have not been used for US genomic evaluation because the small reliability gain achieved did not justify the genotyping cost. In December 2012, the GeneSeek Genomic Profiler HD (GHD) BeadChip was released with 76,867 unique nuclear SNP and 13 mitochondrial SNP. It included 28,376 (63%) of usable SNP from the Illumina BovineSNP50 v2 BeadChip as well as 48,491 BovineHD SNP selected because they had the greatest effects for Holstein net merit. Based on analysis of 1,730 animals with GHD genotypes, 3,153 SNP were not used for genomic evaluation because they were on the Y chromosome or had a low call rate, excess parent-progeny conflicts, or a minor allele frequency of <1% for Holsteins, Jerseys, and Brown Swiss; 73,714 GHD SNP were usable for genomic evaluation, which added 44,925 to the 45,188 currently used (total of 90,113 SNP). Genotypes for those SNP and August 2009 traditional genetic evaluations for 26,200 Holstein bulls and cows were used to predict December 2012 daughter performance of 29 economically important traits for 4,024 bulls with a traditional evaluation since August 2009. Reliability gains from 90,113 SNP were greater than from 45,188 SNP by 2.2 percentage points for yield traits and 0.9 percentage points for calving traits but less by 0.8 percentage points for fitness traits and 0.5 percentage points for conformation traits. Lower gains may result from imputation errors, which will decline as more animals have GHD genotypes. Imputation from lower density chips to 90,113 SNP was about 0.5% less accurate than to 45,188 SNP. More GHD genotypes are needed to achieve adequate imputation accuracy for Brown Swiss and Jerseys, which have few high-density genotypes. The GHD chip allows additional SNP to be included in genomic evaluation without increasing genotyping cost, but higher imputation accuracy is needed before evaluation accuracy can improve for all breeds and traits.

Keywords: Genomic Evaluation, Reliability, Single Nucleotide Polymorphism

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