

Changes in genetic diversity over time in the Dutch Holstein Friesian genome

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The objective of this study was to obtain estimates of changes in genome-wide and region-specific genetic diversity in the Dutch Holstein Friesian (DHF) population over time. Traditionally, genetic diversity has been quantified and managed with genealogical coefficients of inbreeding (F_{PED}) and kinship (f_{PED}). A drawback of this approach is that F_{PED} and f_{PED} only provide genome-wide expectations based on neutral and selection-free loci. In practice, only few (or even no) neutral unlinked loci exist and it is anticipated that there are substantial differences in diversity across the genome due to selection, drift and variation in recombination rate. With the increasing availability of SNP-data, it is possible to quantify these differences. Approximately 5,400 DHF bulls, born between 1996 and 2014 and included in the Dutch gene bank, were genotyped with the Illumina BovineSNP50 BeadChip and imputed to 76 k. Genome-wide levels and rates of F_{PED} and f_{PED} , marker-by-marker homozygosity (H) and similarity (S) and segment-based genomic inbreeding (F_{ROH}) and kinship (f_{SEG}) were estimated and compared. Region-specific levels and rates of H , S , F_{ROH} and f_{SEG} were also mapped across the genome. As expected, substantial differences were observed in (changes in) diversity across the genome. Combined with the increasing knowledge on functional significance of genomic regions, the insight in region-specific diversity will allow for a better and more customised control of genetic diversity in breeding and conservation programmes.

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