

Runs of homozygosity and genomic inbreeding in the German riding horse population

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In Germany, most of the studbooks for riding horses have introduced routine genome-wide SNP genotyping of all registered foals. Together with respective SNP genotype data generated in the context of projects on implementing genomic evaluations and breeders' support through analyses of genetic characteristics, genomic information on over 68,000 German Warmblood horses is stored in the central equine SNP database. Because genetic diversity is an important topic not only for native breeds and small populations, but also for the European Warmblood riding horse with its international and mostly liberal breeding policies, the aim of this study was to determine key parameters needed for assessing genomic inbreeding and development of genetic diversity. 70K+ SNP genotypes of 64,318 German Warmblood horses were used to determine runs of homozygosity (ROH) using PLINK software with its function '--homozyg' (Purcell et al. 2007). Information on 57,286 quality-controlled SNPs entered the analyses performed with a range of lengths of DNA stretches considered as ROH: 0.5 Mb, 1 Mb, 1.5 Mb, 2 Mb, 3 Mb, 4 Mb, 5 Mb, 6 Mb and 10 Mb. The minimum number of SNPs within one ROH was set to 25; no heterozygotes were allowed. For each individual and each scenario, genomic inbreeding based on ROH was calculated according to McQuillan et al. (2008): $F_{ROH} = \text{total length of all ROH} / \text{autosomal genome length covered by SNPs}$. Mean F_{ROH} ranged between 0.9 and 7.9%, with higher values for the scenarios with shorter ROH lengths (highest with 0.5Mb). Considering SNP density across autosomes, results obtained with 2 Mb, indicating a mean F_{ROH} of 6.9%, should best reflect the genomic inbreeding in the German Warmblood population. Low frequency of long ROH of 10 Mb in the population, with only 69.4% of the horses (N = 44,640) having at least one of them (mean $F_{ROH} = 0.9\%$), imply smaller role of recent than more historical inbreeding. Further analyses on the genomic population structure, also separated by breed, and on possible signatures of selection based on ROH are planned. Results are supposed to serve as basis of new tools for support of mating planning and improved breed management, increasing visibility of the benefits of large-scale availability of equine genomic data.

Purcell et al. 2007. PMID: PMC1950838

McQuillan et al. 2008. PMID: PMC2556426