

**Genomic inbreeding based on runs of homozygosity  
in the regional German horse breed Schleswig coldblood**

*M. Wobbe<sup>1,2</sup>, H. Alkhoder<sup>1</sup>, C. Schmidtman<sup>1</sup>, K. F. Stock<sup>1,2</sup>, H. H. Swalve<sup>3</sup>*

*<sup>1</sup> IT Solutions for Animal Production (vit), Heinrich-Schroeder-Weg 1, 27283 Verden (Aller), Germany, <sup>2</sup>University of Veterinary Medicine Hannover (Foundation), Institute of Animal Genomics, Buenteweg 17p, 30559 Hanover, Germany, <sup>3</sup>Martin-Luther-University Halle-Wittenberg, Theodor-Lieser-Str. 11, 06120 Halle (Saale), Germany*

The Schleswig coldblood horse originating from Northern Germany / Southern Denmark was formerly used in agriculture and forestry. With mechanization of these sectors, the number of horses decreased substantially, and the breed was threatened with extinction in the mid-1970s. With around 180 breeding animals, the Schleswig coldblood is today listed as endangered livestock breed (category phenotypic conservation population) by the German Federal Office for Food and Agriculture. The breed has a closed studbook and allows only three other coldblood breeds to maintain genetic diversity: Jutlander, Boulonnais and Southern German coldblood. The aim of this study was to characterize population structure of the Schleswig coldblood in Germany using genome-wide marker data of a large sample from all living horses. Genotypes of 201 horses with 85,401 SNPs were available and used to identify runs of homozygosity (ROH) with PLINK software and its function `-homozyg`. After quality control 57,286 SNPs were retained for analyses with length of DNA stretches considered as ROH set to 2Mb, minimum number of SNPs within one ROH set to 25 and allowing no heterozygotes. For each horse, genomic inbreeding based on ROH was calculated as:  $FROH = \text{total length of all ROH} / \text{autosomal genome length covered by SNPs}$ . Mean FROH was 10.3% (range 0.1-19.9%) in all horses, with no clear trend in inbreeding development over subsequent birth cohorts. However, almost all horses (N=189; 94%) had at least one very long ROH (10Mb), and mean FROH based on this ROH-length was 3.0%, indicating relevance of recent inbreeding. Systematic use of genomic data for genetic diversity monitoring in the Schleswig coldblood and considering of genomic inbreeding in planning of matings can improve management and support preservation of this breed.