Single-step genomic evaluation in German riding horses

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German horse breeding associations started in 2017 under the umbrella of the International Association of Future Horse Breeding (IAFH) a collaboration project with partners from science and practice to advance genomic applications in sport horse breeding. The joint genomic reference population of 5,000 horses, completed at the end of 2020, will now form the basis for implementing a system for estimating genomic breeding values (GEBVs) for a wide range of traits. Harmonization of the routinely used linear recording scheme among the participating associations has ensured that standardized phenotypes are available for all horses in the reference population, including conformation and performance (gaits, jumping) traits. In order to most comprehensively exploit all relevant information, a single step genomic BLUP model (ssGBLUP) was applied using all available phenotype, genotype and pedigree data. The same fixed effects were used as for conventional breeding value estimation for linear conformation and performance traits. First analyses referred to the horses with phenotypic data and the 1,034 stallions with progeny in the reference population. Comparison of phenotypic data between the top and bottom 10% of horses based on their GEBVs revealed promising results for both conformation (e.g. stance of forelimb pastern) and performance (e.g. mechanics of front limbs in trot). Since the reference population was built across breeding associations with varying numbers of pedigree links among each other, ongoing work on validation and optimization must particularly focus on reliability of GEBVs for all breeds.