

Collaboration of studbooks advancing development of genomic selection for sport horses

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High-quality phenotypes and a strong reference population (gRP) are crucial for exploiting the potential of genomic selection. In 2017, horse breeding associations and experienced research partners have joined forces and started an initiative for promoting equine genomic R&D in Germany. Harmonized linear profiling with a comprehensive scheme is delivering the phenotypic data basis. Candidates for gRP have so far been recruited from DNA sampled mares of five studbooks and were required to have linear profiles including performance in gaits, preferably also in jumping. Phenotypes were qualitatively ranked according to proximity to the breeding goal (highest value of assessments under rider). To further optimize gRP composition, pedigree relationships among the horses was considered for selecting horses for SNP genotyping with moderate density (70k+). From the first genotyping cohort, 755 horses and 55,170 SNPs remained after quality testing and were used for preliminary genomic analyses with PLINK software. Discipline and breeding policy related stratification patterns were confirmed, underlining the importance of careful interpretation of first results of association analyses. These revealed significances for several traits including specific aspects of trot and canter like front limb mechanics and stride length. Increase of sample size and the target of 5,000 horses in the gRP will allow refined analyses with the aim of reliable genomic predictions for important traits in sport horses.