WBFSH Standing Committee for
Collaborative Implementation of Genomic Applications
in Sport Horse Breeding (WBFSH-SC CIGA):
Factsheet on parentage testing in the horse

Background

The genetic code of an individual horse is the unique combination of genetic information from the dam and the sire. Certain parts of the equine genome are highly variable and therefore may be used as genetic markers: The pattern of how a number of genetic markers looks is characteristic for the individual horse. This is often referred to as DNA fingerprinting.

For the purpose of parentage testing, information on a relatively low number of genetic markers is enough to either confirm or reject a supposed dam and sire for a given horse. The more variation a single genetic marker is showing (the more possible appearances, so-called alleles, it has), the lower is the overall number of markers which is needed for reliable parentage testing. Microsatellite markers, also often referred to as STRs (short tandem repeats), are a specific type of larger genetic marker which is currently used for routine parentage testing in the horse. Because of high variation (many possible appearances or different alleles) and accordingly high information content of each single marker, approximately twenty STRs or even less are usually enough to check whether or not an indicated parentage of an individual can be confirmed. STR allele data can only be used for parentage testing.

Single nucleotide polymorphisms (SNPs) are the smallest possible type of genetic markers, because it is single positions in the genome that are looked at. Accordingly, the information content per SNP marker is low (usually only two possible appearances or alleles), but the ease of testing in the laboratory makes it straightforward to compensate for this through increasing the number of SNPs considered for parentage control. In a given population of horses, the number of SNPs needed for reliable testing of individuals against supposed parents is in the order of hundreds. SNP allele data can in principle be used for multiple purposes, with the usability being a function of the total number and the distribution of SNPs analyzed. For advanced applications like genomic selection, information on large numbers of SNPs – in the order of thousands to ten-thousands – is needed. Low and further decreasing costs for SNP analyses (SNP genotyping) are stimulating the development of strategies to integrate SNP-based routines which optimize and balance input, i. e. costs for SNP genotyping, and output, i. e. gain in information.

Recommendations

- Be prepared for additional efforts to make the transition from microsatellite-based parentage testing to using SNP data. There are technical and logistical challenges to be met in order to avoid large-scale re-testing of horses.
- Keep in mind the potential of using SNP data for breeding applications. Avoid investments in single-purpose testing systems which include very low numbers of SNPs or other genetic markers. For the same or only slightly higher price, you may get more information out of a differently designed SNP panel.
- Be aware of reasonable opportunities to save time and money by coordinated activities of the studbooks in the transition phase of parentage testing as well as in the development of routine genomic applications for sport horse breeding.