Importance of strong data base systems in the study of genetic characteristics in horses

M. Wobbe[1,], K.F. Stock[1,2], F. Reinhardt[1], R. Reents[1]*

[1]*IT Solutions for Animal Production (vit), Heinrich-Schroeder-Weg 1, 27283 Verden (Aller), Germany;* [2]*University of Veterinary Medicine Hanover (Foundation), ABG, Buenteweg 17p, 30559 Hanover, Germany*

The monitoring of genetic defects plays an important role in many different animal species. It is the responsibility of breeding organizations to consider defects and other genetic characteristics in their breeding programs. In horse breeding some hereditary defects are also known and routinely screened, but not systematically yet in Warmblood breeds. After a case of Warmblood Fragile Foal Syndrome (WFFS) occurred in the USA and was widely discussed in 2018, awareness of breeders increased. The autosomal recessively inherited connective tissue disorder was first described by a US research group in 2012. Since 2013, a commercial genetic test for the point mutation in the PLOD1 gene is available. Homozygous foals are not viable, but little is known about frequencies of WFFS related losses and their timing during foal development. WFFS was therefore chosen to demonstrate how comprehensive data base systems can help elucidating genetic characteristics in horses. Covering data of the last 10 years were provided by 10 German studbooks, so more than 420,000 coverings could be used for analyses of variance using procedures GLM and MIXED of SAS software (version 9.2). The dependent variable reflected the risk of no living foal: It was coded 0 if the foal was born and 1 if it was not born or died within the first two days. In the model, we included WFFS status (carrier or free), individual sire considering his WFFS status, breeding station as fixed effects and a random residual. Assuming a carrier frequency of around 10% in Warmblood horse populations, as previously reported, one would (following Hardy-Weinberg) expect a difference of about 2.8% in the foaling rates of carriers and free sires. Depending on the model and data restrictions (e.g. minimum of 5 potential foals per sire) we found differences of 2.7-3.0% in the foaling rates. These figures fit to the expectations rather well. However, data completeness and recording quality have major impact on the power of statistical analyses, implying the need of strong data base systems especially for more complex genetic characteristics.