Abstracts – Session 2 – Functional Anatomy

Differences in gait quality parameters between Franches-Montagnes and Swiss Warmblood horses

A.I. Gmel^{1,2}, E.H. Haraldsdóttir², M. Neuditschko¹ and M.A. Weishaupt²

¹Agroscope, Route de la Tioleyre 4, 1725, Switzerland, ²Vetsuisse Faculty University of Zurich, Winterthurerstrasse 260, 8057 Zurich, Switzerland; annik.gmel@agroscope.admin.ch

Gait quality is an important selection criterion in many European horse breeds, but is usually evaluated subjectively. The aim was to compare the objective gait quality parameters speed, stride length, maximal protraction (A_{prot}) and retraction (A_{ret}) angles of the fore and hind limbs and suspension duration (SpD) of two Swiss horse breeds. We measured 157 Franches-Montagnes (FM) and 40 Warmblood (WB) horses at three years old with the EquiMoves® system at walk and trot. Speed was recorded with Freelap®. Differences due to breed, sex and breed × sex interactions were analysed using a linear model approach. WB walked faster (1.73±0.07 vs 1.66±0.11 m/s; P<0.0001), with longer strides (1.99±0.11 vs 1.77±0.12 m; P<0.0001) as they were taller (1.65±0.05 vs 1.56±0.03 m). WB had larger A_{prot} of the fore- (34.51±1.52 vs 32.42±2.38; P<0.0001) and hindlimbs (28.51±1.82 vs 27.60±2.11; P<0.05), FM had greater forelimb A_{ret} (41.68±3.02 vs 38.65±3.00; P<0.0001) at walk. At trot, WB had the longer strides (3.27±0.34 vs 2.96±0.29; P<0.0001). FM had greater forelimb A_{prot} (27.59±3.21 vs 24.86±3.34; P<0.01) and hindlimb A_{ret} (24.88±3.13 vs 23.62±3.84; P<0.01). SpD for FM was longer compared to WB (0.039±0.026 vs 0.006±0.030 s; P<0.0001) which was surprising as WB horses are considered the better sport horses. WB showed more limb movement and longer strides at walk, FM had shorter strides but showed more limb movement at trot. Correcting for size and speed should improve our understanding of breed-specific differences.

Differences in joint angles from photographs between six European breeds – preliminary results

A.I. Gmel^{1,2}, M. Stefaniuk-Szmukier³, W. Klecel⁴, T. Martin-Gimenez⁵, A. Cruz⁶ and M.A. Weishaupt²

¹Agroscope, Route de la Tioleyre 4, 1725, Switzerland, ²University of Zurich, Winterthurerstrasse 260, 8057, Switzerland, ³University of Agriculture in Krakow, Al. Mickiewicza 21, 31-120 Krakow, Poland, ⁴Warsaw University of Life Sciences, Nowoursynowska 166, 02-787 Warszawa, Poland, ⁵Universidad de Zaragoza, Miguel Servet 177, Zaragoza 50013, Spain, ⁶Justus-Liebig Universität Giessen, Ludwigstraße 23, 35390 Gießen, Germany; annik.gmel@agroscope.admin.ch

Horse breeds are expected to show differences in their conformation traits due to selection for specific uses and aesthetics. However, these differences have seldom been compared objectively, as each breed is evaluated subjectively by their own judges. Therefore, joint angles were extracted from standardised photographs from the side at stance of 888 horses of six different breeds: 529 Franches-Montagnes (FM), 73 Warmblood (WB), 28 Purebred Arabians (AR), 32 Shagya Arabians (SHA), 228 Lipizzaner (LIP) and 19 Pura Raza Español (PRE) horses. Landmark placement was based on the horse shape space model consisting of 246 2D landmarks. The angles were compared between breeds using ANOVA and Tukey Honest Difference tests (P<0.05). The poll angle was larger (more open throat) in lighter horses (AR=106.30±5.51, SHA=104.76±4.14, WB=106.93±6.55) than in FM=103.25±5.24, LIP=103.12±4.94 and PRE=102.62±5.59. FM and AR were rather buck-kneed (larger carpus angle, >179°), while LIP and PRE were more calf-kneed (<179°). The FM also had straighter hind fetlock angles (>154°) than the other breeds. As expected, AR and SHA had a larger hip angle (more horizontal croup, >80°). The hock angle did not differ between breeds. This dataset is a promising first step to evaluate breed-specific differences in conformation using a consistent method, but more data is needed in breeds with lower sample size. This data should be compared to dynamic conformational data and finally to movement patterns, to understand its functional significance, as well as to genomic data in genetic studies.