

Genetic parameters of functional longevity using a multivariate approach in Austrian FleckviehC. Pfeiffer¹, B. Fuerst-Waltl¹, V. Ducrocq² and C. Fuerst³¹University of Natural Resources and Life Sciences, Vienna, Sustainable Agricultural Systems; Division of Livestock Sciences, Gregor-Mendel Strasse 33, 1180 Vienna, Austria, ²INRA, Bovine Genetics and Genomics, UMR 1313, 78352 Jouy-en-Josas, France, ³ZuchtData EDV-Dienstleistungen GmbH, Dresdner Strasse 89/19, 1220 Vienna, Austria; birgit.fuerst-waltl@boku.ac.at

A longevity subindex is included in the official Austrian total merit index. It is a combination of functional longevity and five auxiliary traits (hip width, body depth, muscularity, feet and legs, udder). Variance components and EBVs for all these traits are estimated univariately. Genetic correlations between longevity and type traits are computed using the approximate method of Calo *et al.* Through the application of this method residual correlations are neglected. This might cause biased EBVs and reliabilities. To solve this problem an alternative method using a multivariate animal model based on yield deviations (YD) was tested. In total, 74,292 YDs of Austrian Fleckvieh cattle (dual purpose Simmental) of five Austrian regions born between 2002 and 2011 were used. The pedigree included 240,268 animals. Variance components were estimated based on an animal model using ASReml 3.0. The log-likelihood converged well. Heritabilities for longevity (0.08 ± 0.006), muscularity (0.36 ± 0.012) and udder (0.30 ± 0.011) differed from the routinely published values 0.12, 0.28 and 0.24, respectively. Genetic correlations between longevity and hip width (-0.08 ± 0.05), body depth (-0.14 ± 0.05) and muscularity (-0.08 ± 0.04) were lower than the ones used in routine evaluation. Genetic correlations between longevity and feet and legs (0.39 ± 0.05) and udder (0.40 ± 0.04) were slightly higher. Genetic correlations within type traits range from -0.27 (muscularity/udder) to 0.64 (hip width/body depth). Results suggest that the approximate multivariate approach based on YDs is feasible and could be introduced in the routine genetic evaluation.

A new mtDNA haplotype of European brown hares (*Lepus europaeus* Pall.) in southwestern SlovakiaL. Ondruska, V. Parkanyi, D. Vasicek, J. Slamecka, M. Bauer, R. Jurcik, K. Vasickova and D. Mertin
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The genetic alterations in mitochondria are common mtDNA, haplotypes that are maternally inherited. Mitochondrial protein coding genes of comprise important components of the oxidative phosphorylation pathway (OXPHOS) and every change in amino acid composition can affect the efficiency of the oxidative phosphorylation. For the analysis of mtDNA we used the samples of liver from 82 adult (male and female) European brown hares of wild population pertain to 10 hunting grounds in the region of south-western Slovakia. The samples were collected from brown hares hunted during winter seasons of 2009-2011. Tissues were stored frozen at -20 °C until DNA extraction. Total genomic DNA was purified by automat Maxwell[®] 16 Tissue DNA Purification kit AS1030 (Promega). The PCR conditions (PTC-200 DNA Engine Cycler; Bio Rad) consist of initial denaturation at 95 °C for 2 min, and 35 cycles of denaturation at 94 °C for 30 s, annealing at 60 °C for 30 s, primer extension at 72 °C for 30 s, with last extension at 72 °C for 10 min. The amplified segments from each sample were subsequently screened for polymorphism in selected regions of two protein coding genes that have been implicated in changes of germinal, generative and somatic cells through ATPase subunit 6 from and a segment of the mitochondrial NADH dehydrogenase subunit 2. For detection of polymorphism we used 2 restriction endonucleases: NlaIII and Sau96I (8 hrs at 37 °C). We detected in ATP6 82 A/D haplotypes and in NADH2 gene were identified 78 A/C/E haplotypes. Moreover we found a new haplotype in NADH2 in 4 samples in two hunting grounds. This new haplotype was discovered for the first time in the hare population in Slovakia.