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P3096 First insight into genetic variation of fatty acids content in flesh of common carp, *Cyprinus carpio* L

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Essential fatty acids (FAs) in food have a positive effect on human health. Hence, high attention has been devoted to improvement of FA content in flesh of farmed animals through nutrition. Information about genetic variation and improvement of FA content is rather scarce. During an experimental breeding program in common carp conducted under semi-intensive pond management, a genetic variation of FA content in fillet of market size fish (1.4 kg) was investigated. For this purpose, 158 individuals from a full factorial mating of 7 females and 36 males were selected. Content of FAs was analysed by gas-liquid chromatography. Multi-trait animal model calculation verified moderate heritability for growth (0.57 ± 0.12). Heritability of selected FAs ranged from 0.0 to 0.34, but the values were not significantly different from zero in most cases. Heritability for monounsaturated FAs (MUFA) was 0.14, and was 0.11 for polyunsaturated FAs (PUFA). Low heritability was observed also in omega-3 and omega-6 FAs (0.09 and 0.08, respectively), and for omega-6/omega-3 FAs ratio (0.12). However, significant heritability (0.34 ± 0.13) was observed for eicosapentaenoic acid (EPA), a highly health-valued PUFA. High and positive genetic correlation ($r=0.74$) was observed between EPA and docosahexaenoic acid (DHA) content, although heritability of DHA content was insignificant (0.05 ± 0.06). Results show that there might be possibility for genetic improvement of some FA content in flesh of common carp, but a better understanding of the bases of individual variation in FA content is needed. A cost-benefit analysis will have to be conducted as well.

P3097 Assessment of genetic diversity and admixture in pony breeds

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Within the context of conservation of Canadian equine genetic resources, we investigated genetic diversity and admixture in the Newfoundland Pony, the Lac LaCroix Indian Pony, and the Canadian Horse. We also included the feral Sable Island horse population, a population from the St-Pierre et Miquelon archipelago, and 11 other pony breeds (Caspian, Connemara, Dale, Dartmoor, Fell, Fjord, Halfinger, Highland, Icelandic, Kerry Bog, and Welsh) several of which are on conservation priority lists. We genotyped 606 individuals at 22 microsatellite markers and 157 alleles were detected. The average number of effective alleles and the average allelic richness were lowest in the Lac LaCroix (2.9 and 4.2) and highest in the Newfoundland (5.0 and 6.3). Unbiased expected heterozygosities were relatively high and ranged from 0.63 in the Lac LaCroix to 0.77 in the Newfoundland and Welsh pony. As expected, 83% of the molecular variance came from within individuals, 5% among individuals and 12% among populations. Phylogenetic reconstructions based on standard genetic distances gave similar topologies supporting a close relationship between the Newfoundland pony, the St-Pierre et Miquelon horse, the Sable Island horse and the Welsh pony. Although 95% of the individuals could be assigned to their own population, 82.5% for the Newfoundland pony, the admixture analysis revealed the presence of 13 clusters as opposed to 16 recognized populations. This study further warrants the close monitoring of the Lac LaCroix, the St-Pierre et Miquelon and the Sable Island populations. The analysis of maternal lineages based on mtDNA sequence data is underway.

P3098 Estimation of genetic parameters of semen quality-related traits in Beijing-You chicken

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This study was conducted to estimate the genetic parameters of semen quality-related traits, using a MTFREML procedure, in 516 purebred Beijing-You (BJY) full-sib male chickens derived from the same hatching, and subsequently to assess the feasibility of genetic selection to improve the semen quality of BGY chickens. Genetic parameters were estimated using an animal model which was considered the result of non-genetic factor analysis. The heritabilities and correlations among semen volume after ejaculation (VOL), semen pH (pH), semen color score (COL), the percentage of live sperm (LP), sperm motility score (MOT), the percentage of abnormal spermatozoa (ABN), and semen concentration (CON) were estimated. The results show that the estimated heritabilities of LP, MOT, and ABN were high (ranging from 0.52 to 0.85), whereas the heritabilities of VOL, COL, and CON were moderate (0.28, 0.19, and 0.12, respectively). In contrast, pH was shown to be a low heritability trait ($h^2 = 0.03$). Genetic correlations between ABN and LP and MOT were both negative (-0.37 and -0.27 , respectively), whereas a high positive genetic correlation was found between LP and MOT (0.88). This indicates that selection for reduced ABN could produce improvements in LP and MOT. Moreover, given the significantly negative genetic correlations between pH and VOL, COL, LP, MOT, ABN, and CON (ranging from -0.36 to -0.66), semen quality could be directly improved by regulating the semen pH.