structure was completed using primer-walking approach applied on a porcine genomic BAC clone isolated with the *ACTC1* primers. The gene is approx. 8 kb long and consists of 7 exons spanning 4163 bp, 1134 bp of which is the coding sequence. A G>A substitution was identified in intron 1. The gene was mapped using radiation hybrid panel (IMpRH) on chromosome 1 with *SW65* as closest marker (41 cR; LOD = 7.73). By real-time RT-PCR, the gene was proven to be significantly overexpressed in porcine foetal skeletal muscles compared to adult ones. The *ACTC1* gene is expected to be involved in muscle development and growth in pigs. (Supported by the Czech Science Foundation 523/06/1302)

Poster 2204

Title: Determination of *IFNG*, *IL2*, *IL4*, and *GATA3* single nucleotide polymorphisms in New Hampshire and White Leghorn chicken and analysis of association with worm burden after artificial infection with *Heterakis gallinarum*

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Abstract:

There is much evidence in chicken, similarly to mammalian species, that antihelmintic worm reactions are driven by an increase of type 2 cytokines and a decline of type 1 cytokines.
The 5'-flanking region of the type 1 cytokine genes *IFNG* and *IL2*, the type 2 cytokine gene *IL4* and the type 2 immune response directing transcription factor gene *GATA3* were analysed for the occurrence of polymorphisms in the two layer lines New Hampshire and White Leghorn. Novel single nucleotide polymorphisms (SNPs) were identified in *IL4* and *GATA3*. For each of the four genes, a SNP was genotyped by PCR-RFLP analysis in samples of New Hampshire (n = 146) and White Leghorn (n = 263) chicken where the worm burden had been determined eight weeks after artificial infection with 100 embryonated *Heterakis gallinarum* eggs. White Leghorn showed a significantly higher number of worms when compared with New Hampshire. Genotyping results of *IFNG* and *GATA3* in New Hampshire were not used for statistical analysis because the two SNPs were nearly monomorphic in this line. Restricted maximum likelihood analysis with fixed effects of line, sex and genotype revealed no association of any of the tested SNP with the worm burden.

Poster 2205

Title: Genetic characterization of the Bracco Italiano (Italian Hound) breed: first results on 22 STRs from the ISAG Canine Comparison Test

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Abstract:

The Società Amatori Bracco Italiano is financing a project aimed at investigating the demographic, genetic and genealogical structure of this old breed. We show an assessment of the genetic variability for 22 STRs typed in a sample of 33 unrelated Italian hounds ("Bracchi") and a sample of 43 dogs from other breeds ("Other dogs"). Individual codes of all subjects were traced in the breed database (20,499 animals), so that the coefficient of relationship was < 0.2 with any other animal.
Three multiplexes were worked out, which allowed analyzing 22 STR markers from the panels recommended for the 2006 and 2008 ISAG canine comparison test. Allele size in bp was determined using the comparison-test reference samples as anchor values. Data were analyzed using ARLEQUIN 3.11. The number of different alleles ranged 3 to 8 (mean 5.2) in the "Bracchi", compared with 6-13 (mean 9.5) in the "Other dogs", whereas the expected heterozygosity ranged 0.41-0.81 (mean 0.65) compared with 0.67-0.89 (mean 0.82). Interestingly, the difference between the observed and expected heterozygosities was lower in the "Bracchi" than in the "Other dogs" (0.65 - 0.58 = 0.07 vs. 0.82 - 0.62 = 0.20), despite the absolute values were lower in the "Bracchi".

Poster 2206

Title: MicroRNA profiles of the fetal pig during skeletal muscle development

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