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Content

Genetic variability of Shagya – Arabian horse derived from pedigree information

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The aim of the paper was to analyze genetic diversity of Shagya - Arabian horse population based on description of probability of identity by gene descent and origin. Reference population created 107 living Shagya-Arabian horses (15 stallions, 92 mares) registered in Shagya-Arabian studbook Slovakia from 2002 to 2007, exploited in provincial breeding. The pedigree data contained information of 1952 animals. The pedigree completeness of reference population was evaluated for each animal by the number of fully traced generations (5.59), maximum number of generations traced (34.18) and equivalent complete generations 9.54. The effective number of founders was 167 and the effective number of ancestors 21. Only 8 ancestors were necessary to explain 50 % of total genetic variability. The average values of inbreeding as well as relatedness in reference population were 4.08 %, respectively 3.03 % and the average increase of individual inbreeding intensity was 0.47 %.

Detection of *Salmonella* spp., *Salmonella enterica* ser. *typhimurium* and *enteritidis* by step one real time PCR in ready-to-eat food

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The aim of this study was follow the contamination of live chickens with *Salmonella* spp. by using the Step One real-time PCR. Detection of food-borne pathogens using conventional culture techniques takes up to 5 days to get a result. This includes primary and secondary enrichment and serological confirmation of colonies grown on agar plates. We used the PrepSEQ Rapid Spin Sample Preparation Kit for isolation of DNA and MicroSEQ® *Salmonella* spp. Detection Kit for pursuance with the real time PCR (Applied Biosystems). The samples were obtained by taking swabs from body of live chickens. In the investigated samples before incubation we could detect strain of *Salmonella* spp. in six out of eight samples, as well as internal positive control (IPC), which was positive in all samples. In the samples after 16 hours incubation we could detect strain of Salmonella spp. in samples, as well as internal positive control (IPC), which was positive in all samples. This Step One real-time PCR assay is extremely useful for any laboratory in possession of a real time PCR. It is a fast, reproducible, simple, specific and sensitive way to detect nucleic acids, which could be used in clinical diagnostic tests in the future.

Procedures of evaluation of genomic breeding value

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The evaluation of an animal is based on highly reliable production records. It is usually in two steps. In the first step the BLUP procedures are used for adjustment of non-genetic systematic effects. In the second step the pseudo-data, like daughter-yield-deviations are used as inputs. Evaluation is by BLUP-AM with random effects of remaining polygenes, with relationship matrix between animals (A), and effects of particular markers. Genomic breeding value (GEBV) is then selection index with combination of polygenic and marker's parts. Including large number of SNP markers (50K) increase the reliability of evaluation of young animals of dairy cattle from 0.30 if only the pedigree value is used to 0.60 when the genomic breeding value is applied. Information about genetic markers can be gathered in realised genomic relationship matrix (G). Similar result of GEBV is then achieved by using in second step only effect of animal, without genetic markers, and substituting G for A. In real population has two step procedure disadvantages, because it is difficult compare genotyped and ungenotyped animals, and second step needs input parameters known without error. Therefore one-step procedure is used, which evaluates both genotyped and ungenotyped animals at the same run, and produces one common ranking of all animals in a whole population. Principal part of one-step procedure is augmented pedigree-genomic relationship matrix. This procedure allows working with usually used models of animal evaluation on national scale.

SSCP detection of rabbit candidate gene

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The aim of this work was to optimise SSCP method to analyse polymorphism in rabbit *MSTN* gene, which is candidate gene responsible for double muscling of different animals (cattle, sheep, poultry). In 2008 was sequenced rabbit *MSTN* gene and there was find one SNP, which seems to be regulation factor of rabbit muscle growth (intron 2, possition 34, C→T). For genotypization was used PCR–RFLP. We optimised silver – stained SSCP method for mutation identification, which is cheaper in a compared to PCR-RFLP.

For optimization was used 12%, 14%, and 16% nondenaturing polyacrylamide gel and running time 5, 7, 9 hours. Because target sequence of *MSTN* gene was only 80bp long, the best concentration of the gel was 14%, running time was 7 hours at 20ºC temperature. It was necessary to use also 5% glycerol to adjust pH. With this method we detected all of three genotypes (*CC*, *CT* and *TT*). Gel was stained with silver and there was needed to change time of staining and fixing solution treatment from 3 minutes as is ussual for this method, to only a few seconds (less than 45 seconds). Results of this detection were verified with PCR – RFLP analyse.

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