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ISBN 978-80-213-2950-8

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Plenary section

AmtDB: database of ancient mitochondrial DNA

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Abstract

In recent years number and quality of ancient DNA samples have been constantly rising. Thanks to advances in ancient DNA isolation and sequencing techniques we are able to access variability of many ancient populations. Today autosomal SNPs and uniparental markers in Y chromosome or mitochondrial DNA provide valuable insight into ancient population genetics. So far genotypes of few thousands of prehistoric samples have been published. The results are spread across many publications in different formats. We have created a hand-curated database of ancient human mitochondrial genomes where the mtDNA sequences and associated sample descriptors can be found at https://amtdb.org.

Recent Advances in Genetic Evaluation of Italian Holstein: Results from Latteco Project

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The evolution of breeding objectives is crucial to reflect future market demands and law requirements, but also to meet farmers' requests operating in different scenarios. Latteco is an ongoing project financed by the Italian Minister of Agriculture, Food, Forestry, and Tourism aiming at maintaining genetic diversity, improving animal welfare, and reducing environmental impact of dairy cattle through animal breeding. The first output of the present project was the development of the udder health selection index, whose aim is to reduce incidence of clinical mastitis by exploiting different patterns of somatic cell score throughout lactation. In this selection index, four different traits, defined from somatic cell score variation, are combined together with different emphasis depending on the genetic covariances existing among traits and between each trait and clinical mastitis. Another output from the project was the revision of the aggregate female fertility selection index by exploiting data from pregnancy scanning, and by including information on body condition score measured on cows as well as heifer fertility. The new aggregate fertility index is a combination of eight traits which are genetically correlated to conception rate at first insemination, which represents the breeding goal of the index. With the official release of December 2018, it was published the third National breeding objective called "Cheesemaking and Sustainability Index – Parmigiano Reggiano" (ICS-PR). This breeding objective is intended for maximizing profit of farmers operating in a market situation in which milk is processed into long-ripened cheeses. The economic values of the traits contributing to the index where estimated based on field data in order to properly quantify the relative emphasis to be placed at each production, fertility, calving ease, longevity, udder health, and type traits. Finally, other relevant parts of the project such as resistance to subclinical ketosis, and feed efficiency, as well as the revision of Production, Type, and Functionality (PFT) breeding objective, are in progress and are expected to be distributed to dairy farmers during 2020.

Keywords: dairy genetics; udder health; bovine fertility; sustainability; breeding objectives

Acknowledgements

Funding from Latteco Project, sottomisura 10.2 of the PSRN-Biodiversity 2014-2020 are gratefully acknowledged.

Sections

STUDY OF COWS' BEHAVIOUR AND WELFARE ON DAIRY FARMS IN SERBIA

Dušica Ostojić Andrić[1], Slavča Hristov[2], Vesna Krnjaja[1], Dragan Nikšić[1], Aleksandar Stanojković[1], Miloš Marinković[1], Nikola Molerović[1]

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Abstract

Modern methods for assessing the welfare of dairy cows are, among other things, often based on the evaluation of animal behaviour. In this regard, behaviour is classified as the most reliable, so-called animal-based indicator as its expression comes from the animal itself and indicates a measure in which it has adapted to the environment. Starting from the need to explore the state of welfare and the ability to demonstrate adequate behaviour in dairy farms in Serbia, the Welfare Quality® Assessment Protocol for Cattle (2009) was used in this study. The overall assessment of behaviour was carried out by analysing four main criteria: social, other forms of behaviour, human-animal relationship and emotional state. The results of the study conducted on a total of 16 dairy farms (N=4,833 cows) show that the conditions for ensuring appropriate behaviour meet only minimum standards and that the greatest welfare risks arise from the impossibility of expressing natural behaviour, such as exploratory behaviour. The most pronounced negative tendencies within the assessment of the emotional status were those expressed to distress, frustration and boredom. Although the estimated general condition does not differ substantially from the same on EU farms, the need for its improvement is imposed first of all in terms of ensuring greater freedom of movement and more stimulating environment in cattle rearing.

Keywords: dairy cows, assessment, welfare, social behaviour, human-animal relationship, emotional state

Acknowledgement

This research was funded by the Ministry of Education, Science and Technological Development, Republic of Serbia within project TR-31053.

PIG BREEDING PRACTICES OF SMALLHOLDER FARMERS IN UGANDA

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ABSTRACT

A household level survey of 199 households conducted between July and August 2018 in Kamuli and Hoima districts of Uganda evaluated the smallholder pig breeding practices. Differences between districts were assessed with a chi-squared test. Farmers mainly relied on animals born on farm, from mating of a sow with and on-farm boar as well as boar service, and animals bought in for use as breeding animals. They were knowledgeable of off-farm sources for fattening and breeding animals. Local and crossbreds of local with 'exotic' types like Large White, Landrace and Camborough pigs were the predominant types of animals accessed by the farmers. The farmers seemed conversant with heat detection methods in the breeding sow. Sow reproductive problems reported by somewhat less than 40% of the farmers were small litter size and few litters farrowed over the sow's lifetime. While important for farm management and breeding purposes, animal identification and record keeping were generally lacking. Main marketing pathways were sales to traders at farm gate. Farmers would benefit from participatory breeding strategies that enhance access to quality genetic material. The local pig is an important resource of the smallholder pig herd and additional studies on important traits (heat tolerance, disease resistance and feed utilization) would add valuable information.

Keywords*:* Smallholder, breeding practices, pig, Uganda

ACKNOWLEDGEMENT

This study was supported by grant funding from the Austrian Development Agency (ADA), and the CGIAR Research Program on Livestock. The authors are grateful to the smallholder women and men pig farmers and officers of the local district administration who participated in the study.

Inferring causal relationships among milk protein fractions in dairy cattle

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Abstract

The quantities and proportion of milk protein fractions have a fundamental role in its nutritional and technological properties. A deeper knowledge of the possible casual relationships among these traits would be useful not only to improve the understanding of their biology but also for setting up management and selection strategies. Aims of this study were: i) to estimate genomic relationships among protein fractions and ii) to infer a Bayesian network structure among them. To achieve these aims, we first fitted a Bayesian multi-trait genomic best linear unbiased prediction (GBLUP) model to infer the genomic and residual correlations among six milk nitrogen fractions (four caseins, namely k-, β-, αs1- and αs2-casein (CN), and two whey proteins, namely β-lactoglobulin and α-lactalbumin), in a population of 1,011 Italian Brown Swiss cows. Animals were genotyped with the Illumina BovineSNP50 Bead Chip v.2. The posterior means of breeding values were used as input to infer putative casual structures among traits by using the Bayesian Max-Min Hill-Climbing (MMHC) algorithm. Strong genomic correlations were found between β-CN and αs1-CN and, between κ-CN and β-CN. The application of the MMHC algorithm pointed out that κ-CN seemed to directly or indirectly influence all the other milk protein fractions (with the exception of β-lactoglobulin), suggesting its possible role of leading trait in the control of milk protein composition. Further and thorough studies are however needed for the validation of the putative causal links among milk protein fractions identified in this study.

Keywords: milk protein composition, genomic correlation, structural equation models

Acknowledgement

The research was funded by Trento Province (Italy), the Italian Brown Swiss Cattle Breeders Association (ANARB, Verona, Italy), and the Superbrown Consortium of Bolzano and Trento.

Genomic differentiation between Simmental and Holstein cattle populations from Croatia

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Abstract

The main goal of this study was to identify the most differentiated genome regions (SNPs), those with largest F_{ST} values, between Croatian Simmental and Holstein cattle populations. Our analyses were based on the high-throughput genomic information (Illumina BovineSNP50 BeadChip) obtained from the individuals sampled in Croatian Holstein (72) and Croation Simmental (229) populations. The most differentiated SNPs were identified on the chromosome 2 (ARS-BFGL-NGS-5831), 3 (Hapmap48051-BTA-69046, BTA-67896-no-rs), 4 (ARS-BFGL-NGS-116590, Hapmap53144-ss46525999, Hapmap51289-BTA-70566), 5 (ARS-BFGL-NGS-39379), 6 (Hapmap60182-rs29025531, Hapmap49292-BTA-75698, ARS-BFGL-NGS-109884), 7 (ARS-BFGL-NGS-11872), 10 (ARS-BFGL-BAC-12251), 11 (ARS-BFGL-NGS-83288, ARS-BFGL-NGS-100141, ARS-BFGL-NGS-89583), 16 (ARS-BFGL-NGS-101656, ARS-BFGL-NGS-106233, BTB-01570194, ARS-BFGL-NGS-22021, ARS-BFGL-NGS-30784,ARS-BFGL-NGS-18487, Hapmap60338-ss46526653, ARS-BFGL-NGS-99802), 20 (Hapmap48214-BTA-121272), 23 (Hapmap54795-rs29014478), 26 (ARS-BFGL-NGS-11271, ARS-BFGL-NGS-101647) and 29 (ARS-BFGL-NGS-115406, Hapmap58266-rs29018037, ARS-BFGL-NGS-29788). In addition, we have identified names and functions of those genes that are in the vicinity of the identified SNPs with extreme F_{ST} values. Our analysis will be extended to the population structure analyses with other worldwide Holstein and Simmental populations and the identification of genome regions that are specific for Croatian populations.

Keywords: cattle, genomics, adaptation, selection

THE ANALYSIS OF REPRODUCTIVE TRAITS IN POPULATION OF THE SLOVAK SPOTTED DAIRY COWS

Jozef BUJKO[1]*, Juraj CANDRÁK[1], Peter STRAPÁK[2], Július ŽITNÝ[1], Cyril HRNČÁR[3] and Anton KOVÁČIK[4]

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Abstract
The aim of study was to analyse the reproductive traits in population of Slovak Spotted cattle from 2007 to 2016 the results for 37,274 dairy cows: days to first service (DFS), days open (DO), number of inseminations per conception (NIC), age of first calving (AFC) and calving interval (CI). The basic statistical analysis were analysed using the SAS version 9.3. For the actual computation a linear models with fixed effects was used: For the actual computation a linear models with fixed effects was used: $y_{ijklm} = \mu + HYS_i + BT_j + F_k + B_l + e_{ijklm.}$ The linear model represents coefficients determination R^2 = 0.452117 % (P<0.001) for DFS, R^2 = 0.377715 % (P<0.001) for DO, R^2 = 0.348442 % (P<0.001) for NIC and R^2 = 0.317128 % (P<0.001) for CI with all fixed effects. Correlation coefficients among DFS with DO, NIC, AFC and CI were r= 0.37275, r= -0.06881, r= 0.06493 and r=0.08348. These coefficients were highly statistically significant (P<0.001).

Keywords: Slovak Spotted cattle, dairy cows, reproduction traits, correlation, coefficient of determination, genetic and non-genetic factors

Acknowledgements
This work supported by the Scientific Grant Agency of the Ministry of Education. Science. Research and Sport of the Slovak Republic and the Slovak Academy of Sciences (VEGA) (Project No. 1/0742/17) and (KEGA) (Project No. 012SPU-4/2019). Authors would like thanks the Breeding Services of the Slovak Republic (B.S. SR. S.E.) for providing data for processing.

Productivity of Krivovir strain and its importance on sheep farming in Republic of Serbia

Bogdan Cekic, Dragana Ruzic-Muslic, Nevena Maksimovic, Violeta Caro Petrovic, Ivan Cosic, Zorica Bijelic, Aleksandar Stanojkovic

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Abstract

The area of central Serbia is very suitable for sheep production, because of it's hilly and mountainous configuration. Such area is rich in pastures for ruminants. In the territory of central Serbia, representative of autochthonous (indigenous) sheep breeds is pramenka (zackel) with its differentiated strains: Sjenica strain, Svrljig strain, Krivovir strain, Karakachan strain, Pirot strain, Lipa strain and Bardoka (White Metohian strain). Aim of this study was to investigate Krivovir strain: number of controlled heads and their part in total sheep population, their productivity parameters and milk parameters. In this study, total of 789 adult animals were observed. Average observed body weight (BW) of lambs were: BW on birth 3.22 kg, BW after 30 days 10.55 kg and BW on weaning 24.99 kg, while BW of adult sheep was 50.52 kg. Fertility index was 1.17 and average wool production was 2.88 kg. Average lactation after weaning lasted for 100 days, with milk production 65.16 kg, 3.91% protein and 6.72% milk fat. Krivovir strain is participating with 0.4% of total number of controlled sheep in central Serbia. Although in small number, this strain is irreplaceable in sustainable systems because they are evolutionary adapted to the conditions in which they are reared and because of their contribution to gene pool and agro-biodiversity.

Keywords: indigenous breeds, genetic resources, sustainable development, zackel, wool, milk

Acknowledgments

This paper was supported by the Ministry of Science and Technological Development, Republic of Serbia [project TR 31053].

THE EFFECT OF FEEDING SYSTEM ON THE CARCASS QUALITY OF CROSSBRED LAMBS WITH TEXEL

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Abstract

The aim of this study was to estimate the effect of feeding system on the growth rate and carcass quality of crossbred Improved Jezersko-Solčava x Texel (JSRT) lambs and to evaluate the effect of sex on these traits. The trial was conducted *in nature* according to the traditional rearing systems. The trial included 44 crossbred lambs, which were born and reared until the slaughter in three different flocks. In the age of 10 days suckled lambs were offered with *ad libitum* corresponding diets according to the feeding system. All lambs were slaughtered in seven consecutive days by the same procedure. The effect of feeding system significantly affected daily gain from birth to slaughter, EUROP carcass conformation and shoulder width. Likewise, the effect of sex significantly affected daily gain from birth to slaughter and internal fatness of carcasses. According to carcass cuts the feeding system significantly affected only the proportion of neck and leg. Considering meat quality traits, feeding system had a significant effect on the pH 45 and CIE a* values. In this study, we could speculate that more than the feeding system the growth and the carcass traits as well as meat traits were affected by the amount of the supplement.

Key words: carcass characteristics, lamb meat, commercial crossing, Improved Jezersko-Solčava sheep, Texel sheep, feeding system

THE CONCEPT OF "ONE HEALTH" IN EDUCATION

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Abstract

One Health, as a new approach to complex public health problems, is based on the recognition that human, domestic animal, and wildlife health are linked, therefore well-functioning ecosystem with appropriate biodiversity is the central element of maintaining the world's health. This adaptive, holistic and forward-looking approach was born in 2004; and to date, it became the most effective system of methods to manage emerging infectious diseases, pollutions and other risk factors that threaten our world. In our paper, we review the history and the main principles of One Health. Through the example of echinococcosis, a severe zoonotic parasitic disease, we demonstrate the mechanism of multidisciplinary teamwork. The important role of animal husbandry professionals are analysed in a holistic view. As a result, we recommend One Health principles to integrate into higher agricultural education. In the end, we present the main skills of One Health professionals, who should lead collaborative work on complex environmental health problems and develop recommendations to policymakers and professionals of different fields of science.

Keywords: One Health, higher agricultural education, multidisciplinarity, teamwork

INFLUENCE OF INBREEDING ON THE GROWTH PERFORMANCE OF MEAT SHEEP BREEDS

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Abstract

The objective of this study was to evaluate inbreeding and inbreeding depression in the Czech populations of 3 major meat type sheep breeds: Suffolk (SF; n = 45 924), Charollais (CH; n = 13 046) and Texel (T; n = 9 490). Growth rate was evaluated based on weight at 100 days of age. All animals were divided into four classes based on the inbreeding coefficient: the first class included non-inbred animals (F=0), the second, the third and the fourth classes contemporized inbred animals ($0 < F \leq 0.10$, $0.10 < F \leq 0.20$ and $0.20 < F \leq 0.30$, respectively). The effect of inbreeding on growth ability of lambs was significant ($P < 0.05$). Non-inbred individuals achieve a higher weight at 100 days of age than inbred individuals in each class. Within the increasing coeficint of inbreeding in individual classes, this weight decreases. The effect of inbreeding depression was expressed on the basis of the regression coefficient. Increasing the inbreeding coefficient by 1% should reduce the weight by 0.04695 kg. There was a high correlation between the breed values of animals with and without the inbreeding coefficient, which shows that there is no significant change in the order of the animals taking into account inbreeding in the estimation of breeding values.

Keywords: lambs, inbreeding, inbreeding depression, growth, Suffolk, Charollais, Texel

Acknowledgements

The study was supported by project MZE-RO0718.

Genomic variation and population structure of Dalmatian Pramenka sheep

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Abstract

Dalmatian Pramenka (DAL) is the largest autochthonous population of sheep in Croatia that belongs to the long tailed Pramenka type of sheep, which are widespread over South-East Europe. We genotyped 28 DAL individuals and 32 mouflons from Croatia (Kalifront) on the Illumina Ovine SNP50 K BeadChip. After the data quality control 26 DAL and 31 mouflons with 40677 SNP remained. We used 478 publicly available genotypes of European and Asian sheep from 18 breeds and three mouflon varieties (European mouflon, Sardinian mouflon and Asian mouflon). Population structure and genetic differentiation were assessed using principal component analysis (PCA) and BAPS software. PCA and BAPS analysis showed that genetic differentiation corresponds well with the geographic origin. At the same time, the clear breed separation was observed. DAL individuals intermingled with other Pramenka type sheep from the geographically neighbouring regions while it was separated from the northern European sheep breeds and mouflon populations.

Keywords: sheep, conservation genomics, population structure,

Evaluation of a dynamic mechanistic growth model simulating the performance of broiler chicken

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Abstract

From a modelling point of view, the differences between mammals and poultry species are due to the magnitude and efficiency of energy transactions, rather than having special metabolic processes. Therefore, a generic dynamic mechanistic model describing the nutrient partitioning in broiler chicken has been developed with the same approach as the pig model, InraPorc®. The model predicts the chemical body composition and the body weight of an average individual chick at any time point of the growing and finishing phase.

The aim of our present study was to evaluate the broiler model in terms of body weight (BW) response to different dietary treatments by using independent literature data. For this purpose, the model was calibrated firstly. For calibration, the daily feed intake (FI) and BW data of Ross 308 and 708 broilers from hatch to day 70 were taken from the breeder's guidelines. The calibrated model was then tested with literature data published during the last three years. The model was challenged with diets containing graded levels of digestible lysine, methionine or threonine. Furthermore, datasets on broilers fed with low protein diets supplemented with or without amino acids and/or dietary fat were tested. To study the reliability of model evaluation the root mean square prediction error (MSPE) was calculated. Based on statistics the contribution of different source of model error attributed to bias, regression and undefined error was also determined.

Our results showed that the model gave a reasonably precise estimation on BW in each trial, the relative MSPE was between 1-5%, except for one trial where it was close to 10% which still could be considered as a good prediction. The reliability of the prediction might be improved further if more precise daily FI data were included to *in silico* experiment. Modelling the main routes of nutrient transformation from absorbed nutrients to body protein and body fat accretion, the model assists for a better understanding of the metabolism and helps to answer questions related to feed use mechanisms.

Keywords: broiler, growth model, model evaluation, amino acids and energy

Acknowledgements

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 633531.

Influence of various effects on fatteners traits

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Abstract

The production characteristics of fatteners in this paper were examined in two farms of pigs in the Republic of Serbia. The research included 1166 pigs of both genders (female animals and male castrated heads) with various genotypes. Research examined influence of sire breed, sire within sire breed, gender of the pigs and the mass at the end of the fattening on the following characteristics of the fatteners: daily gain of the warm carcass side mass (PTP), rump fat thickness (DSK), backfat thickness (DSL) and sum of the fat thickness rump+back (DSKL). The pigs in this research come from the following sires: Large White (LW), Swedish Landrace (SL), Duroc and Crossbreed H × D. Data processing was done using the Harvey computer program. It was determined that all the involved effects in the model show a different level of influence on the researched traits ($P < 0.05$; $P < 0.01$; $P < 0.001$), whereas only one factor, sire within sire breed H × D does not influence the expression of the characteristic gain of the warm carcass side mass ($P > 0.05$).

Key words: influence, fatteners, gain of the warm carcass side mass, fat thickness

Acknowledgements

Research was financed by the Ministry of Education, Science and Technological Development of the Republic of Serbia, project [TR 31081].

Evaluation of the production and reproduction traits in the Czech goat population

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Abstract

Goat breeding has a rich tradition and history in the Czech Republic and is focused mainly on milk production and its subsequent processing on dairy products (cheese, yogurt and kefir) by the breeders.

The aim of current study was to evaluate the effect of reproduction properties on the milk production traits and to evaluate the relationship between dairy properties.

The study was conducted using 254 goats of two goat breeds: White shorthaired and Brown shorthaired, born form 1987 to 2014. Phenotypic data of milk production traits (milk yield in kg, lactation number and protein and fat content in %), and reproduction traits (fertility index, survival rate and number of parturition) were obtained from database of the Association of Sheep and Goat Breeders. The evaluated data were recorded from the 1st to the 7th lactation. The average milk yield reached 1015 kg. The average fat and protein content was 3.60 % and 3.05 %, respectively. The most goats achieved the highest milk yield mainly in the first (99 goats), second (60 goats) or third (66 goats) lactation. The milk yield gradually changed over the years; while until 2006 the average milk yield wobbled around 1100 kg per year, after 2006 the performance started to slightly decline. In the period from 2012 to 2014, milk production has dropped to only 770 kg per lactation. Since 2015 the milk yield has gradually grown. The number of birth averaged 5.67 but also several cases of 12 births were recorded. Average fertility index reached 192 % and the kid survival rate was 172%.

Using SAS® statistical package, the Pearson correlation coefficients (proc CORR) and generalized linear model (proc GLM) were calculated. To the model entered following fixed effects: lactation number, number of parturition, year of birth, year of observation, fertility and survival rate; and a random effect of the individual.

Moderate positive correlation was found out between milk yield and lactation number and between number of parturition and milk production (0.34 and 0.35 respectively). There was weak negative correlation between milk yield and percentage of protein content (-0.21) and weak positive correlation between fat content and protein content in milk (0.14). The weak negative correlation was also ascertained between number of parturition and protein content and between lactation number and protein content (-0.19 and -0.13, respectively). An apparent increasing trend of milk production to the fourth lactation was observed; the milk yield slowly decreased after the 4th lactation. The statistically significant differences were found between the 1st and 2nd, 3rd and 4th lactation and between the 2nd and 3rd or 4th lactation for the estimated milk yield. The lactation number showed no influence on fat content, but on the other hand protein content decreased at higher lactations. An effect of parturition number on milk production was found; goats with more than 3 births achieved the milk yield above 1000 kg. No significant relationship was detected between number of birth and milk components. No significant influence was also found for fertility index or survival rate on milk production traits provided that both observed reproductive traits reached at least 100 %.

The effect of reproduction and production traits on milk yield was found. The results showed that milk production was affected most significantly by the lactation number – with average

increasing 76.5 kg of milk per lactation. Presented preliminary results will be furthermore extended by increased sample size and also the kinship will be accounted in the model.

Keywords: breeding, fertility, milk yield, survival rate

Acknowledgements

Research was supported in the Czech Republic by the MZE RO0718 – V006.

Detection of autosomal hemizygous regions in the Fleckvieh population based on SNP-chip data and parent offspring pairs

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Abstract

A Copy Number Variation (CNV) is a loss or a gain in the DNA sequence, ranging from 50 basepairs to a few megabasepairs. Most studies use whole genome sequencing data to detect deletions. Due to the fact that SNP-chip data is more commonly used in livestock, especially in cattle, the detection of deletions based on SNP-chip data is of interest. In the present study an approach based on SNP chip data and the analysis of Mendelian mismatches in parent-offspring-pairs was developed. Use was made of the fact that deletions appear as homozygous after SNP Chip genotyping. For some SNPs with high number of mismatches, the inheritance of the mismatches could be traced back to one or a few bulls and thereby regions of possible deletions were defined. The study has shown that an approach based on Mendelian mismatches and SNP-chip data is a promising way of detecting deletions.

Keywords: CNV-detection, deletions, Fleckvieh, mendelian mismatches

COMPARISON OF THE TECHNOLOGICAL MEAT QUALITY OF THE BREED WHITE MANGALITSA BRED UNDER THE INTENSIVE BREEDING CONDITIONS

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Abstract

The aim of the experiment was to evaluate the technological meat quality of the breed White Mangalitsa through the pH, electric conductivity, drip loss and meat color parameters. Totally, 20 pigs of the breed White Mangalitsa (10 barrows and 10 gilts) were evaluated. Pigs were bred under the intensive breeding conditions. The animals were fed *ad libitum* using a complete feed compound with the added silage. Pigs were slaughtered upon reaching 110 kg of live weight. The muscles of MLT (*Musculus longissimus lumborum et thoracis*) and MSM (*Musculus semimembranosus*) were evaluated. The meat quality analysis showed that pH_1 was similar between the muscles. The evidently lower pH_2 value was in MLT ($p < 0.01$). The EC_1 value ($p < 0.01$) was evidently higher in the MSM muscle. The EC_2 values in MLT and MSM were similar. Between the muscles, an evidentiary difference was observed in water drip loss ($p < 0.01$), greater losses were recorded in MLT. In the SCI a * and SCI b * values, which express the redness and yellowness of the meat, the values in MSM were evidently higher. The lightness of the meat (SCI L *) was the same in both muscles. The differences between the sexes in the observed qualitative parameters were not evidentiary.

Keywords: mangalitsa, musculus longissimus dorsi, musculus semimembranosus, pork, quality

Acknowledgments

This paper was supported by VEGA 1/0818/16 and KEGA 039SPU-4/2019.

Genomic diversity and characterisation of Balkan Livestock Guardian Dogs.

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Abstract

The main aim of this study was to provide genomic characterisation of the three Balkan livestock guardian dog (LGD) breeds. Thus, we have genotyped dogs sampled in Karst Shepherd (14), Šarplaninac (14) and Tornjak (24) breeds using the Canine HD Bead chip (173,662 SNPs) and analysed them together with four Croatian Grey Wolves; and 432 dogs, representing 45 worldwide dog breeds, with publicly available high-throughput genomic information. Based on multivariate analyses (PCA and DAPC) Šarplaninac and Tornjak were clustered together with other LGD breeds (Anatolian Shepherd, Caucasian Shepherd, Fonni's dog, Great Pyrenees and Pastore della Sila) while the Karst Shepherd was slightly separated towards the German Shepherd Dog. The complex clustering methods implemented in the STRUCTURE were able to distinguish Karst Shepherd, Šarplaninac and Tornjak samples as three separated breeds (populations). TreeMix analyses pointed to the slight influence (introgression) of the German Shepherd Dog to the populations of the Karst Shepherd and Tornjak breeds. Estimated genomic inbreeding ($F_{ROH>2Mb}$) level was low in Šarplaninac and Tornjak breeds while the Karst Shepherd had high inbreeding level comparable with the inbreeding levels observed in some internationally well-known breeds as Cavalier King Charles Spaniel, Collie, Doberman Pinscher and German Shepherd.

Keywords: livestock guardian dogs, conservation genomics, population structure, inbreeding

MANAGEMENT PRACTICES AFFECTING CALVES WELFARE ON FARMS IN SLOVENIA

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ABSTRACT

Calf rearing practices in Slovenian herds were investigated with questionnaire-based survey. The data was obtained from 293 farms in Slovenia about their management, especially milk and colostrum feeding protocol, manner of weaning, housing, hygiene on the farm and biosecurity measures. Majority of respondents think the colostrum supply is very important. In 77% of farms, calves receive the first colostrum meal within 2 hours after birth. Quality of colostrum is not considered in 59% of farms. The temperature of colostrum and milk check 73% of farmers, however majority do it manually without using thermometer. Farmers weans calves gradually, mostly considering the age at weaning (45%). Calves are weaned at mean age of 14.18 weeks. In 57.3% of farms, newborn calves are housed in individual pens. Thirty four percent of farmers are cleaning pens for newborn calves after each calf. Half of farmers observe their calves more than 15 minutes daily. Different biosecurity measures are used in 98% of farms. Many farmers are well aware that calf rearing management bear on later milk and meat production and some would need more persuasion to follow the appropriate management practices.

Keywords: welfare, management, colostrum, weaning, housing, biosecurity, calf

ACKNOWLEDGEMENTS

We acknowledge all the farmers who participated in the survey and veterinarians who helped by distribution of the questionnaires. The authors acknowledge the financial support from the Slovenian Research Agency (research core funding No. [P4-0092]).

Longevity and milk production of Latvian local breeds during last decades

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Abstract

The aim of the study was to analyze the longevity and the amount of energy-corrected milk (ECM) per day of local cows breeds Latvian brown (LB) and Latvian blue (LZ). The study was based on data of LB genetic resources (LBGR) 1770 and LZ 921 cows, which were born from 1st January 2000 till 31 December 2015. Milk productivity and longevity of the LBGR and LZ cows was analyzed by birth year's periods: 2000 – 2005, 2006 – 2001 and 2011 – 2015. LZ culling cows' lifespan was in average 2,762.8 ± 55.14 days, or 7.6 years and significantly higher than for LBGR. Average lifespan of LBGR culling cows was 6.7 years. There are cows which had closed 7 – 12 lactations. On average a lifespan is degreasing during the time. In general, LZ cows' characterized by higher length of productive life and milking days. LZ cows had produced more EC milk during their productive life, however, they had lover milking day ECM productivity than LBGR cows.

Keywords: Latvian brown, Latvian blue, local breed, longevity.

Acknowledgment

This paper was supported by Latvian Ministry of Agriculture [nr. S359]

Changes of the rumination characteristics in dairy cows after change TMR composition

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Abstract

Rumination behavior in cattle is important for health and reproduction management of herd. The aim of presented paper was to evaluate change in rumination behavior between two total mixed rations. Twenty-eight multiparous Red Holstein dairy cows were observed during rumination in first month after calving and in fourth month after calving. Cows were fed different TMR at beginning of lactation in first month after calving and in mid of lactation period in fourth month after calving. Length of the single rumination period and number of jaw movements were recorded. Frequency of jaw movement per minute was calculated from recorded rumination characteristics. Rumination of one bolus TMR2 with higher content of roughage was longer (TMR 1 = 53.97±8.241 sec, TMR2 = 57.57 ± 6.290 sec) and cow perform more jaw movements (TMR1 = 61.0 ± 10.674, TMR2 = 65.99 ± 9.682) than ruminating bolus TMR1. Difference in duration of rumination one bolus as well as number of jaw movement was significant ($P < 0.001$). Frequency of jaw movement was not significantly affected ($P > 0.05$). Rumination was inter-individual stable despite of changes in times of jaw movement and duration of one bolus rumination.

Keywords: dairy cattle, frequency, jaw movement, Red Holstein, rumination

Acknowledgements

Presented work was supported by grants VEGA 1/0724/16 and KEGA 015SPU-4/2019

Effect of Nursing Pattern on the Nursing Behaviour as Does

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Abstract

Rabbit kits consume exclusively the does' milk till the 3rd week of the lactation. Thus the growth and the survival of the kits depend on the milk production and the nursing behaviour of the does. The aim of this study was to examine the nursing behaviour and some production traits of rabbit does which were nursed former as kits once or twice a day. Female kits were nursed once (8am; S group) or twice (8am and 4pm; D group) a day till 21d of age. Later on at 16.5 weeks of age rabbits were artificially inseminated and were housed in flat deck cages. 16h lighting (6am-10pm) and free nursing was applied during the examination. During the first two lactations does were monitored 24h/day by using infrared cameras. Distribution and number of nursing events per 24h were recorded. The suckling kits' body weight was measured, the weight gain and survival of kits were calculated. Frequency of days with more than one nursing events was higher in double nursed does (D). In D group in almost 75% of total observed days ($P<0.001$) multiple nursing per day was noticed while the percentage of multiple nursing days in the S group was only 25.5%. Half (49.6%) of the nursing events occurred during the dark period (2am-6am). Does in group C nursed their kits usually at the end of the dark period, but not later than 2pm. On the other hand in case of group D nursing events were observed during the whole day. In both lactation double nursed does show a clear nursing peak at 4pm, which was the time of the second nursing of the does (when these does were infant). There is a tendency in the body weight of the kits in favour of D group, but the relatively high SD could result the lack of significant differences. There were no differences in body weight gain between the groups. The nursing method of does did not have an influence on the survival of suckling kits. Time of the nursing as a kit could have an effect on the nursing behaviour of the does, double nursed does most likely nurse their kits multiple times/24h. Further studies should cover the following lactation periods. Increased doe number strongly suggested to refine the outcome.

Keywords: suckling rabbits, nursing behaviour, nursing events

Acknowledges:

Supported through the EFOP-3.6.1-16-2016-00007. Authors would like to thank the colleges of the Department of Animal Sciences, Kaposvár University for their help and support.

Level of inbreeding in Norik of Muran horse: pedigree vs. genomic data

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Abstract

The objective of this study was to analyse the level of pedigree and genomic inbreeding in a herd of the Norik of Muran horses. The pedigree file included 1374 animals (603 stallions and 771 mares), while the reference population consisted of animals that were genotyped by using 70k SNP platform (N=25). The trend of pedigree inbreeding was expressed as the probability that an animal has two identical alleles by descent according to classical formulas. The trend of genomic inbreeding was derived from the distribution of runs of homozygosity (ROHs) with various length in the genome based on the assumption that these regions reflect the autozygosity originated from past generations of ancestors. A maximum of 19 generations was found in pedigree file. As expected, the highest level of pedigree completeness was found in first five generations. Subsequent quality control of genomic data resulted in totally 54432 SNP markers covering 2.242 Mb of the autosomal genome. The pedigree analysis showed that in current generation can be expected the pedigree inbreeding at level 0.23 % (ΔF_{PEDi}=0.19±1.17 %). Comparable results was obtained also by the genomic analysis, when the inbreeding in current generation reached level 0.11 %. Thus, in term of genetic diversity both analyses reflected sufficient level of variability across analysed population of Norik of Muran horses.

Keywords: horse, genetic diversity, inbreeding, local population, Norik of Muran

Acknowledgements

This study was supported by the Slovak Research and Development Agency (APVV-14-0054and APVV-17-0060) and VEGA (1/0742/17).

Genetic evaluation of reproductive and metabolic disorders and displaced abomasum in Czech Holstein cows

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Abstract

We estimated the genetic parameters of the most frequent reproductive and metabolic disorders as recorded on-line by 55 milk producers in Czech Holstein cows in the Diary of Diseases and Treatments. The dataset covered the period from July 2015 to May 2019. The coefficients of heritability were estimated for retained placenta (h^2 = 0.01), metritis (h^2 = 0.04), endometritis (h^2 =0.03), cystic ovary disease (h^2 = 0.03), parturient paresis (h^2 = 0.01), ketosis (h^2 = 0.01) and displaced abomasum (h^2 = 0.03). Positive genetic correlations different from 0 were estimated between parturient paresis and displaced abomasum (r_{g1g2} = 0.75), retained placenta and metritis (r_{g1g2}= 0.61), displaced abomasum and endometritis (r_{g1g2}^2 = 0.49), metritis and endometritis (r_{g1g2} = 0.45), and metritis and displaced abomasum (r_{g1g2} = 0.41). Because each farmer recorded a slightly different portfolio of health data, the genetic correlations with metabolic disorders couldn't be estimated in most cases, since the number of observations was not sufficient.

Keywords: dairy cattle; retained placenta; metritis; endometritis; cystic ovary disease; ketosis; parturient paresis; displaced abomasum

Acknowledgements

This paper was supported by the Ministry of Agriculture of the Czech Republic, institutional support MZE-RO0718, and by the National Agency for Agricultural Research, Project No. QK1910320.

Investigation of the connection between the CT estimated total body fat content of rabbits at 10 weeks of age and before the first insemination

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Abstract

The experiment was conducted at Kaposvár University with Pannon Ka rabbits. Divergent selection process was made during four generations for estimated total body fat content. Fat index was calculated at 10 weeks of age by determining the ratio of the total body fat volume (cm^3) estimated by computer tomography (CT) to the body weight (kg). Based on the fat index two lines were formed: the rabbits with the lowest fat index (32.5 - 69.9) belonged to the Lean selected and that of the highest values (76.4 - 136) belonged to the Fat selected lines. The fat index of rabbit does was checked before the first insemination at the same way. In the 1st and 2nd generations there were low positive correlations found (R^2 = 0.325 and 0.260 respectively; P<0.001). In the 3rd and 4th generations correlations were medium (R^2 = 0.548 and 0.689 respectively; P<0.001). According to the results obtained, the selection method based on 10-week-old fat indexes is suitable for selecting rabbits for breeding. The effectiveness of this method can be enhanced if the first insemination occurs at an earlier age (16.5 weeks). It may be worthwhile to carry out the selection in two steps, by filtering out the "outlier" individuals based on the estimated body fat content before breeding.

Keywords*:* divergent selection, rabbit does, body fat content, computer tomography

Acknowledgement

The publication is supported by the János Bolyai Research Scholaship of Hungarian Academy of Sciences and the EFOP-3.6.1-16-2016-00007 project. The project is co-financed by the European Union and the European Social Fund.

Factors affecting accuracy of population imputation in dairy cattle

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Abstract

Animal genotyping is constantly evolving and the demand for obtaining SNP information by commercial arrays is significantly increasing. Information about SNPs are widely used in routine programs for animal breeding. They are mostly used for the determination of regression dependence of productive traits and for adjusting relationship matrix. With increasing genotyping intensity, several methods have been developed for comparison, and one of them is the imputation of missing SNPs. Several factors need to be monitored for imputation accuracy. In the population imputation, a large relationship between genotyped animals is not assumed, but two main factors need to be observed, namely the size of the reference population and the number of missing SNPs. Database, used in this study, was obtained from the Holstein Cattle Breeders Association of the Czech Republic. It contains 1000 animals genotyped with the Illumina BovineSNP50 v.2 panel. Data were reduced by missing SNPs before using it in the simulation to verify imputation accuracy. 250, 500 and 750 animals were randomly chosen for the reference population. 25%, 50% and 75% of SNPs were randomly selected for deletion within animals that were outside the reference population. Nine different files were created and consequently imputed by FImpute software. The imputation accuracy was calculated as the correlation between the original values of SNPs and the values of SNPs after imputation. Since the selection of animals in the reference population and the selection of SNPs was random, the entire calculation was repeated 100 times. The resulting accuracy was average for all repetitions. The resulting average accuracy was ranged from 0.96 to 0.99. The lowest accuracy 0.96 was observed in the highest level of missing SNPs and in the smallest reference population that contained 250 animals as expected. The results are consistent with the assumption that the increasing number of deleted SNPs results in the decrease of average imputation accuracy. This trend can be seen across all sizes of the reference population. The trial has proven, that a sufficiently large reference population is required for good imputation accuracy.

Keywords: accuracy, dairy cattle, imputation, genotyping, SNP

Acknowledgements:

Supported by the Czech University of Life Sciences in Prague (Project No. SV19 – 07 – 21360) and by the Ministry of Agriculture of the Czech Republic (Projects No. QK1810253 and MZE – RO0718)

Comparison of basic internal and external egg quality parameters of brown and white egg-laying hens in relationship to their age

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Abstract

This study was focused on the comparison of the eggs from brown and white egg-laying hens. The aim was to evaluate basic quality parameters of eggs from both groups of hens and compare them. The impact of how age influences the technological value of eggs was also observed. The most important correlations were calculated. Products of Czech original genetic programmes, Dominant Brown D 102 and Dominant Leghorn D 229 hens were included. A total of 1500 eggs were analysed. The egg collection was made for three consecutive days when the hens were at the 28, 35 and 59 weeks of age. The significant effect ($P \leq 0.05$) of genotype was found in all observed parameters, except for the eggshell weight, the albumen index and the Haugh units. The effect of age was found to be significant ($P \leq 0.05$) in all evaluated parameters, with the only exception of the eggshell thickness. Interactions between age and genotype were non-significant only in eggshell and yolk weight. The heaviest eggs were from 59-week-old Dominant Brown D 102 hens (68.89 g) and the lightest eggs were from 28-week-old Dominant Leghorn D 229 hens (57.76 g). Highly significant ($P \leq 0.001$) positive correlations were found between egg weight and yolk, albumen and eggshell weight and between eggshell weight and yolk and albumen weight and eggshell thickness in both genotypes. This research was funded by an „S" grant of the Ministry of Education, Youth and Sports of the Czech republic.

Keywords: age, albumen, Dominant Brown D102, Dominant Leghorn D 229, egg, eggshell, genotype, quality

Acknowledgements

This research was funded by an „S" grant of the Ministry of Education, Youth and Sports of the Czech republic. This study was carried out with the assistance of the Demonstration and Experimental Center of the Faculty of Agrobiology, Food and Natural Resources, Czech University of Life Sciences Prague. We would like to thank to Richard Hardy and Anna Chalašová for the English language correction of the manuscript.

THE EFFECT OF NUTRITION UNDER HOT CONDITIONS ON THE ENERGY COMPENSATION OF THE PIGS

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Abstract

The effects of high long term temperature (30 °C) on fattening parameters and physiological parameters of Large White breed were studied by the nutritional compensation of the diet. Four experiments were realized in the experimental Center of Farm Animals near the Department of Animal Husbandry in Nitra. The pigs were divided into control group housed in standard fattening conditions and experimental groups housed in the climatic chamber with high temperature. In the fourth experiment, the diet in hot conditions was enriched with the fat (BERGAFAT®HTL-306). The pigs housed in the conditions of long-term high temperature obtained better parameters of carcass traits - lower average values of the backfat thickness, the weight of fat from the thigh and the weight of a backfat at $P < 0.05$. The better content of valuable lean meat parts showed pigs with the addition of fat in the diet. The obtained differences between the groups were not statistically significant. Nutritional compensation of heat stress was showed in the lower costs per kg gain in the group under hot conditions with the addition of fat in the diet. The addition of fat in the feed mixture during heat stress can be a good compensation of the energy.

Keywords: pigs, heat stress, energy compensation

Acknowledgement

The project was supported by the Grant KEGA No. 015SPU – 4/2019

Title: Evaluation of immunocastration as a sustainable alternative for the European pork production

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Abstract

Immunocastration is an alternative to surgical castration in pigs which allows in part to maintain boar specific advantages without the sex specific problems. Immunocastration is an active immunization against GnRH, which transiently suppresses testicular functions and consists of two consecutive vaccinations during the fattening phase (Thompson, 2000). The suppression of testicular functions occurs after the second vaccination. Depending on the timing of the second vaccination, both the advantages of the entire male growth potential (feed conversion ratio) and the advantages of barrows (product quality, behaviour) can be utilized. Immunocastration allows a compromise between these conflicting aims and thus may contribute to a more sustainable pork production than with boars or barrows (Kress et al., 2019). Despite these advantages, only 2.8% of male pigs are immunocastrated in Europe (Backus et al., 2018). Within the supply chain, there are still knowledge gaps regarding immunocastration and the potential advantage of this technology (Mancini et al., 2017). To increase the acceptance of this method within the European pork market, immunocastration must be evaluated from the perspective of economy, ecology and society, and conflicting and synergic aims of the interaction between the three pillars of sustainability must be considered (Kress et al., 2019).

Traditionally, barrows are raised for pork production to avoid meat quality problems due to boar taint and to prevent male specific behavior (Zamaratskaia and Rasmussen, 2015). Surgical castration of male piglets is usually performed within the first week of life without pain relief or anaesthesia (Fredriksen et al., 2009). This painful procedure is subject to societal concerns and regarded as a serious welfare problem (Rault et al., 2011). In 2010, stakeholders of the value chain committed themselves in the "European Declaration on alternatives to surgical castration of pigs" to end surgical castration of male piglets until 2018. Despite this commitment of the pork chain, about 63% of all male piglets were still surgically castrated in 2017 (Backus et al., 2018). Even today, these numbers might have hardly changed. Pork production with boars has been regarded as the method of choice to avoid welfare problems, especially as boars reveal a more efficient growth due to the presence of anabolic testicular hormones. Thus boars have a more efficient feed conversion ratio, a higher N-retention and leaner carcasses than barrows (Batorek-Lukač et al., 2012; Van den Broeke et al., 2017), which is cost-effective for producers (Verhaagh and Deblitz, 2019) and better for the environment (Reckmann and Krieter, 2015). During the last years, however, it became obvious that problems in animal welfare and meat quality of boars persist which cannot be reliably managed in practice until now (Weiler et al., 2016b). Along pubertal development, some boars still may develop an off-odour, "boar taint", caused by the two substances

androstenone and skatole (Claus et al., 1994). These substances are perceived by many consumers as unpleasant, even if considerable differences between individuals exist (Font i Furnols et al., 2003; Weiler et al., 2000, 1998). Further boar specific problems in pork production are a high level of aggressive and sexual behaviour which may lead to additional welfare problems, such as lameness or penile injuries (Rydhmer et al., 2006; Weiler et al., 2016a). Immunocastration allows to minimize these boar specific problems while using the advantages of boar fattening until the second vaccination. In order to increase the acceptance of immunocastration in comparison to surgical castration or boar fattening within the European pork market, the superiority of this technique in terms of sustainability (economy, ecology and society and their interactions) must be discussed more offensively.

Keywords: immunocastration; entire males; boar taint; surgical castration; animal welfare; sustainability; pork production; meat quality; food safety

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ECONOMIC VALUE OF FEED EFFICIENCY IN ABERDEEN ANGUS BREED

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Abstract
Estimated breeding values for growth, calving performance and exterior traits are actually combined into simple selection indices of bulls, cows and heifers for Aberdeen Angus breed. To establish a comprehensive economic index for this breed the absolute (EWs) and relative (REWs) economic weights for direct and maternal production, functional, carcass and feed efficiency traits or traits components (16 traits in total) were calculated. The REW of a trait was defined as the trait standardised EW (EW x genetic standard deviation) expressed as percentage of the sum of standardised EWs of all evaluated traits. The highest relative economic importance (64%) showed together the three growth traits, weight gains of calves from birth to 120, from 120 to 210, and from 210 to 365 days of age. Survival rate of calves until weaning and cow productive lifetime reached both 11% of the total traits economic importance indicating that these traits should be considered as a new selection criteria in the future. REWs of the feed efficiency traits, defined as the residual feed intake of breeding heifers and of cows, reached only 4% which corresponded to the low feed costs due to extensive production system of Aberdeen Angus that is mostly based on pasture.

Key words: beef, residual feed intake, longevity, live weight, calving, meat quality

Acknowledgement
The study was funded by the project MZE-RO0718-V003 of the Czech Republic.

SLAUGHTER TRAITS OF CASTRATED, IMUNOCASTRATED AND ENTIRE MALE PIGS ORIGINATING FROM TWO TERMINAL SIRE LINES

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Abstract

The aim of this study was to investigate the influence of gender types (T) and terminal sire line (SL) on meat quality and carcass traits of finishing pigs. The study included 120 pigs divided in two genetic groups according to sire line (A = Pietrain x Large White, and B = pure Pietrain). Pigs were assigned to three groups according to sex type: immunocastrates (IC, n=40), surgical castrates (SC, n=40) and entire males (EM, n=40). After the fattening period pigs were slaughtered at a commercial abattoir where carcass and meat quality traits were measured. The use of terminal sire line B resulted in higher fat thickness($P < 0.001$) , lower lean meat percentage (LMP) ($P < 0.01$), and longer ham ($P < 0.01$) compared to line A. IC, exhibited the longer carcass (length "a") than EM ($P < 0.001$) and intermediate fat thickness and LMP compared to EM (the leanest) and SC (the fattest). Significant interaction between sire line and sex type was observed for both carcass lengths "a" and "b" ($P < 0.001$). As for meat quality, the use of sire line A resulted in higher pH_{45} and drip loss ($P < 0.001$). Compared to the other two sex types, higher pH_{45} was observed for SC ($P < 0.001$) while higher drip loss ($P < 0.01$) and CIE a* ($P < 0.01$) was observed for EM. The interaction between terminal sire line and sex type was observed for pH_{45} ($P < 0.001$), drip loss ($P < 0.001$), CIE a* ($P < 0.001$) and CIE b* colour coordinates ($P < 0.01$). Although statistically significant differences between the investigated groups were found in several meat quality indicators, the overall meat quality was similar across the groups. Since they produce similarly longe carcasses with higher LMP than SC, IC proved to be good alternative to surgically castrated pigs.

Keywords: pig, sire, sex type, carcass, meat quality

Acknowledgement

The authors would like to acknowledge the contribution of the COST Action IPEMA CA15215. The research was partially funded by Croatian Science Foundation, grant number 3396.

The genetic structure of Slovak Spotted cattle based on genome-wide analysis

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Abstract

The objective of the study was to determine the membership probability and level of admixture among Slovak Spotted cattle and historically related breeds (Ayshire, Holstein, Swiss Simmental and Slovak Pinzgau). The analysis was based on the panel of 35 934 SNPs that were used for genotyping of 423 individuals. The optimal number of clusters was estimated in two ways; by analysis of Bayesian information criterion and Bayesian clustering algorithm. The optimal number of clusters ranged from 3 to 5, depending on the applied approach. Subsequently, the population structure was tested by discriminant analysis of principal components (DAPC) and unsupervised Bayesian analysis based on the correlated allele frequencies model. The first discriminant function revealed three genetic clusters in population resulting from the production type and origin of analysed breeds. The unsupervised Bayesian analysis showed similar results, where the highest level of admixture was found between Slovak Pinzgau and Slovak Spotted cattle (0.6 %). Despite that, the results of this study clearly showed that the Slovak Spotted cattle is genetically separated from other breeds that were involved in its grading-up process.

Keywords: *dual-purpose breed, DAPC analysis, membership probability, population structure*

Acknowledgement

This study was supported by the Slovak Research and Development Agency (APVV-14-0054and APVV-17-0060) and VEGA (1/0742/17).

Mitochondrial DNA D-loop sequence analysis of Busha cattle

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Abstract

Maintaining the genetic diversity of autochthonous breeds is very important and should be included in animal breeding strategies and conservation plans with the aim to preserve animals, adapted to variety of husbandry systems and different environmental conditions. Mitochondrial DNA (mtDNA) variation studies were particularly useful in establishing relationship and variability between and within domestic species populations. The mtDNA D-loop sequencing was used to determine the genetic status of 41 Busha cattle from different parts of Croatia along with 21 Busha mtDNA sequences from Genbank, and assessing Busha cattle phylogenetic relationship to the other Croatian autochthonous cattle breeds, as well as to the commercial cattle breeds and main described mtDNA haplotypes. The analysis of Busha cattle mtDNA D-loop sequences revealed presence of 26 different haplotypes, which confirms a high genetic variability of the preserved maternal components. Comparison with major cattle haplogroups sequences revealed that majority of Busha cattle were in the T3 haplogroup (44%), while other haplotypes were present in lesser extent (8% T1, 7% T2, 13% T4 and 5% T6).

Keywords: Autochthonous cattle breeds, Busha cattle, mitochondrial DNA, phylogeny, cattle mitochondrial DNA haplogroups

The effect of socialising piglets during lactation on the performance, suckling behaviour and weaning aggression: a preliminary field study

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Abstract

The post-weaning aggression among piglets is a serious problem in modern pig production which compromises animal welfare and health, as well as could cause considerable economic losses. To prevent post-weaning aggression between piglets an approach of early socialisation of piglets during lactation was tested in the present study. In the group farrowing pen (GFP) three individual farrowing pens were interconnected whereby piglets had free access to move across pens and/or cross-suckled alien sows that were still individually crated – passage between pens was released within 24h postpartum. Piglets/litters in the control group went through the conventional breeding practice (i.e. individual farrowing pen/crate). Altogether, the experiment involved 235 piglets. The preliminary results revealed that the sucking order stability differed between studied breeding technologies (group and individual). About one third of all piglets (31.3%) were found being involved (at least once) in the cross-suckling, *i.e.* suckling by the alien mother. Consequently, suckling stability was found generally lower in the GFP, with a significant drop after two weeks of lactation. Regarding the growth performance, piglets from GFP grew relatively, *i.e.* considering initial body weight, faster both during lactation and after weaning, although their daily weight gain was not significantly higher. The present preliminary study revealed early socialisation of piglets as an effective method to mitigate post-weaning aggression, as well as to improve their growth performance. However, considering mortality in lactation and disturbances in suckling stability, additional studies are needed to optimize the process of early socialisation, particularly in terms of piglets' age when grouping of non-littermates is implemented during lactation.

Keywords: pig, weaning, rearing technology, group farrowing pen, early socialisation, suckling behaviour, performance, aggression, animal welfare

Acknowledgement

The research was founded by the Slovenian Research Agency and Ministry for Agriculture, Forestry and Food (project V4-1604).

Runs of homozygosity as footprints of selection in the Norik of Muran horse genome

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Abstract

The aim of this study was to analyse the genome-wide distribution of runs of homozygosity (ROH) segments in the genome of Norik of Muran horse and to identify the regions under strong selection pressure. Overall, 25 animals genotyped by the GGP Equine70k chip were included in the study. After SNP pruning, 54479 SNPs (75.72 %) covering 2.25 Gb of the autosomal genome were retained for scan of ROH segments distribution. The ROHs were present in the genome of all animals and covered in average 13.17 % (295.29 Mb) of autosomal genome expressed by the SNP loci. The highest number of ROHs was identified on autosome 1 (404), while the lowest proportion of autosome residing in ROH showed ECA31 (38). The footprints of selection, characterized by SNPs with extreme frequency in ROHs across specific genomic regions, were defined by the top 0.01 percentile of signals. Overall, nine genomic regions located on seven autosomes (3, 6, 9, 11, 15, 23) were identified. The strongest signal of selection showed three autosomes ECA3, ECA9 and ECA11. The protein-coding genes located within these regions suggested that the identified footprints of selection are most likely consequences of intensive breeding for traits of interest during the grading-up process of the Norik of Muran horse.

Keywords: autozygosity, horse, genomic data, local population, selection sweeps

Acknowledgement

This study was supported by the Slovak Research and Development Agency (APVV-14-0054and APVV-17-0060) and VEGA (1/0742/17).

Deviation patterns of observed and expected haplotype blocks associated with potential recessive disorders in Tyrol Grey Cattle

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Abstract

Confirmed by phenotypic records, several studies across different breeds in different locations have linked missing homozygous pattern with several defects in the functional system and recessive genetic disorders. Recessive genetic diseases are expressed when the recessive alleles appear in a homozygous state for an individual. One of the indicators to detect the recessive allele is through haplotypes, which have a normal frequency in the population, but never occur in the homozygous state. In this study, we used SNP genotypes of 220 Austrian Tyrol Grey cattle and 80 Italian Tyrol Grey cattle to identify the haplotype blocks (Hapblocks) that possibly carry genes causing recessive disorders. Hapblocks with missing homozygous state in the population were statistically tested as to whether this is very unlikely in Hardy-Weinberg equilibrium. Eight out of all hapblocks passing the threshold had functional genes which are crucial in maintaining the metabolism, production, reproduction, and health of the individuals. These hapblocks had a high frequency of above 13% but never appear in homozygous state. Thus, these are foreseen as potential source of genetic defects. Our finding in this analysis can be used as a reference for further study in haplotype analyses of inherited recessive disease for other cattle breeds.

Keywords: Recessive disease, haplotype, missing homozygous, Tyrol Grey cattle

Acknowledgements

Maulana Naji was granted Erasmus Mundus Alfabet for his MSc and currently receiving Ernst Mach Grant PhD scholarship from OeAd.

The effect of new inbreeding on the number of inseminations per successful kindling in the closed Pannon White rabbit population

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Abstract

Effects of new inbreeding on the number of inseminations per successful kindling was analyzed using 6107 kindling records (collected between 2008 and 2017) of Pannon White rabbits originated from 1379 does and 610 bucks. Pedigree of these does and buck were analyzed back to 1992 using New inbreeding coefficients of the rabbit does were calculated using the the Grain software. Estimating the new inbreeding coefficient the method proposed by Kalinowski (defined as the probability that any allele in an individual is currently autozygous and has been autozygous in previous generations at least once) was used. The new inbreeding coefficients ranged between 0 and 18.7% with a mean of 3.84%. Beside the new inbreeding coefficients the possible influence of kindling season (summer vs other seasons) and parity number (groups to 4 categories: 1, 2, 3-10, 11-) were also considered. The number of inseminations per successful kindling was considered as a trait with Poisson distribution. Kindling data was analyzed using the GLIMMIX procedure of SAS software. Significant inbreeding depression could not be justified ($p=0.5$) for the number of inseminations per successful kindling. On the contrary, season and parity significantly affected the number of inseminations required for kindling. Estimated least square mean of the necessary inseminations (1.15) was significantly higher ($p<0.05$) during summer compared to other seasons (1.11). Parity effects were also significant. The rabbit does in the second kindling showed the highest least square mean of insemination (1.17) which was significantly different compared to all other parities (1.14, 1.11 and 1.10, respectively). Except for the second parity differences among parities 1, 3 and 4 were not significant ($p>0.05$).

Keywords: new inbreeding, inseminations per kindling, Poisson distribution

Acknowledgments: Supported by the OTKA K128177 and by the EFOP-3.6.3-VEKOP-16-2017-00008 project.

Pelvic suspension improves the fresh meat tenderness of common eland

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Abstract

Despite game meat meeting numerous consumer demands in terms of leanness[1] and production systems[8], little is known about the meat quality of antelope species. Common eland (*Taurotragus oryx*) have been identified as a high-potential game species for commercial meat production[9] but their meat is tough[10], even after extended ageing[11]. Thus, the objective of this study was to determine whether pelvic suspension could improve the tenderness of fresh eland meat. Ten male eland (~ 2 years) from the farmed herd at CZU Eland Research Farm (Lány, CZ) were slaughtered with a captive bolt, exsanguinated and dressed. Each carcass was split along the spinal cord and randomly allocated to one of two suspension methods for 24 hours at 4 °C: suspension by the pelvic bone, or by the Achilles tendon. Thereafter, seven muscles were removed from each carcass side and the following quality measurements[12] performed for each muscle: pH (inoLab pH 730, WTW, Weilheim, Germany) CIE Lab cut surface colour (45min blooming; CM-700d, Minolta, Osaka, Japan), drip loss, cooking loss (75°C internal temperature in 80°C waterbath) and shear force determination (6 cores/muscle using Warner-Bratzler blade; Instron, Canton, MA, USA). The GLM procedure was used to analyse each muscle separately for the various quality parameters, using SAS. Normality and homoscedasticity was ensured. The model included animal as a random effect and suspension method as a fixed effect. LSMeans were computed using t-tests and a significance level of 5 % was used. Meat quality of the forequarter muscles were not affected by suspension method, but the Tenderness of two high-value muscles, the *psoas major* (lower pH_{24h}) and *biceps femoris* (lower drip losses) was improved, particularly compared to previous studies on South African male eland of similar age[10]. The *longissimus lumboru*m muscles from pelvic-suspended sides were darker (L*) and yellower (b*) than those from Achilles-suspended carcasses, but these colour differences are unlikely to be detected by consumers. However, the sensory acceptance of fresh eland *psoas major* and *biceps femoris* meat may be improved by using pelvic suspension during carcass cooling.

Keywords: antelope; muscle; shear force; Taurotragus oryx, Warner-Bratzler

Acknowledgements

The authors thank MZE-RO0718, CZ.02.2.69/0.0/0.0/16_027/0008366, IGA 20195011 and GA FTA 20195011 for their support.

[1]Bartoň et al (2014) *Meat Science, 96*, 346-352; [8]Hoffman, & Wiklund (2006) *Meat Science, 74*, 197-208; [9]Charles et al (1981) *The Journal of Agricultural Science, 97*, 453-463; [10]Needham et al (2019) *Meat Science, 152*, 41-48; [11]Needham et al (2020) *Meat Science*, 159. [12]Honikel (1998) *Meat Science, 49*, 447-457.

Behavioural changes of farmed common eland after immunocastration

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Immunocastration of male livestock is a widely used as a management tool not only suitable for controlling reproduction, but also to improve carcass and meat quality[2]. Furthermore, this method also reduces the aggressive behaviour of the males by blocking the production of testosterone. While this effect has been well-documented in swine, and in some extent in cattle and sheep, there is no information available for other non-conventional livestock species. Common eland is one of these species, with high farming potential[4] and attractive meat quality[5]. They are social animals living in fission-fusion dynamics but these groups also show stable hierarchical ranks, which are determined by body mass, age, muscularity, matrilineal genealogy and level of aggressiveness. Immunocastration may potentially be an interesting technique to be applied in this species in order to improve productivity, but it may also negatively influence welfare of the treated animals. An experiment was designed to examine if immunocastration can influence the social rank, aggressive behaviour, affiliative interactions and their activity budget. Thirty common eland were divided into two groups of sub-adults (G1, n=15, 182.9 ± 59.37 kg, ≈ 2 years old) and calves (G2, n=15, 94.18 ± 24.76 kg, ≈ 6 months old). Each group consisted of males (n=10) and females (n=5). In each group, 5 males were immunocastrated with Improvac®, administered at two doses of 2ml/animal, with an intervaccination period of four weeks and the second dose administered three months before slaughter. Behavioural screening was conducted every second week. All occurrence sampling was used to record dyadic social interactions while activity budget behaviours were observed through scan sampling. Social interactions were processed in DomiCalc (matrix manipulation and analysis software) to examine the linearity and hierarchy of the groups, and the proportion of total, dominance, aggressive and affiliative interactions were established. Generalised linear models were designed to test the effects of immunocastration on the behavioural patterns. The immunocastrates showed higher social rank, although they performed aggressive and affiliative behaviours in lower frequencies compared to control males. There was no difference between the activity budget for all behaviours except for social behaviour, which was reduced in immunocastrates. This study suggests that active immunization against GnRH is a practical and non-invasive alternative to physical castration in the behavioural management of common eland bulls.

Keywords: antelope; anti-GnRH vaccine; castration; Taurotragus oryx

Acknowledgements

The authors thank CZ.02.2.69/0.0/0.0/16_027/0008366 and IGA 20195011 for their support.

[2]Needham et al (2017) *South African Journal of Animal Science, 47*, 731-742; [4]Charles et al (1981) *The Journal of Agricultural Science, 97*, 453-463; [5]Bartoň et al (2014) *Meat Science, 96*, 346-352.

Variation in linkage disequilibrium as a signals of artificial selection in local cattle populations

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Abstract

The objective of this study was to identify selection signals within the genome of Slovak Spotted, Swiss Simmental, Ayrshire and Holstein cattle using analysis of linkage disequilibrium patterns between of these breeds. The identification of selection signals left by recent positive selection provides better understanding of selection mechanisms that occurred during the grading up of cattle breeds. The genome-wide scan for selection signals was performed for totally 272 animals genotyped by 50k genotyping platform. After quality control of data, overall 35 989 autosomal loci were retained for analysis. Within genomic regions under strong selection pressure (99.9th percentile of identified signals) 145 genes were found (e.g. BPIFA2B, TSPAN14, BPIFA2B, EGFLAM, CHUK, KAZALD1 genes). The most significant SNPs for production ability, reproduction and fitness were positioned on BTA 1, 11, 13, 20, 26 and 28. The study provides information about the genes and quantitative trait loci modified under the influence of directional selection, aimed at improving milk production and immunity characteristics in analysed breeds.

Key words: *candidate gene, dairy breed, dual-purpose breed, linkage disequilibrium, regions under selection, signatures of selection, variation,*

Acknowledgement

This study was supported by the Slovak Research and Development Agency (APVV-14-0054 and APVV-17-0060) and VEGA (1/0742/17).

ANALYSIS OF CHEMICAL AND FATTY ACID COMPOSITION IN PORK *LONGISSIMUS MUSCLE* OF LATVIAN BREED PIGS

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Abstract

The aim of this study was to investigate the pork chemical composition (protein, intramuscular fat, cholesterol) and fatty acid composition (SFA, PUFA, MUFA) of the longissimus dorsi muscle of purebred Latvian White (Latvian Yorkshire) and crossbred Latvian Yorkshire and Landrace pigs selected from different herds. There were investigated 30 pork samples. The average protein level in pork was 22.8±0.21 g 100 g^{-1} and average intramuscular fat (IMF) 5.6±0.62%. It was found that IMF in investigated meat samples was higher than the ideal level. The saturated fatty acid (SFA) range from 0.7 to 5.2 g 100 g^{-1} and polyunsaturated fatty acid (PUFA) range from 0.1 to 1.2 g 100 g^{-1}. PUFA:SFA ratio of lean meat was 0.24 in average, which is less than recommended minimum and did not exceed the value 0.4. Investigated pork samples contain higher level of omega-6 (n-6) and small level of omega-3 (n-3) with evaluated n-6:n-3 ration 4:1 to 11:1. However, in our investigation were samples of pork in which the IMF was in recommended range 2-3% and with higher protein and omega-3 level. In general, pork chemical and fatty acid composition depended on pigs' genetic.

Keywords: pork, pork quality, intramuscular fat, cholesterol, fatty acid compositions.

Acknowledgments

Investigation supported by VPP 2014-2017 AgroBioRes Project No. 3 LIVESTOCK.

A COMPARISON OF FAT TISSUE PARTITION IN CIKA AND SIMMENTAL BULLS

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Abstract

Cika and Simmental bulls from two different experiments were used to evaluate the effect of breed on fat tissue partition between pelvic and kidney, subcutaneous and intermuscular fat. Bulls (47 Simmental and 50 Cika bulls) were slaughtered at the similar degree of fatness. During the slaughtering process, pelvic and kidney fat were weighted and after slaughter, carcasses were firstly cut into different carcass cuts and then dissected into lean meat, fat (divided into intermuscular and subcutaneous fat) tendons and bones. Cika bulls were slightly lighter than Simmental bulls (live weight 649 kg vs 620 kg) and had slightly higher ($p=0.0637$) percentage of subcutaneous fat in the carcass and higher ($p=0.1368$) percentage of subcutaneous fat in total carcass fat. Cika bulls exhibited higher ($p<0.05$) percentage of subcutaneous fat in rib roast and tended ($p=0.0870$) to have lower percentage in flank.

Key-words: Simmental and Cika bulls, partition, fat tissue, carcass cuts

Cross sectional anatomical, CT and MRI atlas of the Pannon Minipig

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Introduction. The different minipig genotypes became very important as large animal experimental models in biomedical research. For precise planning of different invasive or minimal invasive approaches, detailed knowledge of the animal's morphology is needed. The aim of this study was to create a complete cross-sectional, CT and MR atlas of the Pannon Minipig for preclinical studies.

Materials and Methods. Whole body ante- and post mortem CT and MR scanning were performed on a 2-years-old, female Pannon Minipig. After scanning the body was frozen at -80 °C and embedded in polyurethane foam. This block was sliced using a band saw at a slice thickness of 5 mm. A Canon 5D Mark III camera was used to capture high-resolution (300 dpi and 24-bit color, 7360x4912 pixel) images. The RGB images were post-processed and labeled in GIMP (free software for image processing). Images from CT and MRI were imported into 3D Slicer software where window width and window level values were set, and re-formatting were made if it was necessary. All images were labeled using the official Nomina Anatomica Veterinaria.

Results. Sectioning resulted 112 RGB-images from the whole body in high-detail. Images were paired with their corresponding CT and T1-weighted MR images. During labeling, we created volume rendered images and 3D-models in 3D Slicer using the CT and MR data for the exact identification of the different anatomical structures.

Conclusion. For achieving the best image quality, one has to make precise planning of the diagnostic imaging and handling the specimen during the whole process. There were regions, especially at the head and neck area, where supportive volume rendering from the CT series was crucial for precise anatomical identification. The resulting atlas can serve as an online source for the minipig as a model in biomedical research.

Acknowledgement

All husbandry and experimental procedures were approved by the Institutional Ethics Committee and the Hungarian Directorate for Food Chain Safety and Animal Health (SOI/31/00190-6/2018).
This study was supported by the Bolyai Scholarship of the Hungarian Academy of Sciences.

Genetic analysis of feet and leg conformation and proportion of crushed piglets in Austrian Large White and Landrace sows

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Abstract

Selection for feet and leg traits can increase longevity as well as several performance traits in sows. Moreover, good feet and leg quality contributes to improve animal welfare not only for sows, but also for piglets. Sows with feet and leg problems have a higher risk of crushing their piglets when lying down. Therefore, a feet and leg scoring scheme was derived and applied by trained assessors. Furthermore, piglet mortality rate by crushing was recorded. Genetic parameters as well as breeding values were estimated and the effect of the traits on piglet mortality rate by crushing was investigated. Data of 993 Large White and 299 Landrace sows of 23 nucleus farms were analyzed. Heritabilities ranged from 0.03 to 0.16 for piglet mortality rate by crushing and pastern fore legs. Some genetic correlations between feet and leg traits were significantly highly correlated (0.69 to 0.79). Sows with favorable scores for almost all feet and leg scores had higher estimated breeding values for piglet mortality rate. Higher values indicate less crushed piglets and are thus favorable. An introduction of a feet and leg scoring scheme into routine genetic evaluation may thus contribute to animal welfare improvement for sows and piglets.

Keywords: pigs, genetic parameters, feet and leg conformation, crushed piglets, animal welfare

Acknowledgments

Authors gratefully acknowledge pig farmers for data collection as well as the employees from the breeding organizations for supporting farmers during the data collection period as well as assessing all sows. Many thanks also to Christine Leeb from BOKU University for supporting the training workshop for the breeding organizations' employees

The occurrence of polycyclic aromatic hydrocarbons in different types of Croatian dry-cured hams

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ABSTRACT

Croatian dry-cured hams are traditional meat products with excellent consumer acceptance. One of the phases of production include salting with addition of spices (Istrian and Krk dry-cured ham) and smoking (Dalmatian and Drniš dry-cured ham) which makes them susceptible to polycyclic aromatic hydrocarbons (PAHs) contamination. The aim of this study was to determine PAH content in four types of Croatian dry-cured hams (Dalmatian, Drniš, Krk and Istrian) from four different processing methods (differences in primary leg treatment, salting and smoking phase). Determination and quantification of PAHs was performed by HPLC with fluorescence detection. Out of 15 investigated PAHs, 13 compounds were detected. The total average BaP and PAH4 levels obtained from dry-cured hams ranged from 0.05-0.10 μg/kg and 0.41-0.67 μg/kg. Surprisingly, no significant differences were found between dry-cured hams in terms of BaP, PAH4, PAH8 and PAH 15 contents, although Krk and Istrian dry-cured ham manufacturing processes does not include smoking phase. The majority of PAHs detected in non-smoked dry-cured hams come from spices added in salting phase. BaP and PAH4 contents found in dry-cured ham samples did not exceed the currently legal levels according to the European legislation.

Keywords: dry-cured ham, polycyclic aromatic hydrocarbons, benzo(a)pyrene, HPLC-FLD

Acknowledgments

Funded by the Croatian Science Foundation project: "The application of innovative methods in monitoring of proteolytic, lipolytic and oxidative changes throughout the dry-cured ham process- IM-HQHAM" (HRZZ IP-2016-06-6793)

THE SHARE OF TISSUES IN THE PIG ROUND DEPENDING ON THE GENOTYPE, GENDER AND SEASON

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Abstract

The study included 201 offspring (108 castrated males and 93 females) of Landrace (L), Large White (LW) and Pietrain (P) sires. The studied animals were of following genotype: Landrace (L; n = 48); two breed crosses with 50:50 share of parental breeds (LWxL, n=32; and PxL, n=23), two breed crosses with 75% of paternal breed [Lx(♀LWxL), n=35] and [LWx(♀LxWL) n=38] and three breed crosses [Px(♀LWxL) n=25]. Animals included in this study were born during four seasons: winter (n=38), spring (n=65), summer (n=40) and autumn (n=58). Studies have shown that, at an average weight of warm carcass side of 81.20 kg, the highest average values for the weight of round (RW; 10,204 kg), the weight of intermuscular fatty tissue (RINT; 0.478 kg), bone tissue (RBT; 0.850 kg) and muscle tissue (RMT, 7.552 kg) in the round, were established in three-breed crosses of Px (LWxL) genotype compared to other genotypes. The least skin and subcutaneous fatty tissue (RST; 1,269 kg) was recorded in two breed crosses PxL. They had less skin and subcutaneous fatty tissue by 454 g and 467 grams, respectively, compared to two breed crosses (LWxL) and LWx (♀LxLW). Research has shown that there is a genotype on a farm that gives more muscle tissue in the round by 1.521 kg [Px (♀LWxL): LWx (♀LWxL)] with the same weight of warm carcass side, which is a very large difference. With the same average weight of warm carcass side, female animals had higher average weight of the round and yield of muscle tissue compared to male castrated animals. The effect of genotype ($P<0.001$) on all investigated traits was recorded, also the effect of the season of birth on the skin and subcutaneous fat tissue and on the weight of intermuscular fat in the round was recorded. The effect of sex/gender was significant ($P<0.01$) on the weight of skin and subcutaneous fat and on the weight of the muscle tissues in the round but no significant effect on other tested properties ($P> 0.05$) was observed.

Key words: fatteners, fatty tissue, bone tissue, muscles tissue of the round

Acknowledgment

This review research was financed by the Ministry of Education. Science and Technological Development of Republic of Serbia. project TR 31081.

Mastitis detection from milk mid-infrared (MIR) spectroscopy in dairy cows

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Abstract

Mid-infrared (MIR) spectroscopy is the method of choice for the standard milk recording system, to determine milk components including fat, protein, lactose and urea. Since milk composition is related to health and metabolic status of a cow, MIR spectra could be potentially used for disease detection. In dairy production, mastitis is one of the most prevalent diseases. The aim of this study was to develop a calibration equation to predict mastitis events from routinely recorded MIR spectra data. A further aim was to evaluate the use of test day somatic cell score (SCS) as covariate on the accuracy of the prediction model. The data for this study is from the Austrian milk recording system and its health monitoring system (GMON). Test day data including MIR spectra data was merged with diagnosis data of Fleckvieh, Brown Swiss and Holstein Friesian cows. As prediction variables, MIR absorbance data after first derivatives and selection of wavenumbers, corrected for days in milk, were used. The data set contained roughly 600,000 records and was split into calibration and validation sets by farm. Calibration sets were made to be balanced (as many healthy as mastitis cases) while the validation set was kept large and realistic. Prediction was done with Partial Least Squares Discriminant Analysis, key indicators of model fit were sensitivity and

specificity. Results were extracted for association between spectra and diagnosis with different time windows (days between diagnosis and test days) in validation. The comparison of different sets of predictor variables (MIR, SCS, MIR + SCS) showed an advantage in prediction for MIR + SCS. For this prediction model, specificity was 0.79 and sensitivity was 0.68 in time window -7 to +7 days (calibration and validation). Corresponding values for MIR were 0.71 and 0.61, for SCS they were 0.81 and 0.62. In general, prediction of mastitis worked better with a shorter distance between test day and mastitis event, yet even for time windows of -21 to +21 days, prediction accuracies were still reasonable, with sensitivities ranging from 0.50 to 0.57 and specificities remaining unchanged (0.71 to 0.85). Additional research to further improve prediction equation, and studies on genetic correlations between clinical mastitis, SCS and MIR predicted mastitis are planned.

Key words: MIR spectroscopy, dairy cow, milk, mastitis, somatic cell count, PLS

ACKNOWLEDGMENT

This work was conducted within the COMET-Project D4Dairy (Digitalisation, Data integration, Detection and Decision support in Dairying). That is supported by BMVIT, BMDW and the provinces of Lower Austria and Vienna in the framework of COMET-Competence Centers of Excellent Technologies. The COMET program is handled by the FFG.

Genetic trend of length of productive life in the Holstein and Slovak Simmental cattle in Slovakia

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Abstract

National genetic evaluation of lengh of productive life in Slovakia was carry out from the year 2014 till 2018, three times per year (March, June and October). The survival analysis was performed using Weibull sire model. The heritability obtained from Weibull model was different between populations (0.13 in Holstein and 0.05 in Slovak Simmental, respectively). RBVs of Holstein sires born up to 1999 shows decreasing tendency in all five years. A desirable tendency started from the year 2000. Differences between RBV in particular years are due to descent censored records during the evaluated period. Similar trends showed in Slovak Simmental bulls RBVs. Culled cows reached average 305-day milk yield 6499 kg and 4645 kg in Holstein and Slovak Simmental breeds, respectively. The length of productive life there was 898 days in Holstein and 985 days in Slovak Simmental cows. Age at first calving reached 930 days in Slovak Simmental and 851 days in Holstein heifers. The progress of both traits in the years 2014-2018 was lower in Holstein population, + 288 kg milk and + 76 productive days than in Slovak Simmental cows.

Keywords: Length of productive life, cattle, genetic trends, milk yield

Acknowledgments

This paper was supported by Grant Agency of The Ministry of Education, Science, Research and Sport of the Slovak Republic KEGA - 012SPU-4/2019 and VEGA 1/0724/16.

Variability of mitochondrial DNA in *Testudo hermanni* Gmelin, 1789

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Abstract

The 12S rRNA coding region in *Testudo hermanni* from five geographic locations representing three subspecies of *T. hermanni* was sequenced. The comparison of obtained sequences showed significant variability of this mtDNA region, indicating 24 different haplotypes found in 124 samples which originated from five geographically separated populations of *T. hermanni* representing three different subspecies. In addition to 40 polymorphic sites within the 300 bp long region of the mtDNA, several sites indicating presence of more than one mtDNA haplotype in the same sample were identified. This finding suggested the presence of heteroplasmy in *T. hermanni*. Further experiments are needed to verify this indication by cloning and sequencing of cloned PCR products.

Key words: European turtle, cytochrome oxidase, mtDNA, heteroplasmy

Ultrasound measurement traits and selection of young animals of Aberdeen Angus cattle in the Czech Republic

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Abstract

The evaluation of meat quality is becoming the standard in beef cattle industry. Ultrasonography is a very suitable method for evaluating of live animals. This method of identifying qualitative indicators allows young animals to engage in reproduction and thus in genetic progress. The most important traits are scanning mainly on *musculus longissimmus lumborum et thoracis* (MLLT): eye muscle area, intramuscular fat, rib fat and rump fat. These traits are highly correlated with observation on carcass body too.

Intramuscular fat deposition or marbling in muscle is one of the most important traits influencing beef quality and palatability attributes. Marbling is positively correlated with juiciness, tenderness and palatability of beef. Intramuscular fat content (IMF) in the muscle varies significantly depending on the cattle breed. The highest fat content contains Wagyu, followed by Korean cattle and Angus. The eye muscle area (EMA) is correlated with overall muscular and thus monetization of the animal. The aim of the study is to detect variability in individuals and to enable breeders select animals for breeding based on carcass quality.

The pilot study was realized in February 2019 where a total of 761 animals of the Aberdeen Angus breed were measured at the age of 6-24 months. After data editation (records out of age range 7 to 17 months and crossbreeds were removed) data set contains 675 animals. Animals were measured in 19 farms and also on the 4 performance test stations for young breeding bulls. Four traits were measured according to Breedplan methodology: Eye muscle area (EMA) and Intramuscular fat (IMF) - at the 12/13th rib site; Rib fat- fat depth at the 12/13th rib site and Rump fat - fat depth at the P8 rump site.

Ultrasound measurement traits are influenced by many factors. These factors were analysed by PROC GLM (SAS, 2004). As the most important effect on ultrasound measurement traits was chose management of animals, where for example the feeding, handling and environmental conditions were included. Many breeders had more than one diet for their animals, especially when they had groups of rearing bulls, breeding bulls and young heifers so because of it, effect of Herd – Group (HG) was created. Model equation for EMA contains fixed effects of herd – group (classes), sex*parity (classes), age, age^2, weight (regression). Second model equation for IMF contains fixed effects of herd – group (classes), sex*parity (classes), age, age^2, rib and rump fat (regression).

The goal of the muscle and fat cattle scanning of animals are breeding values of animals but for the very first selection „Utility value“ was determined. Relative utility values for EMA and IMF were adjusted by estimated effects and standardized to mean = 100 and standard deviation = 10.

More than 60% of animals of the corresponding age was scanned this year in the Czech Republic. Breeders have been given a relative utility values, which are adjusted from environmental influences so it is suitable for very first selection. Animal scanning will continue in the coming years to create a database suitable for prediction of breeding values and selection based on the genetic potential of the animals.

Keywords: carcass; beef cattle; intramuscular fat; breeding; selection

Acknowledgement
Supported by NAZV – National agency for agricultural research, project No. QK1910059

THE EFFECT OF SOME NATURAL AND CHEMICAL DISINFECTANTS ON SOME HATCHABILITY PARAMETERS IN LAYER BREEDERS

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Abstract

The aim of the present study was to investigate the effect of different disinfectants from chemical or natural sources on some hatchability parameters (hatchability, egg weight loss, embryonal mortality, hatchling weight, sex ratio) in layer breeders. The trial was divided into two parts. In the trial 1, 3,600 hatching eggs from the layer breeders were randomly divided into eight groups and sprayed with distilled water (negative control) and solutions of 10% NaCl, 96% ethanol, 7% propolis, 0.5% Ecocid S and 3% hydrogen peroxide, respectively. In addition, one group of eggs was fumigated with formaldehyde gas and one group was used as a control and was not disinfected. In the trial 2, 3,150 hatching eggs of layer breeders were treated with 3%, 5%, 7% solutions of hydrogen peroxide and 0.5%, 1%, 2% solutions of Ecocid S. Undisinfected eggs represented a control group. In each group, 150 eggs were individually weighed and chicks were separately hatched and weighed. Hatchability was significantly lower in NaCl and propolis groups compared to hydrogen peroxide, formaldehyde, Ecocid S and control groups. There were no significant differences neither between hydrogen peroxide, formaldehyde, Ecocid S and control groups in the trial 1 nor between groups with different concentrations of hydrogen peroxide and Ecocid S in the trial 2 in terms of egg weight loss, hatchling weight, hatchability of fertile eggs and hatchability of eggs set. It was concluded that solution of 3% hydrogen peroxide could be a good alternative to formaldehyde gas for the disinfection of chicken hatching eggs.

Keywords: poultry, chicken, hatching eggs, disinfection, hatchability, sex ratio, hydrogen peroxide

CANDIDATE ALLELES FOR AGGRESSSIVE BEHAVIOUR IN DOGS

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Abstract

Genetic background of dog aggression is poorly understood. Tendency to aggressiveness in dogs is a complex trait largely influenced by environmental factors. However, differences in behaviour between different breeds suggest that aggressiveness may have a genetic component. Aggressive behaviour is nowadays generally undesirable trait in dogs, but certain aggression-associated characteristics are desired among different types of working dogs (*e.g.* law enforcement dogs). Several candidate alleles in different loci, for example in androgen receptors and dopamine transporters, have been associated with aggression in dogs. Based on literature review we selected several promising candidate loci for detection of aggression-associated alleles in dogs. Cheek swab samples of working dogs, considered selected for more aggressive behaviour (represented by German Shepherd and Malinois), and therapeutic dogs, considered selected against aggressive behaviour (represented by different breeds) were collected and genotyped to assess whether the selected aggression-associated candidate alleles are over-represented in a certain category of dogs or in certain breed(s). Preliminary results suggest that poly(A) expansion in dopamine transporter (*SLC6A3*) and CAG repeat polymorphism in androgen receptor (*AR*) could be associated with aggressive behaviour in dogs. Genotype-based selection for behavioural traits could be a valuable addition to performance testing in selection of reliable working dogs.

Keywords: aggression, androgen receptor, behaviour, candidate genes, dog, dopamine receptor

THE EFFECT OF THE SLAUGHTER WEIGHT ON CARCASS COMPOSITION, BODY MEASUREMENTS AND VEAL QUALITY OF HOLSTEIN CALVES

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Abstract

The aim of this study was to investigate the growth, fattening characteristics and veal quality of MLT from Holstein calves produced from 4 slaughter weight groups (130, 150, 180 and 210 kg). Calves were fed in the same conditions. Average daily gains ranged from 660 g in slaughter weight 130 kg to 840 g in weight 210 kg ($P<0.001$). The most important changes of linear body measurements were revealed in hip height and withers height ($P<0.001$). Slaughter weight had strong impact on average daily gain and most of body measurements ($P<0.01$). Slaughter weight influenced proportion of kidney, rumen and intestinal fat, while highest proportion was found in the group of 180 kg ($P<0.001$). Calves of slaughter weight 180 kg had lowest proportion of bones ($P<0.001$) and highest proportion of meat ($P<0.001$) from right - half carcass. Highest proportion of separable fat had calves of 210 kg as well as 150 kg. In terms of nutritional quality of veal, we found significant and high individual differences in intramuscular fat content ($P<0.01$) as well as between monitored groups. The lightness of the meat was highest in the group of 180 kg ($P<0.05$). Protein content of the loin muscle had negative impact on intramuscular and moisture content ($P<0.001$). Parameter pH strongly positively influenced drip loss value and negatively electrical conductivity.

Keywords: body measurements, carcass composition, correlations, Holstein breed, lightness, pH value, separable fat, veal

Acknowledgement

The project was supported by the Grant KEGA No. 015SPU – 4/2019

Economic viability of the alternatives to piglet castration without anaesthesia - Updating and extension of economic calculations

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Abstract

Farm animal husbandry in Germany is under increasing pressure. In its expert opinion on livestock husbandry in Germany, the Scientific Advisory Council on Agricultural Policy (Wissenschaftlicher Beirat Agrarpolitik, WBA) assumes that "the current husbandry conditions of a large proportion of livestock are not sustainable against the background of social change and new scientific assessment approaches" (WBA at BMEL, 2015 p. 1). Animal welfare is one of the determining issues for the future orientation of animal husbandry operations.

Building on Working Paper 64 (Verhaagh, Deblitz, 2016), the aim of this renewal study is to provide an updated analysis of the economic effects of these alternative methods and to compare their eco-nomic viability. The first step is to specify a reference situation (baseline) with the current practice of castrating male piglets without anaesthesia. The baseline is used as a reference for the quantification of animal performance, revenues, costs and profitability in the alternative scenarios. The typical farms from the German part of the *agri benchmark* Pig network are used as the reference farms for the baseline. The alternatives of the current practice and their effects on performance data and the economics are analysed. The baseline and the alternatives are evaluated as full cost calculations because, apart from direct costs, investments and overheads are also affected. Variation calculations for prices, performance data and application methods complete the analysis. The available information and current studies by the University of Munich von Zöls et al. (2018) indicate that local anaesthesia is not a suitable alternative as it does not ensure effective pain elimination (according to § 5 para. 1 sentence 1 TierSchG, such an elimination is required from 31.12.2020). Thus, local anaesthesia can at best reduce pain, which is "bought" with pain when administered.

The results of the first investigations cannot be confirmed in all cases (Verhaagh, Deblitz, 2019). The costs of immunocastration are compensated by the higher performance of the animals and a better feed-conversion. The boar fattening loses ground against the other options due to the reduction of payment by the German slaughter industry (boar price), but together with boar fattening with vaccination it remains the most profitable measure. In addition, both measures show regional differences. For the surgical procedures, the results between the individual farm classes and regions in Germany are more homogeneous. Injection anaesthesia is the most expensive of the procedures analysed, followed by inhalation anaesthesia with isoflurane. The much-discussed local anaesthesia, on the other hand, is significantly cheaper. In the variation calculations, the costs of measures performed by the farmers themselves are also investigated. If the above sequence is combined with the results from an economic point of view, the immunocastration and boar fattening procedures perform best from the point of view of costs and benefits under the available information and the assumptions made.

German pig production is not only in close competition with European producers, but as one of the largest exporters worldwide (Deblitz, 2018) also in global trade. Competitiveness is determined both by the level of production costs and by profitability as a success factor (Schaper, et al., 2011). The considered alternatives of anaesthetised piglet castration change

the operational framework of the competitiveness of agricultural enterprises. When surgical castration procedures are applied under general anaesthesia, the production costs in piglet production rise sharply, so that piglet exporters from neighbouring countries (Denmark has declared local anaesthesia practicable and the Dutch use the controversial CO2 anaesthesia) become more competitive. The result is rising piglet imports in Germany.
The possible alternatives of immunocastration and boar fattening can strengthen the economic situation of the pig-rearing farms and thus also secure competitiveness. The prerequisites for this are acceptance on the domestic market, by consumers and on the world market. The prerequisites for successful marketing cannot be created by agricultural farms but must be realised through the value chain. The legislative renunciation of the previous castration practice is a challenge for German pig production.

Keywords: piglet castration, boar fattening, immunocastration, castration with(-out) anaesthesia, local anaesthesia, farm economic impact

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A selection index for improving the carcass traits in the Pannon Large rabbit breed

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Abstract

Loin muscle volume and hind leg muscle volume measured by computer tomography are economically valuable traits in rabbit breeding. Hence, genetic parameters were calculated to these new selection criteria, and a two-trait selection index was created in order to modify the current selection process of the Pannon large rabbit breed. The evaluated animals (n=312) were randomly selected from 2014 and 2018, and the total number of animals in the pedigree file was 2758. Loin muscle volume (LMV) and hind leg muscle volume (HLV) were analyzed in a two-trait animal model. The estimated heritability for LMV was h^2=0.4 and h^2=0.42 for the HLV respectively. The selection index was created with desired gains by improving each trait in the selection criteria with one additive genetic standard deviation and the final index was Z transformed. Correlation coefficients between the index and the examined traits were high, 0.86 for LMV and 0.87 for HLV, thus this method could be announced into the breeding program.

Keywords*:* rabbit selection, computer tomography, selection index

Acknowledgements

The publication was supported by the **EFOP-3.6.1-16-2016-00007** project. The project is co-financed by the European Union and the European Social Fund.

INVESTIGATION OF DNA METHYLATION ON PORCINE REFERENCE SEQUENCE GENES FOR BOAR TAINT TRAIT

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Abstract

Boar taint (BT) is an offensive flavor in non-castrated male pigs. However, studies of genome-wide DNA methylation profiles on all reference sequence genes to reveal epigenetic information associated with BT was scare. Reduced representation bisulfite sequencing (RRBS) is an efficient technology to identify candidate epigenetic biomarkers associated with BT. Three different BT levels were analyzed using RRBS data to calculate differentially methylated genes (DMGs). In this study, we found 411 DMGs (Q-value < 0.01) out of 4566 reference genes. Hyper-methylation DMGs were revealed to be mainly enriched in five significant pathways (qvalue < 0.05). These results could contribute to the understanding of methylation levels on reference sequence genes in pigs and the usage of genomic selection for low BT in the breeding programs.

Keywords: boar taint, DNA methylation, reduced representation bisulfite sequencing, differentially methylated genes

Acknowledgment

This study was funded by the AGES project of the Veterinary Department of the Ministry of Food, Agriculture and Fisheries, Denmark. Xiao Wang received Ph.D. stipends from the Technical University of Denmark (DTU Bioinformatics and DTU Compute), Denmark, and the China Scholarship Council, China.

Genomic breeding values for claw diseases/disorders in Czech Holstein cows

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Abstract
Genomic breeding values (GEBV) were predicted for claw diseases/disorders in Holstein cows. The data sets included 6,498, 6,641 and 16,208 cows for the three groups of analysed disorders. The analysed traits were infectious diseases (ID), including digital and interdigital dermatitis and interdigital phlegmon, and non-infectious diseases (NID), including ulcers, white line disease, horn fissures, and double sole and overall claw disease (OCD), comprising all recorded disorders. Claw diseases/disorders were defined as 0/1 occurrence per lactation. Linear animal models were employed for prediction of conventional breeding values (BV) and genomic breeding values (GEBV), including the random additive genetic effect of animal and the permanent environmental effect of cow and fixed effects of parity, herd, year and month of calving. Both high and intermediate weights (80% and 50%, respectively) of genomic information were employed for GEBV50 and GEBV80 prediction. The estimated heritability for ID was 3.47%, whereas that for NID 4.61% and for OCD was 2.29%. Approximate genetic correlations among claw diseases/disorders traits ranged from 19% (ID x NID) to 81% (NID x OCD). The correlations between predicted BV and GEBV50 (84 - 99%) were higher than those between BV and GEBV80 (70 - 98%). Reliability of breeding values was low for each claw disease/disorder (on average, 3.7 to 14.8%) and increased with the weight of genomic information employed.

Keywords: dairy cattle, foot and claw disorders, heritability, genomic breeding values, Holstein breed

Acknowledgements
The work was supported by the project of the National Agency for Agricultural Research QK1810253 and the institutional support MZE-RO0718 of the Ministry of Agriculture of the Czech Republic.

Automated estimation of loin muscle mass in living rabbits using computed tomography

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Abstract

In this paper, a novel technique for the segmentation of loin muscle in the computed tomography images of living rabbits is presented. The segmented muscle volumes are used to estimate the weight of the loin muscle and the regressed weights are compared to the real weights of meat cuts measured after the dissection of the animals. The R^2 value of the proposed technique is 0.74 which is significantly better than the determination coefficients of the methods previously used in practice. The proposed techniques provide acceptable performance to be involved in the breeding selection program of rabbits (Pannon White) at Kaposvár University, Hungary.

Keywords: computed tomography, automated segmentation, loin muscle, rabbit

Acknowledgements

This work was supported by the Emberi Erőforrások Minisztériuma (EFOP-3.6.3.-Vekop-16-2017-00005) and the Bolyai scholarship of the Hungarian Academy of Sciences.

27th Animal Science Days, 18-20 September 2019, Prague, Czech Republic
ASD 2019 - Book of Abstracts
Czech University of Life Sciences Prague, 2019, 77 pp
ISBN 978-80-213-2950-8