

# **Book of Abstracts**

**of the 1<sup>st</sup> Regional Meeting  
of the European Federation of Animal Science**



**Book of Abstracts No. 29 (2023)**  
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# The European Federation of Animal Science (EAAP)

The main aims of the EAAP are to promote, by means of active cooperation between its members and other relevant international and national organizations, the advancement of scientific research, sustainable development and production systems; experimentation, application and extension; to improve the technical and economic conditions of the livestock sector; to promote the welfare of farm animals and the conservation of the rural environment; to control and optimise the use of natural resources in general and animal genetic resources in particular; to encourage the involvement of young scientists and technicians. More information on the organization and its activities can be found at [www.eaap.org](http://www.eaap.org).

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European Federation of Animal Science has close established links with the sister organizations American Dairy Science Association, American Society of Animal Science, Canadian Society of Animal Science and Asociación Latinoamericana de Producción Animal.



# Welcome to the EAAP 2023 in Nitra

On behalf of the Slovak Organizing Committee, it is our honour and pleasure to welcome you to the 1st Regional Meeting of the EAAP, which is taking place in Nitra, one of the oldest cities in Slovakia. This event is organised as a result of a joint initiative of the EAAP Central and Eastern Europe Working Group and represents a new strategy in the development of EAAP activities.

In the past, extended meetings of the CEE WG have been held in the form of satellite symposia at the time of the EAAP Annual Meetings, most recently in Vilnius, Lithuania, in 2008. At a time of rapid development of computing and digital communication technologies, bringing people together is essential for building and developing relationships. The speed of scientific progress and the increase in scientific knowledge only underline the need for active exchange and the formation of broader teams to address people's current needs. It is expected that by 2050 there will be 9.7 billion people on Earth, and more than 60% of them will live in urban agglomerations with no direct connection to the land and their own food production. The science in animal production is currently facing many challenges, such as climate change, the use of marginal land unsuitable for other types of production, the use of raw materials unsuitable for human consumption, increasing production intensity, sustainability and animal health, or the application of biotechnology as a result of human population growth and changing lifestyles. Despite scientific advances, agriculture, and in particular livestock production, remains the main source of food and provides nutrition for humans. The programme of the meeting will include various insights into the field of animal nutrition, genetics, biotechnology, livestock farming systems or animal health and welfare. We believe that the meeting will be full of new and interesting information, will bring interaction and create a space for strengthening existing and establishing new relationships between scientists and teams in the CEE region. In addition to the scientific programme, you can look forward to a welcome drink under our majestic alma mater as well as a gala dinner combined with a presentation of our traditional culture. We hope the 1st EAAP Regional Meeting for Central and Eastern Europe will be a unique opportunity to combine work and social life.

We wish you a pleasant stay in our beautiful city and country!

*Radovan Kasarda*

Chairman of the Slovak Organizing Committee

# Organizers of the 1st EAAP Regional Meeting

## President of the Meeting

### **Radovan Kasarda**

Slovak University of Agriculture in Nitra,  
Slovakia



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## About the University

Slovak University of Agriculture in Nitra (SUA) is a modern, fully-recognized, competitive educational and scientific research institution. The University ranks high in international quality assessment rankings. SUA has been ranked as the fifth-best Slovak university out of 14 universities in the Slovak Republic according to the global SCIMAGO Institutions Rankings 2023 and as the fourth-best Slovak university in Slovakia according to the global University Ranking 2023. SUA offers a wide range of bachelor's, master and doctoral study programs and deals with many research and creative topics. As the only agricultural university in Slovakia, it is unique in its profile, historical roots, but also its future. It is a source of knowledge for the public, building partnerships with other scientific and educational institutions, the community, and companies to help the region. An important landmark in Slovak agricultural higher education was the year 1952. In this year, as part of the reorganization of universities, the government established two separate universities from the two faculties of the University of Agricultural and Forestry Engineering in Košice - the University of Agriculture in Nitra and the University of Forestry and Wood in Zvolen. Act of the National Council of the Slovak Republic No. 324/1996 Coll. In 1996, the College of Agriculture has renamed the Slovak Agricultural University. Since its founding in 1952, more than 100 000 students have graduated at SUA. Currently, 5 621 students are studying at University, 449 teachers are teaching and 664 employees are taking care of the university's operations. It consists of six faculties: the Faculty of Agrobiology and of Food Resources; Faculty of Biotechnology and Food Production; Faculty of Economics and Management; Faculty of European Studies and Regional Development; Faculty of Horticulture and Faculty of Landscape Engineering and Faculty of Engineering.



The basis of SUA's educational and scientific research activities are sustainable development, environmental protection, preservation of natural wealth and biological diversity, but also human health through quality nutrition and safe food production, landscape design, climate change, engineering, and effective development of agriculture and rural areas. SUA provides language education, access to information and communication technologies, courses in a foreign language and the opportunity to complete part of the study at partner universities abroad. Overall, the university provides education in 46 bachelors', 35 engineering, 24 doctoral study programs as well as 16 programs offered in English. The mission of SUA, which is part of the European area of higher education and the common European research area, is to contribute to the development of education, knowledge, science, and culture following the needs of society, to develop knowledge, skills, wisdom, creativity, and goodness of man and thereby contribute to the development of knowledge community. Fulfilling this mission with a focus on the student is the main activity of the university. The main task of SUA in fulfilling its mission is to provide higher education under the needs of society and creative scientific research and creative artistic activity. The basis of pedagogical activities and research activities at SUA Nitra are timeless topics such as: sustainable development, environmental protection, conservation of natural resources and biodiversity, as well as human health through quality nutrition and safe food production, landscape design, ecology, efficient agricultural and rural development. SUA is part of many studies abroad programs including Erasmus+, Jean Monnet, CEEPUS, and the Fulbright Commission among others. It also has partnerships with a number of universities across the world to facilitate staff and student exchanges. SUA provides research and education in agriculture and related research areas such as agrobiological, food resources and technology, sustainable agriculture, biotechnology, mechanical engineering, automation and automation of agricultural equipment, operation of energy equipment for agricultural production, economics and management, international trade in agricultural commodities, marketing, rural tourism development, rural development project management, lifelong education.

Conference website: <https://regional2023.eaap.org/>

# Industry Members Club



EAAP started in 2023 a new initiative to create closer connections between European livestock industries and the animal science network. Therefore, the “EAAP Industry Club” was shaped with the specific aim of bringing together the important industries of the livestock sector with our European Federation of Animal Sciences. All companies dealing with animal production (nutrition, genetic, applied technologies, etc.) are invited to join the “EAAP Industry Club” because industries will have opportunity to increase their visibility, to be actively involved in European animal science activities, and to receive news and services necessary to industries. In addition, through the Club, industries will enlarge their scientific network and will receive specific discounts on sponsoring activities.

The Industries that already joined the “EAAP Industry Club” are:



## The Club gives:

Visibility • Company name and logo at EAAP website and all relevant documents • Slides with name and logo at Official Events • Priority links with EAAP Socials • Invite, through EAAP dissemination tools and socials, people to events organized by your company • Information disseminated through a brand new Industry Newsletter • Networking • Joining the Study Commissions and Working Groups • Suggest topics to be considered for Annual Meetings Scientific Sessions • Organize Professional Panel through the EAAP platforms • Economic Benefits • One free registration to each Annual Meeting and at every meeting organized by EAAP • Five individual memberships at no cost • Many possible discounts (-30%) to increase company visibility through: EAAP Newsletter, EAAP website, EAAP Annual Meetings and workshops • Support young scientist by sponsoring scholarships named by the company • Co-Organize and sponsor webinars

Make yourself more visible within the livestock industry via the animal science network!

For more information please contact [eaap@eaap.org](mailto:eaap@eaap.org)

# YoungEAAP



## What is the YoungEAAP?

YoungEAAP is a group of young scientists organized under the EAAP umbrella. It aims to create a platform where scientists during their early careers get the opportunity to meet and share their experiences, expectations and aspirations. This is done through activities at the Annual EAAP Meetings and social media. The large constituency and diversity of the EAAP member countries, commissions and delegates create a very important platform to stay up-to-date and close the gap between our training and future employer expectations, while fine-tuning our skills and providing young scientists applied and industry-relevant research ideas.

## Committee Members at a glance

- Ines Adriaens (President)
- Jana Obsteter (Vice President)
- Giulia Gislon (Secretary)

YoungEAAP promotes Young and Early Career Scientists to:

- Stay up-to-date (i.e. EAAP activities, social media);
- Close the gap between our training and future employer expectations;
- Fine-tune our skills through EAAP meetings, expand the special young scientists' sessions, and/ or start online webinars/training with industry and academic leaders;
- Meet to network and share our graduate school or early employment experiences;
- Develop research ideas, projects and proposals.

## Who can be a Member of YoungEAAP?

All individual members of EAAP can join the YoungEAAP if they meet one of the following criteria: Researchers under 35 years of age OR within 10 years after PhD-graduation

Just request your membership form ([ines.adriaens@kuleuven.be](mailto:ines.adriaens@kuleuven.be)) and become a member of this network!!!

# EAAP Study commissions



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MINERAL  
OPTIMISATION



## Smart minerals, Smart nutrition, Smart decision



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Thanks to the  
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# Scientific programme

## Session 01. Utilisation of genomics in animal breeding and livestock diversity – differences in the West – East applications

Date: Wednesday 26 April 2023; 13:00 - 16:30

Chair: Grosu / Candrák

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Chair: Dublec / Rolinec

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Chair: Krupa / Zavadilová

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Chair: Kucevic / Kolesárová

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Chair: Cieslak / Gálik

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Chair: Gantner / Tančin

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Chair: Krupa / Zavadilová

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Chair: Potočník / Vostry

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## Session 11. Livestock Farming Systems Free communications / 2

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### Theatre Session 11

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**Single cell RNA sequencing of bovine milk somatic cells**

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The milk yield of dairy cows exceeds significantly the nutritional requirements of the calf. The high efficiency of milk production is essential for the economic use of dairy cattle and provides an important source of animal proteins for human nutrition. The milk yield is a complex trait with significant genetic component that can be efficiently improved with the classical selection approach. Lactation in cattle is a unique model for studying the biology of lactation with the aim of exploring the mechanistic basis of this complex trait at the cellular level. To study the transcriptome of milk at the single cell level, we performed scRNA-seq analysis using the 10x Chromium platform on milk samples from two cows in mid-lactation. Cells were pelleted, fat was removed from the milk and cells were stained with trypan blue in order to estimate the proportion of live cells. The cell suspensions from two cows were then loaded onto each channel resulting in the recovery of 9,953 and 14,557 cells, respectively. Library samples were loaded onto two lanes of the NovaSeq 6000 (Illumina) instrument. After filtering at the cell and gene levels, a total of 8,097 and 16,962 cells remained from each animal, respectively. Based on transcriptome sequencing data we were able to reconstruct nine cell types (milk-producing cells, progenitor cells, macrophages, monocytes, dendritic cells, T cells, B cells, mast cells, and neutrophils) in bovine milk. Genes with most variable expression in somatic cells include genes coding milk proteins (CSN1S1, CSN2, CSN1S2, CSN3). Our work provides a resource to uncover regulatory elements associated with various functions of the mammary gland, such as lactation, tissue renewal, native immunity, protein and fat secretion, and hormonal response.

## Session 01

## Theatre 2

**Genetic evaluation for health traits of Holstein cows in the Czech Republic**

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Genomic breeding values (GEBV) for clinical mastitis (CM) and three groups of foot and claw disorders (CD): infectious digital disorders (IDD), claw horn lesions (CHL) and overall claw disorders (OCD) were predicted for Holstein cows in the Czech Republic. Subsequently, a health index was calculated using predicted GEBVs. The official web application Diary of Diseases and Medication was a source of health records. Datasets included: CM data from 178,107 lactations of 100,873 Holstein cows on 126 farms; IDD 89,727; 50,244; 54; CHL 59,350; 32,687; 35; OCD 121,585; 67,729; 73, respectively, from 2017 to 2022. The linear animal model and single-step genomic prediction were employed for each health trait separately using the Program package BLUPF90 (Misztal et al. 2018). The genomic matrix included 51,381 animals genotyped by the Illumina BovineSNP50. The average of CM GEBVs was for genomic cows and heifers 0.015 (-0.14 to 0.19); for genomic bulls, 0.009 (-0.18 to 0.19). The average reliability of CM GEBVs was for 45,681 genomic cows and heifers 0.29 (max 0.52); 5,701 genomic bulls 0.25 (max 0.90). The results for CD traits were similar. The average health index for genomic cows and heifers was 102.8 (64.9 to 138.7), and for genomic bulls, 100.4 (61.2 to 136.5). Between 2017 and 2022, the average health index based on GEPHs with minimal reliability of 0.2 increased for both bulls and cows. The Ministry of Agriculture of the Czech Republic supported the study, projects MZE-RO0723 and QK1910320.



**Admixture analysis in the Austrian Turopolje pig population**G. Mészáros<sup>1</sup>, B. Berger<sup>2</sup>, C. Draxl<sup>3</sup>, J. Sölkner<sup>1</sup><sup>1</sup> University of Natural Resources and Life Sciences, Vienna, Gregor-Mendel-Str. 33, 1180 Vienna, Austria, <sup>2</sup> HBLFA Raumberg-Gumpenstein, Raumberg 38, 8952 Irnding, Austria, <sup>3</sup> Österreichische Schweineprüfanstalt GmbH, Unter den Linden 1a, 2004 Streitdorf, Austria

The Turopolje pig is a local, endangered breed in Austria, derived from very few animals recovered from Croatia during the Yugoslav war in the early '90s. Due to this origin and no further importations, the population is highly inbred. Recently the routine SNP genotyping was implemented to manage the diversity of the breed. The aim of this study was to assess potential admixture in the population. The data set of Turopolje consisted of 184 animals, genotyped with custom chip with 77,122 SNPs. For comparison, pigs from all commercial breeds in Austria were used, including 82 Large White, 76 Landrace, 74 Duroc and 70 Piétrain pigs, genotyped with a Porcine 60K SNP chip. Only the common SNPs between chips were considered. The data controlled for quality, removing SNP and individuals with more than 10% missingness, as well as pruned for high LD. After the quality control a total of 485 pigs and 33,916 autosomal SNPs remained. The genomic admixture was analyzed with the ADMIXTURE software, assuming  $K = 5$  for the five established breeds. The admixture results showed well separated groups for all breeds. In the four commercial pig breeds a low-level admixture was common. The majority of the Turopolje animals were non-admixed and purebred. A low-level admixture up to a few % was present in 14 animals, while a substantial admixture between 20 and 36% was found in 8 animals. In order to conserve the purebred status of the Turopolje breed, we recommend that the animals with high level of foreign admixture are not used in breeding. We further recommend the continuation of genomic monitoring of the breed.

## Session 01

## Theatre 4

**Gain of muscle and feed-to-gain-of-muscle ratio measured by computed tomography in pig selection**G. Daumas<sup>1</sup>, C. Hassenfratz<sup>1</sup>, M. Monziols<sup>1</sup><sup>1</sup> IFIP - Institut du porc, La motte au vicomte, 35650 Le Rheu, France

Computed tomography is an interesting technology in genetics, because it makes it possible to precisely measure body composition and to access criteria such as the gain of muscle and the feed-to-gain-of-muscle ratio. The aim of the study was to compare muscle growth performance between six purebred populations, females from three sire lines and uncastrated males from three dam lines. The sire lines included a Duroc line and two Pietrain lines. The dam lines consisted of a Large White line and two Landrace lines. Feeding was ad libitum in a biphasic sequence, and consumption was measured individually. Average Daily Gain (ADG) and Feed-to-Gain ratio (F:G) were computed between approximately 35 and 120 kg liveweight. After slaughter, half-carasses were scanned by computed tomography to assess the Lean Meat Content in carcass (LMC), Average Daily Gain of muscle (ADGm) and the Feed-to-Gain-of-muscle ratio (F:Gm). The sample was validated for 119 females from the sire lines and 114 entire males from the dam lines. The criteria tested had coefficients of variation significantly higher than those of the current criteria. The male lines obtained better LMC, ADGm and F:Gm than the female lines, while ADG and F:G were close. F:Gm was well correlated with F:G in the male lines, while the correlation was stronger with ADG in the female lines. LMC was strongly correlated with F:Gm and F:G in the male lines, whereas these correlations were less than 0.5 in the female lines. Almost all correlations between the criteria tested and the current criteria were less than 0.80. Breeder selection could be improved by introducing a precision-composition criterion and a feed-efficiency criterion related to muscle gain, especially in sire line.+

**Genomic selection of pigs in Czech Republic**

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Genomic parameters for boar semen quality traits were estimated. For estimation purposes, only animals with a “call rate” (proportion of identified SNPs out of all SNPs on the chip)  $\geq 90\%$  were used. SNPs with Hardy-Weinberg equilibrium P-value  $> 0.0001$  and minor allele frequency (MAF)  $> 0.05$  were included for further analysis. The total number of genotyped animals was 903 and the number of SNPs was 48991 out of 50697. In terms of data, boars with at least seven defect-free collections between 2010 and 2022 were included in the estimation. A total of 30 400 collections from 599 boars were evaluated. The traits investigated were: semen volume (OB), sperm concentration (KO) and proportion of abnormal sperm (AB). The effects of: month of collection, age of boar at collection, interval between collections, combined effect of insemination station and year of collection, boar breed effect and boar permanent effect were selected as sources to explain the variation in each trait. Estimations were performed by both BLUP and ssGBLUP jointly for the maternal breeds – (Czech Large White, Czech Landrace) by three-trait animal model for traits OB, KO and AB. The estimated coefficients of heritability based on ssGBLUP were 0.28, 0.16 and 0.26 whereas those based on BLUP were 0.26, 0.15 and 0.25 for OB, KO and AB, respectively. Genetic correlations between traits were similar in both methods, statistically significant, but negligible for AB trait ( $-0.01$  to  $+0.01$ ), whereas high significant correlation was obtained between OB and KO ( $+0.63$ ). The study was supported by Czech Republic project QK1910217.

## Session 01

## Theatre 6

**Osborne-Hazel Index to increase the accuracy of selection**

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Selection indexes are great tools in the genetic improvement of the candidates to selection. In the last century a great variety of selection indexes for different species and traits, starting with multitraits indexes and the family indexes, were proposed. The goal of these indexes was to provide a way to rank candidates for selection. Each type of index has its own accuracy of selection. The purpose of this paper is to propose a new index that to combine the characteristics of the two type of indexes, that is, information from many traits and many relatives. I have named this index as Osborne-Hazel Index. The main emphasis was made to show the efficiency of this index, in term of accuracy of selection and the genetic progress for each trait. The demonstration was made on two traits, first with the heritability of 0.30 and the second with 0.25. The genetic and phenotypic correlations between the two traits were 0.40 and 0.20, respectively. The number of sisters per family (n) was 4 and the number of dams per sire was 8. Four indexes were considered in this paper: Osborne Index for each trait Hazel Index for the two traits and Osborne-Hazel Index. The main results showed as follows: The Osborne Index for first trait had an accuracy of selection of 0.658 and 0.623, for second trait; The Hazel Index for both traits was the lowest, 0.570 and the last, the proposed Osborne-Hazel Index, had the biggest accuracy of selection, of 0.673. In conclusion, the Osborne-Hazel index realized the biggest accuracy of selection, among the four variants of indexes. The biggest differences were made versus Hazel Index, with 18 %. If we compared with Osborne indexes, the biggest difference is for the second trait, with low heritability (4%).

**Genomic diversity in selected farms of Holstein cattle in Slovakia**

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The aim of the study was to evaluate the genomic diversity of Holstein cattle in selected farms in Slovakia. Genomic data of 134 cows from three different farms spread in the western part of Slovakia were analysed. After quality control, the dataset included 132 animals and 46195 SNPs. The level of genomic diversity was assessed by calculating expected ( $H_e$ ) and observed heterozygosity ( $H_o$ ) and genomic inbreeding coefficient (FHOM and FROH). In addition, genomic relationships among populations were quantified by Nei's genetic distances and Wright's  $F_{ST}$  matrices. The average  $H_e$  and  $H_o$  values (0.325 and 0.335) indicated a decrease in the overall heterozygosity of analysed populations. On the other hand, based on the observed FHOM value (-0.032) and the fact that  $H_o$  was slightly higher than  $H_e$ , it can be assumed that the decrease in heterozygosity within populations is not so rapid. The current inbreeding in evaluated farms expressed by FROH>16MB and FROH>8MB ranged from 2.34% to 3.17% (on average 2.78%) and 5.18% to 5.87% (on average 5.53%), respectively. Even though FROH values showed differences between farms, it can be concluded that their gene pool was highly affected by selection. As expected, the average values of  $F_{ST}$  and Nei's genetic distance (0.011 and 0.011) pointed to a close genetic relationship among animals and populations analysed. Observed results can be used to control the increase in inbreeding per generation and reduce the potential negative effect of inbreeding depression on analysed farms. This study was supported by the Slovak Agency for Research and Development, grants number APVV-17-0060 and APVV-20-0161.

## Session 01

## Theatre 8

**Genomic Evaluation for Holstein Cattle in Czech Republic**

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Domestic routine genetic evaluation of Holstein cattle in Czech Republic has long tradition reaching first imports of the breed to the country. With advent of genomic evaluation, the development of single-step method for official breeding values of Czech Republic began in 2011. In 2015, all genomic breeding values (GEBVs) included in the national selection index SIH were established and single-step milk production was validated by Interbull for joined international evaluation in gMACE as first national single-step evaluation on the world. Further development was supported by adopting blupf90 family programs for core mathematical procedures of prediction of GEBVs and additionally inclusion of MACE breeding values was applied to routine evaluations for milk production traits, udder health, linear traits, and fertility in 2019. At the present time also GEBVs of linear traits are validated as input to gMACE and genomic evaluation of gestation length was implemented. Furthermore, GEBVs for other traits are in development in cooperation with Institute of Animal Science Prague with main focus on health traits like mastitis resistance, three claw health traits and more in investigation. The genotyped population for prediction of GEBVs counting more than 5.400 bulls and 50.300 cows and heifers is being expanded by bulls' genotyping when registered in herdbook and Fit Cow project for genotyping of heifers and cows.

### The impact of single-step genomic evaluation on breeding values for live animal ultrasound measures in Aberdeen Angus

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Our study investigates the impact of using genomic information on the genetic evaluation of live animal ultrasound measures in the Czech Aberdeen Angus. Breeding values were predicted for body weight at scanning (SCW), scrotal circumference (SC), rump fat thickness (P8FT), rib fat thickness (RBFT), eye muscle area (EMA), intramuscular fat content (IMF) collected on 1,983 animals. The relationship matrix included 6,252 animals, 1,778 animals were genotyped using Geneseek GGP 150K, Illumina BovineSNP50 BeadChipV3, and The EuroG MD beadchips. Common SNPs located on all chips were used for genomic evaluation. The number of effective SNPs was 32,126. The breeding values were predicted by multiple-trait animal model using BLUP and genomic breeding values (GEBVs) using ssGBLUP. Correlations between BVs and GEBVs were 0.90 – 0.98 for non-genotyped animals, 0.91 – 0.95 for genotyped animals with records, and 0.85 – 0.86 for genotyped pedigree animals. No significant changes in reliabilities for non-genotyped animals were found. However, GEBV's reliabilities for genotyped animals were distinctly higher than BV's. For genotyped animals with records, the reliabilities on an average increase from 0.46, 0.51, 0.55, 0.53, 0.45, and 0.41 (BV's) to 0.72, 0.71, 0.76, 0.73, 0.79, and 0.54 (GEBVs). For genotyped pedigree animals, the increase was even higher from 0.25, 0.28, 0.3, 0.29, 0.25, and 0.23 (BV's) to 0.67, 0.67, 0.72, 0.69, 0.64, and 0.5 (GEBVs) for SCW, SC, P8FT, RBFT, EMA, and IMF respectively. These results confirm the benefits of single-step genomic evaluation. This study was supported by the Ministry of Agriculture of the Czech Republic project NAZV QK1910059 and MZE-RO0723.

### Genomic evaluation for fertility traits of limousine cattle in the Czech Republic

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The aim of this study was to develop a genomic evaluation for beef cattle fertility. The genomic evaluation was performed on the performance testing database of the Czech Beef Cattle Association. The evaluated traits were age at first calving (AFC), first calving interval (CI), and productive longevity (PL) at 78 and 150 months. After all edits, the database contained 4,838 records of the CI and 6,736 records of AFC and PL. The relationship matrix contained 21,167 individuals. A total of 1,000 individuals were genotyped using Geneseek GGP 150K or Illumina BovineSNP50 BeadChipV3. Imputation was not used; therefore, the intersection of both SNP chips was used. The number of common SNPs was 41,766. After quality control, the number of SNPs was reduced to 36,622 SNPs. The genomic breeding values (GEBVs) were predicted using the ssGBLUP method. No distinctive changes were found between breeding values (BV's) (predicted earlier) and newly predicted GEBVs. However, it was found that the GEBV's reliabilities were higher than BV's reliabilities. In the genomic evaluation, the increase in reliability varied between animals. For the non-genotyped animals, the maximum increase was by 0.004 for AFC, 0.007 for CI, 0.002 for PL78, and 0.004 for PL150. For the genotyped animals, the reliabilities on average increased twofold compared to BV's. The highest observed differences in reliabilities for genotyped individuals were 0.23 for AFC, 0.15 for CI, 0.28 for PL78, and 0.22 for PL150. The presented results are the first outputs of the effort to introduce genomic evaluation into beef cattle breeding in the Czech Republic. This study was supported by the Ministry of Agriculture of the Czech Republic project NAZV QK1910059 and MZE-RO0723.

### Application of genomic tools in the characterisation of the Vlaško-Vitoroga strain of Pramenka sheep in the Republic of Serbia

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This research aims to apply genomic tools in characterizing the Vlaško-Vitoroga strain of Pramenka breed in the Republic of Serbia. Biological samples of 30 animals (28 ewes and 2 rams) were collected using nasal swabs and genotyped after DNA extraction using a GGP Ovine 50k chip. Data quality control showed that all animals had a call rate above 90%, while 3572 SNPs had a minor allele frequency below 0.01, which is why they were excluded from further analysis. The genetic diversity of the analyzed population was then characterized by the determination of runs of homozygosity (ROH) distribution in the autosomal genome. Across five ROH length classes was identified overall 763 ROH with an average length of 8.09 Mbp. The longest ROH was identified on chromosome 9, while chromosome 3 showed the highest ROH proportion (10.35%). The average value of current genomic inbreeding ( $F_{ROH} > 16\text{Mbp} = 1.45\%$ ) indicated that even if the population is relatively small (less than 1000 animals), their gene pool seems to be not significantly affected by the loss of genetic variability. Manuscript created as a result of research within the framework of the bilateral cooperation Serbia Slovakia (2022-2023) "Genomic tools for conservation of local sheep populations, SK-SRB-21-0013".

## Session 01

## Theatre 12

### Evaluation of longevity by weighted analysis

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Longevity was evaluated from breeding view as production longevity, i.e. from calving to culling. For prediction of genomic breeding value (GEBV) was chosen repeatability model in ssGBLUP. Fixed effects were interaction herd\*year\*season and milk production. Random effects were additive genetic effect, permanent environment effect. Model without and with weights (i.e., weighted analysis) was tested. Totally 9 unevenly long phases were defined. Each survived phase had weight 1 and culled phase had weight  $w = 9 - \sum \text{survived phases}$ . Validation regression was calculated from GEBVs from actual data (April 2021 – GEBV0) and trimmed data (April 2017 – GEBV-4) and correlations were computed with GEBVs for longevity in USA, breeding values of direct longevity estimated by Survival Kit and index of longevity routinely published in Czech Republic for Holstein cattle. Regression coefficient of model with weight was showing less overestimation than regression coefficient of model without weight in all groups of bulls (all bulls: 0.976 and 0.966, active bulls 0.922 and 0.898, active bulls with phenotyped daughters 0.944 and 0.922 respectively). Correlations between GEBV0 and GEBV-4 were higher in model with weight by all evaluated categories of bulls. For group of all bulls correlations were 0.878 (with weight) and 0.866 (without weight). The lowest correlations were for group of active bulls with daughters with phenotypes 0.500 and 0.481 respectively.

### Evaluating alternate model to estimate genetic parameters and breeding values for the calving ease in the Slovak Holstein population

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Calving ease is a complex reproductive trait of economic importance in dairy cattle. This study was aimed to compare of two models of calving ease genetic evaluation in Holstein cattle in the Slovak Republic. The current genetic evaluation of calving ease in Slovak Holstein breed is carried out using threshold sire-maternal grandsire model. The new tested, validated and compared model was threshold animal model. Data included calving difficulty scores provided by The Breeding Services of the Slovak Republic from 512 401 calves born from the first to the sixth parity cows and three randomly selected populations of 10 000 animals each. Included in the model were fixed herd-year, month of calving, parity, sex and breed group and random sire direct and MGS effect (threshold sire-maternal grandsire model) respectively random animal direct and maternal effects (threshold animal model). Predictive ability of the models was defined with the mean square error (MSE). The results obtained using animal model confirmed the slight advantage of threshold animal model over threshold sire-maternal sire model. But statistically significant difference has not been confirmed. Breeding values estimates of bulls were also only slightly more accurate when a animal model instead of S-MGS model was fitted (+ 2 %). This publication was supported by the Operational program Integrated Infrastructure within the project: Creation of nuclear herds of dairy cattle with a requirement for high health status through the use of genomic selection, innovative biotechnological methods, and optimal management of breeding, NUKLEUS 313011V387, cofinanced by the European Regional Development Fund and APVV-20-0161.

### Genetic effect on the prediction of muscle content of purebred pig carcasses

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In the French collective system of pig genetic evaluation the lean meat content (LMC) is calculated by an equation predicting the former EU definition from the proportions of cuts which was established on commercial pigs. In order to improve genetic evaluation the study aim was to develop accurate equations to predict LMC of purebred pigs according to the new EU definition. A sample of 231 pigs was studied, including 119 females from 3 paternal lines and 112 entire males from 3 maternal lines. Paternal lines (2 Pietrain and 1 Duroc) and maternal lines (2 Landrace and 1 Large White) were reared in a phenotyping station and fed ad libitum. Left half-carcasses were scanned by computed tomography to determine LMC. 3 sets of predictors were compared: 2 thicknesses of fat and muscle measured on live pigs around 110 kg by ultrasound (US), 4 thicknesses of fat and muscle measured on carcasses by vision (IM) and the proportions of 4 cuts – backfat, loin, ham and belly – in carcass (CUT). The genetic effect on regressions (partially confounded with sex effect) was tested in a general linear model by including line in fixed effect and in interaction with the predictors. In the entire sample the  $R^2$  of US, IM and CUT was respectively 0.54, 0.63 and 0.82 without the genetic effect and 0.74, 0.73 and 0.93 with the genetic effect. The CUT predictors were the most efficient to predict LMC. With CUT the genetic effect was only additive for the paternal lines; RMSE was 1.04. For the maternal lines, RMSE was 1.27, but genetic interactions with the proportions of loin, ham and belly were significant ( $P < 0.05$ ). Pending possible equipment with X-ray tomography, it could be interesting to consider specific equations for predicting LMC based on the proportions of cuts per genetic population.

**Lactation curves in monitoring cows' resilience**J. Vařeka<sup>1</sup>, L. Zavadilová<sup>1</sup>, E. Kašná<sup>1</sup><sup>1</sup> Institute of Animal Science, Genetics and Animal Breeding, Přátelství 815, 104 00 Prague 10, Czech Republic

The study used Legendre polynomials to describe lactation curves and monitor dairy cows' resilience. Daily milk yield observations (DMY) were analysed from 510 purebred Holstein and 165 Czech purebred Fleckvieh cows. There were monitored via Affimilk software on a farm from 1998 to 2020. The original database included 767 577 observations from 946 dairy cows and 2 795 lactations. After the data edit, it contained 527 966 DMY and 1 839 lactations from cows with days in milk (DIM) from 1 – 305. The highest completed lactation was the eighth. Individual cows' Persistence of Milk Production (PMP) was calculated and then computed to the average PMP by breed and lactation. The average PMP were 97.5 % in Holstein primiparous cows, 88.31 % in older Holstein cows, 93.68 % in Fleckvieh primiparous cows and 81.81 % in older Fleckvieh cows. Average lactations curves were modelled for each lactation by random regression models with Legendre polynomials. Average DMY (according to 305 DIM) and individual DMY were compared with predicted values. Both were assessed for the first and second & further lactations. The average DMY deviated by 8.82 % in Holstein primiparous cows, 9.55 % in Fleckvieh primiparous cows, 19.31 % in Holstein older cows and 22.85 % in Fleckvieh older cows from the modelled lactation curves. Individual DMY deviated 14.29 % in Holstein primiparous cows, 13.96 % in Fleckvieh primiparous cows, 23.54 % in Holstein older cows, and 28.12 % in Fleckvieh older cows. Primiparous cows reported more persistent lactations and less deviated milk yields from modelled lactation curves than older cows, which had inconsistent DMY. Supported by the Ministry of Agriculture of the Czech Republic, the projects QK22020280 and MZE-RO0723.

## Session 01

## Poster 4

**Halothane and sex effect on the prediction of lean meat content of crossbred pig carcasses**G. Daumas<sup>1</sup>, C. Hassenfratz<sup>1</sup>, M. Monziols<sup>1</sup>, S. Schwob<sup>1</sup><sup>1</sup> IFIP - Institut du porc, La motte au vicomte, 35650 Le Rheu, France

Pig carcass grading is compulsory in the EU and based on the lean meat content (LMC). The LMC definition moved from the LMC in the 4 main cuts to the LMC in carcass. This would affect the average LMC and the accuracy of the classification methods. To anticipate consequences of an update, the objective of the study was to test the effect of sex and halothane gene when calibrating the main classification method used in France versus the new LMC. A sample of 79 pigs from crossbred between Pietrain boars and Large White and Landrace crossbred sows was studied. They differed according to sex and halothane status, leading to 4 subpopulations: females NN (n=15), castrated males NN (n=28), females Nn (n=15) and entire males Nn (n=21). Pigs were fed ad libitum in a phenotyping station. They were slaughtered around 120 kg liveweight and classified by the Image-Meater method which included 2 fat depths and 2 muscle depths. The left half-carcasses were scanned by computed tomography to determine the new LMC. The partially confounded sex and genetic effects on regressions were tested in a general linear model by including subpopulation in fixed effect and in interaction with the predictors. Introducing the new LMC would provoke a drop of more than 3 percent points. The new predicting equation would have a RMSE of 2.16 and a R<sup>2</sup> of 0.51, including only 1 fat depth and 1 muscle depth. Interactions between subpopulation and the 2 fat depths were significant. Including sex and halothane status would improve accuracy, RMSE decreasing to 1.88 and R<sup>2</sup> increasing to 0.68. In conclusion, in the next update of pig classification methods it would be worthwhile to control halothane status in the sample and to consider developing separate equations by sex.

**Recessive fertility haplotypes in Serbian Holstein-Friesian cattle**

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The introduction of routine genotyping of cattle populations allows the identification and management of genomic regions affecting economically important traits. In Holstein populations, more than 40 recessive lethal-carrying haplotypes have been identified, and causative genes have been identified for some of them. Holstein haplotype 1 (HH1) was mapped to BTA5. The nonsense mutation truncates 670 AA of the APAF1 protein. HH2 was mapped to BTA1, and the frameshift mutation in the IFT80 gene within this haplotype was identified in 2022. HH3 was associated with a missense mutation in the SMC2 gene on BTA8, HH4 with a missense mutation in the GART gene on BTA1, HH5 with a deletion in TFB1M on BTA9, HH6 with a start-lost in SDE2 on BTA16, and HH7 with a 5-bp deletion in the CENPU gene on BTA27. In this study, we genotyped 1600 Serbian Holstein-Friesian cows with a GGP Bovine 100K SNP array containing known causal mutations for recessive fertility haplotypes (HH1, HH3-HH7). The percentage of cows that are carriers of at least one genetic defect in the studied population is 15.15% (n=242). The most common haplotype in the studied population is HH3 (5.31%, n=85), followed by HH6 (3.31 %, n=53), HH5 (3.13 %, n=50), HH1 (2.31 %, n=37), HH4 (1.31 %, n=21) and HH7 (0.63 %, n=10). In addition, 12 animals carried two deleterious recessive fertility haplotypes. Accurate testing of individuals carrying the lethal allele can be used to avoid carrier-by-carrier matings or to use mating strategies to control the undesirable alleles within the population and keep their frequencies low.

## Session 02

## Theatre 1

**A review: Comprehensive Study Regarding the Mealworm Tenebrio Molitor Worldwide Utilization, Benefits and Recommendation**

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**Abstract** In recent years, the mealworm *Tenebrio molitor* gain interest, especially since 2020 when the European Commission adopted a scientific opinion regarding the *Tenebrio molitor* larva safe alternative as a novel food. The *Tenebrio molitor* is proposed for different aims. Due to its nutritional content, it can be used in human's as well as in animal's food and, in recycling both organic waste and polyether polyurethane foam. Also, it is capable of food bioconversion and feeds contaminated with aflatoxin B1. In this way, it represents an inexpensive pre-clinical model in pharmacokinetics and toxicity. This study aims to review all databases by offering comprehensive information regarding the mealworm *Tenebrio molitor* utilization and recommendations in the way of its potential effects. This research can be used in future scientific studies.



### Dietary supplementation of Stimbiotic improve the growth performance and beneficial gut microbiota population in post weaning piglets

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During the weaning period piglets are delicate with immature immune and digestive system often leading to lower feed intake and weight gain, diarrhoea, stress and increased mortality. Stimbiotic (STB) product shown to improve piglet performance through the modulation of the intestinal microbiota accompanied by a reduced inflammatory response by stimulating fibre utilization specially XOS. This study was designed to see if dietary inclusion of stimbiotic in post weaning diet can enhance piglet performance by improving growth and beneficial microbiota in the faces. Eighty weaned piglets with similar initial body weight (BW,  $8.84 \pm 0.26$  kg) and age ( $28 \pm 1$  days) were allocated to either control diet (CT) or control diet supplemented with 100 g/t of stimbiotic (STB) and fed for 42 days. Piglets in each pen were weighed on days 0, 14, 28 and 42. Blood samples were collected from randomly selected piglets on day 14 and 42 and faecal sample on day 42. STB improved the BW of piglets on days 28 and 42 ( $P < 0.05$ ) and increased daily weight gain and daily feed intake from days 14-28 and throughout the trial ( $P < 0.05$ ). IGF-1 levels on day 42 were also significantly improved by STB ( $P < 0.05$ ). STB inclusion also increased the relative abundance of beneficial bacteria such as *Clostridium sensu stricto* 1 and unclassified *f\_Lachnospiraceae*, norank *f\_Muribaculaceae*, *Rikenellaceae\_RC9\_gut\_group*, *Parabacteroides* and unclassified *f\_Oscillospiraceae*. Stimbiotic improved the beneficial microbiota in the faces, increase plasma IGF-1 levels of piglets, thus improving the growth performance and feed intake of weaned piglets.

### The effects of a grape by-product on the local and systemic antioxidant response in piglets after weaning

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The current challenge for pig sector is the finding of new nutritional alternatives which can promote the intestinal health in piglets. The agro-industrial by-products are low-cost source of bioactive compounds which have anti-oxidant, anti-inflammatory and anti-microbial properties. Of these by-products, grape wastes are sources of bioactive ingredients with potential use in animal nutrition. Starting from these data, the aim of our study was to investigate the effects of a diet included 8% of grape seed meal (GSM) on several parameters of systemic and local antioxidant response in piglets after weaning. Briefly, pigs were fed for 30 days with a control or a GSM diet. At the end of the feeding trial, the plasma and organ samples (duodenum, spleen) were collected, and the activity of enzymes belonging to antioxidant system (catalase CAT, glutathione peroxidase GPx, superoxide dismutase SOD), total antioxidant capacity (TAC) and lipid peroxidation were analysed using specific kits. The obtained results showed that GSM diet increased the activity of SOD (+45%,  $p < 0.001$ ) and TAC (+27%,  $p < 0.001$ ) in plasma samples when compared to Control. Also, in spleen GPx activity and TAC were increased in piglets fed GSM diet versus those fed Control diet (+29%,  $p < 0.001$  and +25%,  $p < 0.001$  respectively), while in small intestine (duodenum) only the GPx activity was increased (+21%,  $p < 0.050$ ). The lipid peroxidation was decreased in plasma and duodenum samples collected from piglets fed GSM diet (-26%,  $p < 0.005$  and -51%,  $p < 0.001$  respectively). In conclusion, these results suggested that grape seed meal could be used to improve the antioxidant responses in pigs after weaning.

### Feeding wheat bran can modify several gut parameters and the excreta composition of broiler chickens

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A feeding trial was carried out with 192 Ross 308 broiler cockerels, kept in floor pens. Two dietary treatments were used in 4 replicate pens of 24 birds each. Beside a commercial corn and soybean meal based control diet (treatment C), diets containing wheat barn (treatment WB) was fed. The wheat bran content of the starter, grower and finisher diets were 3%, 6% and 6% respectively. The diets were isocaloric and isonitrogenous, differed only in their fibre content. No significant effects in the growth rate or feed conversion ratio of chickens were observed. However, feeding the wheat bran containing diets increased the crypt depth in the ileum and caecum. The treatments failed to modify the trypsin, lipase and amylase activity in the jejunum, the pH, the short chain fatty acid (SCFA) content and the bacterial diversity of the caeca. In the caeca treatment WB decreased the abundance of phylum *Firmicutes* by 3.0% and increased the ratio of *Verrucomicrobia* by 5.4%. The strongest change at genus level *Akkermansia* was increased at treatment WB (5.6%). Diet composition affected also the composition of nitrogenous compounds of the excreta. Feeding wheat bran decreased the ratio of  $\text{NH}_4^+$  and uric acid in the excreta and increased the in vitro volatility of ammonia in the first 4 hours of incubation. The reason for this could be the excreta of treatment WB had higher ureolytic enzyme activity.

### Reproductive indices in rabbit does after dietary supplementation with nutraceutical substances: Preliminary data

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Aim of the present work was to investigate the effect of *Chlorella vulgaris* and *Laurus nobilis* on selected reproductive indices in intensive reared rabbit does. Second parity New Zealand White does (n = 60) were enrolled for two consecutive reproductive cycles. Rabbit does were randomly assigned to one of four experimental groups (n = 15 replicates per treatment). The first control group (CON) received a commercial pellet-diet; experimental CHL group received the same diet supplemented with 0.1% of dried *Chlorella* algae powder; experimental LAU group received control diet supplemented with 0.1% of dried bay leaves powder; experimental MIX group received control diet supplemented with a mixture of the same doses of both natural dried plants. Considering data on the first reproductive cycle, dietary treatments did not influence ( $P > 0.05$ ) the number of kits per litter (born alive and dead) and number of animals at the weaning period. A significant effect ( $P < 0.05$ ) was observed on kits mortality rate (percentage of mortality during lactation), with LAU group as the lowest value among all experimental groups. No effect was noticed on parameters regarding weight of litter, weight of single kit and average daily gain during the experimental period. In conclusion, no detrimental effect was observed on reproductive parameters after the use of *Chlorella* algae and bay leaves as feed supplements alone and in combination. Among them, these preliminary data underline a lower mortality of kits during lactation period, obtained in rabbit does fed with *Laurus nobilis*.

### Effects of local oil cakes supplementation on yolk and albumen colour and nutritional value of yolk lipids in Estonian quail eggs

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The aim of the study was to investigate the effects of supplementing commercial diets with rapeseed, hempseed and camelina seed cakes on the yolk and albumen colour and nutritional value of yolk lipids in Estonian quail eggs. A total of 585 eggs from 180 laying females were used to evaluate egg quality of three quail groups each fed a diet supplemented with 10% rapeseed, hemp or camelina seed cakes. The applied CIE L\* a\* b\* and L\*C h colour space system demonstrated high lightness and yellowness as well as a light greenish shading of the yolk in all the groups. The higher lightness (L\*) of the yolk was detected in the group of quail fed the diet supplemented with rapeseed and camelina cakes compared to the hempseed addition. A lower yolk negative a\* value was estimated in the hemp group than in the groups fed rapeseed and camelina seed cake supplements, while the rapeseed group demonstrated lower albumen yellowness (b\*) and colour saturation (C). The highest and lowest proportions of total saturated (SFAs) and monounsaturated (MUFAs) fatty acids, respectively, were found in the yolk lipids of quails fed a mixture supplemented by hemp cake. A higher proportion of polyunsaturated fatty acids (PUFAs) was only found in the hemp group. The highest and lowest n-6/n-3 PUFA ratios were found in the yolk lipids of quail receiving mixtures supplemented with rapeseed and camelina cakes, respectively. The yolk of the quail from the rapeseed group showed more favourable lower and higher atherogenic index (AI) and hypocholesterolemic/hypercholesterolemic (h/H) ratio compared to the hemp and camelina groups. n-3 PUFAs rich diets did not result in reduced cholesterol content.

### Session 02

### Theatre 7

#### Broiler chick's carcass yield and meat quality when supplemented with yeasts bioproducts

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The current study aimed to evaluate the effects of using inactive yeasts as dietary supplements: spent brewer's yeast (SBY), with or without the addition of *Rhodotorula* spp. (Rh) on broiler breast and thigh meat characteristics. During 42 days trial, 320 one-day-old Ross 308 broiler chicks were randomly divided into eight experimental groups (4 x 2 factorial design), with SBY (0, 0.6, 1, and 1.3 g/kg feed) and Rh (0 or 0.3 g/t feed) levels of supplementation. Breast and thigh meat of the slaughtered broilers (n=5/group) were evaluated for pH24, color, chemical composition, and texture profile analysis. Broiler chicks' breast and thigh meat color were improved (p<0.05) by inactive Rh addition, resulting in a predominantly reddish color (a\*). Similar protein content was detected in broilers' breast and thigh meat supplemented with SBY (at levels 0, 0.6, and 1 g/kg feed). The SBY x Rh dietary supplementation interaction positively affected (p<0.05) chicks' breast and thigh meat moisture concentration values. The obtained results allow us to conclude that dietary supplementing inactive yeast products improves broilers' meat's physicochemical attributes.

**Alternative proteins: new trends in nutrition**

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Proteins obtained from alternative sources such as plants, microorganisms and insects have attracted considerable interest in the formulation of new food products that have a lower environmental footprint and offer a means to feed a growing world population and are also relevant in animal nutrition. Compared to conventionally produced proteins, alternative proteins require fewer inputs (soil, water) and generate far fewer negative greenhouse gas emissions. Three types of insects are allowed on the European market as new foods safe for human consumption (*Tenebrio molitor* – yellow mealworm, *Locusta migratoria* – migratory locust and *Acheta domestica* – house cricket). These are allowed in dried whole, frozen and powdered forms. EFSA is currently assessing the safety of another nine new food applications from insects. Insects are also commonly used in animal feed, with the European Commission amending the EU Feed Regulation in 2021 to ban the use of processed insect proteins in poultry and pig feed, likely to make these feeds cheaper and more sustainable. In addition to insect proteins, the compositional, structural, and functional properties of other alternative proteins from plants, algae and fungi are being investigated for nutrition. Recently, the food industry has focused on factors associated with the creation of functional components rich in proteins from alternative sources. In this context, different protein fractions in alternative protein sources have been described, as well as their behaviour under different environmental conditions (e.g. pH, ionic strength and temperature). Available extraction approaches are introduced to produce functional protein components from alternative sources suitable for creating active meat and dairy products.

## Session 02

## Theatre 9

**Insect meal. An effective alternative source of nutrients in animal nutrition?**

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Projected population growth by 2050 could reach 9 billion people. This growth brings with it challenges in terms of increased food production with an emphasis on efficient, eco- and environmentally friendly livestock farming. One possible alternative solution is the rearing of insects for the production of high-quality feed for livestock. Insect farming is a very efficient way of bioconversion of industrial and farm residues of both plant and animal origin. The larvae of most insect species can also act as biological protection against the spread of naturally occurring pathogens in livestock farms. In the process of bioconversion, waste is efficiently converted into alternative feed rich in protein and fat. The protein content varies depending on the insect species, the rearing substrate and the stage of morphogenesis ranges. In terms of essential amino acid content, it is characterized in particular by the high content of the essential amino acid in most animal species, taurine. In terms of the synthesis of unsaturated and saturated fatty acids, the insect metabolism is described by unique processes characterized by a low content of monounsaturated fatty acids and long-chain polyunsaturated fatty acids. The advantage of insect meal is mainly its high content of essential linoleic acid and lauric acid. Insect meal is of interest because of its chitin content, the utilization and digestibility of which is a current issue in both human and animal nutrition. In terms of mineral content, insect meal is particularly characterized by its high iron, zinc and calcium content. Key words: nutrition, alternative sources, insects, quality, utilization

### Alterations in the rumen microbial communities and fermentation patterns of lambs fed diets supplemented with organic zinc

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Modulation of ruminal microbial populations by zinc supplementation improves the productivity of animals. We investigated the effect of diets containing organic zinc on microbial population and fermentation parameters in the rumen of lambs. Twenty-eight lambs were divided into four groups: unsupplemented (Control), supplementation with organic zinc (Zn, 70 mg Zn/kg diet), supplementation with herbs (Herbs, 100 g dry matter (DM)/day) and supplementation with a combination of zinc and herbs (Zn+Herbs). After 70 days all the animals were slaughtered and ruminal fermentation parameters and microbial population were analyzed. The diets did not affect the fermentation parameters of lambs. The number of ruminal ciliated protozoa did not differ significantly between the groups. Nineteen animals had mixed A-B type ciliate populations, consisting of *Polyplastron multivesiculatum*, *Epidinium ecaudatum caudatum*, and *Ophryoscolex caudatus tricornatus*, seven animals had A type populations, consisting of *P. multivesiculatum* and *O. caudatus tricornatus*, and two animals had B type populations, consisting of *E. ecaudatum caudatum*. The total bacterial populations were significantly lower for the Zn group than the Control group, but the relative abundances of *Ruminococcus albus*, *Streptococcus bovis* and *Butyrivibrio proteoclasticus* were significantly higher in the group fed the Zn diets. The adaptation of microbiota in the rumen to the long-term period of Zn supplementation was observed. The study was supported by the Slovak Research and Development Agency (APVV 21-0301).

### Session 02

### Poster 1

#### Investigating the potential of mustard seed as an alternative source of bioactive compounds in feed for piglets

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Mustard seed meal (MSM) is a by-product resulting from the extraction of oil through different processes, used in the food industry, but less in the feed for farm animals. The aim of this study was to investigate the bioactive compounds composition from five MSMs and their effect on the *in vitro* proliferation of epithelial intestinal cells as a marker of epithelial renewal in maintaining the intestinal barrier property. The results showed that the composition in bioactive compounds varies from one MSM to another. MSMs are rich in polyphenols (988.6-2273.6 mg GAE/100g), of which the highest concentration being found for catechin (55.95 to 228.91 mg/100g), one of the most powerful antioxidants, polyunsaturated fatty acids, the highest level being recorded for *cis*-oleic acid (25.83 to 46.25%), followed by *cis*-linoleic acid (15.17 to 34.72g FAME/100gTotal FAME) and linolenic acid (7.32 to 12.96g FAME/100gTotal FAME). MSMs contain mineral elements, essential for the development of a rapid and adequate immune response, such as iron (103.06-179.08 ppm), copper (2.45-6.40 ppm), manganese (28.83-32.83 ppm) and zinc (56.34-64.60 ppm). Carbohydrates (glucose, fructose, sucrose) and organic acids (succinic, malic, citric) essential for modulating the intestinal microflora were also determined in MSMs. MTT test was used to determine the effect of MSMs compounds on cell proliferation. IPEC-1 cell cultured at a concentration of  $1 \times 10^4$  cells/well were treated with MSMs polyphenolic extracts. The low concentrations, regardless of the meal source, did not affect cell proliferation. By contrast, the higher concentration of 100 µg decreases the proliferation below 70%. These results will be used as base estimation for further *in vivo* and *ex vivo* experimentation.

### Separation of soybean fractions in floor warehouses and their influence on the soybean oil and meal quality

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Soybean in animal nutrition is a highly valuable component. When storing soybeans, floor warehouses are often used. Due to the specific method of filling such a warehouse with soybeans, the fractions that accumulate on the edges of the soybean pile are separated and at a given moment enter the production line. Therefore, the goal of the paper is to determine how storage conditions and the fractions formation affect the quality of the soybean oil and meal. The research was conducted in a factory for processing soybeans and producing soybean meal, degummed soybean oil and lecithin. The research in floor warehouses was conducted on American yellow class 2 soybeans stored in a huge pile. Grain temperature, air temperature in the warehouse, outside air temperature, air humidity in the warehouse, humidity of individual soybean fractions, protein, oil, cellulose content and hectoliter weight were monitored. Samples for testing were taken at the top, in the middle and at the bottom of the grain mass. Fractions were taken from the grain samples, which were divided into a light fraction (husk + impurities), a medium fraction (soy + husk + impurities) and a heavy fraction (soybean). Due to the increased ratio of the light fraction, there is a significant decrease in the protein and oil content (2 to 3 times less than in the heavy fraction), and the cellulose content is significantly higher (up to 5 times) compared to the heavy fraction. In the case of lighter fractions, the hectoliter mass also decreases, which indicates poor seed quality and the influence of such seed on changes in oil and meal in terms of quality reduction.

## Session 03

## Theatre 1

### Needs of the dairy sector: an European overview

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The dairy sector is facing to several challenges, including environmental and socio-economic impacts of milk production, and the emergence of new diseases. The aim of this R4D Consortium study was to identify the main needs perceived by dairy farmers, researchers, and stakeholders to improve overall farm resilience and long-term sustainability. An online survey was conducted where respondents were asked to select their level of interest in a range of needs within three fields (technical efficiency; environment, animal welfare, and society friendly production systems; economic efficiency and social resilience). The survey was completed by European farmers and dairy stakeholders. Over 500 responses were received across Europe, from Belgium, Denmark, France, Finland, Ireland, Germany, Italy, Lithuania, Luxembourg, Hungary, Netherlands, Northern Ireland, Poland, Slovenia, and Spain. Work-life balance, welfare conditions of cows, and salary were the main issues identified by respondents, regardless of farm size and level of education. In contrast, innovative devices for animal identification and milking strategies, as well as, special supplements were not identified as crucial needs. The early detection and prevention of animal health problems proved to be the main issues within the technical efficiency field. In the field of environment, animal welfare, and society friendly production systems, the main requirements were the improvement of welfare conditions of calves and cows, as well as, the effective communication of agriculture in society. Within economic efficiency and social resilience, flexibility was considered important, as well as, work-life balance and salary.

**Mountain livestock production – much more than a sustainable agricultural niche**

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Mountain livestock production has a long tradition in connecting different environmental conditions with local livestock resources. These marginal agricultural lands provided an important source of feed to maintain local livestock populations during the summer months. The eco-system services provided by the traditional mountain production systems, along with the positive effects of summer grazing on animal health, justify the efforts to preserve mountain animal production. EAAP established an across-commissions Working Group on Mountain Livestock Farming made of experts on different aspects of animal production and breeding. The group is a welcoming platform for discussion on livestock production in mountain areas in a broad and transdisciplinary perspective. The aim of the group is to identify the most important aspects and problems of animal production in mountain regions and to help preserve it for the future. The mandate of the group is to disseminate relevant outcomes by organizing conference sessions, meetings, and other events with related initiatives that will enable researchers and stakeholders to contribute and exchange their knowledge, experiences and innovations.

## Session 03

## Theatre 3

**Preliminary analysis of beef production systems in central and northern regions of Slovakia**

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We analyzed data from 24 farms producing finishing cattle or weaned calves in order to identify the environmental and economic circumstances of beef production for the year 2021. Database was established based on information about animal turnover, costs and profit calculations, and detailed consultations at the farm site. Geographical position of farms in our research was mostly in regions with highlands and higher sloppiness of farmland (21 farms; count). Mean size of farms was 1276.1 ha (20 farms; count) from which the average share of grassland area represented 68.2 %. Structure of breeds was dominated by Limousine (41.3 % of total; 1487 cows) and Charolais (32.7 % of total; 1177 cows), followed by other breeds of beef cattle. Calf crop was 89 % and average daily gain until weaning was 1085 grams. The highest proportions of costs were linked to feeding (42 %) and workforce (25 %) – 65 livestock units per worker. Reduction of mortality percentage of calves (8 %) and age at first calving (36 months and 22 days) found in this dataset presents an opportunity to increase production efficiency. Emission factors of cows were 93.6 kg, 1.22 kg, and 15.16 kg per animal/year for methane, nitrous oxide and ammonia, respectively. Farm with the average size (150 cows) in our dataset helps to capture 935 tons of organic matter per year in the biogenic conversion of nutrients. Outcomes of this research will provide structure to evaluate larger data views of this database in pursuit of developing the analytical platform for quantifying the impacts of different management decisions in specific regions and farms. This publication was supported by SMARTFARM – 313011W112, cofinanced by the European Regional Development Fund.1111121112

**EuroSheep: Cost benefit and Sustainability analysis of Health and Nutrition Best Practices**

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Within EuroSheep project, Best Practices (BP) answering sheep health and nutrition issues were suggested by partner countries and implemented by farmers in other partner countries to assess their suitability. Alongside this assessment, Cost-Benefit (CB) and Sustainability analyses (SA) were performed by the countries provided the 51 BP selected by stakeholders. CB analysis included additional costs of implementing the identified BP at farm level and/or savings in production costs and monetary benefits. SA assessed the impact of the identified BPs on environmental issues. The CB and SA templates included a description of farm/situation in which the analyses were performed. As several indicators such as energy consumption, farm inputs and productivity rates were common, the SA template was developed as a complement to the CB. Additional indicators refer to benefits, as animal welfare, better work environment, free time, etc. On the 51 BP analysed, 55% lead to an increase in working time, but 27% decrease feeding costs and 37% medicine costs. Most, 88%, lead to an increase of the outputs (meat or dairy). Regarding the SA, the 78% of BP increase the feed efficiency, 88% have a positive impact of animal welfare and 53% a positive impact on the atmosphere.

## Session 03

## Theatre 5

**Agro-ecological practices in a dairy herd simulated digitally in a serious game SEGAE**

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Currently, one of the main challenges facing agriculture is to produce enough food in a way that is as friendly as possible to the environment and farm animals. Agro-ecology is becoming one of the promising solutions to achieve these goals. The above topic was covered by the Erasmus+ project (2017-2020) Development of a serious game for digital learning of agroecology in Europe (SEGAE), carried out by a consortium of six European universities: Agrocampus Ouest (FR), Groupe ESA (FR), Oniris (FR), University of Agriculture in Krakow (PL), University of Bologna (IT) and University of Liège (BE). The model describing the functioning of a farm consists of five modules: soil, crops, animals, ecosystem, socio-economic aspects, created based on mathematical equations and/or expert knowledge. The animal module represents the dairy herd structure and dynamics, animal housing and equipment, feed requirements, milk and meat production, animal health, manure management and environmental impacts from animals. The set of variables and parameters of each module as well as available farm practices and ecosystem services are specific for each country. Steering indicators (technical, environmental, economic and social) are displayed on screen, allowing the player to assess the relevance of implemented agroecological practices and the distance from the objective which is economically, environmentally and socially sustainable development of the farm.



**FaoStat facts about horse gray market in EU countries**

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All Equidae within the EU countries must have an identification document (ID) which is used for identifying the animal, transporting, as the certificate for breeding purposes, and whether the animal is used in the food chain. Recent investigations carried out by the authorities within the EU countries revealed that the ID is used for different frauds. The main fraud represents the illegal use of horses classified as not for human consumption. Such status horses could get if this is a breeder decision, the foal is not registered according to EU legislation, lost ID, or the horse is treated with not allowed medicine. Horses declared as »not for human consumption« often end up illegally in the food chain. The aim of this study was to analyze the FaoStat data on the horse population for each EU country. Data for the analysis included horse population size, annually imported, exported, and slaughtered horses. Records with missing values were excluded, and the obtained data from the year 1994 to 2017 were used for the further analysis. Results showed significant differences for all attributes, both between countries and between years. There were more than 100-fold differences between countries with min and max relative values. Obtained relative values are not comparable and often not logical, suggesting that the presented data on the horse population by FaoStat are not credible. In order to have more reliable data, collection methodology must be improved.

## Session 03

## Theatre 7

**The development of equestrian sports in the Republic of Croatia and in the world**

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Equestrian sport in the Croatia is difficult to compare with equestrian sport in large and economically developed countries such as UK, France, Italy, Czechia, Ireland or Belgium, although recently there has been a revival of horse breeding and thus equestrian sport. 72 equestrian clubs are registered in the Croatian Equestrian Association and about 50 equestrian tournaments are organized annually. Most riders competed in show jumping (52%). Almost a third of them competed in dressage (27.5%), while 18% of riders competed in distance riding and 2.5% of riders competed in team sports. The number of riding licenses for the discipline of jumping was 282, for dressage riding 149, for distance riding 99, and for driving a 14. A total of 137 countries are under the auspices of the FEI, divided into 8 groups according to geographical distribution. A total of 29,898 athletes and 55,098 licensed horses were registered. Most of the riders come from Europe (68%). The leading countries according to the percentage of riders in the world are: France (19%), Germany (12%) and Italy (11%). A full 80% of riders come from eight European countries, USA and Saudi Arabia, while the remaining countries have a share of only 20% of riders. According to the number of licensed horses, France leads the way (10,968 horses), owning 1/5 of all licensed horses. Apart from France the largest percentage of horses can be found in Germany (15%), Belgium (10%) and UK (10%).

**Evaluation of economic indicators on Czech dairy farms in recent years**

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Milk production has a long tradition in the Czech Republic (CR) and has always been considered an integral part of livestock production and the entire agricultural sector. However, a reassessment of factors related to milk production economics is needed due to continuing genetic improvements within main dairy breeds and changes in farm management and economic environment. There is a lack of information concerning milk production economics for different cattle breeds and according to the level of milk yields. The aim of this study was to evaluate the development of economic indicators between 2016 and 2021 on Czech dairy farms using the data obtained by means of questionnaires. The farms were divided into four groups according to breed (Czech Fleckvieh and Holstein) and milk yields achieved in 2016. Overall data from 61 farms were analysed using a mixed linear model in SAS software. Total costs per cow and year were higher ( $p < 0.05$ ) in 2021 than in 2016 in all groups. The costs rose over the period analysed in all groups by 19% to 23% due to increasing milk yields and the associated higher feed consumption as well as rising input prices. In the evaluation period the costs per cow per year have risen faster than inflation in the CR. Due to increasing milk yield, the total costs per litre of milk sold had a slower growth rate. Nevertheless, significant differences ( $p < 0.05$ ) between 2016 and 2021 were observed in all groups with the exception of low-yielding Czech Fleckvieh cows. Profitability and the income over feed costs indicator were the highest on farms with Holstein cows and above-average milk yields.

## Session 09A

## Theatre 1

**Qualitative indicators of sperm evaluation of meat breeds of cattle in Slovakia**

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The reproductive health of a bull in natural breeding has a fundamental impact on the economy of farms. With economic models in natural breeding, the question of the bull's reproductive health is very important, considering the ratio of expected increases in the form of live-born calves. That is why we focused on the qualitative evaluation of the quality of sperm of breeding bulls in natural breeding. In this work, we summarised 3 main andrological factors, namely sperm concentration, progressive sperm motility and average path velocity. The analysis refers to the year 2021 in a total number of 162 examined bulls. The age structure represents bulls after evaluation and is recognised as breeding and ranges from 14 months to 8 years. A total of 9 breeds were analysed: Limousine, Short Horn, Aberdeen Angus, Charolais, Simmental, Salers, Pinzgau, Holstein and Blonde d'Aquitaine. From the results, we can conclude that 51.2% of all examined bulls had high-quality sperm for natural breeding. The average sperm quality in the monitored indicators reached 27.8%. At the level of 21% (which represents 34 out of 163 monitored bulls), which have spermatozoa and overall reproductive health at a low level and which require treatment, or other veterinary-technological intervention. By monitoring the andrological health of bulls, we can intervene and increase the quality of sperm in order to eliminate the effects of infertile bulls on the economy of the farm.

**Influence of metabolic status on ovum pick-up success rate and reproductive capability of cows**

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Lately, more emphasis is placed on biotechnological methods to counter the decrease in the conception rate. The ovum pick-up (OPU) allows for repeated and long-term extraction of oocytes from the best cows for in vitro fertilization. This paper aimed to evaluate the results of oocyte aspiration in relation to the metabolism status of Holstein cows and to investigate the effect of this procedure on the further reproductive capability of tested cows. We evaluated 63 cows on their first lactation (36 to 82 DIM). Each tested cow was aspirated twice in a weekly interval. The energy metabolism status was accessed by the fat/protein (F/P) ratio in milk – average during 25 to 35 DIM. Blood samples were also collected and analysed for cholesterol, triacylglycerol, beta-hydroxybutyrate (BHB) and non-esterified fatty acids (NEFA). The OPU began with ultrasonographic examination of the ovaries. A total of 231 oocytes were aspirated from 95 successful OPU. The mean F/P ratio of tested cows was 1.078 with a range of 0.88 to 1.63. The average cholesterol was 4.36 mmol/l, triacylglycerol was 0.11 mmol/l, BHB was 0.30 mmol/l, and NEFA was 0.62 mmol/l. We observed great variability for the F/P ratio and blood metabolites, which demonstrated existing differences in the metabolic status. Most oocytes (OPU with 5 to 12 aspirated oocytes) were collected from dairy cows with approximately average F/P ratio, BHB, and NEMK values. These initial findings are just the start, and these relationships will be further analysed within the project QK22010270 by NAZV CR.

## Session 09A

## Theatre 3

**Influence of post-mortem time intervals on the quality of spermatozoa recovered from the epididymis of common eland bulls (*Taurotragus oryx*)**

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Common eland bulls are used for trophy hunting in South Africa with farming potential for meat. However, several assisted reproductive technologies (ARTs) can be applied to increase production and preserve their genetic materials, including the epididymal spermatozoa recovery after hunting or slaughtering. For this technique, collection period post-mortem is crucial for survivability and quality of spermatozoa for processing and cryopreservation. Hence, this study aimed to determine the effect of post-mortem collection time on the quality of spermatozoa recovered from the epididymis of common eland bulls. Six common eland bulls (2-2.5 years old; 203±20 kilograms) were slaughtered. Spermatozoa were harvested from the left caudal epididymis after dissection. Sperm concentration, motility, and kinematics (0, 15-35, 45-70, and 80-100 minutes post-mortem intervals), sperm morphometric traits, and viability (0, 20, 40, and 80 minutes post-mortem) were measured using a computer-assisted semen analyzer (CASA). Drastic changes were observed in sperm concentration, motility, and kinematics over time. However, sperm morphometric traits were within the normal range regardless of post-mortem time intervals. Overall, it indicates that spermatozoa should be processed and cryopreserved at 15-35 minutes post-mortem using the caudal epididymal recovery method.

**Milk traits as indicators of energy status in early lactation dairy cows from two farms**M. Štolcová<sup>1</sup>, L. Bartoň<sup>1</sup>, D. Řehák<sup>1</sup><sup>1</sup> Institute of Animal Science, Department of Cattle Breeding, Přátelství 815, 10400 Prague, Czech Republic

The aim of this study was (1) to evaluate the relationship between serum nonesterified fatty acids (NEFA) concentrations and selected milk components in Holstein cows from two farms in the first 5 weeks of lactation, and (2) to find a model predicting serum NEFA concentrations from milk traits valid for both herds. We used serum NEFA concentration as a biomarker to assess the energy status of animals. A total of 121 lactating Holstein cows from two farms (Farm 1; n = 52, Farm 2; n = 47) were included in the experiment. Four blood and milk samples were collected from each cow weekly during the first 5 weeks after calving. Blood samples were analyzed for NEFA concentrations and afternoon milk samples were measured for fat, protein, lactose, and milk fatty acids. Serum NEFA concentrations were correlated most strongly with milk long-chain fatty acids ( $r = 0.50$ ,  $r = 0.54$ ,  $r = 0.51$ ;  $P < 0.0001$ ) and C18:1 ( $r = 0.50$ ,  $r = 0.54$ ,  $r = 0.59$ ;  $P < 0.0001$ ) for Farm 1, Farm 2 and the two farms combined, respectively. The linear model for NEFA (logNEFA) prediction was developed ( $R^2 = 0.51$ ;  $MSE = 0.278$ ). The model included the fixed effect of the herd while milk C18:1, C14:1, fat-to-protein ratio, days in milk, and the quadratic term C18:1<sup>2</sup> were involved as covariates. LSMs of logNEFA were significantly different between farms but the slopes of key fatty acids were the same for both farms. This provides a premise for finding a model with the potential for the early detection of cows with an increased risk of energy-related imbalance diseases, which would be valid for multiple farms.

## Session Plenary

## Theatre 1

**Understanding of the transition period in dairy cows**Z. M. Kowalski<sup>1</sup><sup>1</sup> University of Agriculture in Krakow, Department of Animal Nutrition, Biotechnology, and Fisheries, Al. Mickiewicza 21, 31-120 Krakow, Poland

The transition period in dairy cows lasts from -3 weeks prepartum to 4 weeks postpartum. It is the most difficult and demanding period not only for a cow but also for a farmer. The lecture will pay special attention to the close-up dry period which prognoses future milk yield, health, and reproduction. Important challenges, such as decreased dry matter intake, and increased requirements for nutrients, will be confronted with metabolic consequences, including negative energy balance, insulin resistance, hypocalcemia, oxidative stress, and immunosuppression. The results of these impaired metabolic problems are health disorders, including milk fever and subclinical hypocalcemia, ketosis and fatty liver, retained placenta, and infectious diseases (metritis, mastitis). The current knowledge of these disturbances will be presented. During the lecture, special attention will be given to the program of monitoring of subclinical ketosis conducted in dairy herds in Poland, based on the concentration of ketone bodies in milk (acetone (ACE) and beta-hydroxybutyrate (BHB)). In this program, conducted within the milk recording system we detect the cows in the status of hyperketolactia (elevated milk ACE or milk BHB). Since 2013, we have monitored millions of dairy cows, and the results of this monitoring will be reviewed, and the risk factors discussed. Having milk samples analyzed for ACE, we were able to find among the cows suffering from ketosis, those having elevated ACE, but not elevated BHB (about 8%) as well as those having both ACE and BHB elevated. Milk production and composition of cows suffering from different types of hyperketolactia will be presented.

**Use of infrared spectra of milk for genetic improvement of health traits in cattle**

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Mid infrared (MIR) spectra of milk of dairy cows are used to routinely measure the milk components. Based on 1060 wave lengths and wet chemical analysis, prediction equations were developed and are constantly updated. Upon request, the raw spectra data are provided to milk labs and tools for standardization of the spectra data across types of spectrometers are available. Fine components of milk, including fatty acids, protein fractions, minerals and metabolites, are predicted. Prediction of blood metabolites and energy balance of cows have also reasonably good accuracy. In the framework of D4Dairy, an Austrian project to provide digital support to dairy management via data-driven information systems, we developed MIR equations for state of pregnancy, ketosis and mastitis. These affect milk composition, but not limited to a single or few components. Being able to provide a strong indicator of pregnancy state with milk records would greatly benefit farmers. While results looked promising initially, upon disentangling stage of lactation and state of pregnancy, the accuracy of prediction was not good enough for implementation. Ketosis is caused by strong negative energy balance and results showed that clinical ketosis could be predicted with reasonable accuracy. For clinical mastitis, accuracies were moderate, adding information to somatic cell score, the routine predictor of mastitis. Yet it was not strong enough for inclusion into the udder health index. We conclude that MIR based prediction equations for health traits have moderate accuracies, that may or may not be strong enough to be included in routine genetic evaluation.

## Session Plenary

## Theatre 3

**Implementation of low-cost genomic selection, phenotyping for methane emission and disease challenges using DNA sequencing technology**

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DNA sequencing technology now allows for low-cost discovery and subsequent implementation of parentage assignment, estimation of breed composition, variant discovery, and genomic selection. Examples will be provided using restriction enzyme reduced representational sequencing (RE-RRS) and genotyping-in-thousands by sequencing (GT-seq) methods. Modification of the same sequencing protocols also enable rumen microbial profiling to predict methane emissions and feed efficiency in ruminants. The same methods can be used for quantification of bacterial and viral infections during natural and artificial disease challenges for subsequent use in breeding programmes. Examples and results will be provided. These methods can be implemented at a cost of between 9 and 18 Euro per sample including extraction, analysis and are particularly relevant for minor species because of their very low set-up costs.

**Selecting to lower the environmental impact of livestock production**M. Pszczola<sup>1,2</sup><sup>1</sup> Poznan University of Life Sciences, Department of Genetics and Animal Breeding, Wołyńska 33, 60-637 Poznan, Poland,<sup>2</sup> Centre for Genetics, Polish Federation of Cattle Breeders and Dairy Farmers, Dąbrowskiego 79A, 60-529 Poznan, Poland

Thanks to their abilities to convert otherwise investigable feed into energy i.e. milk or meat, ruminants are essential for delivering nutrients needed to feed the still-growing human population. Methane emission is the side effect of their digestive process. The contribution of enteric methane emissions to the total greenhouse gas emissions ranges from a few to about fifty per cent. Selective breeding is one of the methods to reduce emissions by providing small but cumulative changes. The heritability of methane emissions ranges from 5-25%. The estimated genetic correlations between feed efficiency and methane production suggest that lowering emissions can improve the profitability of production. Additionally, indicator traits, such as milk spectra analysis or the use of rumen microbiome can enhance the reliability of the methane phenotypes. The next step is to run a national genetic evaluation of environmentally important traits and to include these traits in the national breeding goals to lower the environmental impact of livestock production.

## Session Plenary

## Theatre 5

**Mitogenome information in cattle breeding and diversity management: an untapped treasure?**I. Curik<sup>1</sup>, V. Brajkovic<sup>1</sup>, D. Hršak<sup>2</sup>, S. Ristov<sup>2</sup>, V. Cubric-Curik<sup>1</sup>, D. Novosel<sup>1,3</sup><sup>1</sup> University of Zagreb, Faculty of Agriculture, Svetošimunska 25, 10000 Zagreb, Croatia, <sup>2</sup> Ruđer Bošković Institute, Bijenička 54, 10000 Zagreb, Croatia, <sup>3</sup> Croatian Veterinary Institute, Savska cesta 143, 10000 Zagreb, Croatia

Mitochondria, whose mitochondrial DNA (~16.5 Kb) or mitogenome is passed through maternal inheritance, play a critical role in the general functional aspects of mammalian cells, and their dysfunction has been associated with various metabolic phenotypes related to bioenergy. Therefore, it is surprising that information about the mitogenome has been little used in animal breeding and diversity management. In the following, we first provide an overview of the biological aspects of mitochondrial inheritance and its implications for shaping phenotypic variation. Using cattle as an example, we will show how mitogenome information can help to i) estimate the impact on quantitative traits important for cattle production, ii) identify deleterious mutations that cause disease, iii) identify ancient introgression and upgrading, iv) estimate genetic diversity and relatedness of populations, v) screen and/or identify pedigree errors, and vi) estimate mitochondrial effectiveness and its link to productive traits. Finally, we will present some recent developments where mitogenome information has been implemented in the commercial SNP chip. This presentation was supported by the Croatian Science Foundation under the project ANA-GRAMS-IP -2018-01-8708.

**Research on stem cells and their use in conservation of animal genetic resources**

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In general, banking of stem and progenitor cells of human or even other animal's origin is a common method used to cryogenically preserve those cells for their further use. However, stem cell banks should provide a source of stem cell lines that meet high quality and safety standards. Therefore, a proper methodology is required to isolate and characterize these cells. Several farm animal breeds in Slovakia are endangered or at risk based on the monitoring. Therefore, mesenchymal stem cells (MSCs) and endothelial progenitor cells derived from Slovak rabbit breeds (Nitra, Zobor and Zemplin rabbit), and primordial germ cells and MSCs from Slovak chicken breed Oravka have been recently successfully isolated and cryopreserved in gene bank of animal genetic resources at NPPC – RIAP Nitra in collaboration with the Slovak University of Agriculture in Nitra. The stored samples are recorded in the international database CryoWEB (<http://cryo-sk.cvzv.sk/>). This work was supported by the grants: APVV-14-0348, APVV-18-0146, APVV-20-0006 and VEGA 1/0160/18.

## Session 04

## Theatre 1

**Funding of animal genetic resources conservation in Slovakia**

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Financial support for the farmers of local breeds is one of the main measures that support conservation of local animal genetic resources. In the past, support was provided from the state funds in Slovakia. A new funding scheme was applied after joining the European Union in 2004. Support has been paid solely for livestock unit, regardless of sex or level of endangerment. This has been in the contrast to other European countries where different conditions were taken into account. In the period 2014 – 2020 assessment of endangerment was based partly on number of registered purebred breeding females, as well as on effective population size. Aim of this study was to compare the numbers of supported farmers and animals with population data of endangered local breeds in Slovakia. In general, rapid increase of supported animals and breeders was observed in the first years of the period. Although the number of purebred Slovak Pinzgau cows could be considered stabilized, the transfer of cows from milk production to cow-calf system was observed. The number of supported farmers during the period didn't change significantly. In horses, numbers of purebred females were slightly fluctuating. The number of supported animals and horse breeders was slightly increasing during the period. Trends were different in two supported breeds of goats. While the number of purebred White Shorthaired goat females was decreasing, the number of Brown Shorthaired goats was increasing. The change in number of supported animals and breeders was very small. In sheep, number of purebred registered females increased in Askanian Merino and Valachian sheep. Rapid decrease of Tsigai and Improved Valachian registered females levelled off in 2016, when they became eligible for support.

**Genomic regions associated with phenotypic differentiation in European local pig breeds**

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Many local pig breeds have been raised in extensive systems and have adapted to the specific environment causing rich phenotypic and genetic diversity. The present study aimed to detect genomic regions associated with phenotypic differentiation on stature, fatness, growth and reproductive performance in 20 European local pig breeds using a newly developed approach to search selection signatures linked to phenotype at the breed level. The analysis revealed 16 significant genomic regions associated with stature, 24 with fatness, 2 with growth and 192 with reproduction. Among them, several regions contained candidate genes with possible link to biological effect on phenotype. In the stature group, for example, genes *ANTXR1* (interacts with actin cytoskeleton) and *ANXA4* (involved in membrane-related pathways) were identified, in the fatness group genes *POMC* (energy balance via the leptin/melanocortin pathway) and *DNMT3A* (CpG methylation; adipose tissue development), and in the reproduction group gene *HSD17B7* (biosynthesis of sex steroids and cholesterol). To conclude, the genome scan for selection revealed several strong candidate genes with potential implication in adaptation of European local pig breeds to different production systems, which will be helpful for future conservation approaches. Financing of Slovenian Agency of Research (grants P4-0133, J4-3094, PhD scholarship for KP), and project TREASURE (EU H2020 GA no. 634476) is acknowledged.

## Session 04

## Theatre 3

**Inbreeding evaluation in Latvian local breeds**

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In this study, inbreeding and effective population size of the Latvian cattle, sheep and goat local breeds were analysed. Two cattle breeds, Latvian Brown old type (LB) and Latvian Blue (LZ), which has been selected in Latvia for more than 100 years, were included in the analysis. During the last decade, the inbreeding level in cattle populations increased and reached 2.61% for LB and 5.20% for LZ at the time of data selection. Effective population size during the last five years decreased and for LZ was 79 and 112 for LB. At the beginning of the 19th century, coarse-wooled short-tailed sheep were bred in Latvia. The Latvian Darkhead (LT) breed was mentioned for the first time after 1945. Pedigree data for LT started from 1976 with a total of 2296 records. The reference population included 47 males and 502 females that were alive at the time of data selection and defined as GR. In 2019 the effective population size was 122 animals and the inbreeding of animals was 3%. Latvian native goat (LVK) was kept in Latvia since the end of the 19th and the beginning of the 20th century. Pedigree data for LVK started from 1983; the total number of records in pedigree was 3547. The criteria for data selection for the reference population was an LVK abbreviation in pedigree, and the animal was alive at that moment. Over the years, the inbreeding level has increased from 0.36 to 2.3% for LVK offsprings. In the LVK population, there are animals with an inbreeding level higher than 20 %. According to the results in all local Latvian breeds, the level of inbreeding was increased and the number and rate of males and females should be controlled in the local populations. Research was supported by the Ministry of Agriculture of the Republic of Latvia.



**Recent activities for ex situ conservation of AnGR in Poland**

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The important role of ex situ methods in ensuring the conservation of animal resources has been emphasized in the Animal Genetic Resources Strategy for Europe. The role of genbanks, including new technologies, is one of the key recommendations of this document. EU provisions facilitate the possibility of extending the protection of AnGR by ex situ methods. In Poland, the main method is still in situ conservation of a total of 87 breeds of farm animals. In 2014, Poland established a national gene bank as a long-term insurance to maintain AnGR diversity, mainly cattle, pigs, horses, sheep and goats but unfortunately, ex situ conservation is carried out continuously and routinely only for two species: cattle (ex situ in vitro) and poultry (ex situ in vivo). For other species it is used infrequently and on a species basis (pig- embryo collection, sheep -historical semen and embryo collection), or it is impossible because of formal, financial or technical obstacles. There has been an increase in activity in this field recently. Work is underway to adapt the national legislation to the EU, so that ex situ conservation can be carried out to a greater extent based on the available, already existing infrastructure. There has been progress in the development and implementation of the method of cryopreservation of semen from rare bees and poultry lines. The semen collection from stallions of selected conservative breeds has been started. The scope of protection of cattle breeds was increased by adding part of the funds of the agri-environmental program to finance bulls of native breeds for semen collection. We are strengthening cooperation between entities within the network for the long-term conservation of AnGR by signing agreements and building awareness about the importance of ex situ conservation.

## Session 04

## Theatre 5

**Consequences and negatives in the management of local sheep breeds with risk status - threatened with extinction**

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In the context of the new European strategy for AnGRs, this article analyzes the management of local sheep breeds in Bulgaria. The role of the farmer and the role of the breeding organization specialist are emphasized. The role of Regulation 2016 / 1012 for the management of genetic resources in animal husbandry is evaluated. Weaknesses and underdeveloped articles and paragraphs of Regulation 2016 / 1012 are indicated. Special attention is paid to the procedure for the recognition of breeding organizations. The right of farmers to associate and establish breeding organizations in the country was overexposed and the paradox of one endangered local breed being recognized by two or more breeding organizations and two or more breeding programs for an endangered local breed being approved. This leads to the fragmentation of the breed and to a number of negative phenomena, such as the risk of increasing the degree of inbreeding, reducing the potential for building the capacity for management of GHG, migration of farmers from one breeding organization, reduced breeding discipline on the part of some farmers. To a large extent, these negatives are due to the lack of clarity and certainty in certain articles and paragraphs of Regulation 2016 / 1012. To overcome these negatives, proposals for changes and additions to some articles and paragraphs of Regulation 2016 / 1012 have been made.

**Genomic connectedness between local populations of Valachian sheep**

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The Valachian sheep are recognised as an important native group of breeds well adapted to low-input sustainable farming systems. This study aimed to determine the genomic diversity level and connectedness between four breeds belonging to this group from Slovakia (Original and Improved Valachian sheep), Serbia (Pramenka) and Romania (Tsurcana). The database included information about 214 animals and 39960 informative SNPs. A higher level of genomic diversity (total average  $H_o=0.40$ ,  $H_e=0.39$ ,  $F_{HOM}=-0.01$ ) compared to other cosmopolitan breeds indicated that the gene pool of studied breeds includes variants ensuring their adaptability to diverse production environments. The highest level of heterozygosity ( $H_o=0.42\pm0.12$ ,  $H_e=0.42\pm0.11$ ) showed Improved Valachian sheep, whereas the lowest genomic inbreeding was found in the Pramenka population ( $F_{HOM}=-0.03\pm0.04$ ). Even if average  $F_{ST}$  ( $0.05\pm0.01$ ) and  $D_a$  ( $0.05\pm0.02$ ) values confirmed that analysed breeds shared common genetic variants originating from the period before the Valachian colonisation, subsequent analyses showed that they form separate units with limited gene flow. This study was supported by the Slovak Agency for Research and Development (APVV-17-0060, APVV-20-0161, SK-SRB-21-0013) and the project SMARTFARM ITMS 313011W112.

## Session 04

## Theatre 7

**Population structure and genomic characterisation of Czech and Slovak local goat breeds**

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Goat rearing is an important sector of livestock production and managing the genetic diversity of local goat breeds is an important component of genetic improvement and environmental adaptation. The aim of this study was to analyse the genetic diversity based on 46 862 autosomal SNPs of the Czech and Slovak local goat breeds (Czech White Shorthair – CWS, Slovak White Shorthair – SWS, Czech Brown Shorthair – CBS and Czech Landrace – CLA). This analysis was based on 140 individuals representing Czech and Slovak local breeds and sixteen Austrian and Swiss goat breeds (639 genotypes in total). We demonstrated that the Czech and Slovak local goat breeds are genetically similar populations. All Czech and one Slovak local breeds were closely related to other Austrian and Swiss goats. We also estimated genomic inbreeding level ( $F_{ROH}$ ) and effective population size ( $N_eLD$ ) for each breed. Estimated effective population size ( $N_eLD$ ) for Czech and Slovak local breeds ranged from 56 (CLA) to 267 (CWS). We demonstrated that Czech and Slovak local breeds are affected by a loss of genetic diversity, while they are genetically related. The present results show that appropriate management of genetic diversity in local goat breeds is urgently needed to support the conservation of the specific biocultural system of grazing. This study was supported by projects QK1910156, APVV-20-0161, ANAGRAMS-IP -2018-01-8708 and Erasmus+ KA2 grant no. 2021-1-SK01-KA220-HED-000032068.

**Genomic assessment of population structure, admixture and conservation status of two Croatian goat breeds**

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The aim of this study was to determine the position of two Croatian goats in the global context using genome-wide SNP data, while assessing population structure, admixture, and conservation status. All analyses were performed on the genotypes of 11 Istrian and 33 Croatian coloured goats and a sample of 2255 goats from 66 global goat breeds. Neighbor net and admixture results show that two breeds have high genetic diversity, with much of the historical admixture due to an extensive production system. Principal component analysis (PCA) showed clear clustering between the two breeds, while some Istrian goats showed clear clustering with the Saanen breed. The Croatian Coloured goat was most similar to the Greek goats. The results obtained with the Treemix software confirmed these findings and showed gene flow from the Croatian Coloured goat to the Istrian goat. Despite the low Ne for the Istrian goat, both breeds showed a low degree of inbreeding (FROH~0.05). Considering these results, the Istrian goat is at high risk of extinction and should be carefully monitored.

## Session 04

## Theatre 9

**Phenetic classification of some local poultry species using haematological, serum and biochemical indices**

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Taxonomy, the science of classification of organisms, is a system of arranging animals and plants into natural, related groups based on structure, embryology, or biochemistry into kingdom, phylum, class, order, family, genus, and species. This study aimed at using haematological and biochemical parameters of blood of six poultry birds from three different families [Phasiniidae (Chicken, Turkey and Quail), Numidae (Guinea Fowl) and Anatidae (Goose and Duck)] to investigate the effect of species on haematological and biochemical parameters and statistically classify the species into distinct clusters. Blood was collected from the wing vein of five birds each of each specie. Two sets of blood samples on each of the 30 birds across the six species were evaluated for haematology and serum biochemistry parameters. Data from the laboratory were statistically analyzed using Minitab (17) Statistical Software for descriptive, analysis of variance, cluster analysis and discriminant analysis. The method used in the cluster analysis was the Ward linkage, Euclidean distance model. Effect of specie was significant ( $P < 0.05$ ) on all haematological and biochemical indices studied, providing a veritable platform for phenetic discrimination across the six species investigated. However, the three clusters produced by the dendrogram had Duck, Chicken and Turkey in the first cluster, Guinea Fowl and Quail in the second cluster while Goose was alone in the third cluster. There was no misclassification in the discriminant analysis, whereby all six species in the test data were classified appropriately with a 100 percent accuracy. A further investigation of the genetic similarity among the species becomes necessary.

**Estimation of genetic parameters in three horse populations using pedigree and molecular analysis**

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We compared estimation of inbreeding based on pedigree data and STR analysis in three horse populations, Slovenian populations of Lipizzan and American Quarter horses and Czech population of Kladruher horse. The Lipizzan horse is a Slovenian indigenous breed originating from local Karst horses from 16<sup>th</sup> century and at present there are six classical stallion lines Neapolitano, Favory, Siglavy, Pluto, Maestoso and Conversano and 18 classical mare families. The Slovenian population of American Quarter horses contains 2000 animals and represents a fragment of the global AQH population. The Czech population of Kladruher horse represents a historical parallel to the Lipizzan population and has comparable quality and depth of pedigrees as Lipizzan population. For the molecular estimation of inbreeding we applied 17 STR markers recommended by ISAG. The STR genotyped foals served as a reference population in pedigree analysis. In the pedigree analysis of the Lipizzan population we identified 2356 inbred individuals. The lowest FSTR for all three breeds was 0.07 and the highest over 0.25. Average FSTR was between 0.15 and 0.18. Fped values based on pedigree data were lower and there was no significant correlation between the inbreeding coefficients estimated from pedigree and STR data. Based on our results we propose several measures, including regular updating, greater numbers of horses active in reproduction and systematic physical evaluation for all three populations in order to preserve genetic diversity and allow genetic improvement.

**History and present of poultry genetic resources in the Czech Republic**

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Animal genetic resources in the Czech Republic include 3 groups of poultry genetic resources. The original special management of each breed involved in the program is the responsibility of the guarantors. The first group are 3 breeds in hobby breeding. The guarantor is the Czech Breeders' Association in charge of the Breeders' Club of this breed. Czech Golden Speckled Hen. Represented by 37 cockerels and 353 hens from 17 breeders. Rotation of cockerels is organized to minimize inbreeding. In the case of Czech geese, the history goes back to the beginning of the twentieth century. The hobby breeders' club includes 34 flocks with 205 birds of classic Czech White Geese and 9 flocks with 68 birds of Czech Crested Geese. The second group (history from 1955 to 1972) consists of pure lines of commercially implemented hybridization programs of laying hens and waterfowl. These lines are owned by private business operators. All these companies implement their own original management for their own selection program. The third group are highly inbred ( 16) pure layer lines, ( 4) outbred pure layer lines and ( 3) new transgenic layer lines under management of Breeding Centre of Institute of Molecular Genetics, Prague. The history of unique lines for molecular genetic studies dates back to 1932.

### Genotyping of microsatellite markers for the verification of variability in honeybee populations in the Czech Republic

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The aim of the study was to select and test microsatellite markers in honeybee (*Apis mellifera*) populations in the Czech Republic. After optimizations, the microsatellites were assembled into four multiplexes – MP1, MP2, MP3 and MP4 according to the conditions and parameters of the PCR setup. The aim was to develop a system so that testing could be performed under the same cycling conditions for all 4 multiplexes with the aim to develop only one multiplex by selecting the most suitable microsatellites from these 4 used for diversity screening. In the MS1 panel, the average observed heterozygosity and the average number of alleles were 0.561 and 8.67, in MP2 0.6173 and 12.5, in MP3 1.00 and 4.67, and in MP4 1.00 and 3.25. After the genotyping of all samples is completed, the most polymorphic markers will be selected that will be suitable for routine verification of variability in specific bee populations in the Czech Republic. This output has been supported by the project ISAGREED grant no. 2021-1-SK01-KA220-HED-000032068 and the project NAZV no. QK22020324.

### Session 04

### Poster 1

#### Analysis of health and welfare of horses kept in tie stalls and box stalls with paddock

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The aim of the study was to compare animal welfare of horses housed in two types of stables: with tie stalls and box stalls, as well as to analyze the mistakes in rearing and later use. Horses on the analyzed stud farms were used for leisure and breeding purposes. The assessment criteria in both stud farms were: dimensions of the buildings and, respectively, dimensions of stalls or boxes, as well as air data probes in the stables. Given the analysis of the results, it should be concluded that microclimatic conditions in the stud farm affected animal welfare and health. Taking into account the obtained values of physical air parameters in tie stalls and in box stalls, with regard to the recommended animal hygiene standards, it should be noted that more favorable environment for horses health and well-being was found in box stalls. The analysis of all the elements of the microclimate of both stables in winter proves that box stalls should be preferred. In box stalls horses have better living conditions, the possibility of free movement and better microclimatic conditions, especially in winter when it is more difficult to ventilate the rooms. The stalls, where horse is tethered to the manger, reduce the freedom of movement – this system worked well when the horses worked intensively and the stables served as a place of feeding and rest. Nowadays, with the change of horse use, this is the least recommended type of stable. This publication has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. 2021-1-SK01-KA220-HED-000032068 “Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalization”.

**Biodiversity of livestock in Poland**J. Krawczyk<sup>1</sup>, E. Sosin<sup>1</sup>, A. Chelmińska<sup>1</sup><sup>1</sup> National Research Institute of Animal Production, Sarego 2, 31-047 Krakow, Poland

With the ratification by Poland of the Convention on Biological Diversity in 1996, our country committed to protect, among others, biodiversity of livestock, and since 2002 the National Research Institute of Animal Production was appointed by the Minister of Agriculture to coordinate and implement activities in this area. Currently, 48 conservation programs for 87 populations have been implemented in Poland, including: Cattle: Polish Red, Polish Red-and-White, Polish Black-and-White, Białogrzbieta; Horses: Hucul horses, Polish Konik, Małopolski, Silesian, Wielkopolski, cold-blooded horses: Szumski and Sokolski types; Sheep: Świniańska, Wrzosówka, Olkuska, Coloured Polish Mountain Sheep, Coloured merino, Uhruska, Wielkopolska, Żelaznienska, Corriedale, Kamieniecka, Pomeranian, Merino old-type, Podhale Zackel, Blackheaded, Pogórza sheep, White-headed meat sheep, Polish mountain sheep; Goats: Carpathian, Sandomierska, Kazimierzowska; Pigs: Puławska, Złotnicka spotted and Złotnicka white; and 11 breeds/strains of laying hens, 14 geese, 10 ducks, Popielno white rabbits, common pastel and white-necked foxes, polecats, beige chinchillas, coypus and 5 lines of bees. The fragmented structure of farms in Poland and financial support from EU funds are conducive to the preservation of native breeds. Since 2002, the number of native breeds has been showing a constant upward trend, and at the end of 2022, over 116,000 animals and 1882 bee families were covered by the conservation program. A wide range of scientific research is carried out using indigenous breeds, aimed at searching for unique quality features of their products, using ex-situ methods in the protection of endangered breeds and preserving genetically determined traits valuable for breeding.

**Mitochondrial haplotype diversity in Slovak autochthonous sheep breeds**M. Mészárosová<sup>1</sup>, G. Mészáros<sup>2</sup>, N. Moravčíková<sup>1</sup>, I. Pavlík<sup>3</sup>, M. Margetin<sup>1</sup>, R. Kasarda<sup>1</sup>

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The mitochondrial DNA is a relatively small part of the entire genome, residing outside of the nucleus, inherited on the maternal lineage. The aim of this work was to use such haplogroups based on single nucleotide polymorphism data to study Slovak autochthonous sheep breeds. GeneSeek GGP Ovine 50K genotypes from 96 Original Valachian (OVA), 69 Improved Valachian (IVA) and 44 Tsigai (CIG) sheep were used for the study. The quality control consisted of deleting any SNPs with more than 10% missingness, which resulted into 32 mitochondrial SNPs present in all three populations. The loci themselves were polymorphic, but individual genotypes were always homozygous. The occasionally missing SNPs were imputed by filling in the most frequent genotype for that particular locus within the breed. In total 11 mitochondrial haplotypes were found. Haplotype 1 occurred most frequently, in a total of 149 out of 209 individuals (20 CIG, 81 OVA and 48 IVA). Haplotypes 2 and 3 occurred in both OVA and IVA breeds, hinting towards the breed history. Interestingly, haplotype 6 occurred in three CIG and also one IVA animal. A total of three private haplotypes were found for the CIG breed, and two each for the OVA and IVA breeds, all of them up to two individuals. The results of the work will be used to help to describe the diversity, and trace maternal lineages within the Slovak sheep breeds. This study was supported by grants number APVV-17-0060 and APVV-20-0161.

### Impact of genomic information on the genetic evaluation of show-jumping performance of horses in the Slovak Republic

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The evaluation of jumping competition qualities is an important part of the selection of breeding stallions and mares of Slovak Warmbloods selected for equestrian disciplines. Horses are tested and evaluated at a young age and later in real sporting activities. Heritability of many traits in the tests and evaluations is low to moderate. Therefore, these horses should be tested with new genomic methods that can lead to increased accuracy in estimating the true genetic quality of the animals. The aim of this study was to estimate the effect of new genomic information on the genetic evaluation of true jumping performance. For the evaluation we used data from the results lists of jumping competitions from 2017 to the present, data from the Register of Horse Breeding in Slovakia and other data provided by the Slovak Equestrian Federation. In total, 2801 individual jumping competitions of genotyped horses (96 horses) were recorded. Based on the results of our analysis, values of AIC (Akaike's information criterion) and increasing values of coefficients of determination ( $R^2$ ), were statistically significant when genomic information was taken into account. We concluded that the inclusion of genomic information increased the average accuracy of the estimated parameters and breeding values of horses by an average of 6 – 13%. The reliability of the analysis after taking into account the SNPs significantly increased. The  $R^2$  value increased from 0.1697 to 0.2251. This publication was supported by APVV-20-0161 and by the Operational Programme Integrated Infrastructure within the project: SMARTFARM (313011W112), cofinanced by the European Regional Development Fund.

### Population status of Trakehner horses in Lithuania

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Due to rapidly growing importation and use of high-performance stallions, Trakehner (T) horse breed in Lithuania (LT) faces challenges, especially when breeding in small and for many years almost closed population requires special responsibility and planning. Risk of genetic diversity loss arises if selection focuses only on increasing production. Aim was to investigate genetic structure of T horses in LT and possible connections with T Stud (1732) horses, evaluate genetic potential and efficiency of breeding work. Analysis was based on data of Farm Animal Register. Effective population size ( $N_e$ ) via breeding animals was calculated. 4290 pedigree records of T born from 1923 to 2022 were used to set genealogical structure. Live horses were sorted according to pedigree and assigned to related groups, which were divided within genealogical clusters. 62% of live stallions were assigned to lines originating from old T stud, 3% – to thoroughbred (XX) Langraf line formed 40 years ago, 32% to other XX lines mostly bred after 1990, 3% – to Arab lines. 60% of mares were assigned to East Prussian families, 19% – to old T Stud families, 16% to XX families, 5% – to Arab and other families.  $N_e$  of T horses in LT was 61, the population was in vulnerable–maintained state. 57% of population belonged to private breeders, but only 15% of horses were used for breeding. 75% of all T horses born in LT were bred by national stud working under conservation programme. Maintenance of old and new genealogical structures is essential. Use of more different T stallions for breeding would increase  $N_e$ . Strengthening of state-funded selection nucleus functions would ensure more stable state of population and preservation of national genetic resources.

### **Analysis of factors influencing the quality and quantity parameters of milk depending on the cow housing system in selected holdings**

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Milk production in Poland increases year by year, while the concentration of production changes, herds become larger and their number decreases. The aim of the work was to analyze the factors influencing the quality and quantity parameters of milk depending on cow housing systems. Two holdings with Polish Holstein-Friesian cows, located in the region of north-eastern Mazovia were selected for the study. Both herds are subject to milk performance assessment and the animals are under constant veterinary care. Reproduction in both cases was carried out by insemination. Both herds have similar number of cows. For the purposes of the research, farms were named with the first letters of the alphabet, farm A and farm B, respectively. Two food systems were discussed and analyzed: TMR (Total mixed ration) used in the farm B and PMR (Party mixed ration) used in the farm A. The milk yield and milk parameters were compared in both farms. It was noticed that the farm B, using the TMR feeding, showed better yield and better milk parameters compared to the farm A, using the PMR feeding. The PMR feeding was more labour intensive. Milk yield, both daily and annual, was lower in the herd A. The study proved that the use of the TMR feeding on the farm B allowed to obtain higher yield as well as better milk parameters than using PMR feeding. This publication has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. 2021-1-SK01-KA220-HED-000032068 "Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalization".<sup>22</sup>

### **Possible benefits of mare's milk production in Croatia**

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Despite the constant increase in the number of horses, a clear vision of horse breeding is still being look for in Croatia. Horse breeding represents one of the most promising activities in rural development, which is considered a key strategy for restructuring the agricultural sector through innovation. Horses are not only involved in activities related to their use for work, sports and tourism, but also in activities related to the production of food and non-food products. The development of interest in mare's milk and products today exists on the part of milk production companies. It is developing in: Germany, France, Austria, Italy, Greece, traditional Asian (Mongolia, China, Kazakhstan, Kyrgyzstan) countries and many other countries. Mare's milk production is considered as part of the equestrian industry in modern and future societies. Positive consequences would be the preservation of local animal genetic resources, the rural eco-sustainable development of small economies in the micro region, those areas threatened by marginalization. A chain reaction would be transferred to the protection of plant diversity in achieving productive and sustainable use of the landscape. Despite the advancement of knowledge about the nutritional and safety properties of mare's milk, as well as the improvement of technical skills in milk management, detailed research is still needed, especially in terms of human nutrition and animal feeding for this type of production. Due to its potential in human nutrition, rural development, biodiversity and landscape preservation, the production and processing of mare's milk is a promising activity for the microeconomics of marginal rural areas not only in Croatia, but throughout the world.



**Autozygosity islands in the genome of the Slovak wild boar population**

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Slovak wild boar population diversity is currently under significant pressure of ASF expansion and increased hunting intensity to prevent disease transmission to commercial pig farms. Therefore, this study aimed to identify regions under strong selection, in the genome of the Slovak wild boar population through the scan of autozygosity islands distributed across autosomes. Biological samples of animals (N=75) covering all counties in Slovakia were genotyped based on the cross-species approach by GGP Porcine 50k chip. After SNP pruning, a total of 38823 informative markers passed the standard thresholds. For the scan of runs of homozygosity (ROH) distribution consecutive approach was used. Selection signatures were then defined based on the proportion of SNPs in ROH (%) and percentile-based threshold (equal to the 99<sup>th</sup> percentile). Functional annotation of detected autozygosity islands was based on identifying protein-coding genes located directly in the islands region according to the porcine Sscrofa11.1 genome version. The selected approach resulted in the determination of ten signals concentrated in relatively long autosomal islands on chromosomes 1, 6, 8, 12 and 14. These regions contain up to 585 protein-coding genes with different functions in organisms. The longest region on chromosome 6 (50.56-60.13 Mpb) included genes APOE responsible in pigs for hyperlipidaemia, FUT1 controlling susceptibility to oedema disease or PNKP involved in the genetic control of abortion. This study was supported by the Slovak Agency for Research and Development (grants no. APVV-17-0060, APVV-20-0161 and SK-SRB-21-0013).

## Session 05

## Theatre 1

**Does the trace mineral source affect rumen function? A review**

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This presentation will review the impact of different trace mineral sources on rumen function, including solubility trace elements in rumen fluid, ruminal fermentation, total digestibility of nutrients, volatile fatty acid production and rumen ecosystem. Several in vitro attempts have been made to use trace minerals to manipulate ruminal fermentation, and these studies have indicated that higher concentrations of Cu and Zn lower the cellulose digestion. In the last decade, multiple authors have demonstrated the effect of trace mineral source on nutrients digestibility in sheep, dairy and beef on a low/ high forage diets. Studies indicated lower fiber and DM digestibility in cattle supplemented with sulfate sources of Cu, Zn and Mn when compared with animals receiving similar concentrations from hydroxy or organic sources. A recent meta-analysis of 11 studies showed that the effect of trace mineral source (sulfate vs. hydroxy) on NDF digestibility varied depending on the method. Studies using total collection methods showed an increase of  $+2.80 \pm 0.44$  units ( $P < 0.01$ ), studies using uNDF240 as a marker tended to result in an increase of  $+1.70 \pm 0.67$  units ( $p = 0.06$ ), whereas studies using an in-situ incubation method did not show a difference. More recently, authors also shown increased total VFA production when replacing sulfate sources of Cu, Zn and Mn by hydroxy sources in beef cattle. In high forage diets, the replacement of sulfate by hydroxy also impact CP digestibility. Even if limited, new research findings also suggests that trace mineral source may affect the rumen ecosystem, including diversity and relative abundance of certain microbial species. More research is needed to elucidate the full mechanisms whereby trace mineral sources might affect rumen dynamics and function differently.

### The possible impact of punicalagin on ovarian steroidogenesis in animal and human models

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Punicalagin, the most abundant polyphenol found in pomegranate, has been studied for its biological activity. This study has observed the possible effect of punicalagin on the process of steroidogenesis in ovaries. The aim was to determine the punicalagin effect on the secretion of steroid hormones by ovarian fragments of rabbits and on the viability and secretion of steroid hormones by human ovarian granulosa cells HGL5. Ovarian fragments from sexually mature female New Zealand white rabbits (n=20) were incubated with punicalagin (1, 10, and 100 µg/mL), as well as ovarian granulosa cells HGL5 were cultured with punicalagin (10, 50, and 100 µg/mL) for 24 hours. The viability was evaluated by AlamarBlue™ assay, and the secretion of steroid hormones was assayed by ELISA. Our results showed that progesterone and 17β-estradiol secretion (but not androstenedione and testosterone) by rabbit ovarian fragments were significantly affected. Punicalagin increased progesterone level at 100 µg/mL (P<0.05) and decreased 17β-estradiol level at 10 µg/mL (P<0.005). On the other hand, our study revealed an increase in 17β-estradiol secretion by HGL5 cells at punicalagin concentrations of 50 µg/mL (P<0.01) and 100 µg/mL (P<0.05), progesterone was not affected. We did not observe any punicalagin-induced changes in the viability of HGL5 cells. Our results suggest that punicalagin could have a dose-dependent effect on the secretion of steroid hormones by rabbit ovarian fragments and by human ovarian cells and it may be a modulator in process of ovarian steroidogenesis. Acknowledgements: The work was supported by the Ministry of Education, Science, Research and Sport of the Slovak Republic projects APVV-18-0312, VEGA 1/0266/20, KEGA 033SPU-4/2021.

## Session 05

## Theatre 3

### Beyond the rumen. Improving gut integrity and health by ensuring trace mineral source quality and stability

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This presentation aims to review the impact of different trace mineral sources on gut integrity, oxidative stress, and inflammatory response in cattle. Potential dietary mitigation strategies aimed at improving gut health are currently of great interest, especially considering the numerous stressors that impact cattle's intestinal health such as feed restriction, acidosis, heat stress. Several trace elements, such as Cu, Mn, Se, etc., are essential nutrient and play an important role on ruminants' immune response, but among all, Zn is crucial for maintaining epithelial integrity, including intestinal, regulating the renewal of damaged epithelium. From the first Zn demonstrations by improving intestinal health in human models in the 90's, in the last decade multiple researches have highlighted key results in a variety of cattle's stress models including heat stress and feed restriction. Improved Zn source supplementation, such as hydroxy-, has shown altered febrile, cytokine and acute phase protein responses in response to LPS administration and heat stress challenges. Increased DMI and reduced BHBA and NEFA were observed in heat-stressed dairy cows receiving Zn from hydroxy- compared to sulfates. Changes in ileum villi height, oxidative and inflammatory biomarkers were also described in lactating cows submitted into feed restriction supplemented with 75 ppm Zn from hydroxy-. In the same study, Zn hydroxy-fed cows also reduced relative abundance of certain pathogens in feces, including *Treponema* sp. Even if Zn supplementation appears to be a promising strategy to improve gut integrity, more research is needed to elucidate the full mechanisms whereby different trace mineral sources might affect gut health and immune function in cattle.

**The individual differences in dairy cows ruminal pH during the lactation**

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The main goal of the experiment was to monitor the Holstein dairy cows during the lactation period and to point on the health interventions during the monitored period. In detail, 10 Holstein dairy cows had implemented the bolus (Moonsyst International Ltd., Republic of Ireland). The selected boluses were characterized by small dimensions 100 x 32 mm and light weight 200 g. Moreover, for each dairy cow the 120 data points from the rumen pH were recorded. After the data collection were pH values and pH dynamics statistically evaluated by IBM SPSS ver. 23.0 using One-Way ANOVA (descriptive statistics, Tukey Post-Hoc Test for the signification of results). The average ruminal pH in monitored dairy cows during the lactation was 6.35. However, the pH variability was very high and the monitored range was from 5.15 to 8.08. Every dairy cow except of 2 had significantly different pH values. After that, the pH circadian development is very fluctuatable. Thus, the minimal and maximal change in pH in comparison with previous data point was -20.79% and 23.07% respectively. However, the average pH change with previous data point was only 0.02%. To conclude, the pH and pH changes of dairy cows are individual and can be highly variable. This publication was 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, project no. 1/0321/23 (Effective management of the ruminant nutrition using a modern monitoring of the internal environment).

## Session 05

## Theatre 5

**The assessment of amygdalin modulatory effects in different animal models**

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Amygdalin from apricot kernels has found practical application in the prevention of various diseases. The aim of the study was to examine the effect of amygdalin on biological processes taking place in living systems. Possible modulatory effects of amygdalin were tested under in vivo and in vitro conditions. Healthy female rabbits (n=40) and granulosa cells isolated from porcine ovaries were used for the study. The effect of 14- resp. 28-day administration of amygdalin (intramuscular form; 0.6 and 3.0 mg/kg of BW) on hormonal profile (17 $\beta$ -estradiol, progesterone, testosterone), as well as the effect of amygdalin (1, 10, 100, 1000, 10 000  $\mu$ g/mL) on the viability, secretory activity (17 $\beta$ -estradiol, progesterone), and presence of markers (cyclin B1, PCNA, caspase-3, p53) were evaluated. The results showed that plasma concentrations of progesterone, 17 $\beta$ -estradiol, and testosterone in female rabbits evaluated by ELISA were not significantly affected by intramuscular injection of amygdalin after 14, not either 28 days. On the other hand, amygdalin significantly (10000  $\mu$ g/mL;  $P \leq 0.05$ ) stimulated 17 $\beta$ -estradiol secretion, however, with no effect on progesterone. The viability (AlamarBlue test) of porcine granulosa cells was not affected by amygdalin. The immunocytochemical analysis did not reveal changes in the presence of selected proliferation or apoptotic markers. In our study, amygdalin had no modulatory effect on the endocrine profile in female rabbits in vivo but induced significant changes in the secretion of the steroid hormone in porcine ovarian granulosa cells in vitro. Acknowledgements: The work was supported by the Ministry of Education, Science, Research and Sport of the Slovak Republic projects APVV-18-0312, VEGA 1/0266/20, KEGA 033SPU-4/2021.

### The effect of low protein diet on adipose tissue transcriptome in Krškopolje pig breed

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Krškopolje pig is the only autochthonous breed in Slovenia, characterized by a lower muscle growth and higher fat deposition potential. As the genetic regulation for fat deposition can be affected by different diet, the present study aimed to evaluate the effect of low protein (LP) diet on transcriptome of Krškopolje pig's (n=2×12) reared in the outdoor system. Animals received ad libitum standard (i.e. 15, 12.5 and 10% crude protein (CP) from 20 to 80 kg, from 80 to 100 kg and from 100 kg to slaughter, respectively) or LP (i.e. 15% CP from 20 to 60 kg and 10% CP from 60 kg to slaughter) diet. At the average body weight of 167±12.6 kg, animals were slaughtered and backfat samples were collected. After RNA extraction, samples were sequenced with Illumina NovaSeq generating 150 bp paired-end reads. The sequencing yielded app. 82.9 M paired-end reads, from which more than 95.1% of reads uniquely mapped to reference genome. Differential expression analysis revealed 65 genes, among them 28 being upregulated and 37 being downregulated in the LP group. The upregulated genes were mainly involved in lipid metabolism (FASN, ACACA, ACSS2, MOGAT2, ACSM5). This was supported also by functional enrichment analysis with the significant enrichment of fatty acid and acetyl-CoA biosynthetic processes (GO:0006633, GO:0006085). The results of the present study provide the first insight into genetic regulation of Krškopolje pigs fed with low protein diet. Acknowledgement: Slovenian Agency of Research (P4-0133, P4-0053, J4-3094, V4-2201), GERO NIMO (EU H2020 GA no. 101000236). Keywords: local breed, feed stress, backfat, RNA-seq

## Session 05

## Poster 1

### The effects of mycotoxin alternariol on cell growth, division and cell cycle in porcine peripheral blood morphonuclear cells

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Alternariol (AOH), is an Alternaria mycotoxin known as a common natural contaminant of fruits, vegetables, and grain products. AOH can induce the formation of reactive oxygen species causing DNA double strand breaks and oxidative damage, effects associated with the reduction of cell proliferation and cell cycle arrest. In farm animals there are no studies about the effect of AOH in pigs, as the most susceptible specie to the mycotoxins effect due to the high intake of grains in the diet. The aim of our study was to evaluate in vitro the effects of five concentrations of AOH (1-100µg/ml) on peripheral blood morphonuclear cells (PBMCs) of healthy piglets. The cells were stimulated or not with a phorbol 12-myristate 13-acetate-ionomycin (PMAI) mixture in order to analyse the toxin effect on cell proliferation, apoptosis, necrosis and on cell cycle by flow cytometry. Our results show that, in both cases of stimulated and unstimulated PBMCs, a decreasing of cellular viability, directly proportional to the increase in the concentration of the toxin was observed. Regarding the cell cycle, in the case of stimulated cells, the AOH treatments did not cause a significant change compared to stimulated control, but AOH induces an arrest in the G2 phase of the cell cycle of unstimulated PMBCs, starting with the concentration of 10 µg/mL. Taken together, our results have shown that AOH was able to interfere with cell proliferation, apoptosis, necrosis and with cell cycle of unstimulated peripheral blood morphonuclear cells, with important consequences for animal health.

### Nutritional value and bioactive properties of several honey types from Romania

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Beekeeping is an important part of animal husbandry, both as an ancient occupation and as a modern one, of particular relevance and importance. Its importance lies in the fact that bees are the main pollinators of agricultural crops and horticultural sector, but also due to the fact that produce important products with high nutritional value and biological properties. The bee products obtained have a high nutritional value, being generally free of any type of contaminants, but also possessing high biological value, due to the content of active principles from the plants that provide valuable nectar, pollen, resins to the bees' as source of their food. Without talking of all types of honey produced in Romania, we focused here on several types of Romanian honey, with very high potential and bioactive properties: forest honeydew honey, heather honey and Japanese knotweed honey. Harvesting area of these honey types is located in Transylvania region, from the river banks of Cris to the Apuseni Mountains. Determinations of chemical composition, including mineral content, contaminants determination as well as bioactive substances with health benefit properties were made in the Laboratory for Quality Control of Bee Products and Bee Diseases from University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca. The obtained results were comparable, or better to well-known types of honey from other continents which benefits of extensive marketing and high prices.

### Session 06

### Theatre 2

### Production, carcass, meat quality and biochemical traits in Krškopolje pig compared to modern lean crossbreed reared under same conditions

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The Slovenian autochthonous breed Krškopolje pig (KP) is known for its excellent meat. However, a comparison with modern lean pigs (MP) under the same rearing conditions has never been made. Therefore, we aimed to study the productive and qualitative characteristics of KP (n=7) and MP (n=7) fattened in the same environment and equal feeding regime. Starting from the same weight (27 kg), castrates of both breeds were fattened for 179 days with the same amount of commercial feed. Body weight was monitored and carcass, meat and fat quality were evaluated after slaughter. KP exhibited considerably slower growth rate, lower carcass weight, greater fatness and lower muscularity than MP. Regarding meat quality traits (m. longissimus dorsi), KP had higher final pH, darker colour (due to higher myoglobin content), and higher intramuscular fat content. Their fat was had more saturated, monounsaturated and less polyunsaturated fatty acids and lower  $\omega 6/\omega 3$  ratio. However, the degree of fat oxidation (TBARS) was higher in KP than in MP, whereas water-holding capacity and shear force did not differ (nor did total and soluble collagen content). Despite lower performance, KP showed better meat quality and processing suitability. Acknowledgement: Financing of Slovenian Agency of Research and Ministry of Agriculture, Forestry and Food (grants P4-0133, J4-3094, V4-2021) is acknowledged. Keywords: local pig; productivity; carcass; meat quality

**Effect of essential oils on the pH in minced pork meat**

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Plant essential oils (EO) are used in the food industry as natural preservatives mainly for their antimicrobial effects. However, their inhibitory effects depend on many external and internal factors. pH is one of the intrinsic elements influencing the shelf life of meat. Lower pH values hinder bacterial multiplication, whereas higher pH levels encourage it. The aim of our study was to monitor the effect of 1 % concentration of thyme (TEO), marjoram (MEO), and oregano (OEO) EOs on the pH value of pork pure minced meat (PM) and meat preparation (P) (salt, black pepper, ground cumin, fresh garlic) on the 10<sup>th</sup> and 15<sup>th</sup> days of storage at t +2 to +4 °C in comparison to the control (C) untreated with essential oils. In the present study, the initial pH on the 0<sup>th</sup> day (PM: C 6.38; TEO 6.39; MEO 6.44; OEO 6.3; P: 6.24; TEO 6.22; MEO 6.32; OEO 6.18) was slightly reduced in all stored samples for PM and P (p>0.05). The smallest pH value was noted on the 10<sup>th</sup> and 15<sup>th</sup> days of storage (5.93, resp. 5.94) for meat preparation treated with oregano EOs. Keywords: essential oils, minced meat, pH value This publication was supported by the Operational Programme Integrated Infrastructure within the project: Sustainable smart farming systems taking into account the future challenges 313011W112, cofinanced by the European Regional Development Fund. Contact: Ing. Martina Gondeková, PhD., NPPC-VÚŽV, Hlohovecká 2, 95141 Lužianky, Slovak Republic, E: martina.gondekova@nppc.sk

## Session 06

## Theatre 4

**Isolation and characterization of lactic acid bacteria from raw goat milk and farm environment: Assessment of physiological and technological features**

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Goat milk production is a crucial contributor to rural economy in many countries, especially in the Mediterranean and Middle East regions. In the European Union it mainly takes place in the less favored areas of Mediterranean countries, where vast marginal lands with pastures are available. Goat milk dairy products present a favorable outlook in the EU due to their distinctive sensory characteristics. The objective of this study was to isolate and characterize Lactic Acid Bacteria (LAB) from raw goat milk and farm environment, and to evaluate their physiological attributes, technological properties, and safety profiles, within the scope of INDILAB (Production of innovative dairy products with improved characteristics, domestic breeds of small ruminants using indigenous start-up monocultures) project. A total of 200 LAB strains were isolated and identified from goat milk samples and feeding troughs, milking parlor and cheese making equipment surface samples based on their morphological, physiological, biochemical, and genotypic characteristics. All isolates were tested for production of acid, antifungal activity, curd formation, and aroma production at 32 °C and 42 °C after 24 and 48 h. Following the preliminary tests, 30 strains were selected for identification and characterization of their physiological and technological properties. A high proportion of lactic acid bacteria and Gram<sup>+</sup> cocci was found in all samples. INDILAB project is funded through the Research and Innovation Strategies for Smart Specialization (RIS3)-Eastern Macedonia and Thrace 2014-2020.

### Effects of apple pomace in the high-forage diet for dairy cows on ruminal fermentation and methane production in rumen and milk

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Industrial by-products rich in bioactive compounds supplemented with animal diets can reduce greenhouse gas production. This research examined the effects of a diet containing a 6% addition of apple pomace on microbial populations and methane production in the rumen and milk of dairy cows. The four rumen-cannulated Polish Holstein-Friesian dairy cows were used in a 2×2 Latin square design research. The experiment lasted 52 days and included two cycles, each consisting of a 21-day preliminary period and a 5-day sampling period for analysis. Ruminal and milk samples were analyzed. Results have shown a statistically significant ( $P=0.001$ ) increase in the sum of volatile fatty acids and propionic acid. The observed decrease in the methanogen population ( $P<0.001$ ) was related to a reduction of methane emissions by 8% in the experimental group ( $P=0.05$ ). Favorable changes were found in milk yield as well as in fat, protein, and lactose yield ( $P\leq 0.02$ ). The results of the research indicate that apple pomace can successfully serve as an environmentally friendly dietary component for dairy cows. Project CCCfarming National Centre for Research and Development (SUSAN/II/CCCFARMING/03/2021)

## Session 07

## Theatre 2

### Effect of the essential oil blend Rumitech in a high-forage diet on methane production and performance of dairy cows

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The essential oils blend Rumitech was evaluated in three experiments (in vitro, cannulated cows, and lactating dairy cows) to investigate its effects on methane emission, milk production, and milk composition of dairy cows. Initially, an in vitro study (Exp. 1; Hohenheim test) was performed; 0.35 mg of Rumitech (0.1% on diet DM basis) was supplemented to a commercial TMR (rich in brewer's grain and beet pulp; 20% of total diet DM) which corresponded to 20 g/cow per day fed to dairy cows under commercial conditions. The addition of Rumitech decreased methane yield by 6%. Based on the results of the in vitro experiment, two consecutive long-term (39 days) in vivo experiments were conducted using 4 Polish Holstein-Friesian cows fitted with rumen cannulas (Exp. 2) and 22 lactating dairy cows (Exp. 3) fed TMR (76% forage on DM basis) in a replicated 2 (diet) × 2 (period) crossover design. Methane production decreased by 10 and 8% in the groups fed the Rumitech diet compared to the control in Exp. 2 and 3, respectively. Moreover, in Exp. 3 milk yield and milk protein and lactose yield increased (by 5%, 8%, and 8%, respectively) in the groups fed the Rumitech diet. Project CCCfarming National Centre for Research and Development (SUSAN/II/CCCFARMING/03/2021)

**Impact of the long-cut chaff technology on milk yield and methane emission in dairy cows**

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Long-cut-length chaff is a corn silage chaff technology in which the material is cut into 26-30 mm long pieces. This technology enables the mixing of corn silage in TMR as a structural feeding component. Our hypothesis states that using long-cut-length chaff in high-productive dairy cows' nutrition increases milk yield, improves milk composition, and decreases methane emission. In the two-month experiment, 30 dairy cows were randomly selected for the control group (15) fed TMR with wheat straw (0.6 kg per day) and the experimental group (15) fed TMR with long-cut length corn silage chaff (+2 kg). The dairy cows were milked with the milking robots Lely Astronaut A5, Lely Industries, Maassluis, the Netherlands. An increase in the milk yield was observed (+1.4 kg milk per day). A decrease in milk fat and urea concentration as well as methane emission was detected (by 5 %, 17 %, and 9%, respectively). Project CCCfarming, National Centre for Research and Development (SUSAN/II/CCCfarming/03/2021)

**Effect of inoculated grass silage on rumen fermentation and methane emission in dairy cows**

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The study aimed to analyze the effect of feeding dairy cows with a diet containing grass silage preserved with a commercial inoculant based on propionic (*Propionibacterium acidipropionici*, *Propionibacterium thoeni*) and lactate acids bacteria (*Lactobacillus buchneri*, *Lactobacillus plantarum*). The research hypothesis assumed that the inoculant supplemented with grass silage will improve the fermentation process of the ensiled material and, finally, as a component of TMR (23.5% of total components) will stimulate milk production and decrease methane emission. In the two-month experiment, 20 dairy cows were randomly selected for the control (10) and experimental (10) groups. The obtained results confirmed the hypothesis demonstrating the positive impact of commercial inoculant on the ensiling process of grass. The inoculant increased the nutritional value (mainly total protein content) and aerobic stability of the ensiled material. Moreover, the grass silage with inoculant increased daily milk production (by 5%), improved milk composition (higher percentage of protein, lactose, and urea), and decreased methane emission (by 7 %). Project CCCfarming, National Centre for Research and Development (SUSAN/II/CCCfarming/03/2021)



### Greenhouse gases emission from livestock production and its impact on climate change – discussion of the farmers' awareness survey

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The aim of the survey was to present information on the awareness of Polish farmers in terms of using possible technologies to limit the negative impact of animal production on the environment. The survey was carried out on 44 farms in Greater Poland. Each one consisted of 87 open and closed questions which were divided into the following groups: farm characteristics, farmers' experience, knowledge of measures to reduce greenhouse gas emissions, agricultural practices, knowledge of techniques to reduce ammonia emissions, support for environmental protection, general knowledge about greenhouse gas and ammonia. Based on the conducted surveys and interviews, it can be concluded that the awareness of Polish farmers about the risks arising from the above-mentioned phenomena is common but still insufficient. Most of the respondents knew about the existence of the phenomena presented, but did not know the consequences of their occurrence and did not apply solutions aimed at limiting their negative impact on the external environment. The main reason for this situation is the relatively high costs of introducing changes. Project CCCfarming National Centre for Research and Development (SUSAN/II/CCCfarming/03/2021)

## Session 07

## Theatre 6

### Determination of greenhouse gas emissions from pig farming in Slovakia during 2021

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Livestock is one of the main sources of greenhouse gases (GHG). In accordance with valid international agreements, we have to quantify them annually. For determination of GHG, we used methodology 2006 IPCC Guidelines for National Greenhouse Gas Inventories. We quantified emissions from enteric fermentation (methane) and manure management (methane, nitrous oxide). The calculations were based on the emission factors of gases and the number of pigs in the individual categories. To calculate the methane emissions from enteric fermentation TIER 1 method was used. We found the following rates of methane emissions 42.57, 13.23, 0.96, 267.35, 107.33, 103.49, 99.07, and 45.60 t for sows, gilts, boars, pigs up to 20 kg of live weight, pigs 20-49 kg, fattening pigs 50-80 kg, 80-110 kg and 110 kg and more, respectively. In the case of methane emissions from manure management, we used the TIER 2 method with calculated emission factors. We determined the following rates of methane emissions 178.70, 42.10, 2.48, 7.24, 189.51, 128.17, 194.19, 233.97, and 118.49 t for sows, gilts, boars, breeding pigs 21-50 kg of live weight, pigs up to 20 kg, fattening pigs 21-50 kg, 50-80 kg, 80-110 kg and 110 kg and more, respectively. For calculation of nitrous oxide emissions from manure management, we also used the TIER 2 method. We found the following rates of nitrous oxide emissions 0.19, 0.11, 1.01, 6.84, 2.90, 3.67, 6.89, 9.64, and 5.14 t for breeding pigs 21-50 kg of live weight, boars, gilts, sows, pigs up to 20 kg, fattening pigs 21-50 kg, 50-80 kg, 80-110 kg and 110 kg and more, respectively. In the year 2021, 453 076 pigs were kept in the territory of Slovakia, and these produced 1774.46 t methane and 36.37 t nitrous oxide emissions. This article was possible through projects APVV 15-0060 and ÚOP 51-2023.

**Ruminal microbiome and fermentation associated with the gastrointestinal nematode *Haemonchus contortus***

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We investigated the ruminal microbiota and fermentation patterns of lambs infected and non-infected with the gastrointestinal parasitic nematode *Haemonchus contortus* in vivo and in vitro. Twelve parasite-free lambs were divided into two groups: a control group (CON) with six uninfected lambs and an experimental group (EXP) with six lambs inoculated with 5000 infective *H. contortus* larvae. At 48, 49- and 50 days post-infection, sheep were sampled with their corresponding uninfected controls for histological analysis, and rumen fluids were collected for in vitro experiment, pH measurement, ruminal short-chain fatty acids, and microbial community isolation. The ruminal contents, fermentation parameters, and microbiome in vitro and in vivo were determined using molecular and microscopic techniques. Ruminal fermentation characteristics and methane production were affected by infection in vivo and in vitro ( $p < 0.05$ ). The populations of Archaea ( $p < 0.05$ ), Methanomicrobials ( $p < 0.05$ ), and Methanobacteriales ( $p < 0.05$ ) were significantly higher for the EXP than the CON group. Total protozoa in the lambs did not differ significantly ( $p > 0.05$ ) between the groups. During the parasitic load of the *H. contortus* pH increased in the rumen and the abomasum. Subsequently, there was a change in the microbial community of the abomasum, mainly an increase in the anaerobic microbial mass, and at the same time changes in the representation of individual microbial species. The study was supported by the Slovak Research and Development Agency (APVV 18-0131).

***Aronia melanocarpa* mitigate acrylamide induced injury of eukaryotic cell**

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Acrylamide (AA) is a chemical substance with extensive industrial use and is also formed in foods that are rich in carbohydrates during their high-temperature processing. Due to its genotoxic and cytotoxic effects, AA has been classified as a potential carcinogen. In this study, we used a model eukaryotic organism *Schizosaccharomyces pombe* to investigate the toxicity of AA (10 or 20 mM concentration). In *S. pombe*, AA delays cell growth, causes oxidative stress by increasing ROS production, and triggers the excitation of the antioxidant defense system, leading to division arrest. *Aronia* juice supplementation, due to its high content of biologically active compounds, mitigates AA-induced toxicity through depletion of intracellular ROS and protection of the antioxidant enzymatic system of the cell. Cell treatment with several *Aronia* juice concentrations revealed the best protective effect of 1 or 2% *Aronia* juice solutions. Efficiency of *Aronia* juice cell protection is dose dependent as the 2% solution led to significantly higher cellular defence compared to 1%. Our results show that *Aronia* might serve as protecting supplement against toxic effect of AA and due to high similarity of biological processes of *S. pombe* with higher eukaryotes, the protective effect of *Aronia* juice against AA toxicity might also apply for higher organisms. This research was supported by APVV-20-0161.

**The impact of crude protein content in diet of dairy cows to estimate GHG emissions**D. Ruska<sup>1</sup>, L. Berzina<sup>2</sup>, D. Jonkus<sup>1</sup><sup>1</sup> Latvia University of Life sciences and technologies, Institute of Animal sciences, Liela str. 2, LV-3001 Jelgava, Latvia,<sup>2</sup> Latvia University of Life sciences and technologies, Faculty Faculty of Information Technologies, Liela str. 2, LV-3001 Jelgava, Latvia

The importance of data used for the estimation at national emission inventory is described in the guidelines of the Intergovernmental panel on climate change (IPCC) estimation methods and coefficients (IPCC, 2019). On the other hand, these coefficients are based on average data from previous studies in different countries. Therefore, in our study IPCC methodology was used to compare the emission estimation and then two data sets were created. First data set (C) content average from country information used for national inventory, and the second data set (E) content results from a trial conducted in LBTU study farm Vecauce in 2019 (results reported Ruska and Jonkus, 2021). The trial complied into three dairy cow groups, each group was fed with a total mixed ration with different crude protein (CP) content (group A diet 17% CP, group B diet 16% CP, group C diet 15% CP). The amount of feed consumed for milk productivity, manure, and urine excretion was recorded during the trial. The obtained data set was estimated separately for nitrogen (N) and total equivalent to CO<sub>2</sub> emissions by using IPCC methodology. The excreted nitrogen from data set E was significantly lower than data set C by 20% ( $p < 0.05$ ). The total equivalent to CO<sub>2</sub> emission from data set E was lower than data set C but this difference was not significant. After the comparison of the estimation results from both data sets, it was concluded that more trials are required to get a more precise estimation of the emissions as well as data from local research studies could improve the national inventory estimation.

## Session 08

## Theatre 1

**Heat stress at dairy farm level: variability, intensity and frequency of occurrence**V. Bogdanović<sup>1</sup>, D. Stanojević<sup>1</sup>, N. Gligović<sup>1</sup>, R. Djedović<sup>1</sup><sup>1</sup> University of Belgrade - Faculty of Agriculture, Institute of Animal Science, Nemanjina 6, 11080 Belgrade-Zemun, Serbia

With the increasing impact of climate change on livestock production, thermal management at farm level is becoming one of the most important keys for farmers to stay in business. The objective of this study was therefore to analyse the source of variation, frequency and intensity of occurrence of heat stress parameters at the dairy farm level. A systematic measurement of T°C and RH % was carried out on 12 typical dairy farms in Serbia between 2014 and 2021. More than 500,000 individual T°C, RH% and THI values were analysed. To analyse the variability of the heat stress parameters, a fixed model with the effects of the farm, day, month and year of measurement was used. In addition, effects in relation to the breed of cattle, the size of the farm and the type of barns were also tested. For most farms, the average annual THI was below the critical value of 72. However, in the period from May to September, the average THI at farm level was higher than the critical value of 72, especially in June (75), July (77) and August (77), as well as in the second half of May and the first half of September. In other words, the summer season is likely to be extended by one month. The free stall barns have more favorable thermal environment than tie stall barn as well as farms with Holstein breed than with Simmental cattle. In the warmer season, the most critical thermal period of the day for the Holstein farms was from 09.00 to 21.00 (12 hours per day), while for the Simmental farms it was from 09.00 to 02.00 (17 hours per day). It should be noted that the potential for the occurrence of heat stress is particularly pronounced on medium-sized farms that have not adapted the number of animals to the size of the barns.

### Prevalence of udder pathogens isolated in cow milk in Slovakia during the year 2021

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The study aimed to identify udder pathogens and their prevalence in dairy cows during the year 2021. Dairy cows were selected based on the measures taken by veterinarians to prevent mastitis. A total of 467 milk samples from 40 farms in Slovakia were tested. Milk samples were cultured on blood agar and positive cultures were further analyzed in the laboratory. The prevalence of mastitis was found in 95% of cases, and 16 different pathogens were identified. Environmental pathogens formed the dominant group of pathogens causing mastitis. The most frequently isolated pathogens were Coagulase-negative staphylococci (S) (45.7%) followed by *Escherichia coli* (31.8%) and *Streptococcus (Str) uberis* (26.1%). *S. aureus*, which was identified in 32 samples, was among the most common agents causing contagious mastitis. Other identified pathogens were *Serratia marcescens* (4.1%), *Klebsiella pneumonia* (1.8%), and *Pasteurella* spp. (1.1%), *Pasteurella multocida* (<1.0%), *Enterococcus (E) faecium* (<1.0%), *E. durans* (<1.0%), *E. spp.* (<1.0%), *E. faecalis* (<1.0%), *Trueperella pyogenes* (<1.0%), *Yersinia enterocolitica* (<1.0%), *Str. agalactiae* (<1.0%) and *Pseudomonas aeruginosa* (<1.0%). In conclusion, the most of the identified pathogens were environmental origin, thus regular monitoring of the occurrence of mastitis and identification of udder pathogens is the key factor to prevent mastitis in the dairy practice. Keywords: dairy cow, milk, mastitis, pathogens

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### EuroSheep: co-construction approaches to understand main needs of sheep farmers and define innovative solutions to improve the sector's profitability

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In EuroSheep, co-construction approaches are used to exchange knowledge and experience among sheep farmers, veterinarians, advisors and researchers. The aim is to engage stakeholders in a network that facilitates a better understanding of the sector needs and best practices. The main objectives are to improve sheep health, nutrition, and profitability. Stakeholders of the 8 country's involved use both National and Transnational workshops to connect. In each country, farmers' needs were identified, and relevant solutions cross-exchanged by the other countries. Currently, 45 of the 96 technical solutions created have stakeholder feedback on the benefits, and overall acceptance, these solutions were followed by a sustainability analysis. To increase farmer uptake, 26 factsheets, 53 'tips and tricks' and videos were produced.

### Breeding Soundness Examination – as a tool to improve reproductive efficiency and farm yield in extensive systems

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On a farm of Lacaune dairy sheep and their crosses, Breeding Soundness Examination (BSE) were carried out on the rams in two consecutive years to assess the reproductive competence of the rams in the July/August season. In Year-1 (2021), 26 rams were subjected to BSE, and 73.1% were approved for the next breeding season; in Year-2 (2022) 17 rams were submitted to BSE and 82.4% were approved for mating. Of the 19 rams approved in Year-1 and present in Year-2, 57.9% were approved, 10.5% were considered unavailable for the reproductive process and 31.6% were removed from the herd between Year-1 and Year-2 for many reasons including, pathologies, dog attack and age. Of the 6 rams classified as to be reassessed in Year-1 and which were not subject to reassessment because they were not needed for the breeding season, but which were subject to examination in Year 2, 50% passed, 16.7% failed and 33.3% were removed between years. The unavailability of fertile rams at the beginning of the breeding season can lead to lower reproductive rates or to a decrease in the genetic quality of future replacement animals. The need for BSE is even more important when we work with natural mating in groups of synchronized ewes, with paternity control, where an infertile or sub-fertile ram implies the total or partial reproductive loss of an entire group of ewes. The economic impact of these situation is highly relevant.

## Session 08

## Theatre 5

### The development of farm robot in pig breeding

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The application of precise technologies in animal production implies automated detection and monitoring of identified animals concerning the characteristics of productivity, fertility, health and welfare based on the analysis of production data, images, sounds, body weight and condition and various biological parameters in real-time. Furthermore, the application of these technologies enables the early detection of certain disorders, diseases and physiological / health status at the level of an individual animal, group of animals or the level of entire farm. Precision technologies function in such a way that sensors monitor or record information such as images, sound, the temperature of an animal or object, and the activity of groups or individual animals. Sensor data is stored or sent directly to the main processor, followed by analysis using various algorithms. A programming algorithm is a computer procedure that precisely defines to the computer what steps should be taken to solve a certain problem using input information to determine the solution. Programmers initiate the process by writing an algorithm that tells the computer how to perform certain actions needed to solve a problem. An algorithm's value to farmers depends on its ability to transform sensor data into a biological outcome. Ultimately, sensor data combined with individual animal identifications, reference observations and production data are integrated into algorithms to provide relevant information and alerts on pig health, productivity, fertility and welfare. The goal of this paper was to present the possibilities of the development of farm robots for application in pig breeding facilities.

### Effect of cage change on the induction of receptivity of female rabbits under conditions of different photoperiodic regimes

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The goal of the experiments was to investigate the effect of changing the cage (24 h) under different PR (photoperiodic regimes, light 80 lux) on the induction of R (receptivity) in nulliparous does. The R state (level of vaginal discoloration, 1 – 4) was checked before the cage change and 24 hours after. In group ZKN8:16 110 does were kept under PR of 8:16 (light : dark) (min. 30 days). In group ZKN24 112 does were kept under PR of 8:16 (min. 30 days). The PR was changed to continuous light 3 days before the cage change. In group ZKN16:8 104 does were kept under PR of 8:16 (min. 30 days). 7 days before the cage change, the light regime was changed to 16:8. In group ZKNPMSG, hormone treatment (PMSG) was utilized. 101 does were kept under PR of 8:16 (min. 30 days). 7 days before cage change, their PR was corrected to 16:8. The increase in R in the ZKN8:16 group was from  $2.10 \pm 0.38$  to  $2.16 \pm 0.48$  ( $p > 0.05$ ). In group ZKN24, an increase from  $2.21 \pm 0.49$  to  $2.39 \pm 0.61$  ( $p > 0.05$ ) was found. The differences after induction of R between group ZKN8:16 and ZKN24 was without significant differences. The improvement of R in the ZKN16:8 group was from  $2.33 \pm 0.60$  to  $2.70 \pm 0.75$  ( $p \leq 0.05$ ). In the ZKNPMSG group, the improvement after induction of receptivity was found from  $2.31 \pm 0.57$  to  $2.66 \pm 0.76$  ( $p \leq 0.05$ ). The differences of receptivity induction between ZKN 16:8 and ZKN PMSG was statistically insignificant. This publication has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. 2021-1-SK01-KA220-HED-000032068 “Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalisation”.

### Session 08

### Theatre 7

### Seasonal differences in ammonia concentrations and emissions in pig farming

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The experiment was carried out during the fattening period (30-110 kg of live weight) of four pig batches (summer-autumn 1 (SA1), winter (W), spring (S), summer-autumn 2 (SA2)) reared on a slatted floor. We found the highest average ammonia concentration ( $10 \text{ mg} \cdot \text{m}^{-3}$ ) and emission ( $2.4 \text{ kg} \cdot \text{day}^{-1}$ ) in W batch and the lowest concentration ( $4.2 \text{ mg} \cdot \text{m}^{-3}$ ) and emission ( $1.5 \text{ kg} \cdot \text{day}^{-1}$ ) in SA2 batch. The differences in ammonia concentrations and emissions were significant ( $P < 0.001$ ,  $P < 0.01$ ) between batches, expect ammonia emissions in batches SA1 and W. The highest average housing and outdoor temperatures were detected in batches SA1 ( $28.0^\circ \text{C}$ ) and SA2 ( $17.1^\circ \text{C}$ ), respectively. The lowest average housing and outdoor temperatures were found in batch W ( $23.0$ ,  $1.8^\circ \text{C}$ ), respectively. The temperature differences were significant ( $P < 0.001$ ) between all batches, expect batches SA1 and SA2 (housing and outdoor temperatures), and SA1 and S (outdoor temperature). The highest ( $15\,348 \text{ m}^3 \cdot \text{hour}^{-1}$ ) and the lowest ( $10\,335 \text{ m}^3 \cdot \text{hour}^{-1}$ ) airflow rates were found in SA2 and W batches, respectively. The differences in airflow rates were significant ( $P < 0.001$ ,  $P < 0.05$ ) between batches, expect batches SA1 and S, and S and SA2. We detected positive correlation between ammonia concentrations and emissions in all batches (0.756 (SA1), 0.777 (W), 0.903 (S), 0.958 (SA2),  $P < 0.01$ ). Dependence of ammonia concentrations on housing temperature was only confirmed in batch SA1 (0.614,  $P < 0.01$ ). Positive correlation between ammonia emissions and airflow rate was only determined in batch W (0.417,  $P < 0.01$ ). During the fattening of the four pig batches (412 days), 836 kg of ammonia emissions were produced, and ammonia emission factor reached value  $2.1 \text{ kg}$  per pig and year. This article was possible through projects APVV 15-0060 and ÚOP 51-2023.

### The attitudes of consumers and farmers in Ukraine toward animal welfare

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To facilitate the adaption of the EU requirements, current issues in animal welfare in Ukraine should be identified. Totally 147 consumers and 39 farmers were interviewed. Over 60% of the respondents considered animal welfare as important. Consumers had a stricter opinion than farmers regarding animal welfare legislation. Particularly, 93% of consumers and only 52% of farmers believed that the legislation should be improved, and 59% of farmers regarded animal welfare in Ukraine as good as in other countries. The most important welfare issues defined by the consumers were poor housing conditions and feeding, low veterinary care and inhumane treatment. The most important welfare issues defined by the farmers were inappropriate housing, feeding, transport and slaughter conditions, increased production costs and lack of the state support. Keywords: animal welfare, consumer, farmer

## Session 09B

## Theatre 2

### Administration of medicines and performance of sows based on farm data

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The health and longevity of the sows, as well as the vitality and nutritional independence of the piglets, are fundamental pillars of overall breeding efficiency. Parturition and the early postpartum period are critical periods for both sow and piglet. The objective of our study was to evaluate the drug application during these periods and its relationship with sow performance parameters (n = 1902). Basic farm data from 2016 to 2021 and a subsequent performance testing database (377108 records) were considered. The amount and type of application of veterinary prescription drugs were evaluated. The production and reproductive parameters of the evaluated sows were consistent with the level of breeding farms included in the CzePig national breeding programme. On average, 2.10 drugs were administered per litter, including 1.18 oxytocin-containing drugs during farrowing and 0.93 drug administrations in the postpartum period. This treatment was focused on infectious diseases (0.50) and on applied analgesics (0.34) and preventive and supportive drugs (0.09). Slightly higher drug application was found in sire breeds (+7%, i.e. +0.14 applications per litter) compared to dam breeds. Sows were treated the most in the first litter (2.73 drugs), then the number decreased (by one third) with a slight increase in the last eight litter (2.31 drugs). The treatment per sow and litter decreased gradually from 2.45 to 1.55 drugs over the evaluated years. Less treated sows tended to have higher postnatal piglet survival (+0.20 piglets), higher litter size at weaning (+0.44 piglets), reduced insemination interval (-0.18 days) and by 40 days higher production life. The results indicated an improvement in sow health, in piglet survival and litter size and stabilization of insemination interval over the evaluated years. The study was supported by Czech Republic project QK1910217.

**The influence of genotype and sex on the fatty acid composition of the intramuscular fat of pigs fed linseed**

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The aim of the study was to investigate the fatty acid (FA) composition of intramuscular fat (IMF) in gilts and barrows of 3 commercial pig genotypes (PIC, PIC x Swedish Landrace (SL) and SL) experimentally fed linseed as a source of  $\alpha$ -linolenic acid (ALA, C18:3n-3). A total of 90 pigs, equally distributed by genotype and sex, were fattened from 25 to 105 kg on a standard feed mixture supplemented with 3% linseed and vitamin E (100 mg/kg). After slaughtering, carcass traits, longissimus muscle pH and colour, and chemical and FA composition were assessed by standard methods. Data were analysed by GLM procedure with fixed effects of genotype (G), sex (S) and their interaction (GxS). Carcass and meat quality were not affected by G, S or GxS. However, a significant difference was found in the IMF content, which was generally higher in barrows than in gilts and SL compared to genotypes PIC and PICxSL. Barrows IMF also had higher levels of saturated FA (SFA) and monounsaturated FA (MUFA), while gilts had more polyunsaturated FA (PUFA). The genotype SL had more MUFA, PIC more PUFA, while PICxSL was in between. The content of ALA was similar in all pigs, but the content of its longer-chain n-3 metabolites (e.g. C20:5 n-3 and C22:6 n-3) and the total content of n-3 PUFA were higher in gilts and in the PIC pigs. In conclusion, this study shows an evident influence of genotype and sex on the FA composition of the IMF of pigs fed linseed, with a greater accumulation of n-3 PUFA in genotype/sex with less IMF.

**Fatty acid content of cryopreserved and fresh bovine spermatozoa: A comparative study**

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Bovine spermatozoa can be highly sensitive to cryodamage due to their fatty acid composition since these are easily oxidized in the process of lipid peroxidation (LPO). The objective of this study was to examine the fatty acid content and possible changes in their profile between cryopreserved and fresh bovine spermatozoa. All samples were obtained from adult Holstein bulls. The evaluation of fatty acid composition was carried out with GC-FID (Gas-Chromatography with Flame Ionization Detection). Based on the obtained data we identified a major group of fatty acids including docosahexaenoic (DHA), palmitic, linoleic, oleic, stearic and myristic acid. A dramatic decline of DHA acid was observed in the cryopreserved group when compared to fresh sperm cells. DHA is a critical component of mitochondrial and cellular membranes and is involved in the regulation of membrane fluidity and sensibility to oxidative stress. On the other hand, the concentration of oleic acid was higher in the cryopreserved group in comparison to the fresh samples. We may conclude that cryopreservation may stimulate the degradation of DHA in bovine spermatozoa, which may possibly affect the integrity of membranes however an increased content of oleic acid may partially restore the abundance of fatty acid content by its incorporation into the cell membrane. Acknowledgement: This publication was supported by the Operational program Integrated Infrastructure within the project: NUKLEUS 313011V387.



**Effect of diseases on the culling of dairy cows: a case study in Holstein nucleus herd**

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Health issues are the most common reasons for culling dairy cows on farms. The objective of this study was to evaluate the frequency of diseases and effects which influenced the culling rate in the Holstein nucleus herds in Slovakia. High-input, high-intensity production system under the conditions of the university farm VPP Oponice of SUA Nitra has been used as a model. The average production of 375 Holstein dairy cows was 10607 kg (9855 kg at 1<sup>st</sup> lactation) with 3.70 % fat and 3.22 % protein. The average number of lactations is 2.41; the age at first calving is 24 months and 15 days, and the calving interval is 399 days. The farm is currently in 45<sup>th</sup> place in the Top Slovakia Holstein Dairy farms rating. Veterinary records are recorded routinely at the farm in the form of a Veterinary Diary. From veterinary records, the following groups of diseases were evaluated: mastitis, claw diseases (infectious and non-infectious), reproductive disorders and metabolic diseases. Disease incidence was assessed from the period 2017 to 2022. The average percentage of ill animals on the farm was 28.26 %. The highest prevalence was found for retained placenta, 28.10 % and mastitis, 24.79 %. Next followed infectious claw diseases at 17.36 %, metritis at 14.88 %, and ketosis at 6.61 %. The lowest frequency of occurrence was found for postpartum paresis 4.13 % and non-infectious claw diseases 3.31 %. The results of this study show that the production system impacts the culling rate, and results can be used to introduce new traits in future selection indices. This research was supported by the Slovak Agency for Research and Development APVV-17-0060 and APVV-20-0161.

## Session 09B

## Theatre 6

**Challenges of applying selective dry cow treatment on Czech dairy farms**

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Regulation 2019/6 will prevent the routine prophylactic and metaphylactic use of antibiotics in EU in the coming years. For this reason, the possibilities of selective dry cow treatment (DCT) of dairy cows are currently being addressed. The main goal of this contribution is to showcase the screening of the current situation for dry-off on Czech dairy farms. A total of 53 cows from 3 Holstein farms were evaluated within a week before DCT for teat condition (wrinkling, hyperkeratosis, and cleanliness) and milk quality. The blanket antibiotic DCT is used on these farms with a future plan to switch to selective DCT. The milk samples were evaluated for fat, protein, lactose, urea, titratable acidity, citric acid content, free fatty acid content, somatic cell count (SCC) and microbial cultivation. We found significant differences among the farms in all monitored parameters. The average fat content ranged from 3.1 to 3.95% and protein from 3.85 to 4.05%. Lactose content in milk is very stable, we observed 4.75 to 4.87%. However, mastitis infection can slightly lower it, which suggests its potential use as an indicator for selective DCT. The condition of teats was different on monitored farms, with the farm A achieving the best average cleanliness values (1.2) but at the same time the worst hyperkeratosis score (2). These results were also reflected in the average SCC, which ranged from 153 thousand/ml to 189 thousand/ml. Approximately 20% of cows showed a negative result for cultivation, and from 24 to 42% of teats exceeded the limit of 200 thousand/ml SCC. Our results also confirm significant correlations between SCC and the lactose content, titration acidity, and other milk parameters. The most commonly used parameter for selective DCT is SCC. The aim of project QK21010123 NAZV CR is to verify the already used methods and to investigate other possible parameters for optimizing the selection for DCT.

**Dose- and time-dependent in vitro impact of naringenin on the vitality of bovine spermatozoa**

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Naringenin (NAR) is a flavanone widely distributed in citrus fruits with cardioprotective and antiviral properties. This study investigated the in vitro effects of various NAR concentrations on selected quality markers of bovine spermatozoa. Ejaculates from 10 Holstein bulls were diluted in a culture medium enriched with 0, 5, 10, 50, 100 and 200 µmol/L NAR, and sperm motility, membrane and acrosome integrity, mitochondrial activity and reactive oxygen species (ROS) production were assessed at 0, 2 and 24 h of incubation. Our results indicate that while exposure to higher NAR concentrations (50-200 µmol/L) led to a significant ( $P<0.001$ ) inhibition of the sperm motility and mitochondrial activity (2h), lower concentrations (5 and 10 µmol/L) of the flavanone stimulated the sperm motion as well as mitochondrial metabolism ( $P<0.01$ ) (24h). Concentrations ranging from 5 to 10 µmol/L NAR acted as antioxidants ( $P<0.05$ ;  $P<0.01$ ) and offered a higher protection to the sperm membranes and acrosome ( $P<0.05$ ) following 2 and 24h. Our results show that NAR exhibits protective effects on bovine spermatozoa, nevertheless, only when concentrations equal to or below 10 µmol/L are used for in vitro sperm processing. This publication was supported by the Operational program Integrated Infrastructure within the project: Creation of nuclear herds of dairy cattle with a requirement for high health status through the use of genomic selection, innovative biotechnological methods, and optimal management of breeding, NUKLEUS 313011V387, cofinanced by the European Regional Development Fund.

## Session 09B

## Poster 2

**Prevalence of udder pathogens isolated in raw goat milk at late lactation stage**

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Mastitis caused by bacterial intramammary infections is the most common cause of mastitis in dairy goats. Mastitis, which occurs in goat breeding, is as serious a health and economic problem comparable seen in breeding of dairy cows or ewes. Our research aimed to assess the health status of the mammary gland at the end of lactation based on the identification of bacterial pathogens in goat milk. The milk was collected at the specialized dairy farm located in the northwest of Slovakia. Of all the milk samples taken ( $n=242$ ) at the level of semi-udder technique, the pathogens were detected in 16.7% of the milk samples. No contaminated samples were detected. The most frequently identified pathogens were coagulase-negative staphylococci, which accounted for 75% of bacteriologically positive milk samples. The most frequently identified coagulase-negative staphylococcus was *Staphylococcus caprae*, which accounted for 37.5% of the aforementioned group of pathogens. A positive finding was that the contagious pathogens *Staphylococcus aureus* and *Streptococcus agalactiae* were not identified in any milk sample. In conclusion, the bacteriological examination of milk before the drying period could be a key tool for reducing the risk of mastitis in goats and ensuring quality milk production. The possible relationship of pathogens presence before drying with their occurrence after kidding could be important for further study. Keywords: goat milk, mastitis, pathogens, late lactation stage Acknowledgment: This publication was supported by the APVV-21-0134, by the VEGA 1/0597/22 and by the GA FAPZ 06/2023

### Some factors influencing the welfare of dairy cows at the individual level

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The aim of this research was to assess the effect of farm size, milk production level and SCC in milk on selected dairy cows' welfare indicators at individual level. Welfare assessment was carried out in 8 dairy farms rearing Romanian Spotted cows from Timiș County, Romania. Each studied factor had two levels: small and large farms (less and more than 40 cows); low and high milk yield (less and more than 5000 litres/cow/year); and low and high SCC in milk (less and more than 200,000 cells/ml). A modified Welfare Quality<sup>TM</sup> assessment protocol was used. Comparisons among factor levels were carried out using chi-squared test. Results for three indicators are presented in this paper: body condition, rising behaviour and collision with equipment, and cleanliness of hind quarters, udder and tarsus. Rising behaviour and collision with equipment was not influenced ( $p>0.05$ ) by neither one of the studied factors. About 70% of cows had a normal body condition and expressed a normal rising behaviour, irrespective of studied factors. A significantly higher ( $p=0.02$ ) proportion of cows were cleaner on the hind quarters (rump, thighs, tail) in large than in small farms (37.2% vs. 25.7%). The proportion of cows with clean tarsus was 1.8 times higher in farms with high milk yield compared to farms with low milk yield (33.1% vs. 18.1%,  $p<0.001$ ). The proportion of cows with clean udders was by 1/3 significantly higher in farms with low SCC compared to farms with high SCC in milk (49.3% vs. 37.1%,  $p=0.01$ ). It was concluded that cleanliness of certain body regions of dairy cows could be linked with farm size, milk yield level, as well as SCC in milk.

### Session 09B

### Poster 4

### Associations between somatic cell counts (SCC), selected milk production traits and milk production conditions in Slovak Spotted dairy cows

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The aim of this study was to evaluate associations between somatic cell counts (SCC), selected milk production traits, management practices and production areas of entire population Slovak Spotted dairy cows during the years 2014 – 2016. Research dataset, which contained data collected from 64,520 Slovak Spotted dairy cows (952,400 test-day records), was obtained from the Slovak Animal Breeding Services (s.c.). Relations among milk production traits – daily milk yield (DMY in kg), daily fat content (DFC in %), daily proteins content (DPC in %), daily lactose content (DLC in %), somatic cells count (SCC) and somatic cell score (SCS) were analysed by Statistical Analysis System (SAS) version 9.4. The statistically significant effects of SCC on milk yield ( $P < 0.0001$ ) were observed. Impact of the different herd management practices and production areas on the SCC value was confirmed, too. In this study have found that herds breed in lowland areas show high milk yield and low SCC in comparison with herds from mountain and sub-mountain areas. Results also indicate association between organic farming and low SCC values. This study was supported by the Slovak Research and Development Agency No. APVV-17-0060, APVV-20-0161 and KEGA 012SPU-4/2019. Key words: Mastitis, management practices, milk quality, autochthonous breeds, Slovakia

**Observation of changes in heart rate and rectal body temperature of calves during the first hour after birth**T. Hegerová<sup>1</sup>, P. Juhás<sup>1</sup><sup>1</sup> Slovak University of Agriculture in Nitra, Institute of Animal Husbandry, Tr. A. Hlinku 2, 949 76 Nitra, Slovakia

Measuring the vital signs of calves immediately after birth helps farmers determine the immediate health status of calves and predict their possible development. The research took place at the Slovak University of Agriculture Farm in Oponice. Evaluation and analysis of viability signs was performed on a sample of 25 Holstein calves. All statistical calculations and graphical outputs were performed using IBM SPSS Statistics v. 26. The relationship between indicators in individual measurements as well as the relationship between different indicators were analysed by Spearman correlation. The average measured heart rate for all measurements M1–M4 (measurements number 1.–4.) was 165.64 bpm (beats per minute) with a standard deviation of 17.607 bpm. The maximum value for the measurements was 240 bpm and the minimum 136 bpm. No significant differences between measurements M1–M4 were recorded. The most significant variability was found in the M2, where the difference between the lowest and the highest measured heart rate was 96 bpm. This variability was probably caused by the measured values of calf No. 3, which stood up and moved during the measurement. The average temperature for measurements M1–M4 was 38.797 °C with a standard deviation 0.739 °C, the maximum rectal temperature was 40 °C and the minimum was 34.9 °C. The results showed the rectal temperature of calves decreases in first hour after delivery. Significant difference between M1 and M4 measurements (0.692 °C) was recorded ( $P < 0.05$ ). Negative correlation was noted for the relationship between rectal temperature and pulse in measurements M1 ( $\rho = -0.449$ ,  $P < 0.05$ ) and also for measurements of M4 ( $\rho = -0.484$ ,  $P < 0.05$ ). The research was supported by VEGA 1/0572/22.

**Neuronal ceroid lipofuscinosis in a domestic dog on the example of the Golden Retriever breed**J. Kałuska<sup>1</sup>, A. Grochowska<sup>2</sup>, P. Kurowska<sup>1</sup>, J. Osypiuk<sup>1</sup>, D. Wilim<sup>1</sup>, G. Damentka<sup>1</sup>, A. Filipek<sup>1</sup>, M. Michalik<sup>1</sup>, M. Kołpak<sup>1</sup>, B. Grzegółka<sup>2</sup>, J. Gruszczńska<sup>2</sup><sup>1</sup> Warsaw University of Life Sciences – SGGW, Scientific Association of Experimental and Laboratory Animals, Ciszewskiego 8, 02-786 Warsaw, Poland, <sup>2</sup> Warsaw University of Life Sciences – SGGW, Institute of Animal Sciences, Department of Animal Genetics and Conservation, Ciszewskiego 8, 02-786 Warsaw, Poland

Neuronal ceroid lipofuscinosis is a genetically determined degenerative disease of the central nervous system. There are many types of this disease depending on which genes will mutate in the CLN family (CLN1–CLN14). Various types of NCL have been observed not only in humans, but also in domestic dog. The function of the CLN5 protein remains unexplored. The aim of this study was to analyze the genetic background of CLN5 disease in both human and domestic dog of golden retriever breed, as well as to design a molecular test allowing for the unequivocal identification of mutated allele carriers. The following programs were used in bioinformatics analyzes: BLAST, Clustal Omega, Primer3, PCR Primer Stats, NEBcutter, Signal 5.0. Both the nucleotide sequence of the CLN5 gene and the amino acid sequence of the CLN5 protein in the domestic dog (on the example of golden retriever) have been found to be highly conserved, and that the CLN5 protein undergoes similar post-translational processing as in humans. Molecular diagnostic tests were designed to detect pathogenic mutation in the studied species. Project financed under project no. MEiN/2022/DIR/3524 entitled “Best of the best! 4.0.” under the Operational Program Knowledge Education Development co-financed by the European Social Fund (POWR.03.03.0000P019/18).

**Protein profiles in the transfected hen (*Gallus gallus domesticus*) oviductal secreting cells**M. Wu<sup>1</sup>, G. Maiorano<sup>1</sup>, S. Zuo<sup>2</sup>, K. Stadnicka<sup>2</sup><sup>1</sup> University of Molise, Department of Agricultural, Environmental and Food Sciences, Via Francesco De Sanctis 1, 86-100 Campobasso, Italy, <sup>2</sup> Faculty of Health Sciences, Ludwik Rydygier Collegium Medicum in Bydgoszcz, Nicolaus Copernicus University, Łukasiewicza 1, 85-821 Bydgoszcz, Poland

Laying hen is used as a bioreactor for the production of recombinant therapeutic proteins. The oviduct epithelial cell transfection models enable verification of transformation and their effect on cells. 40-week-old laying hens (n=10) were used for the isolation of chicken oviduct epithelial cells (COEC). Nucleofection was used to deliver nonviral plasmid DNA with a reporter GFP and hIFN under the ovalbumin promoter. The transfection rate in cells ranged from 3.1% -10.6%. PCR confirmed the expression of the hIFN $\alpha$ 2a exogen but the hIFN $\alpha$ 2a protein had not been detected. Interestingly, Ovalbumin was highly expressed, especially in the transfected COEC. Proteomics revealed that 60 proteins were up-regulated and 101 proteins were down-regulated in the transfected (>1.5 FC) compared to non-modified cells. Inhibition of metabolite interconversion enzymes and chaperones and upregulation of cell adhesion molecules and collagens were found. GO analysis showed that the majority of differentially regulated proteins (DRPs) came from ribosomes, associated with peptide biosynthetic process and RNA binding. In Reactome pathway analysis, DRPs were mainly involved in the Nonsense-Mediated Decay-related pathway. Unique proteins were mainly participating in Rap1 signaling and Eukaryotic Translation Initiation. The COEC model responds to transfection on cell proteome levels and may serve to assess the effects of genetic modifications in animal bioreactor studies. Fund: Ministry of Science and Higher Education, Poland -UMK Emerging Fields ANTAIO Team

## Session 09B

## Poster 8

**Barn climatic effects on milk production and milking frequency in automatic milking system**I. Knížková<sup>1</sup>, P. Kunc<sup>1</sup><sup>1</sup> Institute of Animal Science, Pratelstvi 815, 104 00 Prague, Czech Republic

The aim of study was to determine the effect of barn climate conditions on milk yield and milking frequency in automatic milking system (AMS). In a period of 3 years, 24 farms with AMS were monitored. The monitored parameters were the milk yield (l.cow<sup>-1</sup>.day<sup>-1</sup>), and the milking frequency.cow<sup>-1</sup>.day<sup>-1</sup> in AMS. These parameters were evaluated depending on air temperature (Ta), and relative air humidity (Rh). The average daily milk yield reached the highest values in the temperature range of 15-25 °C (32.18  $\pm$  4.68 l. cow<sup>-1</sup>). The highest significant (p<0.05) drop in milk was recorded after crossing the 25 °C limit, the drop was 1.22 l cow<sup>-1</sup>.day<sup>-1</sup>. The lowest average daily milk yield was found for Ta in the range of -15 °C to -10 °C (30.8  $\pm$  0.79 l. cow<sup>-1</sup>.day<sup>-1</sup>). The most stable period in terms of efficiency was found in the range of 0-15 °C. Average daily yield was highest at Rh 40-70 %. Low (below 40 %), and high Rh (above 70 %) negatively affected the average daily milk yield, there was a significant decrease in its value (p<0.05). The milking frequency was significantly affected at the temperature range -15 °C to -10 °C, when the lowest frequency was found. Other Ta (from -10 °C to 30 °C) had no significant effect on the milking frequency. The highest milking frequency was found in the range of Rh 40-70%, higher values of Rh meant a significant reduction (p<0.05) in milking frequency. Study funded by MZE-RO0718 and MZE- RO0723.

### Analysis of the calving ease and stillbirth traits in the Slovak Holstein cows

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The aim of the work was to determine the frequency of calving ease and stillborn calves in a group of holstein heifers and older cows in Slovakia. The data file consisted of 918,568 records (347,127 heifers and 571,441 cows) of the Slovak Holstein breed. Four categories of calving ease were defined (1-without assistance, 2-with assistance, 3-difficult, 4-caesarean section) and two categories of stillbirth (1-alive and 2-stillborn calf). The calving ease was evaluated according to heifers and older cows and sex of the calf. In the group of heifers, the highest proportion of heifers born was recorded in the category of calving without assistance (84.17%), which was 2.54% higher than the proportion of bulls born. For older cows, 91.52% females and 89.36% males sex were born without assistance. A higher proportion of born bulls was found in moderately difficult to very difficult calving in both parity. Caesarean section was performed in less than 0.03% of heifers and cows. In the group of heifers, 3.56% of stillborn calves were found, which were born without assistance. In difficult calving and caesarean sections were up to 59.80% and 51.68% of dead calves. Older cows had a lower proportion of stillborn calves than heifers in the category of easy calving (1.1%), on the contrary, this proportion was higher by 6.52% in caesarean-section calving. This publication was supported by the Operational Programme Integrated Infrastructure within the project: Sustainable smart farming systems taking into account the future challenges 313011W112, cofinanced by the European Regional Development Fund and KEGA 017SPU-4/2022.

### Session 09B

### Poster 10

### Relationship between rectal temperature, eye temperature and air temperature

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Based on measurements of eye temperature (ET) (using infrared thermography) and rectal temperature (RT) (digital thermometer) in 83 clinically healthy dairy cows, an analysis of the relationship between these parameters depending on air temperature (Ta) was performed. A change in body temperature is recognized as an important indicator of illness or stress. The eye temperature is considered by experts from human and veterinary medicine to be the only truly relevant data and it can be characterized as a reliable indicator of body temperature and its changes. The measurements were carried out in the field conditions of a dairy farm, at average Ta of 5, 12, 19 and 25 °C. The highest difference between RT and Ta (by 3 °C;  $p < 0.05$ ) was found at Ta 5 °C, the lowest difference between these parameters (1.8 °C;  $p < 0.05$ ) was at Ta 25 °C. Average RT of dairy cows was  $38.21 \pm 0.21$  °C, average ET was  $37.48 \pm 0.69$  °C. A statistically significant difference was found between the two values ( $p < 0.05$ ). The linear regression is in the form  $y = 5.2852 + 0.8427 \cdot x$ , the correlation coefficient is  $r = 0.2559$ , i.e. that there is a low to moderate linear relationship between RT and ET (regression significance  $p = 0.0196$ ). The amount of differences will be related to the body's thermoregulatory reactions to heat and cold, so it is necessary to evaluate the measurement conditions very carefully for the correct interpretation of the measured values. Study funded by MZE-RO0718 and MZE-RO0723.

## Genomic inbreeding and heterozygosity in Austria dog populations

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The maintenance of sufficient genomic diversity is one of the most important tasks in the breeding of companion animals. In dogs especially, the genomic diversity is on the decline in many breeds, due to the small population size and excessive use of favoured animals as parents of the next generation. In our study we aim to screen the selected dog populations from Austria (with at least 20 available genotyped individuals), to determine the genomic inbreeding and heterozygosity levels. The analysed data consisted of 38 Beauceron (BCC), 39 Smooth Collies (SCO), 97 Boxer (BOX), 20 Elo (ELO), 184 Leonberger (LEO), 88 Standard Poodle (SPO), 25 Labrador Retrievers (LR), and 71 Rhodesian Ridgeback (RR) dogs genotyped with a custom SNP chip, containing 57,001 autosomal markers. After removing SNPs and individuals with more than a 10% missingness rate, 56,942 SNPs and all 562 animals remained. Runs of homozygosity with a minimal length of 8Mb were used to calculate genomic inbreeding. The values ranged between  $F(ROH) = 0.07$  ( $sd = 0.04$ ) for LR to  $F(ROH) = 0.23$  ( $sd = 0.07$ ) for BOX. The genomic inbreeding was above 0.1 average for LEO and SCO, and around 0.1 – 0.07 for other breeds. The genome wide heterozygosity, although not restricted to continuous segments as ROH, followed a similar pattern. It was between 0.37 ( $sd = 0.03$ ) for SPO and 0.26 ( $sd = 0.02$ ) for BOX. We conclude that increased attention needs to be given to lowering inbreeding levels and increasing diversity in all breeds, with immediate action, especially for BOX, LEO and SCO breeds.

## Session 10

## Theatre 2

## Genetic parameter estimations for antler traits in a captive red deer (*Cervus elaphus hippelaphus*) population

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Red deer antlers, as one of the fastest growing tissues in the animal world, are an important base material for traditional Chinese medicine, and thus have significant economic value. On the European continent, the antler as a trophy has a prominent role in a hunting culture. According to the latest research results, it has become the focus of attention in clinical medicine, primarily due to its antitumor activity. Regardless of the use, it would be an important aspect to determine the heritability values characterizing the parameters of the antlers, on which there is relatively little literary data available in the case of red deer. The aim of this study was to estimate the heritability of antler characteristic traits which are important either for velvet antler production (antler weight, lower and upper circumferences and the number of tines) or for hunting (antler weight, C.I.C. scores). 377 antler pairs of 101 stags were measured in a farmed red deer population. The age of the stags (2-6 years), the year of antler development (2010-2022) and the mob (6 groups) was taken into consideration. Heritability estimate for hard antler weight was 0.22. Lower circumference showed higher heritability (0.33) than upper circumference (0.24). The number of points had the highest heritability estimates (0.72), while C.I.C. scores had low estimates (0.25). Our results indicate the little potential to respond to phenotypic selection for most of the examined traits; however, selection for the number of antler points should be effective in the free range population too.

### Carcass and meat quality traits of Siciliana chickens, a native Italian breed

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The study aimed to characterize the slaughter performance and meat quality of Siciliana chickens, a native Italian chicken breed. At 180 d of age, 24 birds (12 birds/sex) were weighed and slaughtered. Carcass and the main cuts weight were recorded. On the right pectoral muscle (PM), pH and colour were recorded at 24 h post-mortem. The left PM was used for chemical analyses. Data were analyzed by one-way ANOVA. Compared to females, males had a higher ( $p < 0.001$ ) slaughter weight ( $1511.83 \pm 37.75$  g vs  $1214.17 \pm 35.25$  g), carcass weight and yield (+ 6.2%); while females had a higher breast yield (+ 2.9%;  $p < 0.01$ ) than males. Legs yield and pH were not affected by sex ( $p > 0.05$ ). Higher lightness ( $p < 0.01$ ) was observed in females; while males showed higher ( $p < 0.01$ ) redness and yellowness. Females showed higher ( $p < 0.01$ ) breast moisture, total lipid and ash ( $p < 0.05$ ) contents than males, while a higher protein content was found in males ( $p < 0.001$ ). Males showed a higher content of total saturated fatty acids ( $p < 0.05$ ) and a lower content of monounsaturated fatty acids ( $p < 0.01$ ) than females. No differences were found for total polyunsaturated fatty acids (PUFA) and n-6 PUFA; while, the n-3 PUFA content was higher ( $p < 0.01$ ) in males than in females, leading to a favourable lower n-6/n-3 ( $p < 0.05$ ). As a part of a conservation program for the Siciliana breed, this study was the first contribution to the characterization of carcass and meat quality of Siciliana chickens. Project TuBAvI-2 funded by the Italian Ministry of Agriculture, MIPAAF-TNRDP 2014-2020-Measure 10.2 Biodiversity-Poultry sector (DG DISR-DISR07-Prot. n. 0162350-09.04.2021).

### Examination of the integration efficiency of guinea fowl embryonic gonad-derived cell suspension into the recipient embryonic gonad

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The present tendencies in animal husbandry put more and more emphasis on the gene preservation of the breeds excluded from production. While the mammalian species already have reliable methods for this, avians are problematic due to the homogametic nature of the male (ZZ) animals. The PGC gene banks could be an alternative, but this technique is still not adopted in the case of numerous avian species. To solve this problem, the development of new technologies is necessary. In our experiment, 10-day-old guinea fowl embryonic gonads were isolated and digested to create a cell suspension. This suspension contained various cell types, including primordial germ cells (PGCs). We stained the cells with the PKH26 red fluorescent dye and injected them into the blood circulation of 3-day-old embryos. After four days, we dissected the gonads from the 7-day-old embryos and examined the integration efficiency under a stereo microscope. Our results showed that out of nine successful injections in four cases, we found integrated stained cells in the gonads. Out of these, in three cases, female cells, and in one case, male cells were injected. Our future goal is to include a freezing step into the experiment to check the potential of embryonic gonadal cell suspension injection in gene preservation.



**Statistical discrimination of four Nigerian sheep breeds using haematological and biochemical indices**

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In Nigeria, small ruminant accounts for 63.7% of total grazing domestic livestock, and are widely distributed in rural, urban and peri-urban areas. Serum biochemical and haematological indices constitute important panels in the diagnosis, prognosis and treatment of livestock diseases. This study was conducted to investigate and evaluate differences among four prominent indigenous sheep breeds of Nigeria, using haematological, serum and biochemical parameters to assess their level of disease resistance, adaptation, survivability and genetic similarities. Four indigenous breeds (Yankasa, Ouda, Balami, and West African Dwarf) were evaluated, with six animals were sampled for each breed. A total of 24 animals were sampled by collecting blood from their jugular vein, stored in labelled vacutainers. The samples were subjected to haematological, serum and biochemical properties evaluation. Data obtained from the laboratory analyses were subjected to statistical analyses, which included One Way Analysis of Variance, Post-hoc tests, Cluster and Discriminant analyses using Minitab (17) statistical software. Breed had significant ( $P < 0.05$ ) effect on only two haematological parameters (packed cell volume and neutrophils), and also on only two biochemical parameters (total protein and urea). The Yankasa breed had the best values for all the parameters studied indicating that it is best suited to this locality. A further cluster analysis using the computed values further indicated that the Yankasa breed was aloof from the other three breeds, while the Ouda and Balami were within the same cluster. The discriminant function had a 95.8 percent accuracy in classifying the animals to their respective breeds.

## Session 10

## Theatre 6

**Polymorphisms in CAST genes and their association with feed conversion ratio in Latvian Dark-Head sheep**

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In animal husbandry, feed efficiency is a crucial economic trait. The feed conversion ratio (FCR) is a traditional metric for assessing feed efficiency, defined as the ratio of dry matter intake to average daily gain. Improving the FCR parameter in breeding is highly important for sheep production. Sire rams with better FCR indicators produce offspring with a higher value of this indicator. With the rapid development of science and technology (DNA analysis), more opportunities for breeding using genetic markers associated with various productive traits exist. Calpastatin (CAST) plays a key role in skeletal muscle development and is involved in protein metabolism, muscle growth and development, and fat deposition. This study aimed to analyze CAST gene polymorphisms and their relationship with FCR in the Latvian Dark-head (LT; Latvijas tumšgalve) breed. After control fattening, blood samples were collected from 48 offspring of LT sires for DNA isolation. Exons of the CAST gene and flanking intron regions were sequenced using NGS technology. The CAST gene has been sequenced in LT lambs for the first time; 43 polymorphisms with known ID numbers were identified. From all loci, 18 were rear: minor alleles less than 10%. In the case of two SNPs: rs408766737 and rs161885105, the FCR values of lambs homozygous for the rear allele were statistically significantly lower than the rest of the animals from the experimental cohort. Therefore, CAST gene SNPs have the potential to be molecular markers to predict the FCR value.<sup>2</sup>

### Detection of the 11 bp Insertion Associated with Milk and Reproduction Traits within Slovak Population of White Shorthair Goat

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The CSN1S1 gene is a highly polymorphic gene with different impacts of alleles on the nutritional and technological properties of milk. An 11-bp indel has been observed within the CSN1S1 gene in goats, which has a significant effect on the first-birth litter size of goats and milk performance. The aim of this work was to identify the insertion in the CSN1S1 gene using the PCR method and to evaluate and compare the allele frequencies and genotypic structure of the population for the insertion in the CSN1S1 gene. In this work, we analysed 136 goats of the White Shorthaired Goat breed from the PD Mestečko (44) and ÁBEL Plus (92) breeding farms. In the PD Mestečko farm found 84.09 % representation of the I and 25.91 % of the D allele. Genotype II, which has a demonstrable positive effect on litter size, had 34 individuals (77.27 %). Genotypes ID and DD had 6 (13.64 %) and 4 (9.09 %) goats respectively. In the ÁBEL Plus farm, allelic frequencies for the I allele were 78.80 % and 21.20 % for the D allele. Genotypes ID and DD were found among 15 (16.30 %) and 12 (13.04 %) individuals respectively. The  $\chi^2$  test showed a statistically highly significant difference between the expected and observed frequencies of genotypes in both farms, which means that there is no equilibrium state in the mentioned populations in terms of the Hardy-Weinberg law. This statement is supported by the fact that in breeding farms, breeding males are produced, which are selected only from multiple litters, and thus mothers that have consistently larger litters are selected. This study was supported by the Slovak Agency for Research and Development, grants number APVV-17-0060 and APVV-20-0161.

### Session 10

### Theatre 8

### Ancestral inbreeding and inbreeding-purging models' comparative analysis based on their classification efficiency of the Pannon white rabbit kits' survival at birth

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The authors analysed 22718 kindling records of 5166 rabbits born between 1992 and 2017, respectively. The 25-year-long exanimated period was separated into three different sub-periods (1992-1997; 1997-2007 and 207-2017). The effect of dam and litter inbreeding on the survival of rabbit kits at birth was evaluated with two fundamentally different methods with the same purpose of signalling the possibility of purging. The first method considered the different ancestral inbreeding coefficients (AINB) by applying the generalized linear mixed model extended with model averaging. The inbreeding-purging model (IPM) was based on the purged inbreeding coefficient where the possible purging is accounted for. The parity and season of kindling effects were the same in both methods. The classification abilities of these models were compared based on the ROC Curve where the greater area under the curve (AUC) signals better classification performance. The AUC values of the models using AINB ranged between 0.79 and 0.83. On the contrary, IPM resulted in lower AUC values ranging between 0.54 and 0.57. The optimal threshold was determined by the maximum value of Kappa and depending on the examined period they ranged between 0.87-0.89 for the AINB models and it was 0.94 for the IPM. True positive rate (sensitivity) was high both for AINB-based models (0.93-0.96) and for IPM (0.71-0.82). On the contrary true negative rates (specificity) were generally much lower both for the AINB models (0.25-0.38) and for the IPM (0.23-0.37). Consequently, the proportion of the correctly classified cases were substantially higher (0.91-0.92) for the AINB models compared to the IPM (0.71-0.82).

**Investigation of the effect of heat treatment on epigenetic modification in chicken primordial germ cells**

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Farm animals must adapt to the increased temperatures by climate change. This ability of farm animals is necessary for sustainable agriculture. In addition to gene preservation, primordial germ cells (PGCs) can be used as an in vitro model system to study many molecular processes. The project aims to investigate microRNA expression patterns at the molecular level behind the animals' responses to heat stress. Fertilized eggs are from the Transylvanian Naked Neck Chickens. Three groups were used during the experiment. The first one was the control group (C), the second group (HTHS) was subjected to heat treatment and heat stress, and the third group (HS) was heat-stressed. Our research group isolated 26 PGC lines from these chicken embryos. In our work, RNA was isolated from PG cells, and the expression levels of stem cell specific and heat shock related microRNAs were determined in the samples. Based on our results, it can be said that as a result of heat treatment and heat stress, epigenetic changes occur in the PGCs, which result in gene expression changes that are passed on to subsequent generations.

## Session 10

## Poster 1

**Analysis of chinchilla (*Chinchilla lanigera*) reproduction results on a breeding farm**

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The aim of the study was to analyze the reproduction results of a chinchilla (*Chinchilla lanigera*) from a breeding farm, taking into account the calendar year, the month of birth and colour variety. The analysis included two basic characteristics: the number of born and the number of raised. Throughout this time, chinchillas were kept in families of 4 females plus 1 male. Statistical analyzes of chinchilla reproduction results from 2011-2022 were performed and during ten years, 2 899 litters were recorded. The analysis of variance for the number of born and the number of raised showed a statistically highly significant effect of the calendar year and the month of birth on the number of born and raised chinchillas. When analyzing the number of born and raised chinchillas depending on the calendar year, it was noted that the highest parameters of litter size were obtained in 2018 and 2021. The average litter size in these years was 2.14. The average litter size on the analysed farm ranged between 1.84 (2011) and 2.14 (2018 and 2021), while the average number of raised ranged between 1.57 (2011) and 1.92 (2018). The analysis of the litter size and the number of raised chinchillas depending on the month of birth proved that the highest values were achieved in March and April. This confirms the seasonality of chinchilla reproduction. This publication has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. 2021-1-SK01-KA220-HED-000032068 "Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalization".

**Analysis of factors affecting the quality and length of life of dogs**

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The dog is a diverse species in terms of behaviour, size and lifespan. There are many factors that affect the lifespan of dogs. This paper examines, among others, the effect of breed on the length and quality of a dog's life, the effect of the owner and social environment on a dog's quality of life, the effect of utility on a dog's quality of life, and the effect of nutrition on a dog's length and quality of life. The size of a dog is a well-known factor affecting the length of its life. Purebred dogs are known to have higher health burdens and shorter life spans than non-breed dogs and interbreed hybrids of the same size. The length and quality of life of dogs are also affected by the quality of the bond with the owner and the owner's awareness of preventive veterinary care. A stimulating environment, and proper nutrition taking into account the dog's specific breed or health requirements, are also important for the quality and length of canine life. This publication has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. 2021-1-SK01-KA220-HED-000032068 "Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalization".

## Session 10

## Poster 3

**Interaction of the ovine host genome with *Corynebacterium pseudotuberculosis* infection**

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*Corynebacterium pseudotuberculosis* (Cp) is the etiological agent of caseous lymphadenitis, which has a detrimental impact on the health of small ruminants. The study's goals were the characterization of the ovine whole blood transcriptome and functional comparison of the differentially expressed genes between healthy and affected animals. The blood samples of East Frisian sheep were obtained from Cp serologically positive (3) and negative ewes (3) and the health controls (3) of another herd. Differential gene expression was analyzed by RNA-seq on an Illumina NextSeq™ 550 system using the DESeq2 approach. The DEG sets were annotated with UniProt Knowledgebase and the WEB-based GENE Set Analysis Toolkit. The top unique upregulated genes in the diseased ewes included killer cell lectin-like receptor subfamily B member 1 (KLRB1), immunoglobulin superfamily DCC subclass member 3 (IGDCC3), ADAM metalloproteinase with thrombospondin type 1 motif 13 (ADAMTS13) and BOLA class I histocompatibility antigen, alpha chain BL3-7-like. Extracellular matrix proteins and regulators of lipid metabolism represented the downregulated unique genes. The highest expression of common genes was found for MHC class I polypeptide-related sequence B (MICB) and lymphocyte antigen 6 family member G6C (LY6G6C). The opposite direction between groups showed MHC class I receptor leukocyte immunoglobulin-like receptor subfamily A member 6 and immuno-associated protein GTPase IMAF family member 7-like. There were positive activation and regulation of the adaptive host immunity and the deregulation of some effector components of the diseased compared to the resistant ewes.

### Mutation within the PKLR gene in a domestic cat – molecular test project

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Pyruvate kinase deficiency (PKD) is a genetic disorder causing haemolytic anaemia. In the domestic cat, it is characterised by an intermittent course of the disease and is caused by a single mutation within the PKLR gene. The aim of this study was to identify in silico the mutation within the PKLR gene that causes PKD deficiency in the domestic cat, to identify cat breeds at risk and to propose an appropriate diagnostic test to detect the mutated allele of the tested gene. As a result of analyses performed using bioinformatics programs such as BLAST, NEBcutter V2.0, Primer 3 v. 0.4.0, STRING, it was shown that using the Sau96I restriction enzyme in a molecular test it is possible to identify carriers of mutated alleles of the PKLR gene. The highest risk group includes cats of the following breeds: Abyssinian and Somali, in which mutations of the PKLR gene were discovered for the first time. The results of this study are preliminary studies that can be applied in practice in the genetic diagnosis of PKD in domestic cats. Research funded by project No SKN/SP/536153/2022 “Student scientific circles create innovations” financed by the Ministry of Education and Science.

## Session 10

## Poster 5

### Searching for the DNM1 gene mutation responsible for Exercise Induced Collapse in a domestic dog (Canis lupus familiaris) on the example of the Belgian Shepherd Dog breed

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Due to the highly impulsive and impetuous nature of Belgian Shepherd dogs, dogs of this breed are predisposed to episodes of exercise-induced collapse. In some breeds of dogs, the underlying cause of this disease is a mutation within the gene encoding the protein dynamin 1 (DNM1). The purpose of this study was to analyze the sequence of the DNM1 gene fragment in search of the mutation responsible for the exercise-induced collapse in the Belgian Groendael Shepherd Dog breed. The biological material consisted of hair with roots taken from 5 individuals of the studied breed. DNA was isolated, amplified, purified, and then exons 5 and 6 of the DNM1 gene were sequenced. Using bioinformatics programs: Mega 11, GeneDoc 2.7, BLASTx, SWISS-MODEL, the nucleotide sequence similarity was compared, and then transcribed into an amino acid sequence. The nucleotide and amino acid sequences did not show the presence of variability between the samples and the studied fragment of the sequence of a healthy dog. Based on the data obtained, it was concluded that exercise-induced collapse in the Belgian Shepherd Dog breed is not caused by a mutation within the tested fragment of the DNM1 gene. Research funded by project No SKN/SP/536153/2022 “Student scientific circles create innovations” financed by the Ministry of Education and Science.

**Technological aspects, bee pathologies and bee products in UASVM Cluj-Napoca apiary during 2014-2023**C. Pașca<sup>1</sup>, O. Bobiș<sup>1</sup>, D. S. Dezmirean<sup>1</sup><sup>1</sup> University of Agricultural Science and Veterinary Medicine Cluj-Napoca, Department of Apiculture and Sericulture, 3-5 Mănăstur Street, 400372 Cluj-Napoca, Romania

Apiculture is an important sector worldwide, for its contribution to local ecosystems and to improving approximately 75% of agricultural production of global crops and increasing global crop value by nearly £153 billion. During 2014-2023, the apiary located in University of Agricultural Sciences and Veterinary Medicine of Cluj-Napoca passed through different challenges caused by climate changes, weather conditions, or environmental stressors (contaminated water, feed or flowers, trophallaxis, cleaning activities, bee feces deposited in/on the hive or material with infective spores from infected worker honey bees, etc.). Technologically, the apiary was directly influenced by high temperatures in winter period and reduced amounts of nectar in the active beekeeping season. A honeybee colony, with a young queen, which had developed properly in one year, in the next spring, after April, can die or can be depopulated. We annually control the health status of our apiary, using different alternatives or technologies, which can be useful for beekeepers and also for bee products consumers. We know that beekeepers have some control options for bee disease, but European legislation does not permit the use of antibiotics for the treatment of honeybees, because bee products have to be free of any drug residues. In this context this study presents the technological aspects, the beekeeper role in the honeybee's welfare; the actual bee pathologies for our apiary, and which are the alternative drugs based on natural products, pharmacological and phytochemical properties, which became a priority in the health of honeybee's colony and safety of bee products.

**Farmer experience in transfer from conventional to robotic milking in Croatia**P. Mijić<sup>1</sup>, V. Gantner<sup>1</sup>, M. Gregić<sup>1</sup>, M. Baban<sup>1</sup>, T. Bobić<sup>1</sup><sup>1</sup> Faculty of Agrobiotechnical Sciences Osijek, Department of Animal Production and Biotechnology, Vladimira Preloga 1, 31000 Osijek, Croatia

Automation of milking is an increasingly common situation on dairy farms in Croatia. The milking robots have been among the most important technological solutions and innovations in recent years. Currently, 40 milking robots were installed in Croatia, distributed on 27 farms. More than 47% of the farmers stated that the most common reason for switching from conventional to robotic milking was to reduce the share of human labour and 26% of them wanted to improve one's own quality of life. Along the way, there were various challenges and ambiguities, most often of a financial or bureaucratic nature. However, the first production results encouraged all farmers. After switching from conventional to robotic milking the milk production at the lactation level per cow increased significantly ( $p < 0.0001$ ) by about 500 kg. The somatic cell count were also increased, but not significantly. Furthermore, significant ( $p < 0.0001$ ) reduction in the number of older cows was observed, which indicates an increased selection and selection of cows that are better adapted to the robotic milking. About 68% of farmers managed to adapt most of their cows on the farm within three months, as well as their new commitments to robotic milking. The first year (the year of transition to robotic milking) poses the biggest challenges for farmers in production: adaptation of the facility and installation of robots, habituation of cows to robotic milking, increased herd culling, mastering technical features of robotic milking systems and information, etc. In conclusion, it can be said that the transfer from conventional to robotic milking of cows with Croatian farmers was successful and have a future development potential.

### Teat Condition and Milkability Traits of the Primiparous Cows in Automatic Milking System

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Automatic milking systems and robotic milking are more popular on dairy farms in the recent time. Their popularity are visible in many aspects. Some of them are practicality, more available data per cow per milking, health indicator sensors and other things. The aim of this research was to analyse available data from automatic milking system and compared them with visible change on the teat skin of primiparous cows. These traits were analysed: milkability traits (amount of milk, duration of milking, milk flow rates), electrical conductivity, teat condition scoring (hyperkeratosis, swelling, colour), somatic cell count. It was conducted that primiparous cows in this research had 1.8 milking's per day and average amount of milk per milking 13.70 kg with 7.48 minutes of milking duration. The average milk flow rate per udder quarter were in range from 0.96 to 1.04 kg/min and maximum milk flow rate from 1.42 to 1.56 kg/min. Electrical conductivity were from 3.19 to 4.52, and somatic cell count were 2.62. The amount of the swollen and colour changed teats for all teat positions were between 6 and 10%, and 3 to 11%, respectively. The teat end hyperkeratosis were in average range from 1.91 to 2.09. Despite of the fact that were primiparous cows, there were more than 30% of cows with higher level of hyperkeratosis and a certain number of cows that frequently disrupted the milking ("kick-off" cows).

## Session 11

## Theatre 4

### Variability of daily milk yield in Holstein cows

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We evaluated the variability of daily milk yield (DMY) of cows and estimated its correlations with production, functional and health traits. The dataset included 278,531 DMY records collected on 3 farms between 2004–2020 in 2002 Holstein cows. Cows were required to have records for at least 50 days of the first lactation. All records were used up to 305 days in milk (DIM). The first DIM must have been lower than 150. Herd-year-season (HYS) classes were made with 16 years of calving, 3 herds and 2 seasons (summer, V.–IX; winter X.–IV.). DMY ranged between 2 and 60 kg with a mean of 26 kg of milk per cow and day. The variances of DMY for each cow were log-transformed (LnVar) to achieve their normal distribution. LnVar was affected by the herd, year and season of calving, age at first calving, DIM of the first record and lactation length. Higher LnVar were correlated with lower milk, fat and protein yield per lactation, lower persistency of lactation and a shorter lactation period. We estimated the heritability of LnVar ( $h^2=0.21$ ) and the breeding values (BV) for LnVar with a single animal model and BLUPF90 family of programs. The higher BV(LnVar) of sires with daughters were correlated with higher BV for milk, fat and protein yield (kg), lower BV for milk protein and fat content (%), and a lower BV for the fertility of daughters (cows). The higher BV(LnVar) were also correlated with BVs for a deep body, deep udder, wide rear udder and parallel feet from the rear view. The correlations with other traits (longevity, somatic cells count, retained placenta, metritis, ovarian cysts, clinical mastitis, feet disorders) were not significant. The study was supported by the Ministry of Agriculture of the Czech Republic, project QK22020280 and institutional support MZE-RO0723.

**Effects of housing system (enriched cages vs free range) on external and internal quality of table eggs**

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In this study we investigated effects of two housing systems (enriched cages vs free range) on external and internal quality of table egg from Tetra SL hybrid of laying hens. Eggs (n=180) were collected at the age of laying hens between 34 to 36 weeks. Significantly higher values ( $p \leq 0.05$ ) for hens housed in enriched cage we found in egg weight (67.87 vs 65.12 g), eggshell weight (6.82 vs 6.52 g), eggshell thickness (387.38 vs 382.87  $\mu\text{m}$ ) and albumen weight (40.48 vs 38.62 g). The yolk index (43.53 vs 45.87%) was significantly higher ( $p \leq 0.05$ ) for hens housed free range system. For other parameters – egg shape index (76.99 vs 76.82%), eggshell percentage (10.05 vs 10.01%), albumen percentage (59.64 vs 59.31%), albumen index (11.64 vs 11.76%), Haugh units (88.86 vs 88.72 HU), yolk weight (20.57 vs 19.98 g), yolk percentage (30.31 vs 30.68%) and yolk color (12.68 vs 12.49 °HLR) were comparable ( $p > 0.05$ ). This publication has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. 2021-1-SK01-KA220-HED-000032068 “Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalisation”.

## Session 11

## Theatre 6

**Effect of four types of bedding material on live weight and footpad dermatitis score in broiler chickens**

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The aim of study was to evaluate the effect wood shavings (WS), straw (S), peat (P) and straw pellets (SP) used as bedding materials on the performance and footpad dermatitis (FPD). Trial was performed on 321 hatched chicken Ross 308, randomly divided to 4 groups. Once a week all animals were weighed individually. FPD was assessed weekly using the Swedish scoring system. Data were statistically processed by One Way ANOVA and Chi-Square test. One-day old chicks had the average live weight (ALW) 42 – 43 g. On the 7th day ALW was 210 g (WS), 183 g (S), 223 g (P) and 205 g (WP). On day 35 reached ALW 2476 g (WS), 2442 g (S), 2660 g (P) and 2514 g (SP). Chickens reared on peat had the highest ALW from the first to the last measurement. The first signs of FPD appeared after 21 days of life. On the 21st day 8,5% of chicken raised on whole straw had FPD lesion with score 1. On the day 28 FPD were observed only in a group with wood shavings (69,3 % score 1 and 9,3 % score 2) and whole straw (1,25% score 1). Effect of bedding material on footpad dermatitis occurrence was highly significant ( $P < 0.001$ ). The most suitable bedding materials for reducing the incidence of pododermatitis were peat and straw pellets. Materials that may cause a higher incidence of lesions are shaving and straw. Since animals with foot wounds walk less and consequently eat less, the significant effect on performance was also observed ( $P < 0.001$ ). The highest ALW was observed when peat was used for bedding, followed by SP, WS and S. The publication was supported by VEGA 1/0572/22 and KEGA 017SPU-4/2022.



**Survival of ostrich embryos and chicks until the age of 48 weeks**L. D. Brassó<sup>1</sup>, I. Komlósi<sup>2</sup><sup>1</sup> University of Debrecen, Doctoral School of Animal Science, Böszörményi Street 138., 4032 Debrecen, Hungary,<sup>2</sup> University of Debrecen, Department of Animal Science, Böszörményi Street 138., 4032 Debrecen, Hungary

The study aimed to analyse the survival and vitality of ostrich embryos and chicks and find out the cause of low vitality, culling and death at different stages of life. Embryonic evaluations were carried out on eggs culled on the 38<sup>th</sup> day of incubation. The weight of eggs, egg parts and the embryos, the size of the main body parts and the weight of the heart and the liver were measured. The vitality of chicks was assessed regarding the eight most relevant aspects, according to Tona et al., 2013. The weight of the chicks was also measured as one of the factors that affect chick vitality. For the survival analysis, the effect of the combination of year and season (2019-2021 years, spring, summer and autumn), egg weight, hatching order within the year and hatchability on survival was examined. The abnormalities on the embryos (the lack of eyes, inflammatory exudates and microbial colonies on the internal organs), the weights and sizes of chicks indicated that most embryos were likely to die at the age of four weeks or earlier. According to the vitality assessment, except for the leg condition, most of the chicks were in a good condition. Birds with deformed, oedematous legs and chubby, gaseous abdomens and wet feathers showed low vitality. The results of the survival analysis highlighted that chicks hatching at the onset of the production year with a low hatching rate had the highest relative risk of total loss. The risk increased until the second half of the breeding season, then it was unchanged. Until the age of 48 weeks, 33 % of chicks remained alive. The causes of mortality and death could be the lack of proper hygiene, incubation and husbandry technology.

## Session 11

## Theatre 8

**The frequency of distribution somatic cell count in goat's milk before dry period**K. Tvarožková<sup>1</sup>, V. Tančin<sup>1,2</sup>, B. Gancárová<sup>1</sup>, M. Uhrinčat<sup>2</sup>, L. Mačuhová<sup>2</sup><sup>1</sup> Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 94976 Nitra, Slovakia, <sup>2</sup> Research Institute for Animal Production Nitra, Hlohovecká 2, 95141 Lužianky, Slovakia

The somatic cell count (SCC) is in generally considered an indicator of health status of mammary gland in dairy animals. The aim of the study was to evaluate the frequency of distribution somatic cell count in half udder milk samples of goats before dry period. The study was carried out on a goat dairy farm in northern Slovakia. A total of 175 half udder milk samples (88 goats) were collected during morning milking for determination of SCC in October 2022. SCC were determined using a Somacount 150 (Bentley Czech, USA). Milk samples were divided into four SCC groups on the basis of SCC: SCC<sub>1</sub> < 500 × 10<sup>3</sup> cells/ml; SCC<sub>2</sub> ≥ 500 < 1000 × 10<sup>3</sup> cells/ml; SCC<sub>3</sub> ≥ 1000 < 2000 × 10<sup>3</sup> cells/ml; SCC<sub>4</sub> ≥ 2000 × 10<sup>3</sup> cells/ml. We detected only 9% of half udder milk samples in SCC<sub>1</sub> group (< 500 × 10<sup>3</sup> cells/ml), 12% of milk samples in SCC<sub>2</sub> (≥ 500 < 1000 × 10<sup>3</sup> cells/ml), 22% of milk samples in SCC<sub>3</sub> (≥ 1000 < 2000 × 10<sup>3</sup> cells/ml) and the highest frequency of distribution milk samples was in the last SCC<sub>4</sub> group (≥ 2000 × 10<sup>3</sup> cells/ml) up to 58% of milk samples. SCC in goat's milk is higher compared to SCC in cow's milk or ewes milk. More studies infectious and non-infectious factors of SCC are needed to clarify the physiological value of SCC as an indicator of health status of mammary gland of goats. Key words: goat's milk, somatic cell count Acknowledgment: This publication was supported by the APVV-21-0134 "Subclinical mastitis in ewes and goats: somatic cells and udder morphology", by the VEGA 1/0597/22 „ Etiology of somatic cell counts changes in mammary gland of goats: physiological and pathological aspects“ and by the GA FAPZ 06/2023

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