University of Zagreb Faculty of Agriculture

ASD 2022: Book of Abstracts

30th International Symposium Animal Science Days 2022
21st – 23rd September 2022, Zadar, Croatia

Under patronage of EAAP


Challenges of Animal Science Diversity in Times of Climate and Technological Change

Guest Editors
Dr. Nina Moravčíková
Prof. Dr. Luboš Vostrý
Prof. Dr. Vlatka Cubric-Curik

Deadline
15 December 2022

Special Issue
Invitation to submit

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University of Natural Resources and Life Sciences, Vienna, Austria
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Content

Welcome remarks

Dear colleagues, dear friends,

We are pleased to invite you to the 30th edition of the International Symposium Animal Science Days (ASD 2022) which will be held in Zadar, Croatia from September 21st – 23rd, 2022.

In addition to the symposium there will be the AlphaSimR course from September 18th to September 20th (https://asd2022.agr.hr/group/12/Course).

The ASD Symposium is an annual meeting place for the exchange of experiences and achievements of scientists, researchers and stakeholders in animal production dates back to 1993 and aims to improve animal production in the partner countries Austria, Croatia, Czech Republic, Hungary, Italy, Slovakia and Slovenia. The aim is to create a platform for Central and Eastern European colleagues and for interested academics and professionals from all over the world in the field of animal science to exchange ideas and to enable efficient cooperation. The main topic of the next Animal Science Days will be the challenges of animal science in times of climate change. In this 30th edition of ASD, we would also like to focus on encouraging the new generations of young researchers, scientists and experts and hopefully facilitate their further joint work through the courses organized during the symposium.

Special Issue "Challenges of Animal Science Diversity in Times of Climate and Technological Change"

Dear Colleagues,

The coexistence of humans and animals is deeply ingrained in today's society, as domestication was a hugely influential process that shaped the development and growth of human civilization. Today, the sustainability of modern animal production is strongly influenced by climatic and technological changes. This Special Issue is dedicated to diversity as an important biological and philosophical aspect of sustainable animal production, focusing on the importance of diversity in the face of climatic and technological change. Therefore, this issue calls for contributions that provide information on the genomic aspects of diversity in native livestock breeds, especially those that are threatened by extinction but have potential utility. Theoretical or/and empirical work addressing the estimation or management of genetic diversity, a key component in breeders' genetic improvement, is needed, as even the most productive breeds, such as Holstein cattle, have experienced a decline in diversity. Microorganism diversity is crucial in agriculture because our livestock (hosts) are holobionts, along with various symbiotic microbes and viruses. In addition, almost all animal products (cheese, butter, sausage, etc.) are highly dependent on the presence and growth of various microorganisms. Ultimately, animal production is deeply connected with the diversity of its plant components (pastures and forage crops). Thus, the diversity of the production environment, as an important component of sustainable animal production, cannot be ignored. Farming systems, including animal nutrition and feeding, contribute significantly to the interaction between genotype and phenotype; therefore, papers addressing such issues are encouraged.

We particularly welcome the contributions from the ASD 2022.

diversity

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Scientific programme

Tuesday, 20th 2022	
18:30 - 19:30	**Registration**
Wednesday, 21st 2022	
7:30 - 8:30	**Registration**
8:30 - 9:00	**Opening speech**
8:30 - 8:35	Vlatka Cubric-Curik
8:35 - 8:45	Klaudija Carović-Stanko (Vice Dean)
8:45 - 8:55	ASD's Community History Martino Cassandro
8:55 - 9:00	In memoriam Professor Miroslav Kapš Maja Ferenčaković
9:00 - 10:00	**Invited speakers**
9:00 - 9:30	eDNA metabarcoding: general concepts and practical examples Cristiano Vernesi
09:30 - 10:00	Honesty is the best policy: or how genetic diversity has emerged from the shadows in conservation planning and what we need to do to keep in the spotlight Mike Bruford
10:00 - 10:15	**Coffee break**
10:15 - 12:00	**Animal Breeding and Genetics** (Chairmen: L. Vostry, B. Lukic)
10:15 - 10:30	Male and female autosomal genetic maps of Fleckvieh cattle Abitew Y A, Mészáros G, Duenk P, Druet T, Sölkner J
10:30 - 10:45	Diversity of Slovakian wild boar in European context Kasarda R, Moravčíková N, Lukić B, Raguz N, Curik I, Cubrik-Curik V, Židek R, Hustinová M
10:45 - 11:00	Genetic parameters of growth, feed efficiency and greenhouse gases emissions in Italian Holstein young bulls Benzoni L, Tiezzi F, Finocchiaro R, Galluzzo F, Cassandro M
11:00 - 11:15	Differences in phenotype, wool and semen quality traits between two Slovenian autochthonous sheep breeds Bizjak M, Simčič M
11:15 - 11:30	Genetic variability of two Czech national sheep breeds investigated through haploblocks Machová K, Tichý L, Calta J, Vostrý L

11:30 - 11:45	Mitogenome sequencing of Hungarian Grey cattle by use of founder sampling Maróti-Agóts Á, Wágenhoffer Zs, Fürlinger D, Lancioni H, Kaltenecker E, Gáspárdy A
11:45 - 12:00	Sex difference in the inbreeding level in the Pseudo-Autosomal Region Shihabi M, Vostry L, Ferenčaković M, Cubric-Curik V, Brajkovic V, Drzaic I, Curik I
12:00 - 12:30	**Poster Session** (Chairmen: L. Vostry, B. Lukic)
12:00 - 12:03	Attitudes of dog owners and breeders towards genetic testing Brokés T, Mészáros G
12:03 - 12:06	mtDNA diversity in Hungarian red deer, *Cervus elaphus* populations confirms the knowledge about the origin of the species Kusza S, Khederzadeh S, Bagi Z, Tóth B, Tari T, Náhlik A
12:06 - 12:09	A review on genetic diversity of local chicken population and their adaptation potential to climate change in tropical climate: a case study in East African countries Pius L O, Wanjala G, Strausz P, Kusza S
12:09 - 12:12	Runs of homozigosity patterns in Hrvatica chicken breed Dautanec M, Ferenčaković M, Janječić Z, Cubric-Curik V
12:12 - 12:15	Genomics of dwarfism in Italian local chicken breeds Perini F, Cendron F, Wu Z, Sevane N, Dunner S, Smith J, Lasagna E, Cassandro M, Penasa M
12:15 - 12:18	Genomic differentiation between red and spotted cattle breeds in Slovakia and Czech Republic Moravčíková N, Kasarda R, Prišťák J, Vostry L, Vostra Vydrova H
12:18 - 12:21	Effects of stage of lactation, parity, season and pdo production chain on acidity, composition and fatty acid profile of bovine milk Mariani E, Stocco G, Ablondi M, Summer A, Niero G, Penasa M, Cipolat-Gotet C
12:21 - 12:24	The role of prlr gene polymorphisms in milk production of rabbits Benedek I, Nagy I, Mezőszentgyörgyi D, Molnár T
12:24 - 12:27	The effects of cryopreservation on chicken primordial germ cell viability and germ cell specific marker expression profile Ecker A, Lázár B, Tóth R, Urbán M, Szabadi N T, Várkonyi E, Gócza E
12:27 - 12:30	Genetic and survival analysis of survival time of local chicken ecotypes naïvely challenged with Newcastle disease in Ghana Ampofo I, Soelkner J, Meszaros G, Bovenhuis H, Walugembe M, Dekkers J, Amuzu E
12:30 - 14:00	**Lunch break**
14:00 - 15:30	**Animal Breeding and Genetics** (Chairmen: R. Kasarda, M. Ferenčaković)
14:00 - 14:15	Genomic insights to polledness, wool quality and color traits in Valachian sheep Mészárosová M, Mészáros G, Moravčíková N, Pavlík I, Margetín M, Kasarda R

14:15 - 14:30	Population structure and admixture in closely related Czech Norik horse populations Vostry L, Vostrá-Vydrová H, Hofmanova B, Moravcikova N, Kasarda R, Meszaros G, Shihabi M, Cubric-Curik V, Curik I
14:30 - 14:45	SNP genotyping and genetic analyses of Montenegrin local sheep breeds Đokić M, Drzaic I, Shihabi M, Marković B, Cubric-Curik V
14:45 - 15:00	Individual heterosis for growth traits in Peruvian guinea pig lines Cedano-Castro J I, Wurzinger M, Gutiérrez G, Jiménez R, Huamán A, Sölkner J
15:00 - 15:15	Preliminary study results on the gene expression analysis of intramuscular fat content in Black Slavonian pig Lipavić G, Raguz N, Curik I, Cubric-Curik V, Lukic B
15:15 - 15:30	Analysis of inbreeding effects on survival at birth of pannon white rabbits using inbreeding-purging model Kövér G, Curik I, Vostry L, Mezőszentgyörgyi D, Farkas J, Nagy I
15:30 - 15:45	**Poster Session** (Chairmen: R. Kasarda, M. Ferenčaković)
15:30 - 15:33	Effective population size and population structure in African chicken Xu C, Megens H J, Sölkner J, Kebede A, Bamidele O, Smith J, Hanotte H, Gheyas A, Mészáros G
15:33 - 15:36	Examination of primordial germ cell (pgc) cultures derived from the offspring of heat-conditioned domestic hens: comparison of the RNA expression profile Gócza E, Ecker A, Lázár B, Tóth R, Urbán M, Szabadi N T, Salinas Aponte M T, Várkonyi E
15:36 - 15:39	Contribution of the weighted single-step gblup method for genomic evaluation of udder conformation in Holstein cattle Brzáková M, Bauer J, Přibyl J, Fulínová D, Šplíchal J
15:39 - 15:42	Integration efficiency of GFP-expressing PGCS into chicken gonads Tóth R, Lázár B, Ecker A, Urbán M, Várkonyi E, Gócza E
15:42 - 15:45	Genetic parameters of American Quarter horses registered in the Slovenian stud book Ferme T, Zorc M, Jamnik Cerk K, Tanšek A, Dolinar M, Dovč P
15:45 - 16:30	**Coffee break**
16:30 - 17:15	**Animal Nutrition** (Chairmen: S. Žgur, C. Szabo)
16:30 - 16:45	Effect of dietary olive leaves and pulp on oxidative status in broiler chickens Rezar V, Pečjak M, Salobir J, Levart A
16:45 - 17:00	Dose-dependent effects of the dietary fumonisin b series on the liver membrane lipids of weaned piglets Ali O, Mézes M, Balogh K, Kovács M, Mouhanna A, Szabó A
17:00 - 17:15	Dietary supplementation with olive polyphenols in rainbow trout: effects on growth and fillet quality Bordignon F, Fanizza C, Trocino A, Xiccato G, Fasolato L, Gasco L, Bellezza Oddon S, Caimi C, Balzan S, Novelli E

17:15 - 17:33	**Poster Session** (Chairmen: S. Žgur, C. Szabo)
17:15 - 17:18	Effects of low protein diets and probiotic supplementation on gut health parameters of broiler chickens Strifler P, Horváth B, Such N A, Kisjuhász G, Károly D, Pál L
17:18 - 17:21	Effects of heat stress and high dietary antioxidant supplementation on the ileal digestibility of nutrients and certain minerals in pigs Sol Valmoria Ortega A D, Babinszky L, Ozsváth X E, Humphrey Oriedo O, Oláh J, Szabó C
17:21 - 17:24	Influence of multicomponent transition drench on rumen fermentation parameters of cows Kacsala L, Tóthi R, Tóth T
17:24 - 17:27	Evaluation of early l-threonine supplementation on performance of broilers Tischler A, Áprily Sz, Nagy J, Ács V, Szeli N, Halas V
17:27 - 17:30	The change of microbial diversity and mycotoxins concentration in corn silage after addition of silage additives Kalúzová M, Kačániová M, Bíro D, Šimko M, Gálik B, Rolinec M, Hanušovský O, Felšöciová S, Juráček M
17:30 - 17:33	Feeding corn- or wheat-based diets impacts on perforormance parameters and the caecal microbiota composition of broiler chickens Such N A, Farkas V, Pál L, Wágner L, Strifler P, Horváth B, Dublecz K
17:33 - 17:45	**Break**
17:45 - 18:15	**Animal Production and Welfare** (Chairmen: V. Cubric-Curik, V. Brajkovic)
17:45 - 18:00	Influence of in-ovo injection of methionine on the histomorphometric analysis of jejunum in layer genotypes newly hatched chicks Kachungwa Lugata J, Oláh J, Czeglédi L, Mészár Z, Varga R, Szabó C
18:00 - 18:15	Dead on arrival (DOA) in pigs: a five-year data collection in Italian slaughterhouses Menchetti L, Zappatera M, Padalino B, Nanni Costa L
18:15 - 18:36	**Poster Session** (Chairmen: V. Cubric-Curik, V. Brajkovic)
18:15 - 18:18	Feed preference and feeding behaviour of different mouse species in laboratory housing modelling small domesticated mammals Bárdos B, Kövér G, Szabó A, Mezőszentgyörgyi D, Gerencsér Z, Nagy I
18:18 - 18:21	Contribution of feed source on environmental impact of pig production Martinić O, Karolyi D, Škorput D, Luković Z, Menčik S, Salajpal K
18:21 - 18:24	Diversity and nutrition development of pure chicken breeds in Slovakia Hrnčár C, Bujko J, Kaščák K, Bučko O, Hanusová E, Kasarda R
18:24 - 18:27	Examination of behavioural patterns of laying hens of different genotypes in a pen housing system with scratching area and plastic mesh floor (preliminary results) Farkas T P, Szász S, Orbán A, Mezőszentgyörgyi D, Musincki D, Sütő Z
18:27 - 18:30	Milkability of Holstain dairy cows under practical conditions in Slovakia Tančin V, Uhrinčať M, Mačuhová L, Tvarožková K, Vršková M

18:30 - 18:33	Milkability of Slovak Spotted dairy cows under practical conditions Uhrinčať M, Tančin V, Mačuhová L, Tvarožková K, Vršková M
18:33 - 18:36	Effects of physical and social stressors on some blood biochemistry parameters of common eland (Taurotragus oryx) Musa A S, KundanKumar J, Needham T, Veit N, Kotrba R, Ceacero F
20:00 - 23:00	**Gala Dinner with Klapa Donat**

Thursday, 22nd 2022

8:30 - 9:30	**Invited speakers**
8:30 - 9:00	Animal domestication: Who domesticated whom? Preston T. Miracle
9:00 - 9:15	Use of Combifoss measurements for supporting your selection decision Labena d.o.o.
9:15 - 9:30	Introducing InfiniSeek Bovine - Genome- wide Low-pass sequencing with High- Coverage sequencing at targeted loci Helene Hofeneder-Barclay, NEOGEN
09:30 - 10:00	**Poster Session** (Chairmen: V. Tančin, P. Dovč)
9:30 - 9:33	Maternal phylogeny of Old Serbian shepherd dog based on mitochondrial DNA Dolinar M, Zorc M, Tanšek A, Ferme T, Dovč P
9:33 - 9:36	Natural antioxidants in polutry products Biazik E, Kralik Z, Kosevic M
9:36 - 9:39	Examination of the antioxidant system in knock-out rabbits on cholesterol-rich diet Pintér T, Muhammad F, Major F, Petheő G L, Szeles Z, Skoda G, Kerekes A, Hiripi L, Geiszt M, Bodrogi L
9:39 - 9:42	Predicition of ammonium emission from dairy cow farms according to urea content in milk Papović T, Kučević D, Trivunović S, Janković D, Čobanović K
9:42 - 9:45	The effects of t-2 toxin and zearalenone on the embryonic development of chicken Urbán M, Tóth R, Szőke Z, Ebbin N A, Gócza E
9:45 - 9:48	Influence of genotype and type of muscle tissue of chickens on the content of carnosine and anserine in meat Kralik Z, Kralik G, Galović O, Gvozdanović K, Radišić Ž, Košević M
9:48 - 9:51	Production and investigation of guinea fowl and domestic fowl hybrids for pgc-based cryopreservation programmes Molnár M, Lázár B, Sztán N, Végi B, Drobnyák A, Tóth R, Liptói K, Gócza E, Nandi S, McGrew J M, Várkonyi E
9:51 - 9:54	Effect of season of birth of heifers on milk production and composition Mačuhová L, Tančin V, Mačuhová J, Uhrinčať M, Vršková M
9:54 - 9:57	Dispersion parameters for growth of boars during on-farm test

	Ule A, Kovač M, Malovrh Š
10:00 - 10:15	**Coffee break**
10:15 - 12:30	**One Health** (Chairmen: P. Burger, J. Ramljak)
10:15 - 10:30	Occurrence of mastitis pathogens at dry off period and after calving in dairy cows Vršková M, Tvarožková K, Tančin V, Uhrinčať m, Mačuhová L, Holko I
10:30 - 10:45	The incidence of pathogens in milk of goats and relation with somatic cell count and milk composition Tvarožková K, Tančin V, Uhrinčať M, Mačuhová L, Oravcová M
10:45 - 11:00	Survey of eimeria oocyst and passalurus ambiguus infections at industrial rabbit farms depending on the season Demeter Cs, Matics Zs, Gerencsér Zs, Demeter-Jeremiás A, Sándor F, Német Z
11:00 - 11:15	Human impacts on helminth fauna diversity in wild carnivores Moloi S, Tari T, Nagy G, Csivincsik A
11:15 - 11:30	Exploring microbial communities in haloponic systems at different water salinity Zardinoni G, Stevanato P, Bordignon F, Fanizza C, Trocino A, Xiccato G
11:30 - 11:45	Importance of mid-infrared spectra regions for the prediction of mastitis and ketosis in dairy cows Gruber S, Rienesl L, Köck A, Sölkner J
11:45 - 12:00	Pig as a potential reservoir for Sars-cov-2 infections Tanšek A, Zorc M, Bevec T, Auró Navarro G, Dolinar M, Ferme T, Dovč P
12:00 - 12:15	Investigating the effect of early mycotoxin exposure on the development of non-communicable diseases in an animal model system Major F, Pintér T, Skoda G, Lipták N, Gócza E, Ferencziné Szőke Z, Bodrogi L
12:15 - 12:30	Impact of vaccination against bovine respiratory disease on antimicrobial use in Italian beef cattle Santinello M, Scali F, Alborali G L, De Marchi M, Penasa M
12:30 - 14:00	**Lunch break**
14:00 - 15:15	**Animal Breeding and Genetics** (Chairmen: N. Moravcikova, N. Raguz)
14:00 - 14:15	Assesing among flocks genetic diversity in Istrian sheep to define framework for optimum contribution selection Špehar M, Ramljak J, Kasap A
14:15 - 14:30	MaGelLAn2.0: extending the capabilities for the population genetic analysis Hršak D, Ristov S, Cubric-Curik V, Novosel D, Curik Ino, Brajkovic V
14:30 - 14:45	Genomic adaptation in local Grey Alpine cattle: inbreeding comparison and signatures of selection Gomez Proto G, Mancin E, Tuliozi B, Sartori C, Mantovani R
14:45 - 15:00	Increasing effective population size by strengthening genetic connectedness between flocks: case study on Pag Sheep breed Kasap A, Ramljak J, Špehar M

15:00 - 15:15	Y chromosome illuminates paternal history of modern horse breeds Radovic L, Bozlak E, Rigler D, Brem G, Wallner B
15:15 - 15:30	**Poster Session** (Chairmen: N. Moravcikova, N. Raguz)
15:15 - 15:18	The effect of inbreeding on milk production in Czech Holstein cattle Curik I, Vostra-Vydrova H, Shihabi M, Sölkner J, Brzakova M, Pocrnic I, Gorjanc G, Vostry L
15:18 - 15:21	Genomic analysis of Croatian Goats Orehovački V, Drzaic I, Mikulec N, Vostry L, Curik I, Cubric-Curik V
15:21 - 15:24	Is M. longissimus thoracis colour connected with other traits under selection? Leskovec J, Voljč M, Luštrek B, Žgur S, Čepon M, Malovrh Š
15:24 - 15:27	Analysis of the genetic structure of Slovak Holstein cattle using genes associated with nutritional value and technological properties of milk Miluchová M, Gábor M, Gašper J
15:27 - 15:45	**Coffee break**
15:45 - 17:30	**Animal Production and Welfare** (Chairmen: A. Gáspárdy, G. Kušec)
15:45 - 16:00	Changes in the proportion of eggs laid in the nest and in the litter in an indoor alternative housing system in the case of purebred hen lines during 12 months of production (preliminary results) Farkas T P, Szász S, Orbán A, Mezőszentgyörgyi D, Musinckі D, Sütő Z
16:00 - 16:15	Feather conditions and injuries observed on certain body parts of layer hybrids and purebred hen lines in three way of housing Szász S, Farkas T P, Orbán A, Mezőszentgyörgyi D, Erős A, Garamvölgyi E, Sütő Z
16:15 - 16:30	Estimation of temperament of dairy cows by response to a novel object Juhás P, Vavrišínová K, Dóbi J, Strapák P
16:30 - 16:45	Landings and climbings of pullets in a cage free system at housing: effect of genotype and enrichment Ciarelli C, Bordignon F, Pillan G, Xiccato G, Birolo M, Trocino A
16:45 - 17:00	Non-genetic factors affecting udder health traits in milk of Italian local cattle breeds Magro S, Costa A, Santinello M, De Marchi M
17:00 - 17:15	Physical characterization of ten varieties of hemp to use as animal bedding material Arango S, Guzzo N, Montanari M, Bailoni L
17:15 - 17:30	Carcass traits of bovine animals slaughterd in Slovenia from 2009 to 2021 Leskovec J, Voljč M, Žgur S
17:30 - 17:45	**Break**
17:45 - 18:45	**Animal Production and Welfare & Animal Nutrition** (Chairmen: A. Gáspárdy, G. Kušec)
17:45 - 18:00	The influence of on-farm resting time on stress markers and slaughtering traits of culled sows

	Kušec G, Djurkin Kušec I, Gvozdanović K, Điđara M, Radišić Ž, Bagarić M, Komlenić M
18:00 - 18:15	Effect of acorn feeding on meat quality and expression of myosin heavy chain and some energy metabolism-related genes in the longissimus dorsi muscle of Turopolje pigs Karolyi D, Vrecl M, Salajpal K, Luković Z, Škorput D, Fazarinc G, Čandek-Potokar M
18:15 - 18:30	Lignocellulose roll on performance, animal health and welfare in modern monogastric feed formulation Mayer A, Bosse A, Demeter Cs, Matics Z, Gerencsér Zs
18:30 - 18:45	Effect of grape pomace intake on the rumen bacterial community of sheep Rolinec M, Medo J, Gábor M, Miluchová M, Šimko M, Juráček M, Hanušovský O, Schubertová Z, Bíro D, Zábranský L, Gálik B
19:00 - 21:00	**Zadar walking tour with cheese tasting**
Friday, 23rd 2022	
8:30 - 9:00	**Precision Animal Breeding** (Chairmen: Z. Krupova, G. Meszaros)
8:30 - 8:45	Comparing enteric methane emissions predicted from different equations based on milk fatty acid profile of dairy cows Massaro S, Amalfitano N, Schiavon S, Bittante G, Tagliapietra F
8:45 - 9:00	Fogging system affects microclimate, antioxidant capacity and scrotal characteristics in Frieswal breeding bulls during summer season Sirohi A S, Pande M, Chand N, Mahajan S, Tyagi S, Kumar S, Kumar S, Sarika
9:00 - 10:00	**Animal Breeding and Genetics** (Chairmen: Z. Krupova, G. Meszaros)
9:00 - 9:15	Common selection signatures for heat tolerance in humans, goats and pigs Atrian-Afiani F, Mészáros G
9:15 - 9:30	Optimisation of the Holstein health indeks Krupová Z, Zavadilová L, Krupa E, Kašná E
9:30 - 9:45	Genetic characterization and landscape genetics of local taurine cattle populations in Burkina Faso Tapsoba A S, Ouedraogo D, Barbato M, Yougbare B, Traore A, Koné-Ouedraogo S, Meszaros G, Sölkner J, Soudré A, Burger P A
9:45 - 10:00	MBL2 gene polymorphisms in Mediterranean Italian River Buffalo (MIRB) (Bubalus bubalis) and their association with milk Somatic Cell Count (SCC) Pugliano M, Nowacka-Woszuk J, Stachowiak M, D’Anza E, Matera R, Longobardi V, Peretti V, Albarella S, Szczerbal I, Switonski M, Ciotola F
10:00 - 10:15	**Coffee break**
10:15 - 12:30	**Animal Breeding and Genetics** (Chairmen: Z. Vesela, I. Curik)
10:15 - 10:30	Identification of selection signatures in Croatian Arabian horse Raguz N, Lukic B, Korabi N, Drzaic I, Vostry L, Kasarda R, Moravcikova N, Curik I, Cubric-Curik V

10:30 - 10:45	Management of breeding bulls of Busha cattle in Croatia – a bull:cow ratio trends Menčik S, Piplica A, Ostović M, Ekert Kabalin A, Sušić V, Vlahek I, Čačić M, Ivanković A
10:45 - 11:00	Model selection and estimation of genetic parameters for loin and backfat depth in Czech pig breeding program Calta J, Žáková E, Čítek J, Machová K, Tichý L, Vostrý L
11:00 - 11:15	Morphometric characterization of local goat breeds in two agro-ecological areas of Burkina Faso, West Africa Badjibassa A, Ouédraogo D, Soudré A, Burger A P, Rosen B D, Van Tassell C, Sölkner J
11:15 - 11:30	Phylogenetic background of the reconstruction stock of Szekler horse breed Gáspárdy A, Wágenhoffer Zs, Fürlinger D, Bodó I, Maróti-Agóts Á
11:30 - 11:45	Genetic parameter estimations of fertility traits in Nero di Parma breed Asti V, Sabbioni A, Delmonte F, Mariani E, Ablondi M
11:45 - 12:00	Milk yield and quality at cow udder quarter level as influenced by quarter position, pathogen and somatic cell score Visentin E, Niero G, Bobbo T, Visentin G, Cassandro M, De Marchi M, Penasa M
12:00 - 12:15	Genetic parameters for live animal ultrasound measures in Czech Aberdeen Angus Vesela Z, Birovas A, Brzakova M, Novotna A, Vostry L
12:15 - 12:30	Polymorphism of the tlr2 gene and its relation to clinical mastitis in Czech Fleckvieh population Tichý L, Kyselová J, Sztankóová Z, Calta J, Machová K, Vostrý L
12:30 - 13:30	**Committee meeting**

Session: Animal Breeding and Genetics

MALE AND FEMALE AUTOSOMAL GENETIC MAPS OF FLECKVIEH CATTLE

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ABSTRACT: We constructed genomic maps of Fleckvieh cattle using 38,999 SNPs and 114,228 meiosis events from male parents and 42,706 meioses of females. Meiotic recombination is a source of genetic variation as it shuffles genetic material between sister chromatids, breaking down linkage disequilibrium. Recombination frequencies between neighbouring markers were estimated from 4,600,610 crossovers. The average genome wide recombination rate was 1.04 centiMorgan per megabase with a resulting length of the autosome of 26.05 Morgan in males, corresponding values for female parents were 0.92 cM/Mb and 23.16 Morgan. Longer chromosomes showed lower recombination rates. The genetic map showed pronounced recombination rates around the end position of each autosome in males whereas a gradual decline was observed around the same position in females. The higher number of recombinations observed in males is similar to sheep but unlike many mammals. Using genome wide association study, we identified two previously reported candidate genes (REC8 & RNF212) in chromosome 6 and 10. The strongest signal was found on chromosome 19, near SCO1 gene, not associated with recombination rate so far. Genome wide recombination rate is a highly heritable trait with a chip heritability of 0.51. This estimate was higher than what was found in previous studies for other breeds.

Keywords: *Cattle, Genetic recombination, Map, Morgan, Fleckvieh*

Acknowledgements: We highly appreciate the willingness of the owners of SNP data, the Austrian and German Fleckvieh Breeders Associations, to share data and are grateful to Hermann Schwarzenbacher, ZuchtData EDV-Dienstleistungen GbmH, for preparing the data.

DIVERSITY OF SLOVAKIAN WILD BOAR IN EUROPEAN CONTEXT

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ABSTRACT: African swine fever (ASF) was detected in wild boar in 2/3 of the districts of Slovakia. As a result of the occurrence of the disease, several cases of ASF also occurred in subsistence and commercial pig farms. The high prevalence of ASF in Slovakia led to increased hunting to reduce population density and prevent transmission to livestock. The aim of the study was to provide a first insight into the status of genetic diversity of the wild boar population in Slovakia and to estimate the degree of its genetic differentiation from other European populations. Tissue samples (N=75) were collected from hunting areas in all districts of Slovakia and genotyped using GGP Porcine 50K. As expected, the observed heterozygosity was lower (0.336±0.148) than expected (0.346±0.144). At the same time, the Slovak wild boar population had a low value for F_{HOM} (0.029±0.052). After expanding the database to different regions of Europe, i.e. Croatia (N=16), Southern Balkans (N=20), Northwest Europe (N=20), Iberian Peninsula (N=17), Italy (N=18) and Sardinia (N=20), genetic differentiation analysis was performed. All applied approaches (DAPC analysis, Bayesian clustering, genetic distance matrices) showed clear stratification of Slovak wild boar population from European populations.

Keywords: *African Swine Fever, genomic analysis, population structure, porcine SNP array*

Acknowledgements: Slovak Agency for Science and Development is acknowledged for financial support under project no. APVV-20-0161 and APVV-17-0060.

GENETIC PARAMETERS OF GROWTH, FEED EFFICIENCY AND GREENHOUSE GASES EMISSIONS IN ITALIAN HOLSTEIN YOUNG BULLS

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ABSTRACT: Livestock farming, especially in the dairy industry, accounts for about 50% of GHG of the primary sector. Genetic selection can contribute to reduce its environmental impact. Such selection can be applied directly using breath measurements, but also using indirect indicator traits related to feed efficiency. Purpose of this study is to estimate genetic parameters to verify the feasibility for direct or indirect selection for GHG reduction in Italian Holstein population. The animals involved were 218 young Italian Holstein (genotyped) bulls, candidates to artificial insemination in Italy. Methane and carbon dioxide emissions were collected using the GreenFeed system (*C-Lock Inc., Rapid City, SD, USA*); feed intake and feed behaviour data were collected using the Roughage Intake Control system (RIC, *Hokofarm Group, Marknesse, The Netherlands*); biometric measures were collected by qualified and trained technicians. Growth traits showed the largest estimates of heritability, close to 0.40, while RIC derived traits ranged from 0.167 to 0.306 and emission traits ranged from 0.241 to 0.480. Genetic correlations between growth, RIC and GreenFeed traits were moderate to strong, ranging from 0.60 to 0.99. Results suggest that selection indexes can be estimated in order to reduce GHG emissions without compromising growth, body condition, height and feed intake.

Keywords: *greenhouse gas emissions, laser methane detector, GreenFeed, genomic selection, Italian Holstein*

Acknowledgements: This study was supported by "Latteco2 project, sottomisura 10.2 of the PSRN Biodiversity 2020–2023" (MIPAAF. D.M. no. 465907 del 24/09/2021, project unique code 12C21004080005).

DIFFERENCES IN PHENOTYPE, WOOL AND SEMEN QUALITY TRAITS BETWEEN TWO SLOVENIAN AUTOCHTHONOUS SHEEP BREEDS

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ABSTRACT: The aim of the study was to indicate significant differences in phenotype, wool and semen quality traits between two Slovenian autochthonous sheep breeds, Jezersko-Solčava (JS) sheep and Improved Jezersko-Solčava (JSR) sheep. Forty-four rams of JS sheep and 43 rams of JSR sheep from the same test station in the year 2020 were included in the study. In each ram, body length, wither height, chest circumference, ear and tail length, as well as body weight, were recorded. In addition, ultrasound measurement of eye muscle depth was performed. Wool samples were analysed in the laboratory where several wool quality traits were determined. The concentration of the semen, progressive motility and morphological changes of sperm cells were analysed as well. After analysis of variance, we found that JSR rams had lower wither height, higher chest circumference, and shorter bodies, ears and tails compared to JS rams. A comparison of wool quality traits showed that JSR rams had lower wool fibre diameter, lower spinning fineness, and higher comfort factor, as well as lower fleece weight than JS rams. JSR rams had higher progressive motility of sperm cells compared to JS rams. According to many differences, especially in phenotype, it could be concluded that JS and JSR are two different breeds which are genetically different as well.

Keywords: *Jezersko-Solčava sheep, Improved Jezersko-Solčava sheep, phenotype, wool quality, semen quality*

GENETIC VARIABILITY OF TWO CZECH NATIONAL SHEEP BREEDS INVESTIGATED THROUGH HAPLOBLOCKS

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ABSTRACT: Haploblocks are widely used estimators of molecular genetic diversity. These long stretches of chromosomes have a relatively low recombination rate and variability, and thus allow to follow kinship over several generations. Our study aimed to examine through haploblocks the genetic variability of two Czech national sheep breeds, Sumava (n=48) and Wallachian (n=37), and their potential kinship and continue this way in our previous SNP-based research. After quality control, phasing and imputation of missing genotypes, 36,210 autosomal SNPs remained for Sumava sheep and 32,019 SNPs for Wallachian sheep. Two-marker haploblocks could not span more than 20 kb, and three-marker haploblocks more than 30 kb. Pairs of variants up to 500 kb distance were considered. 1,505 haplotype blocks were found in Sumava and 1,450 in Wallachian sheep. Overall, the Wallachian sheep had a significantly larger number of haploblocks longer than 400 kilobases than the Sumava. Both breeds shared 631 identical haploblocks. Two of these shared haploblocks in Sumava sheep were located inside two different ROH islands. In Wallachian, there were six located inside four ROH islands. Only in Wallachian sheep, there were structural genes present in these regions according to NCBI Oar_V4.0 assembly. Our study found a large proportion of shared haplotypes indicating a genetic flow between the Sumava and Wallachian sheep breeds. This knowledge could improve the management of Czech national sheep breeds in the future.

Keywords: *Haplotype blocks, diversity, genetic reserves, ROH islands, SNP analysis*

Acknowledgements: This research is financially supported by grant QK1910156 from the Ministry of Agriculture of the Czech Republic and an SGS grant SV22-12-21360 from the Faculty of Agrobiology, Food and Natural Resources CZU.

MITOGENOME SEQUENCING OF HUNGARIAN GREY CATTLE BY USE OF FOUNDER SAMPLING

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ABSTRACT: The Hungarian Grey Cattle (HGC) breed went through a serious bottleneck after the World War II, so its stud book registers only 232 surviving maternal lineages. The aim of this pilot study is to evaluate the whole mitogenome of that breed using 22 representative cow families for sequencing. The sample giving individual per maternal lineages were selected by application of the 'founder sampling' method. The mitogenomes were Sanger sequenced in 11 overlapped fragments. With the exception of haplogroups (HG) I, P, Q, T4 and T5, all other HGs (HG(n)- T(2), T1(2), T3(16), T3a(2)) were represented in the sample. The variants of haplotypes T1 and T3 were of that ones which are typical for European taurine cattles. Based on our results, the today mitochondrial diversity of the HGC breed can be considered sufficiently diverse for the maintenance of several within breed varieties. Thanks to the families that have been maintained independently since the 1960s, the mitogenome diversity characteristic of the founding individuals can also be found in today's stock. As one of the representatives of Podolian group of cattle, the mitogenome of HGC also contains a predominantly Middle Eastern HG pattern.

Keywords: *Hungarian Grey Cattle, mitogenome, founder sampling*

Acknowledgements: The project is supported by the European Union, the European Regional Development Fund (ERDF) (VEKOP 2.3.2. 16 2016 00012)

SEX DIFFERENCE IN THE INBREEDING LEVEL IN THE PSEUDO-AUTOSOMAL REGION

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ABSTRACT: While the X chromosome (or Z chromosome in birds) behaves similarly to autosomes in homogametic sex, it recombines only in the pseudoautosomal region (PAR) in heterogametic sex, resulting in a higher recombination rate on PAR than on the rest of the X chromosome, but also in most species than elsewhere in the genome. From an evolutionary perspective, why is PAR the only region on the sex chromosome that still recombines in both sexes? Many authors point out that PAR is simply required for proper segregation of sex chromosomes during meiosis. However, if this were the only reason, then the size of PAR would be very small compared to the rest of the sex chromosomes (e.g., in mice). On the other hand, if PAR is relatively large (e.g., in dogs and sheep), this could be the result of classical forces that favour recombination, such as avoidance of autozygosity and balancing selection. Therefore, in two case studies (metapopulation of East Adriatic sheep; 201 individuals, Illumina OvineHD BeadChip and the Labrador Retriever breed; 273 individuals, Illumina CanineHD BeadChip), ROH-based inbreeding was estimated at PAR and compared with values on the remaining X chromosome and on autosomes. While the average inbreeding in females (F_{ROH_PAR} = 0.057 in sheep and 0.159 in dogs) was similar to that on autosomes, males on PAR showed extremely low inbreeding (F_{ROH_PAR} = 0.023 in sheep and 0.091 in dogs). The obtained results suggest that the higher recombination rate on PAR appears significantly only in heterogametic sex, in species where PAR is relatively large. This could be due to the avoidance of autozygosity, but we also note a high observed heterozygosity (H_O) at/near the end of PAR in males, suggesting the presence of inversion and/or balancing selection, which we will investigate further.

Keywords: *Pseudo-Autosomal Region, inbreeding, high recombination rate, males, females*

Acknowledgements: This study was supported by project ANAGRAMS-IP-2018-01-8708 funded by the Croatian Science Foundation and by the project KK.01.1.1.04.0058 funded by the EU Operational Programme Competitiveness and Cohesion in the period 2014–2020.

GENOMIC INSIGHTS TO POLLEDNESS, WOOL QUALITY AND COLOR TRAITS IN VALACHIAN SHEEP

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ABSTRACT: The aim of the study was to find genomic regions influencing important exterior traits in the Valachian sheep. A genome wide association studies (GWAS) using the GEMMA software was conducted, based on genotypes of 96 Original Valachian sheep from Slovakia, genotyped with GeneSeek GGP Ovine 50 K chip. The phenotypes were polledness (presence vs absence of horns), wool quality (range D to F) and wool color (white vs black). The GWAS of polledness resulted into a single large signal on chr 10 (23.2-30.1 Mb), corresponding to location of QTLs for horns (based on sheep QTLdb), and the gene RXFP2 (chr 10, 29.5 Mb) previously associated with polledness. The results for wool type yielded only one indicative signal, below the Bonferroni significance threshold. The region contained the NRXN3 gene (chr 7, 87.4 Mb) with an indirect association to hair growth in humans, via its connection to the FoxQ1 gene. For the coat color the most prominent gene was the MC1R (chr 14, 14.2 Mb), frequently associated with color traits in multiple species. These results will be used increase our understanding of the exterior traits that are most relevant to breeders of the Valachian sheep.

Keywords: *GWAS, RXFP2, NRXN3, MC1R*

Acknowledgements: This research was funded by Slovak Agency for Research and Development, grants number APVV-17-0060, SK-SRB-21-0013 and APVV-20-0161.

POPULATION STRUCTURE AND ADMIXTURE IN CLOSELY RELATED CZECH NORIK HORSE POPULATIONS

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ABSTRACT: The Silesian Norik and the Czech Norik are Czech local draft horse breeds with a common history. These two Czech Norik breeds originated from the Austrian Norik breed. Although the Silesian Norik has been included in the Czech genetic reserve since 1990, genetic differentiation between these historically related Czech draft horse populations is considered to be low due to their shared history. The aim of this study was to analyse the genetic diversity based on 36 981 autosomal SNPs of the two Czech local Norik breeds (Silesian Norik and Czech Norik) together with the one Slovak local Norik breed (Muran Norik) and the original Austrian Norik breed. Other horse breeds kept in the Czech and Slovak Republics (Old Kladruber horse, Hucul and Shagya Arabian) were also included to study population structure, admixture and genetic relationships between Norik populations. Relatedness and population structure were analysed using Wright's F_{ST} coefficient, unsupervised Bayesian clustering, and multivariate analyses (principal component and discriminant analysis). We also estimated genomic inbreeding rate (F_{ROH}) and effective population size (N_{eLD}) for each breed. We demonstrated that the Czech local Norik breeds are strongly genetically linked. Therefore, in further population management, an appropriate breeding strategy should be applied to preserve the Silesian Norik as a unique Czech genetic reserve, distinct from other Norik breeds.

Keywords: *admixture, genomic diversity, effective population size, horse, population structure*

Acknowledgements: This study was funded by the Ministry of Agriculture of the Czech Republic (grant number QK1910156, MZe-RO0718), the Slovak Agency for Research and Development (grant numbers APVV-20-0161 and APVV-17-0060), and the Croatian Science Foundation (grant number ANAGRAMS-IP -2018-01-8708).

SNP GENOTYPING AND GENETIC ANALYSES OF MONTENEGRIN LOCAL SHEEP BREEDS

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ABSTRACT: Montenegro has a high diversity of autochthonous and locally developed sheep breeds, adoppted to different regions and climatic zones. However, present trend of constant declining of sheep number lead some of them in danger of extinction. Our aim was to investigate the genetic diversity and population structure of five Montenegrin sheep populations, using OvineSNP50 BeadChip. To evaluate admixture contributions and genetic relations from sheep population in Montenegro, a set of worldwide breeds from publicly available genotypes was added to our data. Higher genetic diversity and low inbreeding was observed in Pivska Pramenka and Sjenicka Sheep, $H_o = 0.411$, $H_e = 0.423$, and $F_{ROH} = 0.056$ and $H_o = 0.421$, $H_e = 0.421$, and $F_{ROH} = 0.041$, respectively. While Zetska Zuja has a much lower F_{IS} value (-0.002 to 0.0047) and relatively high F_{ROH} inbreeding (0.090), which indicate small population size and genetic drift. Also, long ROH segments (ROH > 8 Mb) were predominant in all populations. Population genetic structure analyses showed that the Montenegrin sheep populations are genetically distinct populations. This analysis previously revealed the presence of admixture in most sheep population (high heterogeneity), while genetic purity was observed in Zetska Zuja. The obtained results will help in the conservation management of Montenegrin sheep populations, especially for endangered breeds.

Keywords: *Montenegrian sheep, single nucleotide polymorphism, population structure, genomic diversity, conservation*

INDIVIDUAL HETEROSIS FOR GROWTH TRAITS IN PERUVIAN GUINEA PIG LINES

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ABSTRACT: Guinea pigs are a valued source of human food in Peru. Various genetic types or breeds are used, with relatively little information about their relative performance available. As in other livestock species, crossbreeding is deemed a viable solution for genetic improvement. This study aimed to estimate the heterosis for productive traits in a two-way crossbreeding scheme. Four guinea pig lines were selected for the following traits: Two paternal lines, line P1 for growth rate, P2 for feed conversion rate, and two maternal lines, M1 for growth rate of litter and M2 for litter size at birth. Growth traits, including birth weight, weights at 10 days, weaning and 60 days as well as weight gain form birth to 60 days were recorded. Data of 130 pure line animals (P1: 33, P2: 36, M1: 30 and M1: 31), and 68 reciprocal first crosses within paternal and maternal lines (P1P2: 29, P2P1: 16, M1M2: 3 and M2M1: 20) were used for analysis. A linear fixed effects model was applied, and heterosis was estimated as the difference between the average of purebred and crossbred animals within types of lines. For crosses of the two paternal lines, results indicated heterosis in the range of 4.1-8.3% of the parental average for the various growth traits, being significant for weights up to weaning. For the crosses of maternal lines, heterosis was significant for birth weight (13.2%) but not significant at all other ages (heterosis values of 1.5 to 4.0%). These results suggest that, based on growth traits, systematic crossbreeding systems have potential in guinea pig production of Peru. Heterosis for fertility and litter size are yet to be determined.

Keywords: *Guinea pig, crossbreeding, heterosis, reciprocal crosses; growth traits*

IDENTIFICATION OF SELECTION SIGNATURES IN CROATIAN ARABIAN HORSE

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ABSTRACT: Ancient records testify the presence of Arabian horse on Croatian grounds for hundreds of years. Its population size varied depending on the given circumstances of a given time and social events. Today's Croatian Arabian horse originates from the stud farm Borike founded in 1895 which unfortunately ended its existence in 2019. There were four main sources from which today's Croatian Arabian horses derive their ancestry: purebred Arabian horses from Syria, Saudi Arabia, Yemen, Iraq; the horses from the stud farm in Babolna (Hungary), the horses from the stud farm in Slawuta (Poland) and one stallion from the stud farm Radautz (Austria). Nowadays, the Arabian horse is bred at a stud farm Višnjica and by the private owners in Croatia. Due to all these circumstances, we assumed that a special type of Arabian horse was created, adapted to the needs and characteristics of Croatian breeding requirements. For that reason, 70 samples of pure Arabian and Shagya-Arab horses were genotyped using GeneSeek® Genomic Profiler™ Equine SNP BeadChip 70K (73860 SNPs). In order to identify the selection signatures, two approaches were used: 1) detection of extreme Runs of Homozygosity islands (eROHi) and 2) across populations identification of SNPs with extremely high FST values (ehFST). To analyse the FST values, we compared the Croatian Arabian horse population with other international and related breeds populations across the world using data available from other studies. The results from this study will certainly contribute to better understanding of the genomic structure of Croatian Arabian horses as well as a good starting point to implement the genomic information in the existing breeding programme.

Keywords: *Croatian Arabian horse, selection signatures, runs of homozygosity, FST values*

ANALYSIS OF INBREEDING EFFECTS ON SURVIVAL AT BIRTH OF PANNON WHITE RABBITS USING INBREEDING-PURGING MODEL

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ABSTRACT: Mating among related animals is an inevitable consequence of a closed population structure especially when it is coincided with small census size. As a result inbreeding depression may be encountered especially for fitness traits. However, under certain circumstaces the joint effects of inbreeding and selection may at least partly purge the detrimental genes from the population. In the course of this study our objective was to determine the status of purging and to quantify the magnitude of the eliminated genetic load for the survival at birth of Pannon White rabbit kits maintained in a closed nucleus population. The evolution of the survival at birth was evaluated applying the PurgeR software based on the inbreeding-purging model. 22718 kindling records was analyzed for the period of 1992-2017. Concerning the estimated parameters purging coefficient reached the possible maximum value of 0.5 between 1992-1997. Based on the expected fitness and on the expressed opportunity of purging the beneficial effects of purging could be expected after 10 generations where the proportion of the purged genetic load could be between 20 and 70%. These results suggest that large fraction of the inbreeding load may be caused by limited number of genes that could possibly be purged.

Keywords: *inbreeding-purging model, purging coefficient, expressed opportunity of purging*

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ASSESSING AMONG FLOCKS GENETIC DIVERSITY IN ISTRIAN SHEEP TO DEFINE A FRAMEWORK FOR OPTIMUM CONTRIBUTION SELECTION

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ABSTRACT: Long-term sustainability of economically important native breeds depends on sufficient genetic diversity necessary to cope with challenges in environment and breeding programs. The objective of this study was to analyse genetic diversity between and within flocks of Istrian sheep to define baseline population structure before implementation of optimum contribution selection. Altogether 719 animals from 12 flocks were genotyped with the Ovine SNP50 BeadChip. After quality control (SNP call rate > 0.9 and individual genotype call rate > 0.9, exclusion of sex-linked SNPs) 47,793 SNPs were used for further analysis. The snpReady package in the R programming environment was used to calculate genomic population parameters. The average population expected heterozygosity (H_E),observed heterozygosity (H_O) and inbreeding coefficient (F) were 0.357, 0.332, and 0.07, respectively. The average pair-wise genetic differentiation between flocks was moderate (0.194) and ranged from 0.016 to 0.413. The first three PC explained 15.8%, 14.9%, and 10.6% of the variation in the population, showing three genetically disconnected clusters. These results indicate that the Istrian sheep has preserved genetic diversity for the implementation of optimum contribution selection.

Keywords: *Istrian sheep; genetic diversity; SNPs*

Acknowledgements: To Croatian Science Foundation for funding this research under the project Genomic characterization, preservation, and optimum contribution selection of Croatian dairy sheep (OPTI-SHEEP), grant number IP-2019-04-3559.

MAGELLAN2.0: EXTENDING THE CAPABILITIES FOR THE POPULATION GENETIC ANALYSIS

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ABSTRACT: Quantitative genetics (genetics of complex traits) is a field of research that studies the effects of genome on the phenotypic traits in organisms. One of the approaches to follow the phenotype inheritance is the analysis of mitochondrial DNA (mt-DNA), which is conserved only in maternal line. One of the tools for that purpose has been the Magellan software [1], which has found its application in the analysis of population pedigrees in livestock, as well as the selection of individuals best suited for mt-DNA sequencing. Here, we present recent development of the software. The user friendliness has been improved through the implementation of graphical user interface, as well as through the integration of existing modules in the command line interface. The new visualisation module allows for a greater user insight in the structure of important parts of pedigrees. The computational cost of the sampling procedure has been greatly reduced through the implementation of two efficient algorithms. Besides mt-DNA polymorphisms and maternal lineages, the software is now capable of applying the same procedures to Y-chromosome polymorphisms and paternal lineages. A new module has been added for the analysis of pertinent SNPs found in populations, as well as for finding deleterious mutations in individuals' mitogenomes. These advances will enable the software to find a broader audience in the scientific community and wider applications in its field.

Keywords: *quantitative genetics software, pedigree trees, sampling algorithms, SNP, deleterious mutations*

Acknowledgements: This research was funded in part by the Croatian Science Foundation grants ALGSEQ-IP-2018-01-7317 and ANAGRAMS-IP-2018-01-8708.

[1] Ristov, Brajkovic, Cubric-Curik, Michieli, Curik; MaGelLAn 1.0: a software to facilitate quantitative and population genetic analysis of maternal inheritance by combination of molecular and pedigree information; *Genetics Selection Evolution*, (2016) 48:65

GENOMIC ADAPTATION IN LOCAL GREY ALPINE CATTLE: INBREEDING COMPARISON AND SIGNATURES OF SELECTION

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ABSTRACT: Local cattle breeds such as Alpine Grey are able to survive and produce in extreme environmental conditions. The analyses of genomic information allows to better understanding the adaptive mechanisms and better control inbreeding in many species and breeds. This study analyzed the level of inbreeding, based on pedigree and genomic information, and the presence of regions in the genome (runs of homozygosity; ROH) that could explain some adaptive mechanisms. For pedigree-based inbreeding estimates (Fped), 169,434 animals were used. For the genomic-based inbreeding, two different approaches were used: expected heterozygosity (Fhet), and runs of homozygosity (Froh). For this purpose 1,180 genotyped animals, with high (150K), and medium-densities (33K, then imputed to high density) chips were used. Fped was estimated through Inbupg software; Fhet was calculated with PLINK, and Froh was obtained with DetectRuns R package. Pearson correlations between inbreeding coefficients ranged from 0.47 to 0.93. Inbreeding estimates have shown a limited increase over time, suggesting good reproductive management by breeders. Comparisons between the coefficients obtained supported the importance of applying genomics in local populations to complement the missing records in the pedigree. The genes found in the ROH on BTA6 and BTA7 suggested that breeding plans prioritized efficiency and functional traits.

Keywords: *inbreeding, genomic inbreeding, runs of homozygosity, local cattle, adaptation*

Acknowledgements: This research was funded by the Alpin Grey National Breeders Association (ANAGA) within the DUALBREEINDG project (CUP J51J18000000005).

INCREASING EFFECTIVE POPULATION SIZE BY STRENGTHENING GENETIC CONNECTEDNESS BETWEEN FLOCKS: CASE STUDY ON PAG SHEEP BREED

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ABSTRACT: The effective population size (N_e) is an indicator of genetic diversity, and genetic connectedness between flocks is a "proxy" for assessing bias in across-flock BLUP genetic evaluation. We hypothesized that there is a positive correlation between these two parameters in populations under selection and checked our assumptions on data collected in Pag sheep breed (pedigree and flock information of phenotyped ewes). Only animals with sufficiently informative pedigree (>3 full known generations) were used in the inferential statistical analysis (from 1457 to 1833 animals within 4-year spanning generation interval - "sliding window" approach). The N_e estimated from the mean rate of increase in coancestry in the last generation interval was 127 animals, and the overall connectedness estimated with prediction error variance of differences in estimated breeding values (EBVs) between animals belonging to different flocks ($\overline{PEVD_{\iota',j'}}$) was 0.81. By regressing partial (generational) N_e on partial $\overline{PEVD_{\iota',j'}}$ it was estimated that $\Delta\overline{PEVD_{\iota',j'}}$ of 0.01 increased the N_e for 5.5 animals in average. The results suggest that strengthening connectedness in populations under selection, in addition to unbiased ranking of animals' EBVs, has positive implications to preservation of genetic diversity. However, some discrepancies in calculation of these two parameters posed limitations to relate them and make firm conclusions, therefore more research need to be conducted on this issue before generalization.

Keywords: *Effective population size; connectedness; sheep; genetic diversity*

Acknowledgements: To Croatian Science Foundation for fundin this research under the project Genomic characterization, preservation, and optimum contribution selection of Croatian dairy sheep (OPTI-SHEEP), grant number IP-2019-04-3559.

Y CHROMOSOME ILLUMINATES PATERNAL HISTORY OF MODERN HORSE BREEDS

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ABSTRACT: The male-inherited segment of the Y chromosome (MSY) retains information on the paternal ancestry of populations and serves as illuminator of male-driven demography. Historically, horses were repeatedly adjusted to suit human needs, and thus the MSY manifest complex demographic patterns of migrations and breeding strategies. The modern horse population was mainly shaped by the recent breeding influences and carry MSY haplotypes (HT) attributed to the ~2000 year old "Crown haplogroup". Using NGS data and haplotyping, MSY signatures of Thoroughbred and Arabian horses were recently characterized. However, a large portion of Crown HTs remain unexplored. In this project, we delineate MSY HT spectra of modern horse breeds in detail. We utilize an MSY HT topology consisting of 148 HTs and determine HT frequency from 1,665 stallions of 200 different breeds with KASP™ genotyping. Results confirm the prevalance of the Crown in modern breeds, but we report a remarkable broad Crown HT spectrum in Iberian (Spanish) and New World breeds. We reveal discrete grouping of Coldblood and British Pony breeds, and the MSY patterns enlighten the Spanish ancestry of those breeds. Altogether, we demonstrate the power of the MSY as a genetic marker to trace breeding influences in modern horse breeds with pedigree records, as well as the ones with unrecorded ancestry.

Keywords: *Y chromosome, haplotype, paternal ancestry, modern horse population*

COMMON SELECTION SIGNATURES FOR HEAT TOLERANCE IN HUMANS, GOATS AND PIGS

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ABSTRACT: The aim of this study was to get an insight to genomic regions influencing heat tolerance. SNP genotype data from 299 humans, 2689 goats and 1022 pigs were used in selection signature analyses. The data were divided to groups connected to tropical and temperate environments. This categorization was based on grouping in humans, LWK (Luhya, Kenya) and YRI (Yoruba, Nigeria) as “tropical”, and CEU (European ancestry) as “temperate” from HapMap3. GPS sampling coordinates (latitudes) were used in goats and pigs. After quality control of the data was subjected to selection signature analysis using the fixation index (Fst) among categories. The gene content was extracted using the biomaRt R package, and compared between species. Considering the 1% and 0.1% top scoring Fst regions 773 and 46 common genes were identified between humans and goats, 378 and 14 between humans and pigs, 92 and 2 between goats and pigs, and 46 and 0 between all three species simultaneously. The two genes common for the top 0.1% in pigs and goats are the PLCG1 and TOP1, previously connected to heat tolerance. They also appear in the top 1% region in the human data set. The results show links between the biology of thermo-tolerance across species, hold great potential for further exploration in animal breeding and beyond.

Keywords: *Selective sweep, Human, Goat, Pig, PLCG1, TOP1*

OPTIMISATION OF THE HOLSTEIN HEALTH INDEX

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ABSTRACT: Breeding for health traits contributes to sustainable production in times of climate change. Accordingly, the economic health index (HI) of the Czech Holstein was established five years ago. Since then, the breeding process has been encouraged and current population parameters should be updated to revaluate HI for the optimal structure, selection gain and index reliability. General principles of the selection index theory were applied in the study. Current economic weight of the mastitis and overall claw disease incidence were -152 and -134 € per cow and per year, respectively. Based on the optimal index construction the health traits proportion should be slightly reduced from 20% to 14%. The internal 'claw vs. mastitis' traits ratio in the HI could be optionally updated from 1.2 vs. 1 to 1.8 vs. 1, respectively. The expected selection gain in health traits would be -0.02 mastitis and -0.18 claw diseases incidence and the selection reliability would enhance to 80%. It can be concluded that the overall changes that the local Holstein population has gone through are of impact on the optimal HI construction and selection response. To ensure the desired selection gain and selection reliability the HI should be updated in the near future.

Keywords: *clinical mastitis, claw diseases, selection gain, economic weights*

Acknowledgements: The study was supported by project MZE-RO0718-V003 and QK1910320 of the Czech Republic.

GENETIC CHARACTERIZATION AND LANDSCAPE GENETICS OF LOCAL TAURINE CATTLE POPULATIONS IN BURKINA FASO

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ABSTRACT: Taurine cattle breeds including Lobi and Gourounsi are mostly found in the humid Western part of Burkina Faso and have an important socio-economic and cultural role for specific ethnic groups, from which they also draw their name. These small cattle are trypanotolerant, yet, their productivity is low and crossbreeding with Zebu cattle is practiced to increase their body size. The aim of this study is to understand the genetic basis underlying local adaptation and trypanotolerance in the taurine breeds Lobi and Gourounsi as well as their crossbreds. We genotyped a total of 832 cattle from five locations in the Southwest and West of Burkina Faso (Bouroum Bouroum, Kampti, Loropeni, Tenado and Nahouri) with the Illumina Bovine SNP50 BeadChip. To screen admixture between taurine and indicine cattle, we also included genotypes from pure Zebus. We investigated population structure, genetic diversity and admixture. Our preliminary results show limited structure within the taurine populations and high degree of admixture with Zebus. Landscape genomic analyses combined with trypanosome infection status to identify genomic regions underlying environmental and pathogen-related adaptation are still ongoing. Our results are important for the conservation of locally adapted taurine breeds and maintaining their genetic potential also for crossbreeding management.

Keywords: *admixture, local adaptation, Lobi, Baoulé, Gourounsi*

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MBL2 GENE POLYMORPHISMS IN MEDITERRANEAN ITALIAN RIVER BUFFALO (MIRB) (*Bubalus bubalis*) AND THEIR ASSOCIATION WITH MILK SOMATIC CELL COUNT (SCC)

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ABSTRACT: (1) Background: High milk SCC is associated with altered composition and poor technological properties of milk and mastitis. The aim of this study was to search for DNA variants in Mannose-Biding Lectin 2 (*MBL2)* gene and to analyze their association with SCC in milk collected from MIRB. (2) Material and Methods: Blood (for DNA analysis) and milk samples (for SCC analysis) were collected approx. 150 days postpartum from 90 female buffaloes originating from 5 herds. The *MBL2* gene (NC_059179) was sequenced using Sanger method. Distribution of allelic variants was compared between cohorts of females with high (SCC>200,000; N=41) and low (SCC<80,000; N=49) SSC, using odds ratio (OR) test. (3) Results: In total 33 SNPs were detected: 12 in exons (including 7 missense), 8 in the promoter region, 8 in the 3'UTR or 3'flanking region, and 5 in introns. Altogether 3 SNPs, located in non-coding sequences (introns or 3'UTR), were significantly associated with SCC ($p<0.05$). (4) Conclusions: This pilot study showed that *MBL2* gene is highly polymorphic and some of its variants are potentially associated with SCC in MIRB. These preliminary results should be verified on larger cohorts of females producing milk with different SCC and if confirmed could be recommended for the use in selection.

Keywords: *MBL gene, Somatic Cell Count, Buffalo*

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PRELIMINARY STUDY RESULTS ON THE GENE EXPRESSION ANALYSIS OF INTRAMUSCULAR FAT CONTENT IN BLACK SLAVONIAN PIG

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ABSTRACT: Intramuscular fat (IMF) plays an important role in determination of meat quality and directly contributes to the positive technological and sensory characteristics such as taste, texture and juiciness. In Black Slavonian pig (BS), numerous studies reported much higher IMF content compared to other local breeds, therefore, understanding the genetic mechanisms of IMF in BS becomes one of the main challenges in scientific research. Transcriptome and gene expression analyses using RNA-seq technology is approach which enables the identification of genes that are differentially expressed in distinct phenotypes. In the last few years, the majority of gene expression studies has been carried out on modern pig breeds, therefore such analyses on local breeds would significantly contribute to the pig breeding of local breeds, but also to the commercial breeding programs. For the analysis of gene expression for IMF in this study, out of the total of 80 pigs in full-sib design, 10 sib pairs with extremely high and low IMF phenotypes were selected, and also analyzed for performance and meat quality traits. Whole transcriptome analysis was performed using RNA-seq technology, while candidate genes were further verified using quantitative real-time PCR (qPCR) analysis. The results from this study will certainly contribute to the understanding of genetic mechanisms of IMF in BS, and will also provide new possibilities for improvement of breeding program.

Keywords: *Gene expression, intramuscular fat content, Black Slavonian pig, genomics*

MANAGEMENT OF BREEDING BULLS OF BUSHA CATTLE IN CROATIA – A BULL:COW RATIO TRENDS

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ABSTRACT: The Busha cattle breed contributes to a genetic diversity for centuries in Croatia, with the number of breeding cows significantly increasing in the last decades. Successful reproduction of native breeds in outdoor breeding conditions is a multifactorial phenomenon influenced by genetic and non-genetic factors. Improving fertility and conception in native outdoor breeding units with optimal bull:cow ratio is important to reduce costs of production and avoid negative effects of reproductive management in the herd. Herds of the Busha cattle across Croatia were included in the study to calculate the variability and trends in the bull:cow ratio among the herds. The data on 204 active breeding bulls born in the 2007-2020 period were obtained from the Veterinary Information System of the Ministry of Agriculture, Directorate for Veterinary Administration. Observed *vs*. expected frequencies were tested with Chi-sqaured test using the three model approach according to the expected number of bulls *per* cows in the herd; model 1 as 1:10, model 2 as 1:15, and model 3 as 1:20. Analyzing the proportions of the expected bull:cow ratios significant differences were recorded for model 1 (herds with >31 cows, $P<0.01$), model 2 (herds with >61 cows, $P<0.05$) and model 3 (herds with >81 cows, $P<0.01$). Accordingly, a higher number of breeding males is expected in the herds. In this way, it is possible to improve reproductive performance, as well as genetic potential during the productive life, and share positive genes especially for herd fertility management for succesful breeding and genetic diversity of the Busha breed.

Keywords: *Busha, bulls, management, reproduction*

MODEL SELECTION AND ESTIMATION OF GENETIC PARAMETERS FOR LOIN AND BACKFAT DEPTH IN CZECH PIG BREEDING PROGRAM

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ABSTRACT: The selection of livestock is based on breeding values (BV), which represent the genetic value of each animal for a particular trait. The traits of interest are commonly chosen by a national breeding program for their biological or economic importance. In the Czech Large White pig population, the production efficiency is evaluated by lean meat content (LM%). However, this supposedly leads to unintended selection pressure on the LM% components: loin muscle depth (LD) and backfat thickness (BFT). Therefore, this work aimed to estimate genetic parameters for these two traits. For this purpose, data from 178,596 pigs between 2004 and 2020 were analysed. After a preliminary selection of effects for a model equation, BLUPF90 family of programs (Misztal et al. 2012) was applied to estimate genetic parameters using different multiple-trait models. The best performing model contained LD, BFT, and live weight (LW) as correlated traits with fixed effects of sex, year, and apparatus, regression on age, and random effects of herd-year-season, litter, and animal. Heritability estimates were relatively low: 0.17 for LD, 0.24 for BFT, and 0.19 for LW. The genetic correlations were: 0.49 for LD-BFT, 0.68 for LD-LW, and 0.79 for BFT-LW. These results can adjust the national breeding goal to maintain the selection towards meat production and prevent further reduction of BFT.

Keywords: *pig, statistical model, heritability, correlation, breeding value*

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MORPHOMETRIC CHARACTERIZATION OF LOCAL GOAT BREEDS IN TWO AGRO-ECOLOGICAL AREAS OF BURKINA FASO, WEST AFRICA

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ABSTRACT: Goats are the second largest ruminant population in Burkina Faso. They are almost exclusively indigenous breeds reared in extensive production systems in various agroecological zones. This study was carried out to understand the morphological variation of local goat breeds in two agroecological areas. A total of 511 adult female animals belonging to two presumed populations were evaluated based on 9 linear body measurements, including 3 height measurements, 5 length measurements and body weight. Principal Component Analysis (PCA) suggested structure between the Mossi breed on one side and Djallonké on the other. No strict separation was observed suggesting that gene flow is occurring among the different populations. A dispersion map with 4 clusters was built based the first two factors. The least square means of body measurements ranked the 4 groups from small to large body size, namely Djallonké, Sahelian x Djallonké, Mossi and Sahelian x Mossi. Gene flow from Sahelian goat into other populations, based on migration of the Fulani ethnic group from the Sahel into areas with Mossi and Djallonké breeds could explain this configuration and confirms the continuous erosion of genetic identity of these two local breeds.

Keywords: *Characterization, Body measurements, Goat, Breeds, Burkina Faso*

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PHYLOGENETIC BACKGROUND OF THE RECONSTRUCTION STOCK OF SZEKLER HORSE BREED

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ABSTRACT: The Szekler horse was a small sized mountain horse of Carpathians whose official stud book has ceased to exist after WWII. In spite of that nevertheless, individuals really preserving the characters of the Szekler horse remained scattered in remote areas. The aim of this study is to evaluate the mitochondrial D-loop sequence (608 bp) of founder population (n=59) established 2021. DNA samples were Sanger sequenced. D-loop shown 68 polymorphic sites. The number of haplotypes was 34 with haplotype diversity (Hd) 0.966, and nucleotide diversity (Pi) 0.02232. The value of Fu's Fs statistic (-6.566) was significant ($P<0.001$). There were found 13 haplogroups (HG) with a nearly equal number of representatives (HG(n) – A(5), D(1), E(2), G(4), I(4), J(1), M(4), N(2), O'P(4) and R(1)). As exceptions, the Q, L and B HGs occurred with higher number of individuals (15, 9 and 7, respectively). Based on the larger number of polymorphic sites and haplotypes the founder stock is considered diverse. The significant negative Fu's Fs value rejects a stabile population status, supporting a population genetic variability. According to the HG Q characteristic of Asian horses, the examined stock bears the eastern origin of the Hungarian horses brought from the east to a significant extent. Which is complemented by the gene pool of horses from Europe (e.g. L) and the Middle East (e.g. B).

Keywords: *Szekler horse, breed reconstruction program, D-loop*

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GENETIC PARAMETER ESTIMATIONS OF FERTILITY TRAITS IN NERO DI PARMA BREED

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ABSTRACT: Nero di Parma is an endangered Italian pig breed officially recognised in 2016 with nowadays roughly 1,600 alive animals. Since reproductive traits are key in terms of breed sustainability, the purpose of the study was to estimate genetic parameters of several fertility traits in Nero di Parma swine breed. First, a pedigree analysis was performed in Endog 4.8 to investigate the current breed's genetic variability. The dataset consisted of 2484 litters from 1035 different sows. The litter size, mortality rate, number of piglets weaned, and survival rate were evaluated in function of i) inbreeding divided in quartile classes, ii) season, iii) year, iv) herd and v) parity order. Univariate and bivariate animal models were performed using ASReml software (version 4.1) to estimate heritability and genetic correlations among traits. Litter size was found to be the most heritable trait ($h^2 = 0.075$) which was also strongly correlated with weaned piglets and survival rate while a negative correlation was found with mortality. Since inbreeding seemed not to significantly affect fertility, we suspect that in Nero di Parma the increase of inbreeding is still well tolerated probably due to its rusticity. However, breeding strategies must be applied to ensure long-term survival of this breed.

Keywords: *inbreeding, fertility traits, autochthonous breed, genetic parameters*

MILK YIELD AND QUALITY AT COW UDDER QUARTER LEVEL AS INFLUENCED BY QUARTER POSITION, PATHOGEN AND SOMATIC CELL SCORE

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ABSTRACT: Few information on milk from complete draining of individual udder quarters is currently available. The aim of the study was to assess how and to which extent milk yield and quality at udder quarter level are influenced by quarter position, pathogen and somatic cells. Quarter milk samples (n=120) of 10 Simmental cows were collected in three consecutive sampling days. Milks were analysed for bacteriology, chemical composition (fat, protein, casein and lactose, %), pH and urea content (mg/dL). Somatic cell count (SCC) and differential SCC were also determined. Data were analysed with a linear mixed model which included the fixed effects of quarter position (right front, left front, right rear, left rear), pathogens (presence or absence) and somatic cell score (SCS) (4 classes, defined on quartiles of SCS distribution), and the random effects of cow nested within quarter level and residual. Quarter position significantly affected milk yield ($p < 0.05$), with rear quarters being the most productive. Pathogens had a negligible effect on milk yield and quality. Somatic cell score was significant in explaining the variability of fat, lactose, DSCC and pH ($p < 0.05$).

Keywords: *dairy cattle, quarter milk, mastitis, SCC, milk composition*

Acknowledgements: This research was funded by the Ministry of Agricultural, Food and Forestry Policies (Rome, Italy) through project "CowSens" (CUP: C24I19000840001). Technical support of the staff of "Lucio Toniolo" experimental farm (University of Padova, Italy) is gratefully acknowledged.

GENETIC PARAMETERS FOR LIVE ANIMAL ULTRASOUND MEASURES IN CZECH ABERDEEN ANGUS

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ABSTRACT: There is a growing demand for selection on meat quality by Czech Aberdeen Angus breeders. The use of live animal ultrasound measures as indicator traits can be an efficient way to evaluate meat quality. The objective of this study was to estimate heritability and genetic correlations between live animal ultrasound measurements, such as rump fat thickness (P8FT), rib fat thickness (RBFT), eye muscle area (EMA), intramuscular fat content (IMF), and related traits, such as weight at scanning (SCW), and scrotal circumference (SC). Live animal ultrasound measures were collected on 1,949 animals, and SC was measured on 1,021 bulls aged 250 to 500 days through 2019, 2020, and 2022. Estimates of genetic (co)variances were obtained using average information restricted maximum likelihood (REML) as implemented in AIREMLF90 (Misztal et al., 2002). The fixed effects of contemporary group, sex*twin, age of the animal, and age of dam were included in the model equation. Random effects considered were the direct additive genetic effect and the residual effect. The multi-trait animal model was used for estimation. Moderate to high heritability estimates were obtained 0.49 ± 0.08, 0.44 ± 0.07, 0.71 ± 0.01, 0.25 ± 0.03, 0.69 ± 0.05 and 0.77 ± 0.06 for P8FT, RBFT, EMA, IMF, SCW, and SC, respectively. Measures of body fat (IMF, P8FT, and RBFT) were genetically strongly correlated, with correlations ranging from 0.87 ± 0.04 to 0.99 ± 0.01. The correlation between IMF and SCW was 0.70 ± 0.05, between IMF and SC 0.60 ± 0.11, and between IMF and EMA 0.50 ± 0.06. EMA was highly genetically correlated with SCW (0.90 ± 0.05). The heritability estimates obtained in this study indicate that genetic evaluation for live animal ultrasound measures is feasible and genetic improvement through selection should be effective. However, the strong genetic correlation between intramuscular and subcutaneous fat is unfavorable and should be considered in the breeding program.

Keywords: *Aberdeen Angus, ultrasound, genetic parameters, beef cattle, heritability*

Acknowledgements: This research was supported by the Ministry of Agriculture of the Czech Republic (Project No. QK1910059).

POLYMORPHISM OF THE *TLR2* GENE AND ITS RELATION TO CLINICAL MASTITIS IN CZECH FLECKVIEH POPULATION

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ABSTRACT: Inflammation of the mammary gland causes significant economic losses in cow milk production. Despite efforts to prevent, control, and treat, mastitis remains one of the most common cattle diseases. Receptors of immune cells play a crucial role in the attack of an organism by infectious pathogens. The main objective of this study was to determine single nucleotide polymorphism (SNPs) (rs68268260, rs68268250, rs55617172, rs68268263, rs68268268, rs43706433, rs68268256, rs68343167, rs43706434, rs68343168) in gene *TLR2* encoding molecule Toll-like receptor 2, which is considered the candidate immune gene related to mastitis. The primer extension method, specifically its commercial version – SNaPshot (Life Technologies, Thermo Fisher Scientific), was used for SNPs detection in 823 dairy cows of Czech Fleckvieh cattle (CF). Data on the incidence of mastitis in the CF population were obtained from the Cattle Diseases and Treatment Diary (Institute of Animal Sciences, Prague). Collected data were used to analyze the effect of the individual *TLR2* polymorphism on mastitis occurrence during the first lactation. GLM method was used for each SNP separately. The pilot model revealed the significant difference only for SNP rs43706433 ($p=0.0311$). Heterozygous dairy cows carrying genotype "TC" showed the significant difference in the occurrence of clinical mastitis at the first lactation. For a more detailed and accurate evaluation a mixed linear model with animal pedigrees will be used.

Keywords: *Innate immunity, genotyping, mastitis, association, SNP*

Acknowledgements: This work was supported by the Ministry of Agriculture of the Czech Republic, institutional support MZE-RO0718 and Czech University of Life Sciences SGS grant no. SV22-12-21360.

Poster Session: Animal Breeding and Genetics

ATTITUDES OF DOG OWNERS AND BREEDERS TOWARDS GENETIC TESTING

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ABSTRACT: The aim of the study was to gain an insight into the opinions and attitudes of dog owners and breeders related to their preference and practical use of genetics. A total of 330 anonymous responses to 61 questions from 259 pet owners and 71 breeders were analysed, obtained from 19 Hungarian-speaking social media groups. There was a clear sense of importance for genetic diversity and testing in dog breeders, with average ± standard deviation of 4.1±1.0 and 4.3±0.8 on a 1 to 5 scale. Surprisingly, when asked about the necessity of relationship testing before mating, the breeders did not deem it necessary (2.7±1.4), while pet owners found it crucial (4.2±1.2). The respondents were not convinced that tracked pedigrees guarantee the genetic diversity and health of dogs (averages 2.9±1.2 and 2.3±1.3). Moreover, both groups were concerned about disorders. For both the joint problems (e.g. dysplasia) were the most important (3.9±1.1 and 3.3±1.4). Moreover, spine, eyes, circulatory system, skin, and digestion disorders were slightly more concerning to owners (averages 3.2 to 3.6), than to breeders (averages 2.5 to 3.0). In conclusion, the existence of pedigree and certificate of origin makes both owners and breeders moderately confident that the breed is managed properly. Apparently, the breeders are more realistic about the distinction between the existence of certificates and the situation in practice.

Keywords: *dog, genomics, genomic testing, opinion survey, disorders*

Acknowledgements: The participation of questionnaire respondents including their supplementary comments are greatly appreciated.

mtDNA DIVERSITY IN HUNGARIAN RED DEER, *Cervus elaphus* POPULATIONS CONFIRMS THE KNOWLEDGE ABOUT THE ORIGIN OF THE SPECIES

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ABSTRACT: (1) Background: The red deer (*Cervus elaphus*) is one of the most important wild species in Europe. Two effects played a significant role in the development of the current genetic structure of the species. One is a series of extinction and immigration events caused by the cyclical alternation of glacials and interglacials, and the other is a set of human-caused influences that includes hunting, habitat fragmentation, translocations, etc. Regarding the Hungarian red deer, it is assumed that two types are present: Carpathian and Pannonian. However genetic studies with such a number of animals, covering the whole Hungary, have not yet been performed before. We aimed to fill this gap and having information about the diversity of red deer in Hungary; (2) Methods: Sixty-six adult red deer from the managed hunting grounds of south-west and north-east of Hungary were sampled and sequenced a 886-bp part of the mtDNA D-loop and 946-bp region of the mtDNA cytochrome-b; (3) Results: Number of haplotypes in D-loop and cytb region were 25 and 3, respectively; (4) Conclusions: Basic indices for both genetic variability within populations and geographical distribution of the haplotypes clearly indicated separation between red deer populations from the south-west and north-east of Hungary.

Keywords: *Cervus elaphus, genetic diversity, Hungary, mtDNA*

Acknowledgements: Authors thank Gergely Fazekas and the hunters from Szabolcs-Szatmár-Bereg county for sampling and sharing their experience and information about the origin of the sampled populations.

A REVIEW ON GENETIC DIVERSITY OF LOCAL CHICKEN POPULATION AND THEIR ADAPTATION POTENTIAL TO CLIMATE CHANGE IN TROPICAL CLIMATE: A CASE STUDY IN EAST AFRICAN COUNTRIES

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ABSTRACT: (1) Background: Presently, a key objective for sustainable livestock production is breeding for climate change resilience breeds and indigenous genetic resources remain a valuable asset in attaining this important goal. However, the success of this endeavor will depend on our efforts to identify and utilize selection signatures underlying these unique adaptation features in local breeds which indeed remained largely untapped; (2) Methods: In the efforts to understand the local adaptability of indigenous chicken, the present work reviews the published articles describing the genetic diversity and selection signatures underlying tropical adaptability and immunity potential among East African indigenous chicken population and beyond. Further, we also present the utilization of indigenous chicken genetic resources for increased productivity. The noticeable ongoing genetic erosion owing to the currently emerging intermediate production system has also been cautioned, and prospective topics for immediate research are suggested; (3) Results: Our results avers that the indigenous chickens in East Africa are highly genetically diversified and adaptable to different tropical environments. This variation has been exploited through backcrossing, gene introgression, and transgenesis technique with exotic breeds; (4) Conclusions: Further investigations to identify specific selection signatures for local adaptation would enhance the efficiency of breeding for adaptation to climate change.

Keywords: *crossbreeding, East Africa, genetic diversity, indigenous chicken, selection signature*

RUNS OF HOMOZIGOSITY PATTERNS IN HRVATICA CHICKEN BREED

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ABSTRACT: A run of homozygosity (ROH) is defined as a stretch of consecutive homozygous loci in an individual genome. ROH can be caused by a variety of mechanisms, including inbreeding, genetic drift, and population bottlenecks. In chickens, ROH have been associated with several negative outcomes, including increased susceptibility to disease, decreased fertility, and overall inbreeding depression. However, ROH may also confer some advantages, such as increased resistance to parasites and greater tolerance to environmental stresses. The Hrvatica chicken is an autochthonous Croatian dual-purpose breed. It is a medium sized chicken with light brown plumage. One of the most important characteristics of this breed is that it is an excellent forager and does well in free-range conditions. It is a winter-hardy chicken that tolerates cold weather well. Hrvaticas are also known to be good mothers and often go broody. By analyzing the ROH distribution in 24 birds, we get a unique insight into the genetic history of the breed, selection pressure, and specific regions of the genome. All of this provides a good starting point for future selection, conservation, and management of this traditional breed that is capable of withstanding future changes in both the climate and the economy.

Keywords: *Hrvatica chicken breed, Runs of homozygosity, breed genetic history*

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GENOMICS OF DWARFISM IN ITALIAN LOCAL CHICKEN BREEDS

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ABSTRACT: The identification of dwarf phenotype in chicken is based on body weight, shank length and others features, leaving the differentiation between dwarf and small breeds uncertain. A total of 541 chickens from 23 local breeds were sampled (from 20 to 24 animals per breed, 50% males and 50% females, unrelated). All animals were genotyped with a 600 K chicken genotyping array. Three breeds in the dataset were described as "dwarf": Mericanel della Brianza (MER), Mugellese (MUG) and Pepoi (PPP). In order to unravel the genetics underlying the dwarfism, we compared MER, MUG and PPP with the four heaviest breeds in the dataset. After quality control with PLINK v1.9, genome-wide association analyses (GWAS) were performed using the GEMMA software and Manhattan plots were built using the *ggplot2* package in R. GWAS showed significant SNPs in MER and MUG breeds, which shared genomic regions on chromosome 1. Due to this similarity, we also analysed MUG and MER together against the reference population. We observed highly significant SNPs in *LEMD3* and *HMGA2* genes that have previously been reported to be responsible for dwarfism in different species. In conclusion, MER and MUG breeds seem to share a genetic basis of the dwarfism, unlike PPP.

Keywords: *genomic region, local population, chicken, SNP, dwarf*

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GENOMIC DIFFERENTIATION BETWEEN RED AND SPOTTED CATTLE BREEDS IN SLOVAKIA AND CZECH REPUBLIC

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ABSTRACT: As a consequence of the global expansion of high-producing cattle breeds, local autochthonous populations are becoming increasingly rare. Although their lower production efficiency compared to others, they possess unique genetic variants ensuring them a better ability to respond to production environment changes. Therefore, this study aimed to examine intrapopulation diversity level and genomic differentiation between local red and spotted cattle breeds from Slovakia and the Czech Republic. Czech Red (N=40), Slovak Red (N=16) and Norwegian Red (outgroup, N=21) represented a group of red breeds. Spotted breeds were represented by Czech spotted (N=90), Slovak spotted (N=174), and Slovak Pinzgau (N=151) cattle. After standard quality control of genomic data, a total of 24754 SNP genotypes were available for subsequent analyses. Even if all analysed populations showed a similar level of intrapopulation diversity, slightly higher values of diversity parameters were observed for the Slovak Red population (H_o=0.40±0.18, H_e=0.37±0.14, F_{HOM}=-0.08±0.02). As expected due to the origin of breeds, the highest level of differentiation from others showed Norwegian Red and Slovak Pinzgau, while the closest genetic affinity was found between Czech Red and Czech spotted populations. DAPC analysis confirmed also the connection between Slovak Red and Czech Red populations indicating ongoing gene flow between them.

Keywords: *admixture, genetic diversity, gene flow, local population*

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EFFECTS OF STAGE OF LACTATION, PARITY, SEASON AND PDO PRODUCTION CHAIN ON ACIDITY, COMPOSITION AND FATTY ACID PROFILE OF BOVINE MILK

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ABSTRACT: In 2021, Italian dairy industry registered a turnover of about 16 million euro, mainly coming from PDO cheeses. Thus, understanding the variability of nutritional and technological characteristics of milk within each PDO chain is fundamental. The aim of this study was to investigate the effects of lactation, parity, season and PDO chain on milk composition, acidity and fatty acid (FA) profile of Brown Swiss cows. A total of 960 individual milk samples were collected in 48 herds (20 cows/herd) in 3 PDO cheese areas (Parmigiano Reggiano, Grana Padano and Silter). Milk composition, groups and individual FAs were assessed through mid-infrared spectroscopy and acidity (pH and SH°100) through potentiometric titration. Most of the milk components and groups of FAs increased linearly throughout lactation. Among FAs, C18:0, polyunsaturated FAs and trans-FA were the highest in primiparous cows. As regards season, saturated and polyunsaturated FAs were the lowest in summer. The highest acidity was observed in primiparous cows (pH=6.60; SH°100=7.83) and in winter (SH°100=7.95). The PDO chain affected only polyunsaturated FAs ($p<0.05$). The proportion of variance explained by the random effect of herd ranged from 7% to 39%. Exploring new available milk information contributes to improve sustainability and efficiency of the dairy chain.

Keywords: *dairy cattle, fatty acid, mid-infrared, milk quality, sustainability*

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THE ROLE OF PRLR GENE POLYMORPHISMS IN MILK PRODUCTION OF RABBITS

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ABSTRACT: The decreasing amount of milk production from the third week of lactation in rabbits, which is the only source of nutrients until weaning, does not meet the nutritional needs of the young animals. The polymorphisms in the PRLR gene have already been described and linked to milk production in several species. In our study, we performed the sequencing of a 1200 bp long section of the promoter region of the PRLR gene in wild rabbits. We identified four point mutations (SNP1-407G>A, SNP2-496G>C, SNP3-926T> and SNP4-937A>C) and a microsatellite (CTC repeat) at position 574. In our stock, the four SNPs were segregated into four genotypes. Regarding milk production, we found that the homozygous genotype TTAACCCC showed a higher milk production (1564.7 ± 444.7 g) compared to the other three genotypes (GGGGGGTT 1399, 1 ± 326.8 g; GTGACCTT 1403.8 ± 517.1 g; GTGACCCC 1220.0 ± 666.2 g). In the case of the microsatellite, the short variant results in significantly higher milk production (1623.8±525.1 g) compared to the long variant (1300.4±458.6g). Our results provide an opportunity to develop a marker-based selection, resulting in that, the rabbit does especially with larger litters, can better satisfy the increased nutritional requirements of suckling rabbits.

Keywords: *milk production, prolactin receptor gene, wild rabbit, Orictolagus cuniculus*

THE EFFECTS OF CRYOPRESERVATION ON CHICKEN PRIMORDIAL GERM CELL VIABILITY AND GERM CELL SPECIFIC MARKER EXPRESSION PROFILE

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ABSTRACT: Gene preservation becomes more and more important due to the breed uniformization of the poultry industry. To prevent traditional breeds from extinction, gene banks must be established. For poultry gene preservation primordial germ cells (PGCs) are one of the most promising tools. This experiment aimed to inspect the PGCs' viability changes before and after freezing. For the immunohistochemical staining a new antibody, 30B6 was tested, which could become a universal stem cell specific marker in poultry species. For the experiment, chicken primordial germ cells were isolated, cultured and cryopreserved with two special freezing media. The viability was measured with the NanoEntek Arthur Fluorescent Cell Counter before and after freezing. The 30B6 and CVH antibodies were used for the immunohistochemical staining. The results showed that there were no significant differences between the prefreezing and postfreezing viability rates. We could also successfully prove, that the 30B6 antibody expresses from the chicken PGCs. We also found an interesting expression pattern, since the 30B6 expressed both from the cell membrane and parts of the nucleus. In the future we would like to further test the 30B6 antibody's cell specificity on gonad sections and check its universal usage on goose, quail and guinea fowl samples.

Keywords: *chicken, PGC, cell freezing, immunohistochemical staining*

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EFFECTIVE POPULATION SIZE AND POPULATION STRUCTURE IN AFRICAN CHICKEN

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ABSTRACT: African chicken is an important livestock asset with a convoluted demographic history due to multiple introductions. The main goal of this study was to predict the effective population size (Ne) trends for Ethiopian and Nigerian chickens. Data from whole-genome sequences of 234 Ethiopian and 119 Nigerian chicken samples were analyzed. SNPs were limited to about 50K markers for computational reasons, and filtered for quality. For the Ne computation, the SNeP software and a manual script considering recombination rate were used. Moreover, to understand population structure, principal component analysis by PLINK1.9, *Fst* analysis by VCFtools, and admixture analysis by ADMIXTURE1.3 were performed. Migration events were predicted using TreeMix v1.1. The predicted effective population sizes increase looking into the more distant past, from 946 (19 generations ago) to 5325 (700 generations ago) for Ethiopian chickens, and from 668 to 4162 for Nigerian chickens. The estimates are generally lower for Nigerian chickens but the difference decreases looking into the more recent past. The Hugub was identified as a unique population in Ethiopia, with additional geography based clustering, while Nigerian samples were found unstratified. Four migration events were predicted for Ethiopian and one for Nigerian chickens. This study can increase the understanding of the African chicken population history and potentially contribute to local chicken breeding and conservation.

Keywords: *African chicken, effective population size, linkage disequilibrium, admixture, migration*

EXAMINATION OF PRIMORDIAL GERM CELL (PGC) CULTURES DERIVED FROM THE OFFSPRING OF HEAT-CONDITIONED DOMESTIC HENS: COMPARISON OF THE RNA EXPRESSION PROFILE

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ABSTRACT: Adapting to extreme weather is essential for farm animals. Using induced heat stress in domestic chickens, we could examine the stress response. Chicks that have undergone heat treatment have an improved ability to tolerate heat, as they can regulate their internal body temperature more effectively in the event of heat stress, which remains throughout their lifetime because heat treatment affects the heat sensitivity of the hypothalamus. Twenty-four hours after hatching, the chicks were heat-conditioned at an ambient temperature of 38.5°C and 60% humidity for 12 hours. After sexual maturation, heat stress was applied, keeping them at a temperature of 30°C for two weeks. Primordial germ cell (PGC) lines were established from the next generation of animals exposed to direct heat. We isolated DNA and RNA from the PGCs. Among the HSPs, HSP70 has attributed the most significant role. miR-92, miR-181a and miR-138 were also involved in the molecular pathway induced by heat stress. Based on the RNA sequencing results of PGCs established from the embryos of heat-stressed, heat-conditioned, and only heat-stressed animals, we determined gene families and essential genes differentially expressed in PGC cultures. In the case of RUNX2 and miR-6545, we confirmed the results of RNA sequencing with qPCR tests.

Keywords: *Heat stress, Chicken PGC, RNA sequencing, RUNX2, miR-6545*

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CONTRIBUTION OF THE WEIGHTED SINGLE-STEP GBLUP METHOD FOR GENOMIC EVALUATION OF UDDER CONFORMATION IN HOLSTEIN CATTLE

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ABSTRACT: The appropriate udder conformation in dairy cattle is associated with the economic profitability of milk production in commercial dairy farms. Although the udder conformation traits have moderate heritability, selection based on genomic breeding values (GEBVs) significantly contributes to the improvement. Udder morphology has a polygenic background, but also candidate variants were observed. In this study, GEBVs for udder morphology (udder depth, rear udder height, front and rear teat placement, central ligament, fore udder attachment, teat length, and rear udder width) were predicted based on 699,681 cows phenotypes for 1,772,297 Holstein individuals using the single-step genomic BLUP (ssGBLUP) and weighted single-step genomic BLUP (wssGBLUP) method. Genotyping of 25,486 animals was performed by various SNP chips where the common intersection (35,227 SNPs) with Illumina BovineSNP50 BeadChip V2 was used. The comparison of both methods was assessed using validation. Validation reliabilities and regression coefficients were comparable for all traits and both methods. In the wssGBLUP method, the variance of each SNP is used when the genomic relationship matrix is constructed. We assume that the quality of the genomic relationship matrix was comparable for both methods due to the high number of genotyped animals included in the study.

Keywords: *genomic evaluation; validation; udder conformation; dairy cattle*

Acknowledgments: The research was funded by the Ministry of Education, Youth and Sport (Project No.: LTAUSA19117) and the Ministry of Agriculture of the Czech Republic grant ID: MZE-RO0718. We thank to Holstein Cattle Breeders Association of the Czech Republic (Hradištko, Czech Republic) for providing datasets and animal breeding and genetics group from the University of Georgia, USA) for the long-term cooperation and support.

INTEGRATION EFFICIENCY OF GFP-EXPRESSING PGCS INTO CHICKEN GONADS

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ABSTRACT: The development of genetically appropriate gene bank help maintains genetic diversity and prevent the loss of wild populations. The ancient chicken breeds have lower body weight and egg production than the commercial breeds. That is why these breeds will disappear if we do not protect them. Previously we established a chicken primordial germ cell (PGC) based cryobank from endangered Hungarian poultry breeds. The thawed PGCs were characterized (proliferation rate, stem cell and germ cell-specific marker expression). The next step was to analyse the integration efficiency of PGCs into different recipient breeds to find an ideal recipient breed suitable for most of our PGC lines. Three different breeds were selected (White Hungarian, Yellow Hungarian, and Partridge-colour Hungarian). We injected back GFP expressing PGCs into the 3-days-old recipient embryos and examined the integration efficiency on day 14. 365 embryos were injected by GFP expressing PGCs. Two different PGC lines were injected (5ZP=female line; 4ZP=male line). After the injection of 4ZP PGCs, the chimera production was 53,2%, and in the case of 5ZP, we got 43,9% gonadal chimeras. Injecting back 5ZP PGCs, we found a significantly higher number of chimeric gonads in the Partridge-colour Hungarian breed than in the other tested chicken breeds. Our results recommend the Partridge-colour Hungarian breed as a recipient for the PGC-based gene conservation.

Keywords: *PGC, gene bank, chimera, chicken embryo*

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GENETIC PARAMETERS OF AMERICAN QUARTER HORSES REGISTERED IN THE SLOVENIAN STUD BOOK

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ABSTRACT: The American Quarter Horse (AQH) breed was formed in America in the 17th century. The founders were horses of different breeds and crosses with English Thoroughbred horses, however, during the history of the breed, the use of influential stallions led to increased inbreeding in the population. The popularity of AQH has been growing in Slovenia since 1995, when the first AQH was imported, reaching a total number of 1090 AQHs registered in Slovenia by 2022. For genotyping, 63 AQHs were selected from the Slovenian studbook and genotyped at 17 microsatellite loci. A total of 3107 AQHs were included in the pedigree analysis, with 760 AQHs currently living in Slovenia serving as the reference population. The majority of individuals in the Slovenian AQH population have an inbreeding coefficient (F_{str}) based on microsatellite data between 10 and 15%. F_{ped} values based on pedigree data were lower, and there was no significant correlation between the inbreeding coefficients estimated from pedigree and microsatellite data. Several measures, including regular updating, greater numbers of horses active in reproduction and systematic physical evaluation, would preserve genetic diversity and allow genetic improvement of the population.

Keywords: *American Quarter Horse, inbreeding, microsatellites, pedigree*

MATERNAL PHYLOGENY OF OLD SERBIAN SHEPHERD DOG BASED ON MITOCHONDRIAL DNA

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ABSTRACT: Maternal inheritance, lack of recombination, and relatively high mutation rate are important features that make mitochondrial DNA (mtDNA) an important molecular marker for establishing phylogenetic relationships at the species level, as well as within species. Different haplotypes of mtDNA within the species illustrate the genetic diversity of matrilineal contributions to different subpopulations. The control region (CR) is the most variable part of mtDNA, and in dogs, SNPs in this region have been used to differentiate canine mtDNA into six major haplogroups (A, B, C, D, E, and F), which can be further subdivided into subhaplogroups. In our study, we performed Sanger sequencing of mtDNA CR in the Old Serbian Shepherd Dog and compared the obtained sequences with three other Balkan livestock guarding dog (LGD) breeds, the Karst Shepherd dog, the Šarplaninac and the Tornjak, as well as with LGDs from other geographical regions. The mtDNA haplotypes of seven Old Serbian Shepherd dogs were assigned to three canine mtDNA haplotype clusters, four haplotypes in cluster A, two in cluster B, and one in cluster C. This corresponds to the mtDNA haplotype distribution in Šarplaninac and Tornjak, indicating a similar matrilineal gene pool for all three breeds.

Keywords: *Old Serbian Shepherd, mitochondrial DNA, phylogeny, livestock guarding dog*

THE EFFECT OF INBREEDING ON MILK PRODUCTION IN CZECH HOLSTEIN CATTLE

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ABSTRACT: Breeding programmes for dairy cows focus on improving milk production traits and are characterised by intensive use of a relatively small number of elite bulls, resulting in higher levels of inbreeding and inbreeding depression. The aim of this study was to evaluate the effect of inbreeding (per 1% increase) on milk (MY), protein (PY) and fat (FY) yield in the Czech population of Holstein cattle. Our Bayesian approach to statistical animal models included 4749 genotyped cows (effectively providing information on > 40,000 SNPs) with records of milk production in the first lactation. Several different models, depending on pedigree (F_{PED} related to pedigree with complete generation equivalent of 12.5) or ROH-based genomic (ROH>4Mb or ROH>8MB) inbreeding coefficients (covariates), were applied. All values in the high posterior density interval (99%HDI) were negative for the MY estimates, with mean genomic inbreeding depression estimates (expressed per 1% increase in inbreeding coefficient) higher than pedigree estimates, $bF_{ROH>4Mb}$=-30.0 (99%HDI from -36.3 to -23.3) and $bF_{ROH>8Mb}$=-34.4 (99%HDI from -40.5 to -28.2) versus bF_{PED}=-13.2 (99%HDI from -16.8 to -9.6). Negative mean estimates of inbreeding depression were obtained in all models, with only one exception (MY estimates for F_{ROH} > 8Mb) with respect to PY (bF_{PED}=-0.8, $bF_{ROH>4Mb}$=-0.9, $bF_{ROH>8Mb}$=-0.9) and FY (bF_{PED}=-0.7, $bF_{ROH>4Mb}$=-0.1, $bF_{ROH>8Mb}$=0.0), although positive estimates were observed even at an HDI of 95%, which could be the consequence of the low statistical power of the analyses performed. Therefore, the presented results should be confirmed using a larger and more informative data set.

Keywords: *dairy cattle, inbreeding depression, milk production traits, pedigree inbreeding coefficient, runs of homozygosity*

Acknowledgements: This study was supported by the ANAGRAMS-IP-2018-01-8708, ALGSEQ18-IP-2018-01-7317, Project No. QK1810253 and Project No. LTAUSA19117.

GENOMIC ANALYSIS OF CROATIAN GOATS

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ABSTRACT: Native goat breeds in Croatia are considered as an important component of regional biodiversity and are important for the preservation of cultural and traditional heritage. The loss of their genetic diversity could have significant economic, environmental, scientific and social consequences. The aim of this study was to analyse the genetic diversity and conservation status of two native Croatian goat breeds, the Croatian Coloured goat and the Istrian Goat, using genome-wide SNP data. The two breeds are geographically separated, the Istrian goat lives in the Istrian peninsula and the Croatian Coloured goat lives in the area of southern Velebit, Dinara, Kamešnica and Biokovo. Population structure and conversation status were analysed based on 11 Istrian goats and 33 Croatian Coloured goats, as well as an additional 19 breeds of goats and the wild relative Iranian bezoar. The mean observed heterozygosity for the Istrian goat and the Croatian coloured goat was 0.39 and 0.40, respectively. Nei genetic distance with Neighbour-Net graph and PCA were used to reveal population relationships. Istrian goat and Croatian Coloured goat showed that they are two separate breeds. Each of the Croatian native goat breed cluster with different European goat breed. The effective population size calculated with GONE was 5 and 119 and inbreeding level was 0.06 and 0.04, for Istrian and Croatian coloured goat respectively. Despite the lower population size, the two breeds still have relatively high genetic diversity and have potential for a conservation plan in the future.

IS *M. LONGISSIMUS THORACIS* COLOUR CONNECTED WITH OTHER TRAITS UNDER SELECTION?

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ABSTRACT: Colour is considered one of the most important characteristics of beef quality. It is a factor that prevails at the point of sale, while other factors are of lesser importance. Meat colour has medium heritability, so it can be used as a selection criterion. It is also known that meat quality may be negatively correlated with some other traits under selection. The objective of this preliminary study was to analyse the correlations between estimated breeding values (EBVs) for colour parameters (L-lightness, a-redness, b-yellowness) and selected traits of conformation and production in 455 Simmental bulls. EBVs were obtained from the 2021 routine genetic evaluation of Simmental cattle. Lightness was negatively correlated to yellowness (0.30), index of daily gain and carcass traits (0.22), and conformation index (0.13). Redness was positively correlated to lightness (0.55), yellowness (0.50), milk yield (0.20), pH24 (0.19), and rump height (0.11). It was negatively correlated to M. longissimus thoracis area (0.71), conformation index (0.30), and index of daily gain and carcass traits (0.29). Yellowness was positively correlated with milk yield (0.26), pH24 (0.25), rump height (0.19), and negatively correlated to M. longissimus thoracis area (0.70), conformation index (0.18), and index of daily gain and carcass traits (0.11). The results indicate that there is a relationship between meat colour and other economically important traits that should be considered in breeding and selection for high quality beef from Simmental cattle.

Keywords: *cattle, Simmental, carcass and meat quality traits, breeding objectives*

ANALYSIS OF THE GENETIC STRUCTURE OF SLOVAK HOLSTEIN CATTLE USING GENES ASSOCIATED WITH NUTRITIONAL VALUE AND TECHNOLOGICAL PROPERTIES OF MILK

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ABSTRACT: Milk is an important component of a person's diet and its composition and milk yield substantially impact the economics of dairy farms. The basic precondition for livestock breeding is genetic variability, which is commonly used in the identification of individual animals and in selection to improve performance. This report aims at proposing a rapid detection method for genes affecting the nutritional value and technological properties of bovine milk (FADS1, FADS2, FASN, SCD, DGAT1, CSN2 and CSN3) and to analyze Slovak Holstein cattle to widen knowledge on their genetic structure for these candidate genes. Genotyping was performed by the PCR/RFLP and ACRS-PCR methods. Heterozygosity is an important factor for estimating the genetic variability in domestic animals and represents the genetic potential and adaptation abilities to the natural environment. In our study, Holstein cattle showed high heterozygosity values for markers FADS1-07 and CSN2. In contrast, it showed high homozygosity values for markers FADS1-01, FADS2-23, FASN-16024, SCD-T878C, DGAT1-K232A and CSN3. These results suggest that the genetic diversity for the FADS1-01, FADS2-23, FASN-16024, SCD-T878C, DGAT1 and CSN3 markers is reduced, which may be due to breeding effects.

Keywords: *genetic structure, heterozygosity, milk, Holstein cattle*

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GENETIC AND SURVIVAL ANALYSIS OF SURVIVAL TIME OF LOCAL CHICKEN ECOTYPES NAÏVELY CHALLENGED WITH NEWCASTLE DISEASE IN GHANA

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ABSTRACT: Newcastle disease poses a global threat to domestic poultry in low-income countries, where the loss of entire backyard local flocks threatens household food security and income. Thus, improving the survival time of chickens to Newcastle disease together with vaccination is a feasible way of improving poultry production. To investigate the genetics underlying the survival time of local chickens infected with Newcastle disease virus (NDV), three Ghanaian chicken ecotypes were challenged with velogenic NDV at 28 days of age. Estimating genetic parameters was done using survival and a linear model resulting in a heritability of 0.12 for the linear model and somewhat higher heritability of 0.20 for the survival model. Low to moderate genetic correlations between survival time and other traits of disease resilience were observed. Nine suggestive QTL associated with survival time were identified, including QTL previously reported to be associated with NDV viral load. Considering the low to moderate heritability and the trend of genetic correlations between survival time and other traits of disease resilience, we suggest that the survival time of chickens infected with NDV could be improved through selective breeding to enhance vaccination response leading to the production of Ghanaian chickens that are resilient to NDV.

Keywords: *survival model, linear model, heritability, QTL, genetic correlation*

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Session: Animal Nutrition

EEFECT OF DIETARY OLIVE LEAVES AND PULP ON OXIDATIVE STATUS IN BROILER CHICKENS

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ABSTRACT: Olive oil production generates various by-products, such as olive leaves and olive pulp, which can be used in animal nutrition. The aim of the present study was to investigate the effects of olive leaves and pulp on the oxidative status and fatty acid composition of broiler breast meat. One hundred and twenty day old Ross 308 male broilers were randomly divided into 5 experimental groups and fed without (Cont) or with 5% or 10% supplementation of olive leaves or pulp. Blood and breast muscle samples were collected at the end of the experiment. The results showed that supplementation had no effect on the concentration of liver enzymes, malondialdehyde (MDA) and antioxidant capacity of lipid soluble compounds (ACL) in the blood. However, supplementation with 5% olive pulp and 10% olive leaves resulted in lower antioxidant capacity of water-soluble compounds (ACW) in serum of broilers. The addition of 10% of leaves decreased the concentration of α-tocopherol in the breast muscle. Supplementation with different concentrations of leaves and pulp also affected the fatty acid (FA) composition of the muscle. In conclusion, supplementation of broiler diets with up to 5% olive leaves or pulp had no negative effects on the oxidative status of broilers.

Keywords: *broilers, olive leaves, olive pulp, oxidative status, fatty acids*

Acknowledgements: This work was financially supported by a grant from the Slovenian Research Agency and Ministry of Agriculture, Forestry and Food, Slovenia.

DOSE-DEPENDENT EFFECTS OF THE DIETARY FUMONISIN B SERIES ON THE LIVER MEMBRANE LIPIDS OF WEANED PIGLETS

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ABSTRACT: Fumonisin B series (FBs: FB1+FB2+FB3) disrupts sphingolipids and biological membranes of rats in a dose-dependent manner; however, less data is available on other species. 18 weaned Danbred-male piglets (n= 6 individuals) were orally fed FBs-free diet, 15, and 30 mg FBs/kg diet for 21 days. At the end of the trial, growth characteristics were evaluated and livers were sampled for analysis; fatty acid (FA) composition of membrane lipids, lipid peroxidation status, and histopathological assessment. A univariate analysis with an LSD "post hoc" test was performed, whilst a p-value < 0.05 was set as the significant level. Results revealed no marked alteration in growth traits or oxidative stress markers, although hepato-lesional score increased with FBs-intoxication. Minor linear dose-responses were detected in the phosphatidylcholine (increased C16:1n7, C18:1n9, and total monounsaturation), whereas no dose-response was found in other membrane-lipid fractions. However, slight alterations related to FBs-exposure were noticed in sphingomyelin [C12:0 (↑), C20:0 (↓), C22:0 (↑)], phosphatidylethanolamine [increased total omega-3], phosphatidylserine [C12:0 (↑), C20:1n9 (↓), C24:1n9 (↑)], and phosphatidylinositol [decreased C24:1n9 and total omega-3 FAs, whereas the omega-6:omega-3 ratio increased]. In conclusion, perturbations in the liver membrane lipids indicate alterations in desaturases to promote membrane rigidity, perhaps a defense mechanism that limits lipid peroxidation.

Keywords: *Mycotoxins, Fumonisin B series, Swine, Liver, Fatty acid*

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DIETARY SUPPLEMENTATION WITH OLIVE POLYPHENOLS IN RAINBOW TROUT: EFFECTS ON GROWTH AND FILLET QUALITY

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ABSTRACT: Based on its expected antioxidant properties, the present study evaluated the effects of the supplementation with a polyphenol-rich extract from olive oil vegetation water on growth traits and fillet quality at 1, 6, and 13 d of storage in rainbow trout (*Oncorhynchus mykiss*). A total of 480 specimens (initial live weight 95 ± 6.0 g) were randomly distributed into 16 flow-through tanks (4 tanks per treatment; 30 fish per tank) and fed during three months with four isonitrogenous (crude protein: 48.6%) and isolipidic (crude lipid: 14.8%) diets which included increasing levels of polyphenol extract: 0, 200, 400, and 600 mg/kg. The supplementation with polyphenols did not affect the specific growth rate (on average 0.91%/d) and feed conversion ratio (1.40) of trout or the condition (1.00) and viscerosomatic (6.57%) indexes or the fillet yield (56.5%) and quality. Fillet traits changed from 1 to 13 d of storage as pH (+1.40%) and lightness (+5.85%) increased along with total volatile basic nitrogen (+20.9%), and lipid peroxidation (TBARS: +559%) ($P<0.001$). Overall, the dietary inclusion of the tested polyphenol extract up to 600 mg/kg neither affected trout growth nor improved fillet quality and shelf life.

Keywords: *olive oil vegetation water, antioxidants, growth performance, fillet quality*

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LIGNOCELLULOSE ROLL ON PERFORMANCE, ANIMAL HEALTH AND WELFARE IN MODERN MONOGASTRIC FEED FORMULATION

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ABSTRACT: In modern monogastric feed formulas like pig, poultry and rabbit formulas the fiber level has reached a great use of potential. Fiber became an important nutrient contributing to animal health, performance and welfare. Especially since the official date of ban of Zinc Oxide in EU (June 2022) there is an even growing need for structural fiber sources. A major concern when including fiber, is that high fiber diets are associated with dilution effect in energy and reduced digestibility of the feed. That kind of negative attributes are determined by the inclusion rate and the fibrous characteristics of individual feed components or by products sourced from grain milling, sugar, ethanol and oil production. Arbocel® as a unique fiber source was created with a fibrous network structure thanks to a modern state of art milling the so called High Pressure Centrifugal (HPC) fibrillation Technology, unlocks the maximum water binding capacity of the crude fibre concentrate. This pure water binding fiber structure gives a great benefit to the performance of the animal. In this review is going to be taken under focus: how the structure of a non-fermentable and insoluble fiber can raise the performance and digestibility of nutrients at diverse monogastric spices, how it support the growth of the microvilli, the enzymatic penetration and the good bacteria production.

Keywords: *fiber, digestibility, animal health, microflora, microvilli*

EFFECT OF GRAPE POMACE INTAKE ON THE RUMEN BACTERIAL COMMUNITY OF SHEEP

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ABSTRACT: The performance of ruminants is affected mainly by the rumen bacterial community. Composition and properties of rumen bacterial community depends largely on the diet components, which are fed to ruminant. Therefore, the aim of this study was to determine the effect of grape pomace intake on the rumen bacterial community of sheep. Four different diets of which two contained dried grape pomace (DGP) were used in this study. Rumen fluid samples of 12 wethers for 16S rRNA gene sequencing and bacterial identification were used. Rumen fluid was sampled after the end of feeding each of four different diets. From phylum, *Bacteroidetes* and *Firmicutes*, from family *Prevotellaceae* and *Porphyromonadaeceae* and from genera *Prevotella* and *Verrucomicrobia _Subdivision5_genera_incertae_sedis* were most abundant regardless on sampling timepoint. After addition of DGP to the diet, the relative abundance of *Methanobrevibacter*, *Butytirivibrio*, *Fretibacterium* and *Verrucomicrobia _Subdivision3_genera_incertae_sedis* significantly increased, whereas *Succiniclasticum* and *Selenomonas* significantly decreased. The up-regulated pathway of methanogenesis from H_2 and CO_2 is supported with significant increase of *Methanobacteriaceae* after the diet supplementation by DGP. Rumen bacterial community diversity indices (Richness and Shannon) were significantly affected by diet composition. Results of this study shows significant effect of diet composition as well as diet supplementation by DGP on the abundance of some rumen bacteria and on the diversity indices. In addition, diet supplemented with DGP revealed higher activity of methanogenesis pathway in rumen.

Keywords: *wine industry by-products, rumen bacteria, abundance, diversity*

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THE CHANGE OF MICROBIAL DIVERSITY AND MYCOTOXINS CONCENTRATION IN CORN SILAGE AFTER ADDITION OF SILAGE ADDITIVES

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ABSTRACT: In our study presence of bacteria, yeast and microscopic fungi were evaluated. Three forms of corn silage were made including silage without additive, silage with microbial additive and silage with nutritional additive (urea). Silage additives were applied to the matter within the recommended dosage, then the matter was ensiled into plastic bags and stored at a constant temperature. After 5.5 month of storage, average samples for microbial and mycotoxins analysis were taken. From microbiological points plate count agar method for enumeration of total count of bacteria, lactic acid bacteria, enterococci, yeasts, and microscopic fungi and mass spectrometry for microbiota identification were used. Total 43 species of bacteria and yeasts and 6 genera of microscopic fungi were identified from all samples of corn silages. The most isolated species were *Lentilactobacillus buchneri* and *Kazachstania exigua* from bacteria resp. yeasts and *Aspergillus* and *Penicillium* from microscopic fungi. Mycotoxins were determined by HPLC-MS/MS and divided into two groups as regulated and emerging. All corn silages regardless of the addition of the additive were the highest in nivalenol content. Deoxynivalenol and beauvericin with the highest concentrations were present in silage with urea. Although the mycotoxins content of the variants changed, these changes were not statistically significant.

Keywords: *diversity; microbiota; mycotoxin; microbial additive; urea; corn silage*

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Poster Session: Animal Nutrition

EFFECTS OF LOW PROTEIN DIETS AND PROBIOTIC SUPPLEMENTATION ON GUT HEALTH PARAMETERS OF BROILER CHICKENS

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ABSTRACT: The benefits of using reduced crude protein diets and probiotics are well known in the broiler industry. However, the combined effects of these two factors have been hardly addressed so far. Therefore, the interaction between the effects of dietary low protein and a probiotic supplement (*Bacillus amyloliquefaciens* CECT 5940; 500 mg/kg feed) on some gut health parameters of broiler chickens was investigated in the present study. A total of 576 male Ross 308 broilers at 10 days of age were assigned to four dietary treatments (in 6 replicates (pens) per treatment, with 24 birds per pen): control diet with standard crude protein level, low protein diet, probiotic supplemented control and low protein diets. The Eimeria lesion scores were not influenced by the dietary treatments according to the examination of gut health status performed at day 29. Dietary probiotic supplementation significantly reduced the gas production (ballooning) and the presence of inflamed Peyer's patches in the small intestine ($P<0.05$). Besides, the occurrence of the symptom of thin intestinal wall was decreased by feeding the low protein diet ($P<0.05$). A significant interaction between the effects of dietary low protein and probiotic supplementation was not observed in the study.

Keywords: *broiler, nutrition, gut health, probiotic, low protein*

EFFECTS OF HEAT STRESS AND HIGH DIETARY ANTIOXIDANT SUPPLEMENTATION ON THE ILEAL DIGESTIBILITY OF NUTRIENTS AND CERTAIN MINERALS IN PIGS

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ABSTRACT: Heat stress (HS) can impair the pigs' intestinal integrity, jeopardizing their nutrient and mineral digestibility. Our study aim was to investigate HSs' impact on the ileal digestibility of nutrients and minerals in pigs and whether high dietary antioxidant (vitamins C, E, and micro-minerals Se, Zn) supplementation can improve their digestibility. Twenty-four Danbred barrows (65.1 ± 2.81kg) were distributed into four groups and placed in individual digestibility cages under thermo-neutral (TN) (19.5 ± 0.9°C) or HS (28.9 ± 0.9°C) room condition and fed with their respective dietary treatment (TN + control feed (TC); HS + control feed (HC); HS + elevated level dietary antioxidants (HT1); and HS + double elevated level of dietary antioxidants (HT2). Diets and ileal digesta were analysed for crude protein (CP), fat, fiber, ash, organic matter, NFE and minerals (Ca, P, Zn, Se, and Na). HS did not significantly affect the ileal digestibility of nutrients and minerals ($P > 0.05$). However, pigs on the HT1 treatment had significantly greater digestibility ($P < 0.05$) of CP, crude ash, Zn, Se, and Na than those on HC treatment. In conclusion, high genetic potential pigs can be resilient to HS adverse effects on the parameters studied. A high dietary antioxidant-fortified diet could improve pigs' nutrient and mineral digestibility under the HS challenge.

Keywords: *Heat stress, dietary antioxidants, ileal digestibility, fattening pigs*

Acknowledgements: This research was funded by the European Union and the European Social Fund, grant number EFOP-362-16-2017-00001.

INFLUENCE OF MULTICOMPONENT TRANSITION DRENCH ON RUMEN FERMENTATION PARAMETERS OF COWS

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ABSTRACT: Background: Calcium and energy precursors have been used for several years for prevention of metabolic disorders in cows during the early lactation period. However, little information is available regarding the impact of drench supplement on rumen fermentation. Method: 3 non-lactating, rumen fistulated Holstein cows were used to study the effect of a multicomponent drench supplement with low (500 g/cow/day) and high doses (1000 g/cow/day) on some parameters of rumen fermentation. Drench materials were dissolved in warm water, control treatment consisted of only warm water. Before the morning feeding, and then 3 and 6 hours after that, 150 ml of rumen fluid was collected and pH, SCFA and ammonia concentrations were measured. Results: The drench supplement had an effect on the fermentation activity of the rumen microbial population, its elevated dose increased ($p<0.05$) and kept stable the pH value of the rumen fluid until 6 hours after drenching. The concentration of ammonia, the molar concentration of ketogenic SCFAs and the production of acetic acid increased ($p<0.05$) due to the protein-poor, fiber-rich feed and the intensive microbial activity. Conclusion: The results of the rumen fermentation study should be evaluated under operating conditions in addition to the concentrate rich feeding in postpartum period.

Keywords: *supplement, cannula, drench, ca-propionate*

EVALUATION OF EARLY L-THREONINE SUPPLEMENTATION ON PERFORMANCE OF BROILERS

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ABSTRACT: Practically, there can often be a 36-72-hour delay between broiler hatching and installation, during which time the day-olds have no access to solid feed. Therefore, research has led to the development of early feeding methods including *in ovo* feeding. Threonine (Thr) by literature, supports gut tissue development thus may improve broiler performance if provided few days before or after hatch when morphological changes of the intestine are very intensive. We examined the effect of early Thr supplementation such as *in ovo* at 17th day of incubation or as Thr fortified hydrogel provided post-hatch in the transport box while the birds had 48h delayed access to solid feed. The control group were immediately fed with solid feed and the growth performance (body weight and feed intake) was measured during the trial. Our results demonstrate that the low performance due to 48h delayed feed access could not be compensated by early Thr supplementation.

Keywords: *In-ovo, L-Threonine, hydrogel, broiler, growth*

Acknowledgements: The research is greatly acknowledge to GINOP-2.2.1-18-2020-00031

FEEDING CORN- OR WHEAT-BASED DIETS IMPACTS ON PERFORORMANCE PARAMETERS AND THE CAECAL MICROBIOTA COMPOSITION OF BROILER CHICKENS

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ABSTRACT: In this study, the effects of feeding corn or wheat-based diets was investigated on the performance parameters and caecal microbiota composition of Ross 308 broiler chickens. In total, 192 male one-day-old Ross 308 broiler chickens were divided into two dietary treatment groups using six replicate pens of 24 chickens. Beside a corn-soybean based control diet (C) a wheat and wheat bran containing diets (W) were fed. At day 40, two chickens per pen were slaughtered and caecal chymus samples were collected for the determination of microbiota composition with 16S rRNA gene targeted Illumina MiSeq sequencing. Wheat-based diets resulted significantly higher growth rate (2509g vs. 2354g) and lower feed conversion ratio (1.43kg/kg vs. 1.58kg/kg) compared with the control diet. Relative abundance of phylum *Lentisphaerae* was significantly higher ($p < 0.009$, $q < 0.086$) in the case of treatment W (11.8%) compared to the control group (6.8%). The genera of this phylum produce transparent exopolymers, which form from dissolved polysaccharides. Furthermore, this phylum includes members that are importance in the carbon and nitrogen cycle in the caecal content. Our results suggest that differences in the microbiota composition could at least partly responsible for the improved production traits when wheat-based diets are fed.

Keywords: *wheat-based diet, wheat bran, broiler chicken, gut microbiota composition, Lentisphaerae*

Acknowledgements: This research was supported by the Hungarian Government and the European Union, with the co-funding of the European Regional Development Fund in the frame of Széchenyi 2020 Programme GINOP-2.3.2-15-2016-00054 project.

NATURAL ANTIOXIDANTS IN POULTRY PRODUCTS

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ABSTRACT: The human population is projected to be around 10 billion people by 2050. This will result in an increase in total global food demand of 35% to 56% between 2010 and 2050. Therefore, food producers' main goal should be to increase the yield and quality of food products. Consumer income fluctuations can effect changes in diet and the types of food purchased. The use of natural antioxidants may satisfy the growing interest of poultry consumers, on the condition that they prove to be safe and effective. In numerous studies in the food science area, there is a trend toward utilizing natural antioxidants as replacements for synthetic ones. The aim of this study is to provide a review of recent studies which describe the use of natural antioxidants in poultry meat production and their effect on final product quality. The collected data show that natural antioxidants are crucial food additives that could affect the extended shelf life of food, including poultry meat products, and maintain optimal product quality.

Keywords: *natural antioxidants, quality of poultry products, food demand*

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THE EFFECTS OF T-2 TOXIN AND ZEARALENONE ON THE EMBRYONIC DEVELOPMENT OF CHICKEN

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ABSTRACT: The production of good quality food is one of the most critical aspects of animal husbandry. However, mould infection is a growing global problem in grain production. In our experiments, we examined the effects of T-2 toxin and zearalenone in developing Partridge colour Hungarian chicken embryos. We incubated the eggs for three days. After three days of incubation, we injected the embryos with T-2 toxin in 1ng/µl, 8ng/µl, zearalenone in 5ng/µl and 10 ng/µl, and a combination of the 2 toxins in 2.5ng/µl T-2 with 20 ng/µl zearalenone, 5-10 ng/µl and 5-20 ng/µl concentration. We incubated the eggs further to ten days of age, dissected the embryos and took egg white, yolk, liver, and gonad samples. After the toxin treatment in the 8ng/µl concentration treatment group with T-2 toxin, only 52.6% of the embryos were alive, and with the combined toxin treatment of 5-10 ng/µl, only 50% of the embryos survived the treatment. We could also confirm the presence of T-2 and Zearalenone with ELISA test in the yolk, and we could detect T-2 toxin with immunstaining in the gonads of the embryos. Our results show T-2 toxin is highly detrimental in embryonic development.

Keywords: *mycotoxin, chicken embryo, gonad*

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CONTRIBUTION OF FEED SOURCE ON ENVIRONMENTAL IMPACT OF PIG PRODUCTION

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ABSTRACT: Feed source for fattening pigs has major environmental impacts. In the last years world is struggling with food insecurity due to the complex and long supply chain legs, often consisting of cross-continent or international suppliers. The dependance on imports of raw materials increased environmental impacts and costs of animal production and uncertainty for both farmers and end-users. Soyabean meal is the main protein source for the pig, however most of it is imported from South America. In this study, we compare the environmental impacts of pig diets based on locally produced and imported protein sources. Trough life cycle assessment (LCA) we analyzed the differences of three commercial complete pig diets including diet based on imported soyabean meal (1), diet based on locally produced soyabean meal (2), and diet based on locally produced sunflower meal after hydrothermal processing (3). Diets based on locally produced protein source have a lower environmental impact compared to diet with an imported protein source. In addition, hydrothermally processed sunflower meal could be a good source of protein for pig with a lower environmental impact that mainly depends on the cost of energy sources, gas and electricity.

Keywords: *Enviromental impact, pig, feed source, LCA*

INFLUENCE OF *IN-OVO* INJECTION OF METHIONINE ON THE HISTOMORPHOMETRIC ANALYSIS OF JEJUNUM IN LAYER GENOTYPES NEWLY HATCHED CHICKS

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ABSTRACT: The development and maturity of the intestine has a significant impact on the performance of poultry at all stages. In-ovo feeding has been shown to improve the broiler chicks' performance by increasing the absorption of nutrients. However, there is scant information on the influence of *in-ovo* feeding of methionine sources on the jejunum development of TETRA-SL and Hungarian partridge coloured chicks; hence the aim of this study. A total of 120 Tetra SL and 80 Hungarian partridge coloured hen's eggs were used for *in-ovo* treatments. The eggs were candled on the 10th day, and non-fertile eggs were removed. On the 17th day of incubation, eggs were allotted randomly to four *in-ovo* treatments: non injected (N); saline solution (S) injected (0,5 ml); 5 mg DL-Met, or L-Met injected (in 0,5 ml of saline solution) for both genotypes. DL-Met injection facilitated the intestinal development by increasing the villus height, villus width, and villus height/crypt ratio while decreasing the crypt depth in the jejunum of one day old chicks of TETRA-SL and Hungarian partridge coloured hens when compared with the non-injected group ($P < 0.05$). The genotype influence was observed in villus width and villus surface area only ($P< 0.05$). The interaction of methionine sources and the genotype was significant in all parameters measured except for crypt depth and height/crypt ratio ($P < 0.05$). In-ovo feeding of methionine sources influenced the intestinal development and the genotype effect was evident.

Keywords: *In-ovo injection, methionine, layer genotype, intestine, histology*

DEAD ON ARRIVAL (DOA) IN PIGS: A FIVE-YEAR DATA COLLECTION IN ITALIAN SLAUGHTERHOUSES

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ABSTRACT: DOA recorded at slaughterhouses is considered a good iceberg indicator for the welfare of pigs. This study aimed at documenting official data on the mortality related to the transport of pigs for slaughter in Italy from 2016 to 2021. The data were retrieved from the official website of the Italian Ministry of Health. The average DOA and the yearly mortality rate were 5,682 pigs/year and 0.043%, respectively. The mortality rate of the latest two years (i.e. 2020-2021) was higher than the previous ones ($p<0.01$) probably due to the increased accuracy in data recording. The months with the highest DOA were July, August, and September (0.055%; $p<0.01$) confirming that heat stress is one of the major risk factors for mortality during transport. Even if approximately 80% of total DOA were heavy pigs, this category reported the lowest mortality rate (0.037%). Intermediate values of mortality were indeed recorded for sows (0.087%) while the highest one was found for growing pigs weighing 25-50 kg (0.256%). This could be due to the fact that those animals had been excluded from breeding or fattening due to poor physical conditions. Official accurate monitoring of DOA at the slaughterhouse could help identify risk factors for transport-related welfare.

FEED PREFERENCE AND FEEDING BEHAVIOUR OF DIFFERENT MOUSE SPECIES IN LABORATORY HOUSING MODELLING SMALL DOMESTICATED MAMMALS

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ABSTRACT: The feed preference of two species of wild mice, the house mouse (*Mus musculus*), and the mound-building mouse (*Mus spicilegus*) was investigated kept in our laboratory for 25 generations. Our interest focused on the feed preference (i.e. if the mice chose the type of feed closest to their natural food). The analytical composition of the two granulated feeds differed minimally; the crude fat and crude fibre content of the natural feed mixture was higher, and only this feed contained insect protein. Based on the obtained results, both wild mice approached for the natural feed mixture more frequently than the two other granulated feeds. The same tendency was observed for the feed consumption where the animals mostly consumed the natural feed mixture. During the 5-day long study, the consumption of the natural feed mixture increased continuously, while the consumption of the granulated laboratory feed significantly decreased. The average feed consumption was also influenced by temperature but the difference between the feed consumption in the two temperature altered significantly for the examined species. The reported differences could be explained with the characteristics of their original habitat. Our studies can help develop the indoor keeping and breeding of small domesticated mammals.

CHANGES IN THE PROPORTION OF EGGS LAID IN THE NEST AND IN THE LITTER IN AN INDOOR ALTERNATIVE HOUSING SYSTEM IN THE CASE OF PUREBRED HEN LINES DURING 12 MONTHS OF PRODUCTION (PRELIMINARY RESULTS)

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ABSTRACT: The research was conducted with laying hens of two genotypes provided by Bábolna TETRA Ltd. [pure-line maternal offspring group (Maternal); pure-line paternal offspring group (Paternal)]. N = 212; n = 106 hen/genotype; 53 hen/pen. 14 nests with artificial grass were provided on two levels per pen (3.8 hens/nest). We recorded separately the number of eggs laid in the nests on the lower and upper levels, as well as in the litter. Based on the results, we found a significant difference between the tested genotypes in the total number of litter eggs during the 12 months of production (Paternal: 41.1%; Maternal: 10.2%; $p < 0.05$). In the case of the Paternal genotype, even in the first month of production, the proportion of eggs laid in the litter was high (75.8%). In contrast the Maternal genotype laid only the 20.8% of the eggs there. A significant difference was obtained between the two genotypes in the proportions of eggs laid at the lower (L) and upper (U) level during the 12 months of production (Paternal: L: 88.0%, U: 12.0%; Maternal: L: 71.4%, U: 28.6%; $p < 0.05$). During the time spent in production, the proportion of eggs laid in the litter gradually decreased for all three genotypes, according to our conclusions, because the laying hens learned to use the egg nests over time and got used to them.

Keywords: *laying hen, non-caged, production, litter eggs, behaviour*

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FEATHER CONDITIONS AND INJURIES OBSERVED ON CERTAIN BODY PARTS OF LAYER HYBRIDS AND PUREBRED HEN LINES IN THREE WAY OF HOUSING

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ABSTRACT: The aim of this study was to obtain data on the effect of different way of housing on the change of the plumage of hybrids and purebred hen lines during the production. At the MATE Kaposvár Test Site, three different genotypes from Bábolna TETRA Ltd. [Commercial hybrid; maternal and paternal pure-line offspring] were investigated. The non-beak-trimmed layers, were placed in the intensive poultry house at 19 weeks of age. Three different housing way (furnished cage, conventional cage, alternative compartment) were located in one room. The status of the plumage was examined at 30, 60, 72 weeks of age. The plumage condition was rated on nine main body parts based on a reference table. By summing up the plumage points of the different body parts, a total plumage point was calculated for each hen, which could vary between 9-36. The obtained results confirmed that the condition of the plumage deteriorates with advancing age, and the feather wears out. In all cases, the alternative pen produced the best (31.99-35.73 point) while the traditional cage housing the worst (28.85-35.44 point) results. It was statistically proven that there were significantly fewer feather injuries in the alternative housing than in the two cage systems.

Keywords: *hen, non-beak-trimming, plumage, housing system*

Acknowledgements: This research was supported by the ’2018-1.3.1-VKE-2018-00042’ and the ‘EFOP-3.6.3-VEKOP-16-2017-00008’ project, funded by the Hungarian Government. The genotypes required for the research were provided by Bábolna TETRA Ltd.

ESTIMATION OF TEMPERAMENT OF DAIRY COWS BY RESPONSE TO A NOVEL OBJECT

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ABSTRACT: The presented study aims to design on-farm test temperament for dairy cattle due to the individual differences in behavior during approaching the novel object - a red cycling light in 11 m distance. Behavior traits (duration of walking and standing) with numeric modifiers (distance of 1st stop and number of stops) were analyzed from the video records. Individual differences in the behavior were evaluated by differences in duration of approaching the novel object. A group of 53 tested cows was split into 4 distinctive clusters by duration of approaching (DA). Cluster 1 with 28 members of calm temperament, voluntary approaching novel object, mean DA was 23 s ± 41. Cluster 2 with 14 members of curious temperament, voluntary approaching was recorded in 8 of them, mean DA was 52 s ± 71. Cluster 3 with 9 members of vigilant temperament, mean DA was 98 s ± 128. Cluster 4 with 2 members of fearful temperament, mean DA was 250 s ± 312. Results showed the possibility of on-farm temperament type measure by simple test. Testing discovered inappropriate type of temperament in 2 of tested dairy cows with higher risks of problem with habituation to novel objects or during manipulation.

Keywords: *dairy cattle, novel object, on-farm, temperament, test*

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LANDINGS AND CLIMBINGS OF PULLETS IN A CAGE FREE SYSTEM AT HOUSING: EFFECT OF GENOTYPE AND ENRICHMENT

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ABSTRACT: To evaluate the adaptability of hens at housing in a cage free system, 1800 pullets (17 weeks of age) were allocated in 8 pens of an aviary according to a tri-factorial arrangement with two genotypes (Hyline brown vs. Lohmann white) and two types of pens (enriched or not with additional perches). At 17 and 20 weeks of age, the number and rate of successful landings at ground and climbings to the aviary were scored (10 min/hour; 9.00 to 21.00). Unsuccessful movements were associated to collisions. The number (218 vs. 67.6) and the success rate (93.3% vs. 83.8%) of landings were higher in white vs. brown hens ($P<0.001$) and increased from 17 to 20 weeks (89.8 to 196, $P<0.001$; and 85.1% to 92.0%, $P<0.01$, respectively). Similarly, the number (177 vs. 21.6; $P<0.001$) and success rate (99.1% vs. 96.5%; $P<0.10$) of climbings were higher in white than brown hens and increased with age (58.4 to 141, $P<0.001$; 95.7% to 99.8%, $P=0.01$). The enrichment with additional perches did not affect landings or climbings. In conclusions, large differences in the movement activity were measured between genotypes, while the adaptation of hens to the aviary increased with age.

Keywords: *laying hens, perches, adaptability, movement, collisions*

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NON-GENETIC FACTORS AFFECTING UDDER HEALTH TRAITS IN MILK OF ITALIAN LOCAL CATTLE BREEDS

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ABSTRACT: No studies have been carried out on the new udder health trait differential somatic cell count (DSCC) in the Burlina and Alpine Grey local breeds so far. Milk DSCC represents the proportion (%) of polymorphonuclear neutrophils out of the total somatic cell count (SCC). The present study investigated the factors determining the phenotypic variability of SCC and DSCC in such breeds. Restrictions allowed outliers elimination and, finally, 4,355 test-day records from 257 Alpine Grey and 434 Burlina cows in 62 herds were available to estimate the least square means of udder health-related traits through a linear mixed model. The fixed effect of breed, parity (1, 2, 3 and ≥4), lactation stage (6 classes), and sampling season were considered together with the first-order interaction between breed and other fixed effect. The random effects were: cow, herd-test-date, and residual. DSCC was greater for Alpine Grey (66.20±0.77 %) compared to Burlina (63.70±0.70 %) and both SCC and DSCC tended to increase across lactation and parity regardless of the breed. In both breeds the greatest DSCC percentage was estimated in summer. Results suggest that the conventional DSCC threshold proposed for Holstein cows (65%) should be adjusted to better fit the udder health status of local breeds used for milk production.

Keywords: *Alpine Grey, Burlina, udder health, somatic cell count, differential somatic cell count*

Acknowledgements: The Breeders Association of Veneto Region (ARAV, Vicenza, Italy) is gratefully acknowledged for supporting the study.

PHYSICAL CHARACTERIZATION OF TEN VARIETIES OF HEMP TO USE AS ANIMAL BEDDING MATERIAL

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ABSTRACT: Hemp (*Cannabis sativa* L.) hurds, the inner bark of the stem, is a poorly appreciated part of the plant that typically represents a waste. The aim of this experiment was to describe the physical characteristics, such as moisture (M), water absorption (WA) and ammonia absorption (AA), of 10 hemp varieties (Fibranova, Codimono, USO31, CS, Futura 75, Eletta Campana, Carmaleonte, Felina 32, Santhica and Ferimon) cultivated in Italy along 2 years. Samples of hemp hurds were ground to 8mm obtaining hemp shives. The M, WA and AA values were determined following the official procedures. The results showed an average of 7.78%, 251.9% and 50.0% for M, WA and AA resp. The M values were similar among varieties and over the two years. A high variability of WA was observed among varieties, with the highest value for Felina 32 (317.9%) and the lowest value for Eletta Campana (211.4%). Furthermore, no differences were found between years for this parameter. The AA values ranged from 45.0% (Fibranova) to 55.5% (Ferimon), but were very similar in both years. In conclusion, hemp shives have similar physical characteristics to other commercial bedding materials, but on-farm trials will be required to have a full assessment.

Keywords: *hemp, animal bedding, water absorption, ammonia absorption*

Acknowledgements: This research was funded by a Ph.D. grant of Fondazione Cassa di Risparmio di Padova e Rovigo (CARIPARO) and by the project Produce hemp in the food and agro industrial chain-Veneto Region-Rural Development Programme (RDP) 2014-2020

CARCASS TRAITS OF BOVINE ANIMALS SLAUGHTERD IN SLOVENIA FROM 2009 TO 2021

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ABSTRACT: Meat production and especially beef and veal production is an important part of agricultural production in Slovenia. In the last decade, many structural changes in livestock production took place in Slovenian agriculture. In the present study, an analysis of cattle born and slaughtered in Slovenia in the last thirteen years was conducted. The total number of slaughtered animals increased from 110,515 in 2009 to 116,382 in 2021. The percentage of slaughtered Simmental and Brown breed animals decreased, while the percentage of Holstein animals increased. The structure of slaughtered animals by category remained relatively stable over the years, but differed significantly between breeds. In the Holstein breed, a higher percentage of animals were slaughtered as calves and older calves (39%), while in Simmental breed only 8% of animals were slaughtered as calves and older calves, and vice versa, with 38% of Simental and 21% of Holstein breed animals slaughtered in category of young bulls. The average carcass weight of young bulls increased from 351 kg to 359 kg from 2009 to 2021, the age at slaughter remained relatively constant, so the daily carcass gain increased slightly, and the carcass conformation slightly increased (0.4 subclasses), and the carcass fatness decreased (0.1 subclasses). In the calf category, even a relatively larger increase in carcass weight was observed (from 92 to 110 kg). At the same time, the slaughter age increased from 135 to 177 days, so the daily carcass gain decreased from 720 to 645 g/day. Carcass conformation also increased slightly and carcass fatness decreased. These changes also differed in the categories of young bulls and calves between the Simmental, Brown and Holstein breeds.

Keywords: *cattle, slaughter, carcass traits, Slovenia*

THE INFLUENCE OF ON-FARM RESTING TIME ON STRESS MARKERS AND SLAUGHTERING TRAITS OF CULLED SOWS

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ABSTRACT: The aim of the study was to investigate the effect of time spent on farm before slaughter on stress markers, as well as on fattening, carcass and meat quality traits of culled Large White x Landrace (LWxLD) sows. Twenty-four (24) sows were equally divided into three groups according to the duration of on-farm resting period: control group (no rest), 1st experimental group – EG1 (14 days rest) and 3rd experimental – EG2 (28 days rest). The duration of on-farm resting period had significant effect ($p<0.05$) on the levels of cortisol and all measured blood parameters with exception of glucose. As expected, the sows from EG2 group had the most favorable carcass traits due to the highest dressing percentage, carcass length, ham circumference and lean meat percentage in 4 dissected parts (ham, loins, shoulder and neck) when compared to EG1 and control group. On-farm resting time generally improved the meat quality of sows under investigation. The highest initial and pH values measured in s*emimembranosus* (SM) and *longissimus thoracis et lumborum* (LTL) muscle and the lowest drip loss, indicating dark-firm-dry (DFD) meat, were recorded in control group that had no on-farm rest. Statistically significant differences between the groups were found for color parameters CIE a* and CIE b*, both being the highest in 2nd group of sows. Although no effect of resting time could be observed for CIE L* values, darker meat (≤50) was detected in all groups. The results of present study show that on-farm resting can improve certain production traits of culled sows, such as meat quality and carcass composition, in the sense of increased production of lean meat with improved quality.

Keywords: *pigs/sows, on-farm resting time, stress indicators, carcass composition, meat quality*

Acknowledgements: This work was funded by QualSec research team of Faculty of Agrobiotechnical Sciences Osijek.

EFFECT OF ACORN FEEDING ON MEAT QUALITY AND EXPRESSION OF MYOSIN HEAVY CHAIN AND SOME ENERGY METABOLISM-RELATED GENES IN THE LONGISSIMUS DORSI MUSCLE OF TUROPOLJE PIGS

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ABSTRACT: The Turopolje pig (TP) is a fatty pig breed traditionally reared in an outdoor system linked to local oak forests and marsh meadows in Central Croatia. There is limited information on meat quality and skeletal muscle myofibers characteristics from TP, including the impact of locally available feed. Therefore, the present study investigated the meat quality and contractile/metabolic properties of longissimus dorsi muscle (MLD) from TP fed either conventional (C) or acorn-supplemented (A) finishing diets. The MLD quality traits (pH, color, drip loss, intramuscular fat (IMF), fatty acid (FA) profile) were determined by standard methods, and expression of selected genes related to myofiber contractile/metabolic properties by qPCR. The results showed no significant effects of acorn feeding on meat quality, and myofibers contractile phenotype determined by expression of myosin heavy chain (MyHC) isoforms, except for lower pH_{24} and higher saturated FA content (SFA) in group A. Among the genes related to metabolic phenotype, a 2-fold increase in the expression of FASN (FA synthase) was found in group A compared with group C. This is consistent with the higher saturation of IMF in acorn-fed pigs, thus suggesting an up-regulatory effect of acorns on SFA synthesis. GYS1 (glycogen synthase) also tended to be more strongly expressed under acorn supplementation, which is in line with the observed pH differences.

Keywords: *Turopolje pigs, acorn, meat quality, MyHCs, metabolic phenotype, qPCR*

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EXAMINATION OF BEHAVIOURAL PATTERNS OF LAYING HENS OF DIFFERENT GENOTYPES IN A PEN HOUSING SYSTEM WITH SCRATCHING AREA AND PLASTIC MESH FLOOR (PRELIMINARY RESULTS)

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ABSTRACT: The examination was carried out at the Poultry Farm of the MATE Kaposvár Campus with three genotypes of Bábolna TETRA Ltd. [Commercial hybrid (K); pure-line maternal offspring group (Maternal); pure-line paternal offspring group (Paternal)]. N=159; n=53 hen/genotype. We placed 53 19-week-old non beak trimmed hens in each of the 3 alternative pens (5.52 m^2). 1/3 of the base area was scratching area and 2/3 was plastic grid. Infrared camera was installed above the 3 pens, and 24-hour recordings were made (96 times/pen). In our results, the hens spent 60% of the light period resting, 20% scratching, and 7% eating. In the light period, all three genotypes were located on the scratching area in greater proportion than the plastic grid floor, while in the dark period the Commercial (90%) and Paternal (75-80%) genotypes preferred the plastic grid floor. The scratching activity of the maternal line varied between 10-20%, while that of the Commercial hybrids varied between 10-40%. A maximum of 4% of the hybrids, while up to 8% of the Maternal genotype dealt with the beak abrasive material at the same time. We found that the enrichment of the environment clearly defines the behavioural repertoire of the laying hens and ensures the possibility of expressing natural behaviour patterns.

Keywords: *laying hen, non-caged, behaviour, scratching area, plastic mesh*

Acknowledgements: This research was supported by the ’2018-1.3.1-VKE-2018-00042’ and the ‘EFOP-3.6.3-VEKOP-16-2017-00008’ project, funded by the Hungarian Government. The genotypes required for the research were provided by Bábolna TETRA Ltd.

MILKABILITY OF HOLSTAIN DAIRY COWS UNDER PRACTICAL CONDITIONS IN SLOVAKIA

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ABSTRACT: Milkability is one of the most important response to machine milking depending on many external and internal factors. Selection on milk production including nucleus herds and milking routine belong to this factors. Thus the aim of the study was to evaluate actual milkability of Holstein dairy cows bred in Slovakia and possible effect of bimodality. On four dairy farms using Lactocorder there were obtained data from randomly selected 334 cows with standard milking routine during evening milking. Milk yield, peak flow rate, time of milking and duration of milk flow phases were evaluate. Milk yield ranged from 11.02±3.88 kg (farm 4) to 16.17±5.45 kg per milking (farm 3) on selected farms. Peak flow rate ranged from 2.92±1.00 kg/min (farm 1) to 3.96±1.01 kg/min (farm 3), which correspond to the significantly longest milking time on farm 1 (8.37±2.09 min) and shortest on farm 3 (6.13±1.48 min). Bimodality of milk flow was significantly related to the reduced milk yield and milking time but increased peak flow rate in all farms. Increase phase was significantly longer, plateau phase shorter and descending phase did not changed in bimodal milk flows. In conclusion, milkability should be regularly evaluated at dairy farms especially to improve milking routine.

Keywords: *Holstein cows, milkability, bimodality*

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EFFECTS OF PHYSICAL AND SOCIAL STRESSORS ON SOME BLOOD BIOCHEMISTRY PARAMETERS OF COMMON ELAND (*TAUROTRAGUS ORYX*)

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ABSTRACT: The gradual transition of some wild antelopes such as common eland (*Taurotragus oryx*) to domestication is necessitating a more comprehensive understanding of their welfare and management. The present study was conducted for 12 months using 12 growing calves (135.1±2.25kg body weight; ≈ 9 month; females n=6 and males n=6), aimed at examining the effect of physical and social stressors (short and long-term stressors) on the blood biochemistry profile of eland. The research animals were routinely handled once per month during which their temperament was scored. Afterward, they were driven to the barn where their social interaction was observed and analysed for dominance and linearity. The blood chemistry parameters served as markers for stress and were analysed using standard VetTest chemistry protocols. A generalized linear mixed model was designed to test the effect of temperament and social hierarchy on the blood chemistry parameters while considering age, body weight, body condition score as covariates. The outcome shows that the blood chemistry profiles were not influenced by long term stressors except for albumin. However, some of the blood parameters were influenced by physical stressors of which most decrease overtime due to habituation to the system of handling. Meanwhile, all profiles where within the normal range for eland. Thus, the study would provide a guideline for management, welfare and health care in eland and other related antelopes.

Keywords: *Creatinine, Eland, Glucose, Stress, Temperament, Welfare*

MILKABILITY OF SLOVAK SPOTTED DAIRY COWS UNDER PRACTICAL CONDITIONS

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ABSTRACT: In recent years, breeding goals in dairy cattle are not only focussed on at increasing milk production, but also at the functional traits of dairy cows. One such functional trait is milkability. Information on milkability will also help breeders in the selection of offspring for further breeding both in commercial and nucleus herds. The aim of the study was to evaluate milkability of Slovak Spotted dairy cows and possible effect of bimodality. Milk flow profiles from 595 cows randomly selected from six farms were recorded by Lactocorder during evening milking. The total milk yield was on average 11.09±3.84 kg per milking, ranged from 6.40±1.50 kg (farm 5) to 12.13±3.83 kg (farm 6). The total milking time was on average 7.10±2.38 min and peak flow rate 2.85±0.93 kg/min. The 25.4% of total curves were classified as bimodal. Bimodality of milk flow significantly increased the duration of the ascending phase and reduced the peak flow, duration of the plateau phase and amount of milk within the first minute. The increase in the duration of the ascending phase due to bimodality was significantly manifested on every farm. In conclusion, when selecting animals, it is more appropriate to focus on individual milkability.

Keywords: *Slovak Spotted dairy cows, milkability, bimodality*

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INFLUENCE OF GENOTYPE AND TYPE OF MUSCLE TISSUE OF CHICKENS ON THE CONTENT OF CARNOSINE AND ANSERINE IN MEAT

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ABSTRACT: Carnosine (β-alanyl-L-histidine) and anserine (β-alanyl-1-methyl-L-histidine) are dipeptides that play a significant role in physiological functions in the human body. They are present in the skeletal muscles and brain tissue of many vertebrates, and from the literature it can be seen that white chicken meat has high concentrations of these peptides. By designing a feed mixture with an increased content of the amino acids L-histidine and β-alanine, their concentration in the meat can be increased. The aim of this study was to examine the influence of genotype and muscle tissue on meat colour and content of carnosine and anserine. The research was conducted on Cobb 500 and Ross 308 broilers during 42 fattening period during which broilers were fed with commercial fodder mixtures. After slaughtering and processing the carcass, the colour of the breast and shoulder meat was measured (CIE L*, CIE a*, CIE b*). Obtained results showed that muscle tissue has a statistically significant influence on meat colour ($P<0.05$), while genotype has influenced only on CIE b* value (<0.001). The content of carnosine and anserine in the meat samples of breast and shoulder indicate that genotype has no influence on the content of the mentioned dipeptides in the meat ($P>0.05$), while the muscle tissue has a significant influence ($P<0.001$) on their deposition. A significantly higher content of carnosine and anserine was found in breast meat compared to shoulder meat in both genotypes.

Keywords: *chickens, genotype, muscle tissue, color, dipeptides*

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PRODUCTION AND INVESTIGATION OF GUINEA FOWL AND DOMESTIC FOWL HYBRIDS FOR PGC-BASED CRYOPRESERVATION PROGRAMMES

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ABSTRACT: Related to the avian gene preservation programmes, the aim of our research was to produce infertile interspecific hybrids (recipient), to investigate and tested their ability hosting the primordial germ cells (PGCs) from native poultry breed (donor). To achieve our goals, Hungarian guinea fowl x Hungarian yellow chicken hybrids were produced, the crossing was repeated inversely then the hatching time and rate, the sex ratio, the presence of own germ cells, the fertility and the phenotype of viable hybrids and the incidence of chromosomal abnormalities of dead hybrid embryos were described. Crossing of Guinea fowl females with roosters resulted 6.65% viable offspring but crossing of domestic fowl hens with Guinea fowl males was unsuccessful (only 0.14% viable offspring). The hybrids hatched between the 21st and 27th day of incubation and raised until maturity. Results of histological analysis show that the observed offspring from the successful crossing were sterile male hybrids and their gonads may be suitable for hosting of donor PG cells and to produce gametes. 3 days old hybrid embryos were tested by injecting fluorescently labelled chicken PGCs. 17 (5.23%) individuals reached hatching and 85% of the examined gonads contained fluorescent labelled donor PGCs. 2 of them are being raised to investigate their ability to produce donor-derived gametes.

Keywords: *interspecific hybrids, primordial germ cells*

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EFFECT OF SEASON OF BIRTH OF HEIFERS ON MILK PRODUCTION AND COMPOSITION

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ABSTRACT: The effect of birth season (spring, summer, autumn, and winter (astronomical)) on milk prodution and milk composition (lactose, fat, protein, and sum fat and protein (kg, %) was analyzed based on milk production records of first lactation Hostein cows on two farms (farm 1 and farm 2) in west part of Slovakia. The analysis model also included the effects of heifer birth year (from 2012 to 2018 and from 2013 to 2017 on farm 1 and farm 2, respectively), calving age, and season calving. The birth season of heifers had no effect on their milk composition and production on both farms evalueted. The calving age had a significant effect on fat, protein, and sum of fat and protein (all in kg) on farm 1. The significant effect of birth year of heifers was observed on all evalueted parameters except on percentage of lactose and protein on farm 1. Milk yield of heifers, depending on the year of birth, ranged from 8781.92±130.45 to 9791.90±131.21 kg on the farm 1 and from 6734.39±318.80 to 9165.83±360.55 kg on the farm 2. Milk production and milk composition of first lactation cows depends mainly on management on the farms evaluated.

Keywords: *Holstein heifer, milk production and composition, influence factors*

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DISPERSION PARAMETERS FOR GROWTH OF BOARS DURING ON-FARM TEST

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ABSTRACT: The aim of this work was to evaluate the dispersion parameters for growth of boars. Longitudinal measurements of body weight were analyzed using random regression models (RRM) and compared with results from single trait (STM) and multiple-trait models (MTM). Data included 24591 records for terminal boars from on-farm performance testing. Two covariates litter size and age, dam parity and year-month interaction as season on test day were treated as fixed effects. The random part of the model included common litter environment, direct additive genetic, and permanent environment effect. Legendre polynomials were used to model random effects, based on eigenvalues, second-order polynomials were found to be sufficient. Covariance components were estimated using REML as applied in VCE6. The estimated heritability in RRM ranged from 0.26 at weaning to 0.67 at the end of the test and was lower than in STM (0.34-0.84) and MTM (0.36-0.84). The proportion of common litter effect was greatest at weaning (0.36) and decreased with age. The proportion of variation due to permanent environment was the lowest at weaning (0.05) and increased with age. Additive genetic correlations estimated by RRM were the highest between adjacent age classes and decreased with time. The lowest correlations were between weight at birth and weight at other age classes (0.07-0.17). Estimates did not differ much between the methods used, with only some variation at the end of test period due to non-random sampling of slow-growing boars in the last two age classes. RRM estimates were less sensitive to non-random sampling and were numerically less unstable than MTM.

Keywords: *boars, on-farm test, random regression models*

DIVERSITY AND NUTRITION DEVELOPMENT OF PURE CHICKEN BREEDS IN SLOVAKIA

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ABSTRACT: (1) Background: This study examined carcass characteristics, chemical composition, amino acid and fatty acid structure of breast and thigh muscles from pure chicken breeds (Australorp Black, New Hampshire, Oravka Yellow-brownish, Plymouth Rock White, Sussex Light). (2) Methods: Ten cocks and ten hens of each chicken breeds after the end of the reproductive cycle were then slaughtered for the carcass characteristics: live weight at slaughter, hot carcass weight, and chilled carcass weight were determined. Portion yields and dissection characteristics were measured. To evaluate the chemical composition, we removed the pectoral muscle (*musculus pectoralis major*) and the thigh muscle (*musculus biceps femoris*) without skin. Selected indicators of the chemical composition of meat were determined by spectrophotometric method on a sample of 100 g of breast and thigh muscle. (3) Results: It is clear from the study that there are differences in the content of some amino acids and fatty acids in the breast and thigh muscle among dual chicken breeds. (4) Conclusions: Quality of meat from native chicken breeds obtained from post-production cocks and from hens in their post egg-laying stage has shown that there are chances for their use in meat production.

Keywords: *chicken breed, carcass, chemical composition, amino acid, fat acid*

Acknowledgments: This publication was financially supported by projects APVV-17-0060 and APVV-20-0161.

Session: One Health

OCCURRENCE OF MASTITIS PATHOGENS AT DRY OFF PERIOD AND AFTER CALVING IN DAIRY COWS

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ABSTRACT: (1) The aim of the work was to study the occurrence of mastitis pathogens before and after calving in the same dairy cows. (2) The Holstein cows suspicious on subclinical mastitis (positive California Mastitis Test) were sampled at quarter level under practical farm with high level of milk yield (11,278 kg). The cows were treated with antibiotics (Cefquinomum) before drying. In total 84 samples before drying and 107 samples after calving from the same dairy cows were collected. The samples were cultured on blood agar (MkB Test as, Rosina, SR). MALDI-TOF MS (Bruker Daltonics, Germany) was used to identify mastitis pathogens. (3) Bacteriologically positive (BP) samples from dairy cows before drying were found in 35% of the milk samples. The most frequent pathogens in BP milk samples were coagulase-negative staphylococci (CNS) (77.38%). The most common CNS was *Staphylococcus (S.) xylosus* (41.54%). *S. aureus* was detected in 5.95% of BP samples. After calving, we found BP samples in 14.02% of dairy cows. The most common pathogens in milk samples were CNS (13.08%). *S. aureus* was detected in 0.94% of BP samples. (4) Antibiotic treatment during the drying period clearly reduced the occurrence of CNS and *S. aureus* in dairy cows at the beginning of lactation.

Keywords: *dairy cows, mastitis, pathogens*

Acknowledgements: This research was supported by the APVV-18-0121 project in response to the Slovak Research and Development Agency and by the SmartFarm (313011W112) and NUKLEUS (313011V387) project implemented within the Research and Development Operational Program funded by the European Regional Development Fund.

THE INCIDENCE OF PATHOGENS IN MILK OF GOATS AND RELATION WITH SOMATIC CELL COUNT AND MILK COMPOSITION

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ABSTRACT: The study aimed to evaluate somatic cell count (SCC), pathogens and relationship of SCC and the presence of pathogens and milk composition of goats. Totally 394 milk samples at half udder level (100 goats) were collected during June and July. According SCC in milk the samples were divided into groups: SCC1 $< 400\times10^3$; SCC2 $\geq 400 < 1000\times10^3$; SCC3 $\geq$ 1000 cells.mL^{-1}. Pathogens were evaluated by cultivation and MALDI TOF MS. In June and July we detected the lowest frequency of milk samples in SCC1 (25.89%, 13.20%, resp.), higher frequency in SCC2 (32.49%, 40.10%, resp.) and the highest frequency in SCC3 (41.62%, 46.70%, resp.). Intramammary infection caused by minor and major pathogens was detected in 10.41%. Minor pathogens were identified in 92.68% and major pathogens in 7.32% of bacteriological positive samples. The significant higher somatic cell score was observed in samples with the presence of pathogens (6.37±0.25) compared to samples without pathogens (5.81±0.18) ($p=0.0094$) in SCC3 group. We detected significant lower content of lactose in SCC3 group compared to content of lactose in SCC1 group ($p=0.0453$). In conclusion, low count of bacteriological positive samples with high SCC opens a discussion about the reasons of high SCC in milk of goats.

Keywords: *goats, milk, somatic cell count, pathogens*

Acknowledgements: Supported by the Project VEGA 1/0597/22 „Etiology of changes somatic cell count in the mammary gland of goats: physiological and pathological aspects."

SURVEY OF *EIMERIA* OOCYST AND *PASSALURUS AMBIGUUS* INFECTIONS AT INDUSTRIAL RABBIT FARMS DEPENDING ON THE SEASON

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ABSTRACT: Nowadays, one of the main problems of large-scale rabbit farms is the digestive diseases of rabbits. The aim of the study was to evaluate the incidence of *Eimeria spp.* and *Passalurus ambiguus* infection at industrial rabbit farms according to the season. The survey was made between 2018 and 2022 at 29 Hungarian and 2 Slovakian rabbit farms. Altogether 7612 faecal samples were examined. *Eimeria* oocystes and *Passalurus ambiguus* were also detected on the large-scale rabbit farms studied, although in relatively small portions of faecal samples. *Eimeria* oocysts and *Passalurus ambiguus* were found in 32 % and 6 % of the samples, respectively. According to season, the highest proportion of *Eimeria* positive samples occurred during the summer (35.3 %) and autumn (36.2 %) periods. In winter significanly lower infection ratio was found (29.5; $P<0.05$). The most favorable results were observed in the spring 25.1 %; $P<0.05$). As for *Passalurus ambiguus*, the highest ratio of infection was measured in spring (8.4 %) and the lowest in summer (4.5 %;$P<0.01$). The autumn and winter periods showed intermediate results (6.7 % and 5.5 %, respectively). Based on the results obtained, the parasitological monitoring of rabbit farms is extremely important.

Keywords: *parasitology, coccidiosis, pinworm, animal health*

HUMAN IMPACTS ON HELMINTH FAUNA DIVERSITY IN WILD CARNIVORES

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ABSTRACT: Background: Wild canids are the most widely distributed hosts of zoonotic diseases on the planet. These species are the source of many human infections with their intestinal helminths. The direct link between zoonotic helminth infection and human activities is well known. We assessed the human impacts on helminth diversity of wild canids, which could contribute to the elevation of human infection. Methods: A necropsy-based parasitological investigation was conducted. The helminth species were collected and identified from red fox, and golden jackal hunted in Hungary and Croatia. We performed a multiscale geographically weighted regression model to explore the connection between the helminth diversity (response variable) and human impacts (explanatory variables: distance from the nearest settlement, citizens' number in the nearest settlement, population density of the nearest settlement, and proportions of different land cover types). Results: We have found 13 potentially zoonotic helminth taxa (one trematode, nine cestodes and three nematodes). From the explanatory variables, the distance ($\beta=-0.304$, $p<0.0001$) and the wet habitats' proportion ($\beta=0.132$, $p=0.026$) had a significant effect on helminth diversity. Conclusions: The results revealed that in the vicinity of human settlements, wild carnivores carry more zoonotic helminth species than farther from them.

Keywords: *wild carnivores, helminth diversity, human impact*

Acknowledgements: We are very thankful all of the huntmasters and the professional hunters who contributed to our investigation.

EXPLORING MICROBIAL COMMUNITIES IN HALOPONIC SYSTEMS AT DIFFERENT WATER SALINITY

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ABSTRACT: Haloponics is a form of aquaponics, a multi-trophic production system based on the dynamic integration among fish, plants, and microorganisms in brackish water. To understand the role of water salinity on bacteria structure in a low-tech haloponic system, we performed a 16S rDNA multi-amplicon sequencing to compare microbial community profiles in nine tanks where rainbow trout and catfish were kept at three water salinity concentrations (0.5‰, 3‰, and 6‰). The overall microbial profile was represented by different functional groups, involved in plant growth and protection, and nitrification processes, but also bacteria found in the guts of freshwater fish. Potential fish and human pathogens such as *Pseudomonas*, *Vibrio*, and *Aeromonas* were detected. The core microbiomes revealed the absence of beneficial and plant-associated bacteria such as *Bacillus*, *Lactobacillus*, *Massilia*, and *Thermomonas*, in the tanks at 6‰ salinity. Principal Coordinate Analysis showed no significant separation between bacterial communities according to salinity, suggesting a common structure among samples. These results enhance our understanding of the composition of bacterial populations in haloponic systems and their relationships with water salinity. Brackish water up to 6‰ did not severely impact the microbial ecosystem, resulting in an alternative source for the establishment of sustainable and healthy aquaponic systems.

Keywords: *Aquaponics, Next-generation sequencing, Microbial communities, Salinity*

Acknowledgements: The research was funded by the University of Padova, Italy (BIRD 179231; CUP: C52F17000140005).

IMPORTANCE OF MID-INFRARED SPECTRA REGIONS FOR THE PREDICTION OF MASTITIS AND KETOSIS IN DAIRY COWS

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ABSTRACT: Mid-infrared (MIR) spectroscopy is a standard method to determine major milk components such as fat, protein and lactose. Further, it has been applied to predict fine milk composition and various traits relevant for breeding and animal health. MIR spectra express the absorbance of infrared light at 1,060 wavenumbers in the region from 926 to 5,010 cm^{-1}. It was reported that specific regions of the spectra are less informative because of water absorption. The objective of the present study was to identify which MIR regions are of importance in the prediction of clinical mastitis and ketosis. Four statistical methods, partial least squares discriminant analysis (PLS-DA), least absolute shrinkage and selection operator (LASSO), random forest (RF) and support vector machine (SVM), were compared. Data from 59,002 dairy cows, collected within the routine milk recording and health monitoring system (GMON), were used. Test-day data, including MIR spectra, were linked to diagnosis data, considering clinical diagnoses of mastitis and ketosis. Specific wavenumbers were identified to be of particular importance in the models to predict clinical mastitis and ketosis. Variation was found regarding traits and also across the four different methods. Results indicate a potential advantage by applying variable selection analyses prior to model development.

Keywords: *dairy cows, mastitis, ketosis, MIR spectroscopy, variable selection*

Acknowledgements: This work was conducted within COMET-Project D4Dairy (Digitalisation, Data integration, Detection and Decision Support in Dairying, project 872039), which is supported by BMK, BMDW and the provinces of Lower Austria and Vienna in the framework of the COMET-Competence Centers for Excellent Technologies. The COMET program is handled by the FFG.

PIG AS A POTENTIAL RESERVOIR FOR SARS-COV-2 INFECTIONS

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ABSTRACT: Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) infections have occurred in several animal species, and transmission from humans to animals and back to humans has been confirmed, supporting the importance of the One Health principle. Animal species that are in constant and close contact with animal caretakers are particularly at risk. The major entry point for SARS-CoV-2 into host cells is angiotensin-converting enzyme 2 (ACE2). Its amino acid sequence is highly conserved in vertebrates, allowing SARS-CoV-2 to use the orthologous forms of ACE2 to enter different cell types in different host species. Sanger sequencing of four crucial regions of ACE2 was performed to identify polymorphisms that cause amino acid changes. Samples from two local pig breeds (Krškopolje pig and Schwäbisch-Hällisches pig), a commercial pig line (Large White x Swedish Landrace), and a wild boar were included in the study. We identified a missense variant within exon 9 of the ACE2 gene in the Krškopolje pig. Our results indicate that there is some genetic variation in the coding region of the ACE2 protein in *Sus scrofa* species. *In silico* structural modelling of different genetic variants of the ACE2 protein will allow prediction of host cell susceptibility to SARS-CoV-2 penetrance.

Keywords: *SARS-CoV-2, COVID-19, ACE2, One Health, Sus scrofa*

INVESTIGATING THE EFFECT OF EARLY MYCOTOXIN EXPOSURE ON THE DEVELOPMENT OF NON-COMMUNICABLE DISEASES IN AN ANIMAL MODEL SYSTEM

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ABSTRACT: Background: Fusarium toxins are widely distributed in the European food chain. Mycotoxins pass through the placenta affecting the development of the offspring however, little data is available about mycotoxin exposure of preimplantation mammalian embryos. To our knowledge evaluation of long-term effects of low level and short duration mycotoxin exposure at this very early developmental stage is not available. **Aim:** Investigating the effect of mycotoxins on gene expression profiles in connection to non-communicable diseases and disorders that besides genetic background have environmental factors, for example autism spectrum disorder. **Methods:** Rabbit embryos were derived 10 hours after insemination. An increasing amount of mycotoxin was administered to the culture media (T2-toxin, Zearalenone and combined toxin groups). Embryo development was monitored and photo-documented in 24-hour intervals for 96 hours. The ratio of developmental stages was compared to non-toxin control group. Design and optimisation of quantitative PCR for gene expression profiling have started. **Results and conclusion:** Sublethal concentration of 2,5 ng/ml was determined for T2-toxin. In case of zearalenone there was no significant toxin effect on rabbit embryo development in the studied range (5-20 ng/ml). The combination of T2-toxin and zearalenone had a synergistic effect on embryo development based on blastocyst development rate.

Keywords: *preimplantation rabbit embryo, mycotoxin, T2-toxin, zearalenone*

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IMPACT OF VACCINATION AGAINST BOVINE RESPIRATORY DISEASE ON ANTIMICROBIAL USE IN ITALIAN BEEF CATTLE

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ABSTRACT: Antimicrobial use (AMU) in the livestock sector is a major driver of antimicrobial resistance. The Italian beef industry is based on the import of young bulls from France, reared on several farms, commingled together in collection centres and transported to Italy. These factors induce stress in the animals and lead to higher risks of bovine respiratory disease (BRD) and AMU. The aim of this study was to investigate the effect of a BRD vaccination programme in Italy on AMU. Slaughter performances, AMU and vaccination treatments (number and time of first BRD vaccination) were available for 48,642 young bulls of different breeds between May 2015 and April 2019. AMU was estimated using a treatment incidence. Data were also collected on overall mortality rate and mortality rate due to BRD. A generalised mixed linear model was used to quantify the effects of the number of vaccines and the time of first treatment on AMU and mortality. The number of vaccines did not impact AMU and mortality but anticipating the first vaccination significantly reduced AMU. Thus, even if the vaccination programme is essential to tackle the BRD in Italy, it is suggested to apply the vaccination programme prior the commingling procedure in France.

Keywords: *beef, young bull, antibiotic, vaccine, antibiotic resistance*

Acknowledgements: The authors would like to thank Associazione Zootecnica Veneta (AZoVe, Cittadella, Italy) for providing the data used in the study.

Poster Session: One Health

EXAMINATION OF THE ANTIOXIDANT SYSTEM IN KNOCK-OUT RABBITS ON CHOLESTEROL-RICH DIET

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ABSTRACT: There is a lot of research available on the relationship between hypercholesterolemia and oxidative stress. Overturning of the oxidant-antioxidant system induces processes such as apoptosis, necrosis, ischemic damage, fibrotic processes, neurodegeneration and tumor changes. NADPH oxidases (NOX) are responsible for the production of endogenous ROS in animal organisms. Our studies were performed on NOX4 knock-out and wild-type animals. During the experiment, the animals were fed with 1% cholesterol enrichd food for 10 weeks. We took blood from the animals for RNA isolation immediately before the start of feeding and then at the 5th and 10th week. In the samples, genes playing a more important role in the functioning of the oxidant-antioxidant system, such as NOX4, NOX5, SOD1-3, GPX, CAT, KEAP, NRF2, TGFß, are examined by rt-QPCR. Our aim is to summarize the complex, chronic effect of hypercholesterolemia on the regulation of the body's oxidant-antioxidant system in a rabbit model, as well as to explore the role of the Nox4 gene in the regulation of the body's metabolic processes, answering the question of how the NOX4 gene affects the harmful effects of a high-cholesterol diet loss of function.

Keywords: *antioxidant systen, NADPH-oxidase, rabbit*

Session: Precision Animal Breeding

COMPARING ENTERIC METHANE EMISSIONS PREDICTED FROM DIFFERENT EQUATIONS BASED ON MILK FATTY ACID PROFILE OF DAIRY COWS

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ABSTRACT: Nowadays the livestock sector is blamed by public opinion for its contribution to the GreenHouse Gas Emissions. This study aimed to test different equations proposed in literature to predict enteric methane emissions (EME) of dairy cows from milk fatty acid (FA) profile. A database composed by milk production, composition, and FA profile of 992 dairy cows classified according to days in milk (DIM), parity order (PO), and 4 dairy systems, was used to compare EME values obtained from 21 equations proposed in literature. A mixed model was used to evaluate the effect of DIM, PO, and dairy system on EME expressed in term of intensity (16.05 ± 2.76, g/kg of milk), yield (20.63 ± 2.26, g/kg of dry matter intake), and daily production (385.43 ± 68.21, g/day). EME predicted by different equations were not correlated, except for 2 cases. EME predicted by 19 equations were significantly influenced by DIM and 13 by PO. Farming system showed significant differences in EME data (17 equations), especially comparing modern and traditional farms. New EME predicting equations based on milk yield and composition and also the maintenance requirements of dairy cows are needed.

Keywords: *methane emissions; dairy cows; predicted equations; milk fatty acid profile*

FOGGING SYSTEM AFFECTS MICROCLIMATE, ANTIOXIDANT CAPACITY AND SCROTAL CHARACTERISTICS IN FRIESWAL BREEDING BULLS DURING SUMMER SEASON

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ABSTRACT: The present study was conducted to assess the effect of fogging system of cooling on the performance of Frieswal crossbred (Holstein Friesian X Sahiwal) bulls during summer season. The experimental bulls (n=12) were equally distributed into treatment (F) and control (C) group with and without fogging system of summer management, respectively. Daily climatic variables and fortnightly scrotal surface and ocular temperature were recorded during the entire study period. Semen samples were evaluated biweekly for semen quality parameters. Blood samples were collected for analysis of total antioxidant capacity (TAC). Significant ($p<0.05$) reduction in THI value was observed in F than in C sheds. The bulls in F sheds had lower ocular temperature and higher ($p>0.05$) scrotal thermal gradient than in C sheds. F group bulls had significantly higher semen volume with lower sperm abnormalities ($P>0.05$). Significantly higher ($p<0.05$) TAC was found in the bulls of F than in C. The bulls of C had higher ($p<0.05$) testicle peduncular length than F bulls. In conclusion, fogging system had significant effect on THI, semen volume, total antioxidant capacity and testicle peduncular length in crossbred bulls during summer season.

Keywords: *Crossbred bull, Semen quality, Summer management*

PREDICITION OF AMMONIUM EMISSION FROM DAIRY COW FARMS ACCORDING TO UREA CONTENT IN MILK

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ABSTRACT: The objective of this study was to determine the variability of daily milk yield, and evaluation of milk urea nitrogen to assess the potential of ammonia pollution from farms and to test was it affected by the stage of lactation and the dietary crude protein (CP) concentration, using a precision dairy farming methodology (test day records). The research was conducted under production conditions in four different sizes of agricultural holdings located in various places in the Province of Vojvodina and represent different animal housing and feeding technologies. Milk content parameters for total 8.700 milk samples were analysed in accredited milk quality laboratory at the Faculty of Agriculture in Novi Sad. The statistical analyses were performed with the Statistica program package. The results emphasized that the optimum amount of urea in milk is 15-30 mg dL-1, and there was a strong relationship between ammonia emission and MUN which was not different among lactation stages. By using these data, each farm may make calculations and should control urea content in milk yielded from each individual cow on regular basis so test day records can be used not just for evaluating animal productivity but also for monitoring of ammonia pollution from dairy cattle farms.

Keywords: *MUN, precision dairy farming, ammonia emission, dairy cattle*

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Conference venue

The symposium will be held in Zadar, Hotel Kolovare (address: Bože Peričića 14, 23 000 Zadar, Hrvatska, phone: +385 23 211 017, +385 23 203 200, e-mail: info@hotel-kolovare.com) placed on the beach, five minutes’ walk from the city center. Special rates will be offered by the Hotel Kolovare for the participants. Accomodation in Hotel Kolovare **** from 18 to 23 of September (possible extension for 23 - 25 September).

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