

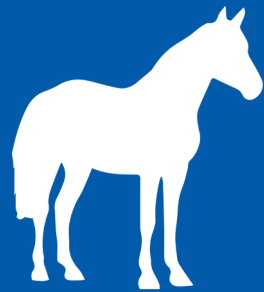
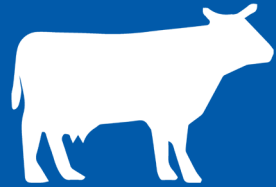
INTERNATIONAL CONFERENCE

MICROBIOTA
AND ANIMAL:
INTERACTION,
HEALTH,
WELFARE AND
PRODUCTION

Programme and Abstracts

Kaunas

29 September, 2022





Kuriame
Lietuvos ateitį

2014–2020 metų
Europos Sąjungos
fondų investicijų
veiksmų programa

Renginys organizuojamas Lietuvos mokslų akademijai kartu su partneriais įgyvendinant projektą „Nacionalinės mokslo populiarinimo sistemos plėtra ir įgyvendinimas“, kuris finansuojamas Europos socialinio fondo lėšomis.

INTERNATIONAL CONFERENCE

MICROBIOTA
AND ANIMAL:
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AND PRODUCTION

LITHUANIAN ACADEMY
OF SCIENCES

LITHUANIAN UNIVERSITY
OF HEALTH SCIENCES

VETERINARY ACADEMY

INTERNATIONAL CONFERENCE

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THE CONFERENCE IS DEDICATED
TO THE 30th ANNIVERSARY OF THE RESEARCH
CENTER OF DIGESTIVE PHYSIOLOGY AND
PATHOLOGY OF THE DEPARTMENT
OF ANATOMY AND PHYSIOLOGY
OF LSMU VETERINARY ACADEMY

THE CONFERENCE SPONSORS & SUPPORTERS

Lithuanian Academy of Sciences (LMA)

Lithuanian University of Health Sciences (LSMU)

Lithuanian Association of Veterinarians (LVGA)

CJSC “VetMarket”

GENERAL INFORMATION

Conference organizer:

LMA,

The Research Centre of Digestive Physiology and Pathology
of the Department of Anatomy and Physiology
of LSMU Veterinary Academy, Kaunas, Lithuania

Main topics of the Conference:

1. Animal health and welfare
2. Animal nutrition and productivity
3. Quality of production

Conference language: English

Type of the presentation: oral or poster

INTERNATIONAL SCIENTIFIC COMMITTEE

Jan JANKOWSKI, academician, prof. dr., LMA, UWM, Poland

Antanas SEDEREVIČIUS, academician, prof. dr., LMA, LSMU VA, Lithuania

Vita RIŠKEVIČIENĖ, prof. dr., LSMU VA, Lithuania

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Ilma TAPIO, dr., LUKE, Finland

Asta TVARIJONAVIČIŪTĖ, dr., UM, Spain

DEAR COLLEAGUES,

The primary purpose of scientific and educational conferences is to share research achievements in animal physiology, disease diagnosis, treatment, and welfare, examining the interaction between the microbiota and the animal in relation to health, welfare, and the quantity and quality of production.

The conference focuses on animal holobionts and microbiomes of the same individual in different body parts and their interrelationships. Microbial ecosystems are known to affect ruminant phenotypes, the gastrointestinal tract, especially the large stomach, the composition of the distal intestinal feces, the upper respiratory tract, milk quality, gas emissions, and others.

The twentieth-century second half's and the twenty-first century's fundamental scientific discoveries have significantly changed the understanding of food assimilation and the genesis and treatment of some common farm animal diseases. In terms of micro- and macromolecular transport, lysozyme and membrane digestion, non-microbial animal studies, the role of microflora and microfauna in nutritional processes, and stomach and intestines in immunology, these and other physiological studies have led to the new advances not only in physiology theory but in practice.

As the productivity of farm animals increases, so do their health problems, and new diseases are emerging, especially gastrointestinal dysfunctions. Diagnosing these diseases is still difficult today because there are still no effective ways and means to diagnose diseases, especially subclinical forms, and normalize the physiological processes. This educational conference aims to approach this growing problem by seeking new diagnostic methods and tools for treatment. Much attention will be paid to feeding programs which are determined not only by theoretical and practical but also by social motives. Feeding affects the quality of animal production, health, and breeding and is also a critical factor in livestock productivity, profitability, and economic rationality of feed.

The problems mentioned above have been successfully studied by the researchers of the LSMU Veterinary Academy since its establishment. The most productive

research was started in 1992 when the Center for Digestive Physiology and Pathology was founded. Celebrating its 30th Anniversary this year, the Center plans to organize the sixth scientific-educational international two-day conference, "Microbiota and the Animal: Interaction, Health, Welfare, and Production." On the first day of the conference, the remote discussions and sharing of knowledge on the latest research and advances in animal health, nutrition and productivity, product quality, and food safety with scientists worldwide will be held. The second conference day will provide the latest practical knowledge for veterinarians, livestock professionals, farmers, and other participants.

Current knowledge and practical innovations will allow professionals to find the most appropriate solution to problems in agriculture. Farm animals' health, quantity, and quality can be significantly improved and increased by using scientifically based methods to regulate physiological processes.

On behalf of the organizing Committee
Chairman of the International Scientific Conference
academician, prof. dr. ANTANAS SEDEREVIČIUS

MIELI KOLEGOS,

Pagrindinis mokslinių ir edukacinių konferencijų tikslas – dalintis tyrimų pasiekimais gyvūnų fiziologijos, ligų diagnostikos, gydymo ir gerovės srityse, nagrinėjant mikrobiotos ir gyvūno sąveiką sveikatos, gerovės, produkcijos kiekybės ir kokybės atžvilgiu.

Konferencijoje pagrindinis dėmesys skiriamas gyvūnų holobiontams ir to paties individo mikrobiomams skirtingose kūno dalyse ir jų tarpusavio ryšiams. Yra žinoma, kad mikrobinės ekosistemos veikia atrajotojų fenotipus, virškinimo traktą, ypač prieskrandį, distalinių žarnyno išmatų sudėtį, viršutinius kvėpavimo takus, pieno kokybę, dujų išmetimą ir kt.

Dvidešimtojo amžiaus antrosios pusės ir dvidešimt pirmojo amžiaus esminiai moksliniai atradimai gerokai pakeitė supratimą apie maisto asimiliaciją ir kai kurių įprastų ūkinių gyvūnų ligų atsiradimą ir gydymą. Kalbant apie mikro- ir makromolekulinį transportą, lizocimo ir membranų virškinimą, nemikrobinis tyrimas su gyvūnais, mikrofloros ir mikrofaunos vaidmenį mitybos procesuose bei skrandžio ir žarnyno vaidmenį imunologijoje, šie ir kiti fiziologiniai tyrimai lėmė naujus pasiekimus ne tik fiziologijos teorijoje, bet ir praktikoje.

Didėjant ūkinių gyvūnų produktyvumui, didėja ir jų sveikatos problemos, atsiranda naujų ligų, ypač virškinamojo trakto veiklos sutrikimų. Šias ligas diagnozuoti ir šiandien sunku, nes vis dar nėra veiksmingų būdų ir priemonių ligoms, ypač subklinikinėms formoms, diagnozuoti, fiziologiniams procesams normalizuoti. Šia edukacine konferencija siekiama spręsti šią augančią problemą ieškant naujų diagnostikos metodų ir priemonių gydymui. Daug dėmesio bus skiriama maitinimo programoms, kurias lemia ne tik teoriniai ir praktiniai, bet ir socialiniai motyvai. Šėrimas turi įtakos gyvulių produkcijos kokybei, sveikatai ir veisimui, taip pat yra svarbus veiksnys gyvulių produktyvumui, pelningumui ir pašarų ekonominiam racionalumui.

Minėtas problemas LSMU Veterinarijos akademijos mokslininkai sėkmingai nagrinėja nuo pat jos įkūrimo. Rezultatyviausi tyrimai pradėti 1992 m., kai buvo

įkurtas Virškinimo trakto fiziologijos ir patologijos centras. Šiemet 30 metų jubiliejų švęsiantis centras planuoja surengti šeštąją mokslinę-educacinę tarptautinę dviejų dienų konferenciją „Mikrobiota ir gyvūnas: sąveika, sveikatingumas, gerovė ir produkcija“. Pirmąją konferencijos dieną vyks nuotolinės diskusijos ir dalijimasis žiniomis apie naujausius tyrimus ir pasiekimus gyvūnų sveikatos, mitybos ir produktyvumo, produktų kokybės ir maisto saugos srityse su viso pasaulio mokslininkais. Antroji konferencijos diena suteiks naujausių praktinių žinių veterinarijos gydytojams, gyvulininkystės specialistams, ūkininkams ir kitiems dalyviams.

Dabartinės žinios ir praktinės naujovės leis specialistams rasti tinkamiausią žemės ūkio problemų sprendimą. Ūkinių gyvūnų sveikata, kiekis ir kokybė gali būti žymiai pagerinta ir padidinta naudojant mokliškai pagrįstus fiziologinių procesų reguliavimo metodus.

Organizacinio komiteto vardu
Tarptautinės mokslinės konferencijos pirmininkas
akademikas, prof. dr. ANTANAS SEDEREVIČIUS

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(Moderator Ingrida Monkevičienė)

*Representatives of the Lithuanian Academy of Sciences,
The Lithuanian Health Sciences University and other institutions*

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**16:00–17:00 DISCUSSION AND PREPARATION
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ABSTRACTS

ORAL CONTRIBUTIONS

HISTORY AND PERSPECTIVES OF THE RESEARCH CENTER FOR DIGESTIVE PHYSIOLOGY AND PATHOLOGY

Antanas Sederevičius* and Rasa Želvytė

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The origins of the Research Center for Digestive Physiology and Pathology began in 1972 with establishing a scientific research laboratory at the Department of Physiology, Pathological Physiology, and Pathological Anatomy. The Laboratory activities extended, and the branch Laboratory of Use of Enzyme Preparations in Veterinary and Animal Husbandry in 1984 and the Laboratory of Bovine Problem Digestive Biotechnology in 1989 were established. In 1992, the Research Center of Digestive Physiology and Pathology (Center) was founded by merging the mentioned two laboratories. To date, the Center has developed research in the following main areas to address the issues of digestive physiology and pathology in cattle (1):

1. Investigation of the impact of various feed, feed additives, and their different rations, and feeding technologies on biochemical and microbiological processes in cattle rumen contents, the digestibility of organic matter (OM), and quantity of D and L-lactic acid isomers in blood, milk, and urine (2, 3).
2. Analysis of biochemical, microbiological, and OM digestibility indices of bovine rumen contents in cattle with various forms of gastric dystonia of alimentary origin and in cases of experimental acidosis (3, 4).
3. Research of the influence of enzymatic preparations, probiotics, B group vitamins, peptides, amino acids, ammonium sulfate, and other synthetic compounds on the *in vitro* digestibility of feed OM and the normalization of impaired pathological processes in the rumen contents of cattle (1,4).
4. Development and improvement of diagnostic tools and methods for the research of physiological and pathological parameters of the cattle rumen content (1–5).

At the Center, 13 doctors of science, of which 4 are professors, 2 associate professors, and one academician have been trained. The Center has made 12 inventions and improved eight scientific products approved by the Pharmacological Council and released into production. The Center researchers have published over 400 scientific articles and over 30 scientific publications. Every five years,

the Center organizes specialized international scientific conferences to publicize the results of the Centre's activities (there have been six conferences in total).

Over the last five years, the Centre's staff has organized five conferences to promote research awareness and competitiveness and implemented the following national and international scientific projects: "Application of Non-Invasive Measures for The Assessment of the Physiological Condition of the Mammary Gland and Presentation of Recommendations for The Detection of Early Pathologies in the Technological Process of Milk Production" (MT-15-9); "Studies on the Influence of Various Factors on the Change of Casein Content in Raw Milk" (R&D No. MT-13-18); "Determination of the Relationship between the Fat Content of Raw Milk and Dairy Products Derived from It" (MT-17-13); KTU-LSMU joint scientific project "Application of Acoustic Vibrations for Prevention and Treatment of Bovine Mastitis (VIPGAMA)" (No. 2021-V-0156); Animal Health and Welfare (ANIHWA) (No. 187838); and "Understanding Microbiomes of the Ruminant Holobiont (HoloRuminant)" (No. 001791, Horizon 2020).

Also, the Center conducts commercial research and consults the interested businesses on health and productivity issues for dairy herds.

In the future, the Center plans to carry out the research under the LSMU 2017–2021 approved strategic direction "Molecular Technologies for Animal Health and Productivity" and develop the diagnostic tools that are necessary to analyze physiological and pathological processes in animals and allow to evaluate metagenomic changes in bacterial diversity and model the digestive processes of dairy cows with feed and feed additives for improving milk composition and quality.

Keywords: digestive physiology and pathology, history, research areas, perspectives

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ASSOCIATING GUT MICROBIOME WITH FEED EFFICIENCY PHENOTYPE

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The gut microbiota in ruminants is fundamental for feed digestion, but the role of microbiota in defining animal feed efficiency phenotype is still not fully understood. The objectives here were to 1) assess rumen microbial community composition in dairy cows, 2) generate machine learning model for feed efficiency prediction by Extreme gradient boosting (xgboost) method, 3) identify bacterial taxa that have strong impact on feed efficiency. Residual energy intake (REI) was calculated for 100d period after calving and was based on a multiple linear regression model with energy corrected milk, metabolic bodyweight, and piecewise regressions of BW change on the metabolizable energy intake (1). Rumen bacterial community composition was determined by 16S rRNA gene V4 amplicon sequencing and processed using Qiime 2 (2). In xgboost modelling (3), bacterial composition was included as dimension reduced components regularized to positive values only. The number of predictors reduced by two thirds while the omitted variation was only one third of the total variation. Simpson diversity statistics were included as ecological predictors. Data from 87 primiparous Nordic Red cows was randomly split in proportions 8:1:1 to training, validation and test data, respectively. Training and validation data were used to fit and tune xgboost regression models. Final model was used to predict REI in the test data. Overall rumen community differences had no simple association with REI estimates. The model explained 1/3 of the variation in REI in the test data. In total, 19 predictors, including the diversity values, had non-zero marginal contributions to the predictions. The four most important features were dimension reduction components demonstrating approximately monotonous impacts on REI predictions. Each of the top component had non-zero contribution from 10–20% of the total OTUs, that were affiliated with *Acetitomaculum*, *Bacteroidales* RF16, *Christensenellaceae* R-7, *Lachnospiraceae* NK3A20, *Methanobrevibacter*, *Paraprevotella*, *Prevotella*, *Rikenellaceae* RC9, *Succinivibrionaceae* UCG-002 genera. The results can be used to infer microbial metabolic networks involved. However, the component ranks are sensitive to hyperparameter settings, and caution is necessary.

Keywords: ruminants, gut microbiome, feed efficiency

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EFFICACY OF COPPER, ZINC AND MANGANESE NANOPARTICLES IN TURKEY NUTRITION

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This report presents the results of four experiments performed on female Hybrid Converter turkeys to test the research hypothesis postulating that Cu, Zn and Mn added to turkey diets as nanoparticles are characterized by higher bioavailability than their conventional sources. The study involved a comprehensive analysis of bird performance, carcass quality, meat quality, bioavailability of minerals (intestinal digestibility), blood mineral concentrations, selected diagnostic indicators, major parameters of tissue redox status, selected indicators of immune status, and the heavy metal content of selected tissues. In the experiment with Mn, protein nitration parameters and epigenetic changes were also determined. The first three experiments had a two-factorial design (3 x 2) with three inclusion levels of the analyzed micronutrients (100%, 50% and 10% of the amounts typically added to practical turkey diets, close to BUT recommendations) in the form of nanoparticles or conventional sources. The impact of nanoparticles was not unequivocally positive, but it was found that the amounts of supplemental micronutrients added to turkey diets can be reduced by at least 50%. The last (fourth) experiment compared the efficacy of a simultaneous decrease in the inclusion levels of supplemental Cu, Zn and Mn (both nanoparticles and conventional sources) to 10% of the levels recommended by BUT; the negative control group did not receive any supplemental micronutrients. The inclusion levels of the analyzed micronutrients, decreased to 10%, had no negative influence on the values of the tested physiological parameters, bird performance or carcass quality, regardless of their physical form. Turkeys fed diets without supplemental micronutrients were characterized by lower rates of lipid peroxidation in the small intestinal wall and in the liver.

The amounts of supplemental Cu, Zn and Mn recommended by breeding companies and added to practical turkey diets are too high and may exert adverse

effects on both the birds and the natural environment. However, the possibility of radically reducing the use of the analyzed micronutrients in turkey nutrition requires further research, including under unfavorable management conditions and in commercial farms.

Keywords: turkeys, nanoparticles, copper, zinc, manganese

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SALIVA, ORAL MICROBIOTA AND PATHOLOGY

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Saliva for long years was considered merely a part of the digestive system with very simple functions such as helping in the formation of food bolus in the mouth and moistening and protecting the oral structures. However, the advancement of research and technology is turning saliva from a simple digestive fluid into a crucial tool capable of reflecting health and wellness (1). The advancement in saliva research in the last decades was fostered because of its 3 main features:

1. COMPOSITION. Saliva is a very rich sample in proteins, enzymes, electrolytes, and oral microbiota and their products among others.
2. COLLECTION. Saliva collection is easy, safe, non-invasive, and stress-free.
3. COST-EFFECTIVE. Saliva collection does not require specialised personnel nor specific material thus saliva obtaining and processing costs are lower than those of blood.

Therefore, saliva is further gaining enormous attention in biomedical sciences from the basic (such as biochemistry, microbiology, anatomy and histology) to applied (such as epidemiology, prevention, diagnosis, and treatment) fields of knowledge.

The interest in saliva in microbiota studies lies mainly in the fact that saliva contains oral microbiota and its by-products in the host environment permitting close interaction between microbiota and the host so constituting an oral microecosystem (2). The role of the oral microbiome in a number of human and animal pathologies has been investigated in the last years. The studies report that homeostasis of oral microbiota is disrupted in different local and systemic diseases. In most cases, it is still not clear whether it is a cause or a consequence, although different authors have suggested its involvement in the development pathways of the disease.

In this presentation, the leading general applications of saliva will be indicated and the studies made with oral microbiota outlined.

Keywords: analysis, non-invasive, oral biofluid, saliva, sample, disease

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FEED FERMENTATION – INFLUENCE ON PIGLETS FECES MICROBIOTA AND MYCOTOXIN BIOTRANSFORMATION *IN VIVO*

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Lactic acid bacteria (LAB) are beneficial microorganisms, which can ferment carbohydrates and produce organic acids, which suppress pathogenic bacteria growth (1). In addition, fermentation can reduce toxins in feed, and, during the fermentation, some of the microbial starters excrete enzymes that may transform mycotoxins into non-toxic compounds. However, fermentation can lead to the formation of masked mycotoxins (2). The aim of this study was to apply a combination of the microbial starters *L. uvarum*, *L. casei*, *P. acidilactici*, and *P. pentosaceus* for feed fermentation and to analyse the influence of fermentation on feed parameters, as well as on the piglet feces microbiota and mycotoxin biotransformation *in vivo*. The 36-day experiment was conducted using 25-day-old Large White/Norwegian Landrace (LW/NL) piglets with an initial body weight of 6.9–7.0 kg, which were randomly distributed into two groups (in each 100 piglets): control group, fed with basal diet, and treated group, fed with fermented feed at 500 g kg⁻¹ of total feed. It was found, that fermented feed can modify microbial profile change in the gut of pigs, and fecal microbiota analysis showed an increased number of beneficial bacteria in the treated group, particularly *Lactobacillus*, when compared with the

control group at the end of experiment. Mycotoxin analysis showed that alternariol monomethyl ether and altenuene were found in 61-day-old control piglets' feces and in fermented feed samples. However, alternariol monomethyl ether was not found in treated piglets' feces. Finally, feed fermentation is a promising means to modulate piglets' microbiota and to increase mycotoxin detoxification *in vivo*.

Keywords: fermentation; feed; piglets; microbiota; mycotoxins

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OCCURRENCE OF SOME C18:1 FATTY ACID ISOMERS IN GOAT'S MILK AND SERUM

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Milk fat contains over 400 fatty acids (FAs) with a different number of carbon atoms, various degrees of saturation: saturated (SFA), monounsaturated (MUFA), and polyunsaturated (PUFA), with *cis* and *trans* configuration and straight or branched carbon chains. Natural *trans* FAs typically arise from ruminant microbiota activity during the ruminal biohydrogenation of dietary FAs. Mainly C18 monoenoic *trans* FAs are formed with predominance of the 11 isomer *trans*-vaccenic (C18:1*t*-11) and *trans*-elaidic FA (C18:1*t*-9). The FA composition of milk has numerous effects on milk quality including its physical properties and nutritional value. Approximately half of the FAs in the milk are sourced from the blood. The aim of this study was to determine C18:1 isomers in goat's milk and serum. The research was carried out on 15 clinically healthy Saanen goats in two lactational phases (early, around 30th lactational day, L1; late lactation, around 150th lactational day, L2) and dry period (D). After the extraction of total lipids from the milk and serum samples, the analysis of methyl esters of FAs was performed using gas chromatography. The most predominant isomer in goat's milk, expressed as % of total FAs in milk (mean \pm SD), was C18:1*c*-9 (20.2 \pm 3.4%), followed by C18:1*t*-11 (6.6 \pm 1.7%), then by C18:1*t*-9 (1.8 \pm 0.8%) and C18:1*c*-11 (0.8 \pm 0.2%). Only C18:1*c*-9 showed significant difference in representation in two lactational phases, being significantly higher in L1 compared to L2 (22.9 \pm 2.6% vs. 17.8 \pm 1.9%; $p < 0.01$). The percentages of C18:1*t*-11 in L1 was positively correlated with that of C18:1*c*-9 ($r = 0.66$, $p < 0.05$) and negatively with SFA ($r = -0.7$, $r < 0.05$). In goat's serum the pattern of predominance of C18:1 isomers was similar as in milk (C18:1*c*-9, 16.9 \pm 8.1%; C18:1*t*-11, 3.3 \pm 1.4%) with the difference of C18:1*c*-11 being more represented than C18:1*t*-9 in serum than in milk (0.9 \pm 0.5%; 0.8 \pm 1.5%, respectively). Signif-

ificantly higher percentages of C18:1*t*-9, C18:1*c*-9 and C18:1*c*-11 were determined in L1 compared to D period ($1.1 \pm 2.3\%$ vs. $0.3 \pm 0.3\%$, $p = 0.04$; $19.5 \pm 8.0\%$ vs. $9.1 \pm 2.4\%$, $p < 0.01$; $1.1 \pm 0.5\%$ vs. $0.6 \pm 0.1\%$, $p < 0.01$, respectively). Furthermore, significantly higher percentages of C18:1*t*-9 and C18:1*c*-9 were determined in L2 compared to D period ($0.8 \pm 0.5\%$ vs. $0.3 \pm 0.3\%$, $p = 0.03$; $18.6 \pm 8.0\%$ vs. $0.6 \pm 0.1\%$, $p < 0.01$; respectively). Since *trans* FAs have both positive and negative effects on obesity, insulin resistance, cardiovascular disease, cancer and inflammation in human organism, there is a general suggestion to reduce their consumption. There is also interest in the role of *trans* isomers of 18:1 in mediating the milk fat depression associated with certain dairy diets.

Keywords: C18:1 isomers, milk, serum, goat

POSSIBILITIES OF FEED SUSTAINABILITY INCREASING ADDITIVES – FLAXSEED SQUEEZES AND EXTRUDATE – IN ORDER TO IMPROVE CARCASS AND MEAT QUALITY IN LITHUANIAN BLACK-HEADED SHEEP

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The aim of the experiment was to investigate the effect of the adding of flaxseed squeezes and commercial extrudate “Nutex” to feed on the carcasses and meat quality of sheep offspring. The experiment was performed in Šėduva Lithuanian blackhead sheep breeding department of of JSC “Genetiniai ištekliai”.

Four groups contained 8 lambs in each of them were used in this experiment. Every day for feeding of each group 300 grams per lamb of concentrated feed was used. First group (1) was fed with ration, including 10% flaxseed squeezes. Second group (2) was fed with ration including 10% flaxseed extrudate “Nutex”. Third group (3) was fed with commercial ration, prepared for growing lambs. All experimented sheep groups can eat hay *ad libitum*.

Fourth sheep group (4) was used as control. The lambs of this group were fed by ration, including homemade concentrates, consisted from 90% of barley and 10% of peas meal and grazed in pasture *ad libitum*. The weights of all groups lambs were 18–20 kg, in the beginning experiment and 43–46 kg in finish.

After slaughtering of lambs, the carcasses quality was evaluated according to the SEUROP system. Meat protein amount and fatty acid composition were determined by standard methods.

It was detected that the lambs feeding and keeping methods have an influence on lamb carcass quality. It is important to note that in experimental lambs' groups carcass yield, was 3.9–5.7% higher, conformation and fat classes of carcasses were in 1–2 units better than control group carcasses respectively. Differences between groups were statistically significant ($p < 0.05$).

This study data showed, that the content of saturated fatty acids in the intramuscular fat was 1.18% and 0.97% lower in experimental lambs groups, which were fed with flaxseed extrudate “Nutex”, and flaxseed squeezes compared

to control group ($p < 0.05$). Polyunsaturated fatty acids amount in experimental groups varied from 4.5% up to 5.1% of total fatty acids, at average 1.5% more than in control groups ($p < 0.05$).

In conclusion: Housing and feeding had an effect on carcass yield, conformation and fat classes and composition of fatty acids content in Lihuanian Blackhed Sheep offspring.

Keywords: lamb meat, carcass yield, conformation and fat classes. fatty acids, flaxseed squeezes flaxseed extrudate

ABSTRACTS

POSTER CONTRIBUTIONS

NUTRITIONAL LIPID QUALITY INDICES IN MILK OF DIFFERENT ANIMALS

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The components of milk provide valuable nutrients for the human body. Milk fat is one of the most complex natural fats that consist of approximately 400–500 fatty acids (FAs). According to the number of double bonds, the FA are classified in saturated fatty acids (SFA), monounsaturated fatty acid (MUFA), and polyunsaturated fatty acid (PUFA), where sum of MUFA and PUFA are total unsaturated FAs (UFA). The aim of the study was to evaluate the nutritional lipid quality indices in milk of different animals. Milk samples were collected from Croatian Lipizzan mares (N = 17), Simmental cows (N = 15), Istrian donkey jennies (N = 30) and Saanen goats (N = 15). Total lipids from the milk samples were extracted and the analysis of methyl esters of FAs was performed using gas chromatography. Indices of concern were: the PUFA/SFA, the hypocholesterolemic/hypercholesterolemic index ($h/H = [(C\ 18:1+PUFA)/(C14:0+C16:0)]$), index of atherogenicity ($AI = (C12:0+4*C14:0+C16:0)/UFA$), the index of thrombogenicity ($TI = C14:0+C16:0+C18:0)/[(0.5*MUFA)+(0.5*n-6)+(3*n-3)+(n-3/n-6)]$), and the peroxidation index ($PI = (\text{monoenoic acid} * 0.025) + (\text{dienoic acid} * 1) + (\text{trienoic acid} * 2) + (\text{tetraenoic acid} * 4)$). Mare's milk showed the highest PUFA/SFA index, while cow's milk had the lowest ratio. The h/H index was the highest in mare's milk; mean values were calculated for goat's and donkey's milk, while the lowest index was found in cow's milk. The higher concentration of C12:0, C14:0, and C16:0 in cow's milk can increase the cholesterol concentration in serum by inhibiting the activity of low-density lipoprotein receptors. The AI as well as TI were the lowest

in mare's milk, mean values were calculated for goat's and donkey's milk, while the highest index was found in cow's milk. These indices depend on the SFA concentration due to C12:0, C14:0, and C16:0 favour the adhesion of lipids to cells of the circulatory and immunological systems and have pro-thrombogenic effect in blood vessels. Mare's, donkey's, and goat's milk had n-6/n-3 ratio below 4.0, which is recommended level by the World Health Organisation; while in cow's milk it was 4.54. In mare's milk PI was 41, which compared to PI values for donkey's (19), goat's (10) and cow's milk (3.4), makes it very sensitive to oxidation. Based on results it can be concluded that mare's milk has the most favourable nutritional lipid quality indices, but due to high PI, it is recommended to be cooled down quickly, and when fresh, to be used within 6–9 hours after milking.

Keywords: milk, nutritional quality indices, fatty acids

EFFECT OF DIET WITH GENETICALLY MODIFIED SOY TO GUINEA PIG LIVER MORPHOLOGY

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Introduction. There are limited data in the scientific literature on the role and metabolism of genetically modified soy in guinea pigs. Researchers have found that soy reduces total plasma cholesterol and reduce atherosclerotic lesions in guinea pigs (1, 2). The aim of this study was to investigate the effects of genetically modified soy, on histomorphological liver changes in guinea pigs.

Material and methods. Average weight of guinea pigs was 911.7 ± 1.24 g, they were divided in to two groups. Guinea pigs of group I (n = 6) were fed with commercial pellets without genetically modified components, animals of group II (n = 6) were fed with ration from soya meal, made from genetically modified soy for six months. In pellets of group I crude protein was 19.91%, crude fat 12.05%, crude fibre 2.79% and all animals get high quality of hay and water *ad libitum*. In pellets of group II crude protein was 21.50%, crude fat 6.00%, crude fibre 3.96% and all animals get high quality of hay and water *ad libitum*. Guinea pigs of group I and group II have got of 20 mg of vitamin C kg⁻¹ of body weight daily. The specimens of liver of all examined guinea-pigs were collected during the autopsy for histopathological examination. The samples were immediately fixed in 10% buffered formalin. The paraffin blocks were made using the tissue processor (Shandon Pathcentre, UK, 2004) and paraffin block embedding centre Tess 99” Medite, USA. Serial 4- μ m sections were prepared with a “Sakura Accu-Cut SRM” microtome. Every specimen of the liver was stained with haematoxylin-eosin (HE). The histopathological analyses were performed using the Olympus microscope supplied with the digital Olympus DP72 image camera with CellSensDimension software. Confidence interval (CI) was calculated for evaluation of pathologies rate in the liver. Data were considered statistically significant at $p < 0.05$.

Results. No significant hepatic changes were observed on histopathological examination. The following pathologies in liver of group II were found: hepatocyte swelling (hydropic degeneration), liver hyperaemia and mild inflammatory

response. Swelling of hepatocytes was found in the majority of cases and accounted for 75% (95% PI: 48-93), a mild inflammatory response was observed in 44% (95% PI: 20–70) of guinea pigs, hepatic hyperemia were observed in 31 proc. (95% PI: 11–59). No statistically significant difference was found between pathologies ($p > 0,05$). Mild and severe swelling of hepatocytes predominated. In cases of hydropic degeneration almost all hepatocytes were enlarged, irregular in shape, pale in color, with pressure on adjacent capillaries. In the case of inflammatory response, borderline leukocyte adhesion in the blood vessels, or heterophils aggregation in the vascular lumen, or stroma (acute course) were found. Less frequently small focuses of lymphocytes in the stroma of the liver were seen. No lipidosis was observed in guinea pig liver.

Conclusion. In our experiment guinea pigs that received genetically modified soy had swelling of hepatocytes and mild inflammatory response. A mild inflammatory response may be associated with damaging of hepatocytes or unidentified infectious agents.

Keywords: guinea pig, diet, liver histopathology

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INFLUENCE OF METABOLIC DISORDERS ON DYNAMICS OF MILK YIELD IN COWS

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According to research data, approximately 80% of productive cows on dairy farms suffer from metabolic diseases, which can be caused by cows' productivity, housing conditions and feeding (1). The development of certain metabolic disorders initially occurs without certain clinical signs, making it often difficult to detect reduced cow health and to diagnose certain diseases (2). In this case, regular blood and milk tests help. In dairy farms, cows that calve or are present for several days after calving are particularly observed, as cows lose large amounts of trace elements during this period (3).

Objective and tasks: The aim of this work is to evaluate the dynamics of cow milk yield under the influence of metabolic disorders in various Lithuanian dairy farms. In order to achieve this goal, the following tasks were set: to collect the results of the established indicators of the quantity, composition and quality of cow's milk and blood biochemical testing in different Lithuanian farms; analysis and comparison of milk quantity, composition and quality indicators of collected cows; analysis and comparison of blood biochemical parameters of collected cows; evaluation of the influence of metabolic disorders on the dynamics of cow milk yield in various Lithuanian dairy farms.

Material and methods: The study involved 165 dairy-type cows from ten Lithuanian farms suspected of having metabolic diseases based on clinical symptoms. Metabolic diseases were identified and differentiated according to changes in milk and blood biochemical parameters. Milk samples were collected at the one breeding company in the "Power BI" system. Blood samples were tested and analyzed in different laboratories and submitted to this breeding company. Interpreting the obtained blood biochemical parameters, cows were divided into three main groups according to the milk fat/protein ratio: <1 – acidosis, 1–1,5 – healthy animal, >1,5 – ketosis. The influence of metabolic disorders on milk intake was analyzed.

Results and conclusions: From all tested cattle, 67.2% of cows had fat/protein ratio within the normal range – the animal was healthy (1–1.5), 17.4% had acidosis when a fat/protein ratio was (<1), meanwhile 15.4% – had ketosis at

a fat/protein ratio (>1.5). Blood biochemical tests showed that all cows had low levels of Cu (100.0%), more than half of cows had low levels of GLU (64.0%), Fe (60.0%), and T-Pro (54.3%). Increased levels of T-Bil (63.0%), Mg (98.3%), and Na (88.9%) were also found for most cows. An increase in blood T-Bil (100.0%) was observed in all cows with ketosis. The amount of milk received per day varies in cows with acidosis, ketosis, and healthy cows. It was found that cows with ketosis (48.22 ± 10.8 L/d) and acidosis (43.18 ± 10.9 L/d) produced significantly more milk per day than healthy cows (41.48 ± 11.2 L/d) ($p < 0.05$).

Keywords: milk yield, ketosis, acidosis, metabolic diseases, metabolic disorders, cows, indicators of cow milk quantity, composition and quality, blood biochemical indicators

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EFFECT OF *LACTOBACILLUS PLANTARUM* (LUHS135) AND *THYMUS VULGARIS* ESSENTIAL OIL ON SUFFOLK LAMB BREAD MEAT (*MUSCULUS GLUTEUS*) QUALITY PARAMETERS

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The aim of this study was to evaluate *Lactobacillus plantarum* (LUHS135), *Thymus vulgaris* essential oil (0.1% v/v) and their combination were used to treat *Suffolk* lamb meat. Changes in the microbiological profile and physicochemical parameters of meat were evaluated after 24 h of treatment at 4 °C. The results showed in significantly lower mould/yeast, total enterobacteria (by up to 45%) counts, water-holding capacity (by 21–55%) and cooking loss (by 17–20%) in all samples. Moisture content increased, on average, by 14.5% in the *Suffolk* meat. Polyunsaturated fatty acid content increased after all treatments. Experiment and breed significantly affected the content of malondialdehyde and some biogenic amines. Sensory analysis showed that raw lamb meat colour was more acceptable after all treatments, while the odour acceptability was ranked highest after combined treatment. These findings suggest that the applied treatments could be used to improve microbiological safety and some quality characteristics and to increase the PUFA content of lamb meat.

Keywords: lamb meat, thymus essential oil, lactic acid bacteria

EARLY ADMINISTRATION OF BOVINE COLOSTRUM INDUCES IN THE DIVERSITY OF INTESTINAL MICROBIOTA OF THE CALVES

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Introduction. Intestinal microbiota plays an important role for the health and early survival of neonate calves. Bovine colostrum (BC) is rich in numerous bioactive molecules that could play a role in maintaining the healthy composition of intestinal microbiota of the calves. In this study we aimed to characterize longitudinal changes of intestinal microbiota in neonate calves that received BC and artificial colostrum replacer (CR).

Methods. The composition and diversity of fecal microbiota in neonatal calves was evaluated by using amplicon-based 16S rRNA metagenomic analysis. The total fecal genomic DNA was isolated from snap frozen fecal samples collected from calves undergoing feeding with BC ($n = 5$) or CR ($n = 5$). Samples were collected at day 1, 7 and 30 post partum to represent early, mid and late metagenomes. The amplicon was generated by using universal primers and sequenced with Illumina NextSeq 2000.

Results. Early administration of BC in neonatal calves resulted in the significant changes of intestinal microbiota in comparison to CR. BC administration resulted in higher abundance of probiotic *Clostridium IV*, *Anaerostipes*, and *Bifidobacterium*. Interestingly lactic acid producing *Kandleria* was only found in animals treated with BC.

Conclusion. Bovine colostrum plays an important role in the early development of intestinal microbiota in neonatal calves. Further studies are needed to

better understand the BC mechanism of action on the host, microbiota, pathogens and signals sent to intestinal immune response.

Keywords: calf, fecal microbiota

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ANALYSIS OF THE INFLUENCE OF QUAIL SEX AND AGE ON BIOCHEMICAL BLOOD PARAMETERS AND CHEMICAL COMPOSITION OF MEAT

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The gourmet meat of quail is successfully competing in the world market with chicken broiler and turkey meat, because of high nutritional value and medical reasons (1). The nutritional value of meat can be assessed by examining its chemical composition, which is influenced by many different factors such as breed, genotype, feeding characteristics and subclinical infections, age, and sex of the slaughtered birds (2, 3).

This study was selected to determine the age- and sex-dependent changes in the chemical composition of quail's meat, considering the optimal time of slaughter of quails of the respective sex, and to evaluate changes in blood biochemical and morphological parameters associated with quail sex and age.

Objective and tasks: To collect blood and meat samples of the subject groups (quails of different age and sex); to determine, analyze and compare both the biochemical and hematological blood parameters in subject groups; to determine the meat chemical composition in subject groups.

Material and methods: Data has been collected from the blood and meat samples of 72 Japanese quails from X farm, which were raised under the same conditions and were different ages (5, 6, 7, 8 weeks old) and sex. Hematological analyzer IDEXX ProCyte Dx®, clinical biochemical blood analyzer Dialab Autolyser and food analyzer FoodScan™ were used for the study.

Results and conclusions: It was determined that all male quails (no matter the age) had higher levels of blood haematocrit (HCT) 12.8% ($p < 0.05$), red blood cell count (RBC) 6.7%, hemoglobin (Hgb) 3.9%, mean corpuscular volume (MCV) 5.0% ($p > 0.05$), high-density lipoprotein (HDL) cholesterol 323% ($p < 0.001$), aspartate aminotransferase (AST) 12.0% ($p > 0.05$) and lower levels of mean corpuscular haemoglobin (MCH) 2.1% ($p > 0.05$), mean corpuscular hemoglobin concentration (MCHC) 7.5% ($p > 0.05$), alanine aminotransferase (ALT) 47.1% ($p < 0.001$), total protein (TP) 58.4% ($p < 0.001$), triglycerides (TGL) 513.0% ($p < 0.001$), calcium (Ca) 161.0% ($p < 0.001$), phosphorus (P) 49.0% ($p < 0.05$) and alkaline phosphatase (ALP) 94.2% ($p > 0.05$) than female quails. With age levels of HCT ($p < 0.05$), RBC

and Hgb ($p > 0.05$) get higher, and AST ($p > 0.05$) activity slows down both in female and male blood. As females grow, their concentration of Ca ($p < 0.05$) and TP ($p > 0.05$) in blood consistently increase. Regardless of age at slaughter, male quails had 28.5% more salt ($p > 0.05$) in their meat compared to female quails. Sex didn't have any significant impact on other chemical characteristics of meat (moisture, fat, protein, connective tissue, collagen and proteins without collagen). With the increase of age, moisture in meat decreases ($p < 0.05$), and fat increases ($p > 0.05$).

Keywords: quails, hematological and biochemical parameters, chemical composition of meat

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THE EFFECT OF ADMINISTRATION OF A PHYTOBIOTIC CONTAINING CINNAMON OIL ON MICROBIOLOGY AND HISTOLOGY OF JEJUNUM OF BROILER CHICKENS

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In poultry farming, additives are sought after to improve the health and growth performance of birds while meeting their nutritional requirements. Phytobiotics play a growing role as potential alternatives to antibiotic growth promoters (AGP) because they are natural, easily available, nontoxic, and residue-free. Phytobiotic additives can stimulate the appetite, increase secretion of digestive enzymes, stimulate immunity, and exert bactericidal, antiviral, and antioxidant effects, as well as improve growth performance and the quality of animal products [1].

It was postulated that the addition of a phytobiotic preparation containing cinnamon oil and citric acid to drinking water for chickens in a suitable amount and for a suitable time would beneficially modify the microbial composition and morphometry of the small intestine. The aim of the study was to determine what dosage of the phytobiotic and what duration of administration would have the most beneficial effect on the histology and microbiological composition of the intestine of broiler chickens.

The experimental procedure was approved by the Second Local Ethics Committee for Experiments with Animals in Lublin (approval no. 38/2018). The experimental design for administration of the phytobiotic preparation is shown in Table 2. The experiment was carried out on 980 chickens assigned to seven experimental groups of 140 birds each (seven replications of 20 individuals each). The control group (G-C) did not receive the phytobiotic. The phytobiotic preparation containing cinnamon oil was administered in two different application modes: continuous (CT-continuous application) and periodic (PT-periodic application). Groups CT-0.05, CT-0.1, and CT-0.25 received the phytobiotic in their drinking water in the amount of 0.05, 0.1, and 0.25 mL/L, respectively, at days 1–42 of life. The birds in groups PT-0.05, PT-0.5 and PT-0.25 received the probiotic in the same amounts, but only at days 1–7, 15–21, and 29–35 of life (21 days in total).

The samples of the jejunum were collected and placed in sterile containers. The material was then subjected to microbiological analysis to determine the number of aerobic bacteria, the final identification of the bacterial colonies

was performed using API tests (bio-Mérieux, Warszawa, Poland), according to PN-ISO 4832, PN-EN ISO 7218, and PN ISO 4832. Intestinal samples collected during dissection were subjected to histological evaluation. From each intestinal sample, 20 intestinal villi were selected. A representative section 2 cm in length, cut 1 cm behind Meckel's diverticulum toward the caecum, was collected for histological examination. A computerized microscopic-image-analysis system was used to estimate villus length and crypt depth. A light microscope (Nikon Eclipse E600) with a digital camera (Nikon DS-Fi1) and a PC with image analysis software (NIS-Elements BR-2.20, laboratory imaging) were used.

Of the three doses (0.05, 0.1 and 0.25 mL/L water) of the phytobiotic containing cinnamon oil administered to chickens, the most beneficial was 0.25 mL/L water administered for 42 days. Chickens receiving the phytobiotic at 0.25 mL/L had the best growth performance, which was linked to the beneficial effect of the preparation on the microbiome and morphometry of the small intestine, on the metabolism, and on the immune and antioxidant systems.

Keywords: phytobiotic; cinnamon oil; nutritional supplement; microbiological parameters

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COMPARISON OF TWO BEHAVIORAL TESTS ON THE CHINCHILLA'S RESPONSE TO HUMANS

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The aim of the study was to determine the reaction of farm chinchillas to humans based on the results of two behavioral tests: the hand test and the empathic test, as well as to calculate the correlation between results of these two methods.

The experiment was carried out at the chinchilla breeding farm in southern Małopolska. The chinchillas were kept in accordance to the national regulations, in a polygamous system, in the standard cages with a wire floor. 252 chinchilla females (2, 3 and 4 y.o.) of the standard variety were included in the research. For 6 months, a hand test and an empathic test were carried out alternately every two weeks. The hand test (HT) was performed by placing the hand into the cage [2, 3], while the empathic test (ET) consisted of inserting a stick with a ribbon tied at its end inside the cage, without the door opening [4, 5]. The mean scores of both tests were used to classify the animals' responses to human as a: confident, cautious, nervous, aggressive.

The vast majority of the tested females were characterized by a cautious response to human (138 ind. classified by HT and 161 ind. classified by ET). Consequently, there were 87 nervous animals according to HT and 67 according to ET. An interesting situation occurs when we take a look at the extreme types of reaction, i.e. a confident and an aggressive animals. On the basis of the hand test, 9 confident and 18 aggressive were distinguished, while according to the empathic test, 21 confident and 3 aggressive were distinguished.

It is worth noting that when using the ET to assess chinchilla's response to humans, animals were more often classified as confident and cautious than in the case of the hand test. Despite some differences between the two tests for animal response to humans, their results were correlated. The value of the coefficient of correlation for the performed tests was $r = 0.4979$ ($p < 0.01$). On this basis, it can

be concluded that the tests performed with both methods confirm each other. On the other hand, presented research showed that chinchillas' response to the empathic test was less pronounced, which made it less suitable for assessing chinchilla temperament type and response to human. The hand test gave much more unambiguous results and, in our opinion, it is more useful in the assessment of the human–animal relationship as an important determinant of animal welfare.

Keywords: chinchilla, behavioral tests, human-animal relationship, animal welfare

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INVESTIGATION OF ATTENUATION VALUES IN HEALTHY AND BENIGN PROSTATIC HYPERPLASIA DIAGNOSED INTACT MALE DOGS

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Introduction. Benign prostatic hyperplasia (BPH) is the most common disease in older intact male dogs. It is important to note, that BPH in many cases are asymptomatic and no clinical signs can be present [1]. Ultrasonography is used in veterinary practise as a “golden-standard” method for prostate gland evaluation. However, computed tomography (CT) nowadays is frequently used in veterinary practise. It has been described that CT is a valuable method in examination of reproduction tract organs, including prostate gland [2,3]. Our study goal was to evaluate the attenuation values of the prostate gland in 4 different contrast phases in healthy and BPH diagnosed intact male dogs.

Material and methods. 20 large breed, private-owned, older than 5 years intact male dogs were included in the study. All male dogs were examined clinically. No male dogs showed any clinical signs and no medical history in past year based on reproductive tract organ disorders were presented by the owners. Breeding history was provided and none of the male dogs were bred in the last 3 months. All examinations were performed under the request of the owners. At first, prostate glands were examined using ultrasound. Then ultrasound-guided fine needle aspiration was performed and prostate gland tissue specimens were collected using technique proposed by Kustritz et al. [4]. Two study groups were formed: 10 male dogs (experimental group) diagnosed with BPH by cytological examination of prostate gland tissue. Other 10 males (control group) were clinically healthy based on cytological findings. Then computed tomography (CT) was carried out based on protocols proposed by Pasikowska et al [3]. Four contrast phases were recorded: arterial, native, venous and accumulation. Attenuation values were calculated by CT software and referred in Hounsfield Units (HU)

Results. Our results showed, that mean \pm SD attenuation values in experimental group were 64.18 ± 14.79 HU in venous phase, 37.47 ± 7.84 HU in native phase, 52.59 ± 15.77 HU in arterial phase and 64.53 ± 12.59 HU in accumulation

phase. In contrariety, these values were lower in control group: venous phase 53.67 ± 13.10 HU, native phase – 34.33 ± 4.64 HU, arterial phase – 45.67 ± 9.46 HU and accumulation phase – 56.33 ± 9.18 HU.

Conclusion. Study results suggested that attenuation values of prostate gland in different contrast phases can be used as a marker for BPH diagnosis. However, further investigations with larger sample size are recommended.

Keywords: prostate gland, benign prostatic hyperplasia, computed tomography

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BACTERIA ISOLATED FROM BROILERS SUBCUTANEOUS TISSUE OF MYOPATHY AFFECTED AREA

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Introduction. Myopathies of *m. anterior latissimus dorsi* (Dorsal cranial myopathy – DCM) and *m. pectoralis major* (Pectoral myopathy – PM) are mainly evidenced in fast-growing, heavy weight broilers (1, 2). These muscle pathologies not only alter meat visual appearance, but also downgrade meat quality. The presence of bacteria in carcasses of broilers with myopathies has not been widely investigated. Various microbiotas are hosted in the digestive tract, lungs, skin, feathers of broilers. In slaughterhouses, the surfaces, air and liquids also encompass bacteria. An increase in faecal indicator microorganisms may be noted during the slaughtering process, with a subsequent contamination of the environment by microorganisms, which may be a source of contamination for industrialized food (3, 4).

The aim of this study was to isolate bacteria from subcutaneous tissue which covers *m. pectoralis major* and *m. anterior latissimus dorsi* which are affected by myopathy.

Methods and materials. Male and female chickens (n = 24), bred and raised in Lithuania, 41 days old, Ross 308 broilers were slaughtered at a commercial slaughterhouse according to standard industrial practices. All broilers used in this study were raised without antibiotics. Broilers were macroscopically examined in slaughterhouse in order to assign them to particular group according to type of myopathy, samples were taken for microbiological analysis. I group (n = 12): broilers (n = 6) with DCM and broilers (n = 6) with no DCM lesions (control group) were selected. II group (n = 12): broilers (n = 6) with PM myopathy and broilers (n = 6) with no PM myopathy (control group) were selected. Samples for microbiological study were collected aseptically with sterile cotton swab from subcutaneous tissue of the myopathy affected area. The samples were placed into Amies transport medium and taken to the laboratory in less than 12 hours. The obtained samples were cultured aerobically on selective and differential

media. Microorganisms were identified according to biochemical and antigenic characteristics.

Results. Overall incidence of PM and DCM in Lithuanian poultry farms (in Ross 308, meat-type broilers) is 1,9–29,8% and 0,6–9,2% respectively. During microbiological analysis *Hafnia alvei* was isolated from samples of broilers with PM myopathy (100%), whereas *Enterococcus viikkiensis* was isolated from samples which were taken from broilers with no evidenced PM myopathy (100%). *Enterococcus viikkiensis* (33,33%), *Escherichia coli* (33,33%), and *Hafnia alvei* (16,67%), were isolated from samples which were taken from broilers with DCM myopathy. In one of the samples which was taken from broilers with DCM myopathy bacteria were absent (16,67%). *E. coli* was isolated from samples of broilers with no evidence of DCM myopathy (100%).

Conclusions. This study revealed that bacteria, including faecal indicator microorganisms, were isolated from all investigated groups of broilers belonging to the non-pathogenic environmental microbiota. *Enterococcus viikkinesis*, *Escherichia coli* and *Hafnia alvei* were isolated from all groups of broilers with and without myopathies. Regular cleaning and disinfection of all equipment, even during slaughtering, are necessary, and their respective efficiency must be checked.

Keywords: broilers, myopathy, bacteria

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VARIATION OF QUALITY PARAMETERS OF CURED MEAT SAUSAGES REVELLED BY HISTOLOGICAL ANALYSIS

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The objective of this study was to evaluate the quality of cured meat sausages by quantification of skeletal muscles, adipose tissue, connective tissues and blood vessels and spices by histological analysis and automated image analysis.

Sample collection. Sausages of two local producers (A and B) were collected within a one-month period at retail shops in Kaunas, Lithuania. Sampling included 28 sausages samples of first and extra quality categories as indicated by the producer on the label.

Histological analysis. Samples of each cured sausage were fixed in 10% neutral buffered formalin and routinely processed for paraffin embedding (1). Three histological sections (5 µm thickness) of each cured sausage sample were stained with Calleja method (2). The histological sections were examined with a BX43 light microscope with digital camera DP73 (Olympus, Tokyo, Japan).

Image analysis. One of three prepared sections was used for image analysis to quantify the amount of individual animal tissue content. Different tissues were detected and scored with automated and manual colour threshold image analysis by use of an Olympus BX43 light microscope and image analysis program “Olympus Stream Essentials” version 1.9.1 (Olympus, Tokyo, Japan).

Statistical analysis. Statistical analysis was performed using SPSS Inc., SPSS 24, Chicago, IL, USA and mean values, standard deviation and statistical significance at $P < 0,05$ were calculated.

The histological evaluation of the cured sausage samples revealed different types of tissues (skeletal muscles, adipose, connective, blood vessels, nerves, glandular) found together with spices. Also, the study showed differences of the tissue composition of cured sausages of two producers and differences between sausages assigned to the first and extra quality categories. The highest mean values of skeletal muscles were found in cured sausages of extra quality of producer A (42,8%), first quality of producer A (41,37%), extra quality of producer B (43.49%), and first quality of producer B (45.49%), respectively. The content

of adipose tissue varied from 48.37% (extra quality) to 46.42% (first quality) in sausages of producer A and from 35.23% (extra quality) to 27.22% (first quality) of producer B, respectively. Whereas the content of connective tissue varied between 10.02% (first quality, producer A) and 12.63% (first quality, producer B). Most of the blood vessels and spices found in the sausages of first quality produced by producer B (98.75%).

We have detected glandular tissues and nerve fibres only in 4 samples. No cartilage and bone tissues were found in any of the examined samples.

This study shows that histological analysis was very useful to identify tissue components of sausages and quantify tissue content. Automated image analysis enables to perform quantitative evaluation of tissues contents of meat products. However, it is recommended to validate histological analysis results with additional methods.

Keywords: cured meat sausages, quality, animal tissues, histology

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INFLUENCE OF HERBAL RUMEN – PROTECTED CHOLINE ON DAIRY COWS' INSEMINATION TIME, INCIDENCES OF MASTITIS AND UTERUS INFECTIONS

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Rumen protected choline plays an important role in dairy cattle reproduction performance after calving [1]. A recent study showed less incidences of metritis, endometritis, pyometra and retention of placenta [2]. The objective of this study was to evaluate the influence of organic herbal preparations containing choline analogues on time from calving till first, second, third insemination and incidences of udder and uterus infections. One hundred similar yielding (9000–10000 kg/lactation), lactation (2–4), BCS (3.75–4) Lithuanian Black and White healthy dairy cows were grouped into two equal groups: experimental (RPC) and control. Both groups were fed TMR and the RPC group was supplemented with rumen protected choline from – 21 day to 60 DIM. Cows were inseminated when standing reflex was determined (cows' oestrus were monitored 3 times per day for 15 min). Mastitis was diagnosed by increased SCC and clinical signs: mammary gland swelling and local fever. Uterine infections were diagnosed by uterine discharge (metritis considered till 21 DIM, endometritis – from 21 DIM). Cows with mastitis, metritis and endometritis were treated according to routine farm practice. RPC group cows had earlier 8.08% first and 8.14% second inseminations ($p < 0.05$). Clinical mastitis and uterine infections incidences were determined 12.0% less in RPC group ($p < 0.001$). Uterine infections have occurred 31,15% more times till 32 DIM in RPC group ($p < 0.05$). Metritis and endometritis treatment time was 6.7% shorter in RPC group ($p < 0.05$). In conclusion, supplementing RPC improve reproductive parameters due to shortest time before first and second inseminations and reduce incidences of mastitis, uterine infections and reduced uterine infection treatment time.

Keywords: choline; endometritis; mastitis; metritis; RPC; uterine infection

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EFFECT OF A DIET SUPPLEMENTED WITH *ASPERGILLUS ORYZAE* AND YEAST ON RUMINAL PROTOZOA, PH AND VFA PRODUCTION

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The aim of this investigation was to define the effect of diet supplementation with *Aspergillus Oryzae* and active yeast on the ruminal protozoa, pH and VFA production in cows. For this purpose 15 clinically healthy crossbreed (Lithuanian Black-and-White & Holstein) mid-lactation dairy cows were selected and divided into 3 groups (5 cow/group) applying the principle of analogous (considering lactation, parity, productivity during former lactation, animal's weight, milk production). All cows were fed basal diet balanced to meet maintenance and production needs. Cows were divided into the groups according to the dietary supplement: the control (C) group – basal diet with no supplementation; the test group 1 (T-1) – basal diet supplemented with prebiotics mix of *Aspergillus oryzae* fermentation extracts, inactive *Saccharomyces cerevisiae*, and *Kluyveromyces marxianus* (5 g/cow/day); and test group 2 (T-2) – basal diet supplemented with combination of prebiotics mix (*A. oryzae* fermentation extracts, inactive *S. cerevisiae* and *K. marxianus* (5 g/cow/day)) and live dry yeast *Saccharomyces cerevisiae* CNCM-1077 (1 g/cow/day). Supplements were topdressed on the basal diet.

The experiment lasted for 30 days. At the end of the experiment the rumen fluid of was collected and analyzed. The rumen fluid samples were collected by a stomach tube 3 hours after morning feeding from cows of each group. The rumen fluid was analysed for protozoa count, pH and total volatile fatty acids (VFA).

Protozoa were counted in a Fuchs-Rosenthal chamber (Blaubrand, Wertheim, Germany) and identified morphologically to the genus level. Ruminal pH was measured immediately after sampling by pH-meter (Horiba-Twin pH, Spectrum Technologies). Total VFA amount was defined by rumen fluid distillation in a Marcmagus apparatus. Statistical analyses were carried out using SPSS (IBM

Corporation, USA) and mean values, standard deviation and statistical significance at $p \leq 0.05$.

The results of the studies assessed all tested ruminal parameters were within the physiological norm in all three groups.

At the end of experiment (d30) total count of protozoa in the rumen of cows group T-2 increased by 58.8% ($p = 0.001$) while in group T-1 protozoa count increased by only 0.3% ($p > 0.05$) compare to the results of C group. Following genera of protozoa: *Diplodinium*, *Entodinium* and *Enoploplastron* were predominated in the rumen of all groups of cows. At the d30 count of the genus *Diplodinium* in the rumen of cows group T-2 increased 2.2 ($p = 0.001$) and genus *Entodinium* – 2.4 ($p = 0.001$) compare to the results of the group C.

The pH was in 10,09% higher of T-1 group to compare with T-2 group with values 6.74 ± 0.16 and 6.06 ± 0.389 respectively. The ruminal pH value was 0.19 higher ($p = 0.001$) and in 0.31 lower ($p = 0.009$) of groups T-1 and T-2 respectively to compare with group C.

The highest detected VFA production was in group T-2 fed (140 ± 11.55 mmol/L at day30) and it was higher in 26.7 mmol/L ($p = 0.001$) and in 6.7 mmol/L ($p = 0.026$) to compare with group C and T-1 respectively.

In conclusion, the basal diet supplemented with combination of prebiotics mix of *A. oryzae* fermentation extracts, inactive *S. cerevisiae*, *K. marxianus* and live *S. cerevisiae* has statistically significant effect on the total count of protozoa and genera *Diplodinium* as well as *Entodinium* in the rumen fluid of cows and increased ruminal pH within optimal physiological ranges. Consequently, active yeast supplement positively effected total VFA production in rumen.

Keywords: protozoa, pH, VFA, Aspergillus Oryzae, yeast, rumen

RUMEN ARCHAEA INTERACTION WITH VOLATILE FATTY ACIDS

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Methane gas is one of the climate changes affecting gases. CH₄ emissions from ruminants account for about 81% of methane emissions from the livestock sector, of which 90% are the result of methanogenesis by rumen microbes. As rumen archaea is involved in fermentation process is important to know which of biochemical fermentation parameters it could be related. For this reason, we calculated correlation by using DNA sequencing and fermentation biochemical parameters data from 54 rumen samples.

The DNA was isolated from the rumen contents using a solution of phenol, chloroform and isoamyl alcohol. The QIAquick PCR Purification kit (Qiagen, Germany) was used for DNA isolation and purification. Libraries of bacterial 16S ribosomal RNA gene (rRNA) V4 region were prepared following the “16S metagenomic sequencing library preparation” protocol (Illumina), by using 515 F and 806R primers with Illumina adapters. Libraries were sequenced with Illumina MiSeq (Finnish Functional Genomics Centre, Turku) using PE approach and 2 x 250 bp chemistry. Sequencing data were further processed using Qiime v 1.9.1

The pH of a sample of rumen contents was measured immediately after collection using a Twin pH meter (Horiba, Japan). Volatile fatty acid (VFA) levels in rumen contents samples were determined by gas chromatography. Acetic, propionic, isobutyric, butyric, methyl-valeric, valeric, caproic and enanthic levels (mmol/L) were measured in rumen contents. A GC-2010 Plus gas chromatograph

(Shimadzu Corp., Kyoto, Japan) with a mass spectrometry detector GCMS-QP2010 (Shimadzu Corp., Kyoto, Japan) was used for VFA analysis.

Statistical analyses were calculated using the open-access online software Calypso, Version 8.84. The correlation coefficient (r) was calculated using Pearson. The strength of correlation was determined from the calculated r -value: strong: $r > 0.7$; medium strength: $0.4 \leq r < 0.7$; weak: $r > 0$. Results are considered statistically significant at $p < 0.001$, $p < 0.01$, and $p < 0.05$.

The five archaea species *Methanobrevibacter gottschalkii*, *Methanobrevibacter ruminantium*, *Methanosphaera ISO3.F5*, *Methanomassiliicoccaceae Group8*, *Methanomassiliicoccaceae Group10* were found which correlating with biochemical rumen parameters. *M. ruminantium* had positive correlation with propionic ($r = 0.397$; $p < 0.01$) and methhyl-valeric acids ($r = 0.403$; $p < 0.01$), negative correlation with butyric ($r = -0.355$; $p < 0.01$) and caproic ($r = -0.364$; $p < 0.001$) acids. *M. gottschalkii* correlated positively with butyric ($r = 0.384$; $p < 0.001$) and caproic acids ($r = 0.44$; $p < 0.001$). Negative correlation was estimated between *M. Group8* and caproic acid ($r = -0.380$; $p < 0.001$), *M. ISO3.F5* and rumen pH ($r = -0.316$; $p < 0.05$), *M. Group10* and propionic acid ($r = -0.285$; $p < 0.05$).

In conclusion, correlation results revealed that rumen archaea participate in rumen biochemical metabolism by interacting with VFA. Also, we can conclude that archaea species use VFA as energy sources, and archaea species abundance depends on VFA levels.

Keywords: cow, rumen, archaea, volatile fatty acids

SEMEN PARAMETERS OF THE POPIELNO WHITE RABBITS VS. MALE REPRODUCTIVE PERFORMANCE

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The aim of the study was to evaluate the basic semen parameters of White Popielno rabbits in relation to the breeding results obtained. Rabbits of this indigenous breed are included in Poland in the Programme for the Protection of Genetic Resources of Farm Animals. The study was performed on 24 ejaculates that were collected from 4 males using an artificial vagina and a provocateur. Each ejaculate was subjected to macroscopic and microscopic evaluation. On the basis of breeding cards as well as records of born and weaned offspring, mating efficiency, number of rabbits born per mating and born per litter were determined for each breeder. On average, the semen volume of individual males ranged from 1.15 ml to 1.5 ml. In contrast, sperm concentration and total sperm count in the ejaculate ranged from $158 \cdot 10^6/\text{ml}$ to $380 \cdot 10^6/\text{ml}$ and from $203 \cdot 10^6$ to $482 \cdot 10^6$, respectively. An average of 52% to 82% motile spermatozoa were observed in ejaculates. Morphological evaluation of spermatozoa showed that semen from one of the males contained more than 29% of abnormal spermatozoa. Additionally, it was characterised by low values of other sperm microscopic parameters. This individual achieved the lowest mating efficiency (40%), but the highest mean number of rabbits born per litter (9.25). For the remaining males, mating efficiency took values ranging from 47% to 73.5%. Breeders from a single mating produced an average of 3.21 to 6.72 offspring, while litter size averaged 6.43 to 9.14 offspring. The male with the highest mating efficiency and the most rabbits born from one mating had the highest average semen volume.

Keywords: Popielno rabbits, semen parameters, breeding results

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EFFECT OF LOW FREQUENCY OSCILLATIONS ON MILK YIELD, QUALITY AND COMPOSITION OF DAIRY COWS

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Carefully selected physiologically resonant frequencies can both suppress disharmonious fluctuations that occur in affected cells during inflammation, and normalize metabolic processes, accelerating the transport of inflammatory products due to the known effect of increasing vascular permeability [1], while recording weak currents caused by potentials of the udder cells themselves [2; 3]. The use of non-invasive methods ensures animal welfare and health, and the effects of acoustic low-frequency vibrations on the mammary glands are likely to stimulate blood circulation in cow udder and reduce the incidence of subclinical mastitis in dairy cows.

The objective of this study was to investigate the impact of low-frequency oscillations on milk yield, quality and composition of dairy cows.

The study was carried out on an organic dairy herd of 1330 Holstein-Friesian cows in 2021. The dairy parlors were equipped with an online computerized DeLaval Herd milking system. Fifteen multiparous lactating Holstein cows in middle lactation were used in the experiment.

According to the somatic cell count (SCC) in milk, determined by the California Mastitis Test, cows were assigned to three groups (5 cows per group). The Group I (control) consisted of clinically healthy cows with no evidence of mastitis (SCC < 200 000 cells/ml); the Group II consisted of cows diagnosed with subclinical mastitis (SCC > 200 000 cells/ml) and the Group III consisted of cows with clinical mastitis (SCC > 300 000 cells/ml). Cows of II and III groups were treated with low-frequency (X-axis – 25.0; Y-axis – 41.0 Hz) vibration devices on cow's udder during the automatic milking. Milk samples were collected from each cow for the milk's composition and quality analysis. For determining SCC and total bacterial count (TBC), the milk samples were analyzed by the flow cytometric analysis

according to the standard methods. The lactose, urea, fat, and milk protein levels were determined using the spectrophotometric method. One-way ANOVA were used to analyze the results of milk parameters. Significance was declared at $p \leq 0.05$.

Exposure of low frequency vibration on udder during milking process within a period of seven days significantly decreases the number of somatic cells in milk with clinical mastitis. During the first 5 days of the trial, the number of SCC has decreased from 2 million. up to 221 thousand/ml ($p < 0.001$), and on day seven amounted to 206 thousand/ml ($p < 0.001$). The total number of bacteria in milk with clinical mastitis over a 7-day period decreased from one million up to 25 thousand CFU/ml ($p < 0.001$).

Low-frequency vibrations reduced the number of somatic cells in the first 5 days of cows with subclinical mastitis from 453 thousand up to 227 thousand/ml ($p < 0.001$) on day seven has decreased to 196 thousand/ml ($p < 0.001$). The total number of bacteria in cow's milk with subclinical mastitis over a 7-day period decreased from 84 to 29 thousand CFU/ml ($p < 0.05$).

Low frequency oscillations were not affected SCC and TBC in the Group I (control) cow's milk. Used low-frequency vibrations did not significantly affect milk yield, milk composition indicators (fat, protein, lactose, urea).

Keywords: low frequency oscillations, cow, milk quality

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THE INFLUENCE OF AGE AND SEX ON THE INCIDENCE OF UROLITHIASIS IN DOGS

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Urolithiasis is a common and often recurrent problem in dogs (1). Urolithiasis is a multifactorial disease with implied epidemiological aspects influenced by different risk factors. These include breed, sex, age, diet, anatomical and functional urinary alterations, metabolic disorders, genetic predisposition, and bacterial urinary tract infection (2). Urolithiasis can occur at any age, from puppies to geriatric animals. Animals between five and eight years old are considered at greater risk. Perhaps in this age group, animals can commonly present systemic or metabolic diseases, including urinary tract alterations that can cause changes in its defense mechanisms and thus favor the presentation of urolithiasis (2). The aim of this study was to analyze the influence of sex and age on the incidence of urolithiasis in dogs and the most common clinical signs. Dogs (n = 69) with urinary tract stone were selected from the data system. The research was performed in accordance with the provisions of the Law on Animal Welfare and Protection of the Republic of Lithuania. The dogs were divided according to: breed, sex, age, manifestation of clinical signs depending on the type of crystals and uroliths localization; methods of visual diagnosis of urinary tract stone, crystal type, localization of uroliths. Statistical analysis was performed with SPSS v25.0 (IBM, USA) and Microsoft Excel programs. Data was statistically significant when $p < 0.05$. The results of the study showed that purebred dogs are more likely to have urinary tract stones than crossbreeds. Males (63.77%) were 1.76 times more likely to have urolithiasis than females (36.23%). Dogs suffer from urolithiasis 24 times more often than neutered dogs. The highest number of cases was found in the 6–10-year age group, the average age of a sick dog was 7.7 years. The most commonly detected crystals were struvite's (44.93%). Struvite's occurred 1.5 times more frequently in males than in females. There is a connection between the localization of uroliths and the type of urine crystals ($p < 0.05$). The most common symptom in urolithiasis was pollakiuria (25.39%), and the second most common symptom was hematuria (20.21%). In conclusion, the results of this study indicate that urinary tract stone disease was 1.76 times more common in males than in

females. Uncastrated dogs are 24 times more likely to develop urolithiasis than castrated dogs. Females aged 6–10 years suffer from urinary tract stone disease 2.4 times more often than females aged 11–14 years.

Keywords: age, sex, urolithiasis, dogs

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RELATIONSHIP BETWEEN MILK PRODUCTION, COMPOSITION AND SOMATIC CELL COUNTS

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Mastitis, which manifests as inflammation of the mammary gland, is currently one of the most widespread diseases affecting dairy cattle (1). The inflammation of mammary gland results in an influx of somatic cell, predominantly polymorphonuclear neutrophils, which lead to the elevation of the somatic cell count (SCC) in milk (2). Therefore SCC, which is a universally accepted parameter in the evaluation of udder health status, is widely used for monitoring milk quality and raw milk pricing in dairy farming (3). The aim of this work was to investigate relationship between somatic cell counts with milk production and composition. The study was carried out on 200 Holstein lactating dairy cows, in accordance with the Law on the Care, Keeping and Use of Animals of the Republic of Lithuania. Milk production was determined by control milking. Milk composition (milk proteins, milk fat, lactose concentration and somatic cell count) were performed in the laboratory at Joint Stock Company "Pieno tyrimai". According to the data cows were divided into fourth SCC groups (with SCC up to 100×10^3 cells/ml – group I, $100\text{--}200 \times 10^3$ cells/ml – group II, $201\text{--}400 \times 10^3$ cells/ml – group III and more than 401×10^3 cells/ml – group IV). The statistical analysis was performed using computer software SPSS 22. Data was statistically significant when $p < 0.05$. The results of this study showed that somatic cell counts are negatively correlated with milk production. Increased somatic cell count was found to decrease milk production ($p < 0.05$). The milk yield of the fourth group cows decreased by 11,5 percent compared to the first group of cows. The lowest milk fat, protein and lactose's count was found in milk with high somatic cell count (more than 401×10^3 cells/ml) ($p < 0.05$). In the fourth group of cows, the fat of milk (0,31%), proteins (0,17%), lactose (0,11%) concentration decreased compared with the first group of cows. Fat percentage had no significant relationship with protein yield ($p > 0.05$). High somatic cell count has a significant negative effect on protein, fat and lactose content in milk ($p < 0.01$). In conclusion, the results of this study

indicate, that the lowest milk yield and milk composition were observed in milk when SCC was more than 401×10^3 cells/ml).

Keywords: milk production, composition, SCC, cows

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EVALUATION OF ESSENTIAL OILS EFFICIENCY AGAINST *M. PACHYDERMATIS IN VITRO*

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According to the history, the benefits of aromatic oils were known of ancient Egypt people, who successfully used aromatic oils in medicine and cosmetics. Although essential oils have been known for a long time, we started to study the chemical and biological structure, pharmacokinetics and application of essential oils in modern medicine and everyday life, probably only a few decades ago [1].

With the increasing resistance of microorganisms to antifungal and antimicrobial agents, it is becoming increasingly important to discover alternatives that would also be effective in inhibiting pathogenic microorganisms. It is a public secret that due to the increasing resistance of bacteria and fungi, there may be a severe shortage of drugs in the future that will effectively provide the antimicrobial effects required for treatment.

For the determining whether the essential oil under test has antibacterial or antifungal activity different techniques could be used. The antibacterial activity of essential oils is effectively tested by the agar diffusion method, where the essential oils are added to agar in which the bacterial strain is uniformly infected. The result obtained is evaluated according to the size of the disc area and it is determined whether the essential oil has an antimicrobial effect. After incubation, the inhibition zone reflects the antimicrobial effect [2].

In this study 11 samples of the dogs were collected from both ears. Nine dogs were not identified with clinical symptoms consistent with otitis symptoms characteristic of otitis media in two dogs shaking of the ears, digging, discharge, unpleasant odor. The samples taken were collected using TransSwab bacteriological tubes. All samples were inoculated on petri dishes using dextrose agar. Samples are grown for 5 days at 30 degrees. In all the samples the *Malassezia* was observed, following a cytological test *M. Pachydermatis* was identified.

Efficiency evaluation results of the different essential oils in various concentrations on the *M. Pachydermatis* will be presented.

Keywords: essential oils, *M. pachydermatis*, antifungal activity, resistance

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THE EFFECT OF DOG AGE ON BACTERIAL COUNT IN SEMEN SAMPLE

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In literature, compared to human medicine the microbiota of dog semen is described uncertainly (1). It is known that some bacteria such as *Escherichia coli*, *Staphylococcus aureus*, *Mycoplasma canis*, *Pseudomonas aeruginosa* and *Streptococcus spp.* are normal flora in canine sperm and bacterial contamination up to 10⁴ CFU/mL are considered physiological for a dog semen sample (1, 2). In earlier researches it has been notified that bacterial count can impact sperm motility in other animal species (3). The aim of this study was to investigate bacterial count of dogs semen sample and the effect of dogs age to semen sample microbiota. In this study 30 canine semen samples from dogs of different age groups were collected manually and analysed. The range of dogs age was from 10 month to 12 years old. Dogs were divided into two age groups (young Y < 6 years; old O ≥ 6 years). The ejaculates (10 µL with serial dilutions) were cultured on blood agar and were incubated for 24 to 48 h at 37 °C in aerobic environment. Colony-forming units (CFU) were counted per millilitre of sperm sample. Bacteria identification was performed according to colony morphology, Gram staining and biochemical testing. The samples were divided into three groups according to bacterial count (group 1: < 10⁴ CFU/mL; group 2: 10⁴–10⁵ CFU/mL; group 3: > 10⁵ CFU/mL). Results of data analysis showed that smaller number of bacteria was detected in Y dog age group rather than in O group samples (1.67 × 10⁵ CFU/mL and 4.8 × 10⁵ CFU/mL respectively) (p < 0.05). Pearson correlation analysis showed that dog age and semen sample bacterial number correlates moderate (r = 0.422; p < 0.05). Overall, with age canine semen sample bacterial count changes significantly. Our study results proved that comparing samples of two different age group, bacterial count increases in senior dog sperm samples. This can be associated with dog prostatic problems which are more common in elder

age. According to that canine age significantly affects bacterial count in semen samples an assumption can be made that with age bacterial count can impact sperm motility to decrease.

Keywords: canine, semen, microbiota, age

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RUMINAL BACTERIA CORRELATION WITH BLOOD BIOCHEMICAL PARAMETERS

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The rumen microbiota is the most dynamic and largest gastrointestinal ecosystem in the animal kingdom which plays a major and critical role in cow production performance. Also, we think that ruminal bacteria are related to animal health and could correlate with blood biochemistry parameters. The aim of this study was to investigate ruminal bacteria correlation with blood biochemical parameters. The rumen contents and blood of 54 cows were taken. DNA was isolated from the rumen contents using a solution of phenol, chloroform and isoamyl alcohol. The QIAquick PCR Purification kit (Qiagen, Germany) was used for DNA isolation and purification. Libraries of bacterial 16S ribosomal RNA gene (rRNA) V4 region were prepared following the “16S metagenomic sequencing library preparation” protocol (Illumina), by using 515 F and 806R primers with Illumina adapters. Libraries were sequenced with Illumina MiSeq (Finnish Functional Genomics Centre, Turku) using PE approach and 2 x 250 bp chemistry. Sequencing data were further processed using Qiime v 1.9.1.

Blood biochemical tests were performed using a dry chemistry biochemical blood analyzer Spotchem EZ (Arkray, Japan) for total protein (TPro), albumin (ALB), total bilirubin (TBil), aspartate aminotransferase (AST), alanine aminotransferase (ALT), lactate dehydrogenase (LDH), Alkaline phosphatase (ALP) levels measurement. Glucose (GL) and β -hydroxybutyrate (BHB) levels were determined using a FreeStyle Optium Neo (Abbott Laboratories, USA) blood glucose and ketone meter.

Statistical analyses were calculated using the open-access online software Calypso, Version 8.84. The correlation coefficient (r) was calculated using Pearson. The strength of correlation was determined from the calculated r -value: strong: $r > 7$; medium strength: $\pm 7 > r \geq \pm 0.4$; weak: $\pm 0.4 > r > 0$. Results are considered statistically significant at $p < 0.001$, $p < 0.01$, and $p < 0.05$.

The results showed that positive correlation was estimated between ALB and *Succiniclacticum spp.* ($r = 0.295$; $p < 0.05$), Tbil and *Succiniclacticum spp.* ($r = 0.333$; $p < 0.05$). AST had positive relation with *Prevotella spp.* ($r = 0.360$; $p < 0.01$) and

Coprococcus spp. ($r = 0.362$; $p < 0.01$), negatively correlated with *Butyrivibrio spp.* ($r = -0.384$; $p < 0.01$), *Ruminococcus spp.* ($r = -0.419$; $p < 0.01$) and *Selenomonas spp.* ($r = -0.304$; $p < 0.05$). ALT correlated positively with *Treponema spp.* ($r = 0.311$; $p < 0.05$) and negatively with *Bifidobacterium spp.* ($r = -0.347$; $p < 0.05$), *Selenomonas spp.* ($r = -0.423$; $p < 0.01$). Blood LDH had positive relation with *Bifidobacterium spp.* ($r = 0.312$; $p < 0.05$), *Prevotella spp.* ($r = 0.370$; $p < 0.01$), *Coprococcus spp.* ($r = 0.539$; $p < 0.001$) and negative with *Fibrobacter spp.* ($r = -0.47$; $p < 0.001$).

The correlation results revealed, that the most abundant ruminant bacterial species influence cow blood parameters. In conclusion, keeping animals healthy and blood biochemistry parameters in optimal ranges is possible by maintaining ruminal bacteria.

Keywords: cow, rumen, bacteria, blood biochemistry

ANALYSIS OF COW MILK QUALITY INDICATORS IN DIFFERENT SIZE FARMS

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A very important indicator of quality for milk processors is the content of somatic cells and the total number of bacteria. An increase in the number of somatic cells in raw milk is associated with mastitis, an inflammatory reaction of the udder, most often due to bacterial infection (1). Somatic cell count is broadly used as an indicator for mastitis or intramammary infection and is the basis for udder health management programs (2,3).

The aim of this study was to analyze the milk quality indicators of cows in farms of different sizes.

Methods and materials. During the research, milk quality indicators of 12 farms in one district were analyzed: total number of bacteria, thousand CFU/ml, somatic cell count, thousand/ml, milk freezing point, m °C and milk pH. Dairy farms were divided into 4 groups according to the number of cows available: up to 10 cows; 11–50 cows; 51–100 cows; 101 and more cows. 3 farms were randomly selected in each group. Statistical analysis was performed by analysis of variance (ANOVA) using the statistical package SPSS 20. Mean values, mean errors and statistical reliability of the data were calculated. The results were considered reliable at $p \leq 0.05$.

Results and conclusion. We found that the highest total number of bacteria was in dairy farms keeping 101 and more cows, and it was 44.6 thousand CFU/ml higher than in farms keeping 11–50 cows ($p < 0.05$) and 21.8 thousand CFU/ml are higher in farms with 51–100 cows. After estimating the season of the year, we noted that the largest differences in the total number of bacteria in milk on different farms were during the autumn season and the smallest differences were during the winter. The highest number of somatic cells in milk was found in farms with up to 10 cows and was 136.1 thousand/ml higher than in farms with 11–50 cows ($p < 0.05$) and 73.4 thousand/ml higher, than 51–100 cows farms. Only in the autumn, the number of somatic cells in these farms was found to be 162.6 thousand/ml lower than in the farms with 51–100 cows. The highest milk freezing temperature was found in farms keeping 11–50 cows, and it was 0.01 m°C higher than in farms keeping up to 10 cows ($p < 0.05$). Milk pH was found to be

0.08 larger in farms with 101 and more cows than in farms with up to 10 cows. After evaluating the correlations between milk quality indicators, a weak positive (0.288) correlation was found between the number of somatic cells in milk and the total bacterial contamination of milk ($p < 0.01$).

Keywords: dairy cows, somatic cell count, total bacteria count

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THE IMPACT OF INCREASED DIETARY DL-ALPHA- TOCOPHEROL AND INORGANIC SELENIUM INTAKE ON RABBIT GROWTH PERFORMANCE

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The rabbit industry has made significant contributions to regional socioeconomic development in numerous nations over the last several decades (1). There is a substantial amount of multidisciplinary agricultural research on rabbits, covering meat quality, their behaviour and welfare, as well as growth performance. Many studies have investigated the impact of many factors on rabbit meat quality and growth performance, which can include variables such as housing conditions (2), limiting feed intake (3), and various feed additives (4,5). So, the aim of this study was to see how increased levels of DL-alpha-tocopherol and inorganic selenium additives can affect rabbit growth performance. The feeding trial started with a total of 16 Californian rabbits (42 days old), which were selected by weight and divided into 2 groups ($n = 8$ rabbits/group). Rabbits in the control group were fed a standard compound diet (SCD) + 50 mg/kg DL-alpha-tocopherol + 0.50 mg/kg inorganic Se, while rabbits in the experimental group were fed SCD + 100 mg/kg DL-alpha-tocopherol + 0.50 mg/kg inorganic Se. During the feeding trial, the following rabbits' growth performance indicators were evaluated: body weight, average daily gain (ADG), growth rate, daily feed intake (DFI), feed conversion rate (FCR), and total feed intake over the different feeding trial periods (42–112 days of age). Feeding trial results showed that the body weight of rabbits in the experimental group was 6% lower than in the control group at 84 days of age and throughout the whole feeding trial period (42–112 days of age) ($p < 0.05$). The ADG and growth rate of rabbits were lower in the experimental group over the whole feeding trial and separate trial times, although there were no significant differences between the groups assessed ($p > 0.05$). When compared to the control group, DFI in the experimental group was 5% lower at 42–56 days of age and 2% lower at 70–84 days of age, but 6% higher at 98–112 days of age ($p > 0.05$). Rabbits fed 100 mg/kg DL-alpha-tocopherols and 0.50 mg/kg inorganic Se (experimental group) consumed more feed and had significantly greater FCR and total feed intake compared to rabbits fed 50 mg/kg DL-alpha-tocopherols and 0.50 mg/kg inorganic Se (control group) at 56–70 and 98–112 days of age

of feeding trial ($p < 0.05$). According to the current findings, increased levels of DL-alpha-tocopherols and inorganic selenium additives influenced some growth features over separate feeding trial periods. However, no significant trend was observed, indicating that there is no evidence supporting the specific or direct impact of experimental additives on rabbit growth results.

Keywords: DL-alpha-tocopherol, inorganic selenium, productivity, rabbits

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RELATION BETWEEN RUMEN BACTERIA AND MILK PRODUCTION PARAMETERS

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Cows' milk production depends on diets and the fermentation process in the rumen. The digestive processes in ruminants are the most complicated compared to other animals. It is very important to know which rumen bacteria is beneficial for milk production. For this reason, we estimated the correlation between rumen bacterial composition and milk parameters. We tested 54 rumen content and milk samples in this study.

The DNA was isolated from the rumen contents using a solution of phenol, chloroform and isoamyl alcohol. The QIAquick PCR Purification kit (Qiagen, Germany) was used for DNA isolation and purification. Libraries of bacterial 16S ribosomal RNA gene (rRNA) V4 region were prepared following the "16S metagenomic sequencing library preparation" protocol (Illumina), by using 515 F and 806R primers with Illumina adapters. Libraries were sequenced with Illumina MiSeq (Finnish Functional Genomics Centre, Turku) using PE approach and 2 x 250 bp chemistry. Sequencing data were further processed using Qiime v 1.9.1.

The taken milk samples were sent to the laboratory of UAB "Pieno tyrimai". Milk fat, protein, lactose, urea and milk pH were determined using a LactoScopeFTIR infrared mid-range meter (FT1.0. 2001; Delta Instruments, Netherlands). Somatic cell counts were determined by cytometry using a Somascope meter (CA-3A4, 2004; Delta Instruments, Netherlands). The amount of milk per cow was recorded daily according to the readings of the milk scales at the milking parlor (Delaval, Sweden).

Statistical analyses were calculated using the open-access online software Calypso, Version 8.84. The correlation coefficient (r) was calculated using Pearson. The strength of correlation was determined from the calculated r -value: strong: $r > 0.7$; medium strength: $\pm 0.4 < r \leq \pm 0.7$; weak: $r > 0$. Results are considered statistically significant at $p < 0.001$, $p < 0.01$, and $p < 0.05$.

The results showed that *Ruminobacter spp.* correlated positively with milk yield ($r = 0.364$; $p < 0.01$), milk fat ($r = 0.363$; $p < 0.01$), milk protein ($r = 0.900$; $p < 0.05$), milk lactose ($r = 0.466$; $p < 0.001$). The daily milk yield negatively correlated with *Fibrobacter spp.* ($r = -0.293$; $p < 0.05$) and *Succiniclasticum spp.* ($r = -0.352$; $p < 0.05$). Positive correlation was determined between with milk lactose and *Ruminococcus spp.* ($r = 0.297$, $p < 0.05$), somatic cell count and *Fibrobacter spp.* ($r = 0.387$; $p < 0.01$). Negative correlation was observed between milk urea and *Butyrivibrio spp.* ($r = -0.299$; $p < 0.05$), *Succiniclasticum spp.* ($r = -0.301$, $p < 0.05$).

Our study results revealed, that the most positive influence on milk production parameters has *Ruminobacter spp.* – maintaining this bacterial species would be beneficial for milk production aspects. Also, by this study results, we can confirm that exist relation between the rumen microbial community and milk production.

Keywords: cow, rumen, bacteria, milk production

COMPARATIVE EVALUATION OF RECTAL AND MAMMARY GLAND SURFACE TEMPERATURES IN COWS WITH SUBCLINICAL MASTITIS

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Mammary gland inflammation – mastitis – is one of the significant problems on dairy farms. In the cases of mastitis in cows, the dairy farmers suffer financial losses due to deteriorating quality and yields of milk, the costs of treatment and veterinary services, and early culling of cows. The State Food and Veterinary Service (SFVS) reports that mastitis affects 21.06% of all dairy cows. According to the SFVS reports on the productivity of controlled cow herds, an average of 10,05% of the controlled cows are culled each year due to various udder diseases (1, 2).

Microorganisms are a significant cause of inflammation. However, multiple other factors, such as hygiene, climate, premises, milking equipment, feed, genetics, etc., are involved in creating conditions and directly relate to causing infection. These factors favor microorganisms' entering the mammary gland and allow them to establish themselves to such an extent that they result in inflammation. (3, 4).

The purpose of the study was to investigate the physiological state of the milk gland by using infrared thermography, compare the obtained results with the parameters of the animal's rectal temperature and somatic cell count (SCC) in the milk gland, and propose the methods for diagnosing mastitis in cows.

The research was conducted at the LSMU Training and Testing Center in Muniškės, Kaunas district. In cows, rectal body temperature was measured with a Brannan digital thermometer (DB). The udder's surface skin was examined using a FLIRT 640 thermal imaging infrared camera, and the SCCs were determined using a somatoscope. The samples for studying mastitis were inoculated into Petri dishes with selective nutrient media and blood agar.

Based on the rectal temperature assessment, the highest reading was 38.9 °C, and the lowest – was 38.0 °C, which was within the physiological range,

and 35.09% of the 57 cows tested had subclinical mastitis. The SCCs ranged from 206 thousand/ml to 981 thousand/ml, and in clinically healthy cows ranged from 10 thousand/ml to 184 thousand/ml. In the tested cow group with mastitis, the *Staphylococcus spp.* genus microorganisms were prevailing. Other microorganisms such as *Corynebacterium spp.*, *Streptococcus spp.*, and mixed microflora distributed evenly.

According to the test by the FLIR method results, the mammary gland temperature in different zones of the mammary gland was as follows: in clinically healthy cows, the highest temperature reading was on the venous ring (32.55 ± 1.06 – on its right, and 32.41 ± 1.20 – on its left); the lowest – in the right side of the teat canal (28.95 ± 1.45) and on the left side of the udder (29.38 ± 1.52). In cows with subclinical mastitis, the highest temperature reading was in the area near the venous ring (34.11 ± 0.57 on the right and 34 ± 0.56 on the left), and the lowest – was in the area near the teat canal on the right (31.61 ± 0.66) and the left side of the udder (31.07 ± 0.78).

When comparing the cattle rectal temperature with the temperature of the mammary gland surface, no correlation was observed and/or found between the studied data ($p > 0.05$).

A correlation was found when evaluating and comparing the mammary gland surface temperature and SCCs. It showed that the number of somatic cells increased with increasing temperature in cows' mammary glands ($p < 0.05$). And, when the udder temperature of healthy and diseased cows increased by 1°C , the number of somatic cells increased by 11.6 thousand/ml.

Keywords: cow, subclinical mastitis, microorganisms, infrared thermography

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THE INFLUENCE OF DIFFERENT DIETS ON BLOOD PROTEIN CONCENTRATION AND GUT MICROBIOTA IN RATS

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Rats have become as experimental animal model of choice for most biomedical studies and are extensively used for investigation of gut microbiota (1). Numerous studies demonstrated that different dietary components affect the blood profile values, can change gut microbiota, might contribute to the alterations of liver disorders, disrupt metabolic homeostasis and cause many other impairments of body function in rats. It is recognized that blood proteins are as indicators of liver functions. Albumin accounts for more than 50% of the total serum proteins and maintains oncotic pressure and transports hormones, vitamins and drugs throughout the body. Globulins make up the remaining percentage of proteins and are either produced by liver or by the immune system, help the body fight infections and also transport nutrients. Globulin, as a major serum protein component, is synthesized and secreted mostly by the liver and plasma cells in response to inflammatory and infective reactions. Moreover, many studies displayed that diet components can alter the protein fractions of blood and interact with gut microbiota (1, 2, 3). In addition gut microbiota influence not only gastrointestinal physiology but also central nervous system function and behavior of animal through the microbiota-gut-brain axis (4). Thus, the main aim of this study was to evaluate the effects of different diets on blood protein concentration and gut microbiota in rats.

The study was conducted in 12 adult male Wistar rats. Six rats were allocated to the group I (control) and were fed for 6 months with standard commercial pellet diet containing 19.91% crude protein, 12.05% crude fat and 2.79% crude fiber, six rats were allocated to the group II (experimental) and got diet with 21.50% crude protein, 6.00% crude fat and 3.96% crude fiber. It is noticed that experimental group animals diet include genetically modified soya. All rodents had

ad libitum access to water. Housing room temperature was maintained between 21–24 °C and relative humidity between 50–70%, with a 12:12 h light/dark cycle. The procedures with rodents were approved by the national ethics commission license no (G2-73/2017). Collection of blood and faeces samples was performed at the end of the experiment. Blood samples were collected in microtubes without anticoagulant by puncturing of the lateral tail vein. The serum protein biomarkers (total protein, albumin (A), globulin (G), and A/G ratio) were evaluated between two groups. Serum was separated by centrifugation (4000 x g, 10 min.) in a EBA-200 centrifuge (Germany) and stored at –20 °C until analysis. Biochemical parameters as total protein (T-Pro) and albumin (Alb), were analyzed by automated biochemical analyzer. For calculation of A/G ratio albumin globulin ratio calculator was used (<https://www.mdapp.co/albumin-globulin-ratio-calculator-463/>). 1 gram of faeces was needed for analysis of faecal microbiota. Faeces samples were homogenized in 9 ml 0.9% NaCl solution by vortex mixing (IKA mini shaker, MS2, USA). The serial decimal dilutions were made and as parallel duplicate cultures were inoculated into Plate count agar (Liofilchem, Italy) – for enumeration of *aerobic and facultative anaerobic bacteria*, plates were incubated at 30 °C for 24 hours (LST EN ISO 4833:2003); MRS (de Man, Rogosa and Sharpe) agar (Biolife, Italy) – for enumeration of *Lactobacillus spp.*, plates were incubated at 30 °C for 72 hours under microaerophilic condition (Thermo Scientific™ Oxoid AnaeroGen 2.5L Sachets are anaerobic gas generating sachets for use with Thermo Scientific™ Oxoid 2.5L jar), (LST ISO 15214:2009); Slanetz and Bartley agar +TTC (Liofilchem, Italy) – for enumeration of *fecal streptococci*, plates were incubated at 35 °C for 48 hours (ISO 7899-2:2000); Violet red bile glucose agar (Liofilchem, Italy) – for enumeration of *Enterobacteriaceae*, plates were incubated at 37 °C for 24 hours (ISO 21528-2:2004). Bacteria enumeration was performed by standard method (EN ISO 7218:2007). The mean value of the colony counts (colony forming units (CFU/g ± SD)) in the two duplicates was calculated. The numbers of CFU were expressed as log₁₀ CFU per gram feces. Statistical analysis was performed using *t-test*, *one-way ANOVA* and Pearson correlation. For analyzing and visualizing data RStudio software was applied. The statistical significance of difference was taken as $p \leq 0.05$. T-Pro value was 67.667 ± 2.1707 g/l and 74.00 ± 1.1831 g/l, Alb value 35.667 ± 0.3331 g/l and 41.333 ± 2.0764 g/l, and A/G ratio 0.938 ± 0.038 and 1.267 ± 0.0763 in rats blood samples of group I and II, respectively. Total protein value increased by 9.36% and albumin content by 15.88% in group II rats when compared to group I rats ($p = 0.043$). A/G ratio difference of 0.329 unit was observed between groups. Data of gut microbial profile revealed *total count of aerobic and*

facultative anaerobic bacteria of $5.55 \pm 0.35 \log_{10}$ CFU/g and $6.08 \pm 0.53 \log_{10}$ CFU/g, *Lactobacillus spp.* $4.81 \pm 0.63 \log_{10}$ CFU/g and $4.84 \pm 0.63 \log_{10}$ CFU/g, *Enterobacteriaceae* $4.23 \pm 0.45 \log_{10}$ CFU/g and $4.17 \pm 0.38 \log_{10}$ CFU/g, and *fecal streptococci* $4.63 \pm 0.56 \log_{10}$ CFU/g and $4.618 \pm 0.13 \log_{10}$ CFU/g in group I and II, respectively.

The increment of $0.53 \log_{10}$ CFU/g ($p = 0.072$) for *total count of aerobic and facultative anaerobic bacteria* was fixed in group II, whereas increment of $0.45 \log_{10}$ CFU/g ($p = 0.063$) for *fecal streptococci* was noticed in group I. Statistically insignificant differences between groups were found in *Lactobacillus spp.* and *Enterobacteriaceae* results. One-way ANOVA analysis showed that genetically modified soya had a statistically significant effect on the amount of *fecal streptococci* in the faeces of rats ($R^2 = 0.3438$; $p = 0.0451$). Pearson's correlation analysis on gut microbial parameters exhibited the highest negative correlation in group I between *Enterobacteriaceae* and *fecal streptococci* ($r = -0.52$; $p = 0.285$) and in group II between *Enterobacteriaceae* and *fecal streptococci* ($r = -0.7$; $p = 0.122$). Whereas, the highest positive correlation was found in group II between *Lactobacillus spp.* and *fecal streptococci* ($r = -0.61$; $p = 0.199$), however in group I there was no correlation between these gut parameters.

To sum up, diets with genetically modified soya did not have deleterious influence on blood protein values and gut microbiota in rats, thus diet composition of group II can be suitable for laboratory rats nutrition.

Keywords: diet, rat, blood protein, gut microbiota

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THE EFFECTS OF DIFFERENT DIETS ON GUINEA PIG HEALTH, HAIR MORPHOLOGY AND BLOOD PROTEIN CONCENTRATION

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Guinea pigs (*Cavia porcellus*) have biological similarities to humans, which make them a suitable animal model in multiple fields of research. Guinea pigs have contributed to 23 Nobel prizes for medicine with studies leading to the discovery of vitamin C, the tuberculosis bacterium, as well as the development of vaccines for diphtheria and tuberculosis, replacement of heart valves, blood transfusion, kidney dialysis, antibiotics, anticoagulants, asthma medicines, etc. The majority of studies highlighted that diet components can have significant impact on gut microbiota, liver functions, homeostasis, metabolism and other functions in guinea pigs organism (1, 2, 4). We aimed to investigate the effect of different diets on guinea pigs health, hair morphology and protein value in blood. Twelve short-haired guinea pigs of 911.7 ± 1.24 g initial body weight were employed in this study. Environmental parameters of housing guinea pigs were: an ambient temperature of 20–24 °C, relative humidity of 55% ($\pm 10\%$), ventilation – 15 fresh air changes per hour and a 12h light/12h dark light cycle. Guinea pigs of group I (n = 6) were fed for 6 months with commercial pellets (free of genetically modified organisms sourced ingredients), whereas animals of group II (n = 6) got rations containing genetically modified soybeans. The crude protein, crude fat and crude fiber of the pellet in group I and group II were 19.91% and 21.50%, 12.05% and 6.00%, and 2.79% and 3.96%, respectively. Access to high quality of hay and water in both groups was *ad libitum*. In order to avoid vitamin C deficiency all guinea pigs were administrated daily intake of 20 mg of vitamin C/1000 g of body weight. For monitoring general health status in guinea pigs, health inspection checklist of 7 parameters (nose, eyes, ears, mouth, fur, fecal/urine, behaviour) was used. Blood samples were collected once at the time after six month from the beginning of feeding two different diets Serum total protein (T-Pro) was estimated using refractometry method. Hair samples were taken by clipping 1 cm from the dorsal spine and shoulder region/scapula on the right and left sides. Before use, the hairs were cleaned by distilled water and degreased using ethanol at 70% for

2–3 minutes to remove dirt and air-dried prior to further microscopic analysis (Olympus SZx7, Japan). Hair diameter (μm), cuticle, medullary diameter (μm), and medullary index (MI) were evaluated in 36 hair samples. MI was determined by measuring the diameter of the medulla and dividing it by the diameter of the hair (3). All conducted tests meet ethical principles and comply with animal welfare standards. The procedures with guinea pigs were approved by the national ethics commission (permission number G2-127/2019). Statistical analysis was performed using MedCalc (<https://www.medcalc.org/calc/>, Version 20.015; 2021) and EndMemo statistical softwares (<http://www.endmemo.com/statistics/kurtosis.php>). A difference was considered significant when the P value < 0.05 . Applying health inspection checklist was noticed that noses of guinea pigs in both groups were clear, no discharge, eyes clear, symmetrically open and shiny, ears clean, mouth closes easily, tooth was not overgrowth, fur clean, no hair loss area on body, faeces oval shape and urine clear. All animals were active, no signs of decreased appetite or abnormal behaviour. The morphometric measurements of cuticle were $1.48 \pm 0.127 \mu\text{m}$ (skewness -0.4895 , excess kurtosis -0.6981) and $2.15 \pm 0.09 \mu\text{m}$ (skewness -0.8451 , excess kurtosis -0.6981 ; $p = 0.0015$) in guinea pig hair samples of group I and II, respectively. Medullary diameter of $67.28 \pm 13.02 \mu\text{m}$ (skewness -1.4542 , excess kurtosis 2.9011) was noticed in group I and $116.91 \pm 10.133 \mu\text{m}$ (skewness 0.4652 , excess kurtosis -1.615 ; $p = 0.0006$) in group II. Diameter of hair in group I was $68.75 \pm 1.253 \mu\text{m}$ (skewness -1.7777 , excess kurtosis 3.7826), in group II $-118.96 \pm 10.12 \mu\text{m}$ (skewness 0.4532 , excess kurtosis -1.5812 ; $p = 0.006$). Increments of 73.03% of hair diameter and 73.76% of medulla diameter was fixed in group II, but MI has remained stable (MI varied from 0.97 to 0.98 between groups). T-Pro value was $51.00 \pm 5.11 \text{ g/l}$ (95% CI 38.99–63.01, median 46, kurtosis 1.377) and $44.5 \pm 2.22 \text{ g/l}$ (95% CI 39.28–49.72, median 42, kurtosis 2.759, $p = 0.0638$) in group I and II, respectively. Pellets for guinea pigs containing genetically modified soybeans did not have harmful impact on guinea pigs fur coat, morphological elements of hair and MI. Amount of T-Pro value was 12.75% lower in group II but in appropriate physiological norm.

Keywords: guinea pig, diet, health, hair, blood protein

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TARPTAUTINĖS KONFERENCIJOS

MIKROBIOTA
IR GYVŪNAS: SAŪVEIKA,
SVEIKATINGUMAS,
GEROVĖ IR PRODUKCIJA

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