# MEETINGS AND ABSTRACTS OF THE CZECHOSLOVAK BIOLOGICAL SOCIETY IN 2006 YEAR

# SCHŮZE BRNĚNSKÉ POBOČKY ČESKOSLOVENSKÉ BIOLOGICKÉ SPOLEČNOSTI V ROCE 2006

**Členská schůze 18. ledna 2006**

*(Schůze konaná ve spolupráci s Českou anatomickou společností a Anatomickým ústavem Lékařské fakulty MU při příležitosti životního jubilea prof. MUDr. Libora Páče, CSc.)*

*P. Dubový* (Anatomický ústav LF MU): **Jubilant profesor MUDr. Libor Páč, CSc.**

*P. Dubový* (Anatomický ústav LF MU): **Somatosenzorická tělíska – model pro studium buněčných a molekulárních procesů reinervace**

*L. Horáčková, L. Vargová* (Anatomický ústav LF MU): **Lékařsko-antropologický výzkum kosterních pozůstatků vojáků z napoleonských bitev na Moravě (1805–1809)**

*L. Veverková* (I. chirurgická klinika LF MU a FN u sv. Anny v Brně): **Klinicko-anatomické studie – naděje 21. století**

**Členská schůze 15. února 2006**

*(Schůze konaná ve spolupráci s Českou anatomickou společností a Anatomickým ústavem Lékařské fakulty MU při příležitosti životního jubilea doc. MUDr. Antonína Zechmeistera, CSc.)*

*L. Páč* (Anatomický ústav LF MU): **Doc. MUDr. Antonín Zechmeister, CSc. jubilující**

*P. Handlos, L. Páč* (Anatomický ústav LF MU): **Ultrastruktura kardiomyocytů excitomotorického aparátu u člověka**

*K. Kovačičová, D. Kučera, K. Poloková, J. Pořízka, M. Richterová* (Anatomický ústav LF MU): **Akutní infarkt myokardu a základní variety věnčitých tepen**

**Členská schůze 8. března 2006**

*(Večer Oddělení lékařské genetiky FN Brno, Pracoviště dětské medicíny na téma Genetická vyšetření u hematologických malignit)*

*A. Oltová a kol.* (Oddělení lékařské genetiky FN Brno): **Cytogenetická vyšetření kostní dřeně u pacientů s diagnózou mnohočetný myelom**

*H. Filková a kol.* (Oddělení lékařské genetiky FN Brno): **Molekulárně cytogenetická vyšetření pacientů s mnohočetným myelomem**

*J. Vigášová a kol*. (Oddělení lékařské genetiky FN Brno): **Relativní kvantifikace nádorově specifických antigenů MAGE u mnohočetného myelomu**

**Členská schůze 12. dubna 2006**

*(Využití molekulárně-genetických metod a jejich aplikace v genetice a šlechtění zvířat na Pracovišti genetiky živočichů Ústavu morfologie, fyziologie a genetiky zvířat AF MZLU v Brně)*

*K. Bílek* (Pracoviště genetiky živočichů AF MZLU v Brně): **Zkoumání genové exprese s využitím Real-time PCR**

*J. Verner* (Pracoviště genetiky živočichů AF MZLU v Brně): **Analýza vybraných genů ovlivňujících masnou užitkovost prasat**

*P. Humpolíček* (Pracoviště genetiky živočichů AF MZLU v Brně): **Aplikace dat molekulární genetiky ve šlechtění prasat**

*M. Burócziová* (Pracoviště genetiky živočichů AF MZLU v Brně): **Molekulárno-genetická charakteristika plemien Český teplokrvník a Slovenský teplokrvník**

**Členská schůze 26. dubna 2006**

**9. Babákova přednáška**

*(Schůze pořádaná Hlavním výborem Československé biologické společnosti)*

*K. Smetana* (Ústav hematologie a krevní transfúze Praha): **Jsou nukleoly užitečnými márkry stavu jedné buňky? Strukturální a cytochemické poznámky**

**Členská schůze 31. května 2006**

*(Vzpomínkové odpoledne při příležitosti 80. výročí úmrtí Edwarda Babáka spojené s vernisáží výstavy dokumentů z Babákova života a díla; uspořádala Veterinární a farmaceutická univerzita Brno, Masarykova univerzita, Československá biologická společnost, Česká fyziologická společnost, Společnost veterinárních lékařů a Společnost pro dějiny vědy a techniky)*

*J. Doubek* (Veterinární a farmaceutická univerzita Brno): **Trvalá inspirace Babákovým dílem**

*P. Bravený* (Masarykova univerzita): **Edward Babák a brněnské vysoké školství**

*B. Ošťádal* (Česká fyziologická společnost): **Česká evoluční fyziologie jako Babákův odkaz**

*A. Svoboda* (Československá biologická společnost): **E. Babák – zakladatel Biologické společnosti**

*H. Hrstková* (Masarykova univerzita): **Babákův význam pro českou pediatrii**

**Členská schůze 28. června 2006**

*(Schůze konaná ve spolupráci s Českou anatomickou společností a Anatomickým ústavem Lékařské fakulty MU při příležitosti životního jubilea doc. MUDr. Pavla Matonohy, CSc.)*

*L. Páč* (Anatomický ústav LF MU): **Doc. MUDr. Pavel Matonoha, CSc. šedesátiletý**

*L. Vargová, L. Horáčková, M. Menšíková** (Anatomický ústav LF MU, *Museum města Brna): **Anatomická a patologická pitva v 18.–19. století v Brně**

*L. Páč* (Anatomický ústav LF MU): **Založení Anatomického ústavu Masarykovy univerzity v roce 1919**

*I. Svíženská, I. Čižmář*, P. Višňa*** (Anatomický ústav LF MU,*Klinika úrazové chirurgie FN Brno, **Chirurgická klinika 2. lékařské fakulty UK Praha): **Parciální denervace kloubů zápěstí a musculus pronator quadratus**

**Členská schůze 15. listopadu 2006**

*M. Vojtíšková* (Biofyzikální ústav AV ČR, Brno): **Příčiny a důsledky nestability lidského genomu**

**Členská schůze 6. prosince 2006**

*L. Novák* (Oddělení preventivní a sociální pediatrie Ústavu sociálního lékařství a veřejného zdravotnictví LF MU): **Dynamický fenotyp komplexních znaků a jeho význam pro hodnocení růstu zvířat i člověka**

*L. Kukla, M. Čuta, L. Novák* (Oddělení preventivní a sociální pediatrie Ústavu sociálního lékařství a veřejného zdravotnictví LF MU): **Modelování růstu dvojčat z růstového potenciálu rodičů a dynamických fenotypů tělesné výšky a hmotnosti**

*P. Mareš, J. Vavrečka, M. Sikora, L. Zeman, L. Novák* (Ústav výživy zvířat a pícninářství Agronomické fakulty MZLU v Brně): **Růst hybridní kombinace prasat PIC v různých ročních obdobích hodnocený dynamickým fenotypem hmotnosti**

*P. Kratochvílová, M. Sikora, L. Zeman* (Ústav výživy zvířat a pícninářství Agronomické fakulty MZLU v Brně): **Vliv hladiny *Vicia faba L.* v pokusné dietě pro růst brojlerových kuřat a jeho hodnocení dynamickým fenotypem hmotnosti**

**14. prosince 2006**

**Symposium Aktuální otázky bioklimatologie zvířat 2006**

*(Uspořádala Česká bioklimatologická společnost při RČVS – Sekce bioklimatologie zvířat a Výzkumný ústav živočišné výroby v Praze ve spolupráci s Ústřední komisí pro ochranu zvířat a Brněnskou pobočkou Československé biologické společnosti)*

## ABSTRACTS

*J. Vigášová[1,2], J. Kadlecová[2], R. Spěšná[2], R. Gaillyová[2], M. Penka[3], R. Hájek[1,4]* ([1]Laboratory of Experimental Hematology and Cellular Immunotherapy, The Faculty Hospital Brno; [2]Department of Medical Genetics, The Children's Medical Center of the Faculty Hospital Brno; [3]Department of Clinical Hematology and [4]Clinic of Internal Medicine – Hematology, Center for Adult Medicine of the Faculty Hospital Brno): **Relative quantification of tumor associated antigens MAGE in pacients with multiple myeloma** [vigina@seznam.cz]

Multiple myeloma (MM) is a malignant plasma cell neoplasm that often is preceded by a common pre-malignant monoclonal expansion of plasma cells called monoclonal gammopathy of undetermined significance (MGUS). MGUS is reported to be present in 1% of the adult population and to progress to MM at a rate of 1% per year. MM is an incurable tumor characterized by clonal expansion of malignant plasma cells in the bone marrow. The MAGE genes encode antigenic peptides that are presented by HLA class I molecules and that are recognized on human tumors by T lymphocytes. They are activated in a variety of malignant neoplasma while remaining silent in normal tissues with the exception of testis and occasionally placenta. Because MAGE is expressed in many kinds of cancers and MAGE gene expression is highly specific to cancer cells, it has been studied as an important marker for cancer diagnosis. Presence of RNA transcripts encoding members of the MAGE gene family in myeloma tumor cells and cell lines has been documented.

The aim of the paper was to evaluate the possibility of using these genes as molecular markers of the progression MGUS to multiple myeloma and the early relapse of the MM. Total of 50 samples from bone marrow were examined: 25 samples from myeloma patients, 8 samples of patients with early stage of MM who did not required treatment (smouldering MM 2x, stage IA 6x), 5 samples of MGUS patients, 9 samples of normal healthy donors served as control group. All samples were kept on ice until RNA extraction. Total RNA was evaluated by RT-PCR and then by real-time PCR using FRET probes on the LightCycler instrument (Roche). For relative quantification authors used G6PDH housekeeping gene as external standard. As positive control served myeloma cell line U266.

None from samples of 9 healthy donors did show expression of MAGE. Only 1 (20%) of 5 samples from MGUS patient showed expression of MAGE-A1. Five (62.5 %) from 8 patients with early stage of MM (IA and smouldering) showed expression of MAGE. On the contrary 11 (44 %) of 25 samples from MM patients showed expression of at least one gene MAGE-A1 or MAGE-A3 or both (7 cases).

The method seems to be useful for monitoring minimal residual disease in patients with MM.

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*K. Bílek* (Department of Animal Morphology, Physiology and Genetics, Faculty of Agronomy, Mendel University of Agriculture and Forestry Brno): **Investigation of the gene expression using Real-time PCR method**

Investigation of the gene expression helps to understand mechanisms of organism or tissues development. The aim of this study was to verify and quantify the different gene expression of the selected genes in *musculus longissimus dorsi* of fetus using the real-time quantitative PCR. On the bases of sequences obtained from subtractive hybridization clones and the results of linkage and comparative mapping, the specific primers were designed to analyze expression of genes *ACTB, ACTC, CDK4, CNN, GNAS* and *POST*.

The skeletal muscle specific RNA was isolated from adult pigs and 50 day aged fetuses. Samples were homogenized in FastPrep FP 120 (ThermoSavant) and the total RNA was isolated using the FastRNA Pro Green Kit (Q-BIOgene). The first-strand cDNA was synthesized from 1μg total RNA using Omniscript RT (QIAGEN). All samples were analyzed using SYBR Green PCR Master Mix (Applied Biosystems) and reactions were run on a PTC-200 and Chromo 4 Detector (MJ Research). From three primary-used potential housekeeping genes two the most stable were selected by geNorm programme (*HPRT*, *PPIA*). These genes and their relative quantities were used for normalizing of quantity in samples by qBase programme.

It was determined that two genes are down-expressed (*ACTB, GNAS*) and four of them were over-expressed (*ACTC, CDK4, CNN, POST*) in studied tissue. Obtained results are helpful for better understanding of skeletal muscle development and growth in pigs, with the prospect of their application in selection.

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*M. Burócziová, J. Říha* (*Department* of Animal Morphology, Physiology and Genetics, Faculty of Agronomy, Mendel University of Agriculture and Forestry Brno): **The molecular-genetic characterisation of Czech and Slovak Warmblood horse breeds**

Authors compared the genetic diversity between two horse breeds (the Czech and Slovak Warmblood ones) by means of 17 microsatellite loci /AHT4, AHT5, ASB2, HMS3, HMS6, HMS7, HTG4, HTG10, VHL20, HTG6, HMS2, HTG7, ASB17, ASB23, CA425, HMS1, LEX3 – recommended by ISAG. In different size of population /100 individuals of Czech Warmblood, 100 individuals of Slovak Warmblood, 98 individuals of Kladruben, 97 individuals of Arabien, 69 individuals of Quarter Horse, 67 individuals of Paint Horse, 50 individuals of Haflinger and 42 individuals of Shetland Pony/ the allele frequencies, observed and expected heterozygosity and polymorphism information content have been calculated for each breed. In conclusion, the main objective of the study was to show the level of genetic distance among the Czech and Slovak Thoroughbred horse breeds with very short history of breeding. Genetic distance and diversity between them was analysed on the basis of the dataset of highly polymorphic set of microsatellites representing all autosomes using a set of PowerMarker v3.28.

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*P. Humpolíček* (Department of Animal Morphology, Physiology and Genetics, Faculty of Agronomy, Mendel University of Agriculture and Forestry Brno): **Applications of molecular data to animal breeding**

Rapid development of new technologies in genetics leads into speculations how the freshly available information can be utilized in the livestock breeding. There are many different types of information (e.g. linkage markers, functional markers, candidate genes) and each of them is useful for a different purpose and under different conditions. The most useful are candidate genes or direct markers

that are in population-wide disequilibrium. Many researchers and breeders have suggested what the most efficiency way is. The methods as marker assisted selection (MAS), marker assisted introduction (MAI), gene assisted selection (GAS), candidate gene assisted selection (CGS), gene pyramiding and many others were making up. Each of aforementioned methods has some strong point and some weakness. Molecular data are useful mainly in situation when the classical breeding methods are not effective. That means in cases when the selected traits have low heritability, they are detectable in one gender only or after slaughter, and in some others situations. The practical use in different species is limited not only by economics but by the contemporary situation in animal breeding. The molecular data provide many advantages but the application is conditioned by integration to contemporary animal breeding techniques.

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*J. Verner* (Department of Animal Morphology, Physiology and Genetics, Faculty of Agronomy, Mendel University of Agriculture and Forestry in Brno): **Analysis of the selected genes influencing quality pork production**

Porcine *MYF-4*, *MYF-5* and *IGF-2* genes play key roles in growth and muscle development regulation and are considered to be candidate genes in relationship to meat performance in pigs.

The objective of the study was to verify the occurrence of polymorphic variants of analysed genes, determine single genotype and allele frequencies and assess associations between ascertained polymorphisms and performance traits in pigs. 187 pigs (143 Czech Large White and 44 Czech Landrace breeds) were included into the analysis. DNA was isolated from porcine blood samples, was amplified, and digested using PCR-RFLP method. The genotypes of all genes were detected using *Msp*I, *Hpa*II and *Bcn*I restriction endonucleases. PCR products of expected lengths were controlled on 1.5 % agarose gel. Fragments of digested amplicons were visualized on 2–3 % agarose gel using ethidium bromide.

To evaluate the associations between obtained genotypes and selected meat traits, the mixed models procedure of SAS 8.2 including fixed effects of *MYF-4*, *MYF-5* and *IGF-2* genes, breed, sex and year of the slaughter was used. There were studied following meat characteristics: weights of neck, loin, shoulder and ham, lean meat content and backfat thickness.

There was verified a cleavage with the restriction endonucleases and thus confirmed occurrence of analysed polymorphisms. There was not identified genotype *AA* in *MYF-5* gene. In Czech Large White breed no statistical differences were observed, while in Czech Landrace were found in *MYF-4* highly significant differences in backfat thickness and lean meat content; and in *IGF-2* significant difference in neck weight was registered.

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*L. Kukla, L. Novák, M. Čuta* (Department of Preventive and Social Paediatrics at Medical Faculty, Masaryk University, Brno): **Twins growth modelling from parent growth potential and body height and weight dynamic phenotypes**

Most of the previously proposed growth modelling methods was based on a curve function calculated using sophisticated mathematically defined constants. The modelling method proposed by Novák *(Scripta medica Brno 78, 2005, 366–367)* used in present study describes a human growth curve by three components which correspond with Karlberg's I, C, P phases *(Karlberg 1987)* but are mathematically easily calculated and what is an advantage for a practical physician or biologist, they are each defined by biologically easily comprehensible constants. Each component is described by the following constants: starting weight or height (G0, D0), genetic limit weight or height given by parent or genetic growth potential (GLi, DLi) and maximum weight or height gain (dGmax, dDmax). In our department, we have been following a study set of over 5000 families and their children since their

birth (and before) until present, i.e. 15 years of age of studied children. The study internationally follows over 40000 children, its nature is longitudinal, hence the name – European Longitudinal Study of Pregnancy and Childhood. The introduced bioversion of growth functions has been tested on the set of ELSPAC children and its reliability in modelling child growth has been proven *(Čuta et al, Scripta medica Brno 78, 2005, 368)*.

ELSPAC study set also contains a unique set of twins and their longitudinal growth curves obtained from empiric data. These growth curves have been smoothed through the calculated curve using dynamic weight and height phenotypes allowing the confirmation of expected similarities and dissimilarities between mono – and dizygotic twins. The model not only can exactly describe the growth curve and its derivations from the determined growth channel, with quality nutritional, socioeconomic and health-status data but it offers exact cause determination of such derivations. In the next research phase, authors plan to collect such nutritional data and in combination with the extensive range of background data already obtained to indicate the causes of individual growth derivations and to establish general factors negative and beneficial for child development. Further twins studies using the bioversion of growth functions supported by quality nutritional data promises to contribute in the field of study of genetic and environmental sides of human growth and development influence.

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*L. Novák* (Department of Preventive and Social Paediatrics at Medical Faculty, Masaryk University, Brno): **Dynamic phenotype and its significance for animal and human growth assessment**

The growth of living organisms is a deterministic process executed in genome and proteome cooperation. Weight genotype development then is dependent on growth necessity adequate nutrition and an environment capable of absorbing all the excess body heat produced by the physiological processes biochemical reactions that cover the preservation and growth needs. Weight growth has a shape of sigmoid curve and can be derived from quadratic or exponential differential equation (*Table 2*). By use of an original approach the growth curve course from birth until maturity can be characterized by three directly measurable „dynamic phenotype" variables. These are as follows: the genetically limited weight of the mature individual (GLi, kg), maximum weight gain in the growth curve inflexion point (dGmax) and the beginning of the direct growth assessment – birth weight (G0, kg). The maximum weight gain is defined from the organism viewpoint by the amount of metabolizable energy (PMEP, MJ/d) acquired from ingested food. In relation to the environment, it is necessary that the environmental cooling effect (ECE, MJ/d) in the optimal case is equal to the total heat production (THP, MJ/d). The dynamic phenotype (G0, GLi, dG max) defines the classic growth functions constants (*Table 1* and *Table 2*).

*Table 1*

| Function type | Differential equation | Weight growth |
|---|---|---|
| Logistic | $dG/dt = a.G-bG^2$ | $G = GLi/(1+C.\exp(-a.t))$ |
| Exponential | $dG/dt = \alpha.G-B.G.\ln G$ | $G = GLi.\exp(-C.\exp(-B.t))$ |

*Table 2*

| Function type | Anabolism coeff. | Catabolism coeff. | Integration constant |
|---|---|---|---|
| Logistic | $a = 4.dG\ max/GLi$ | $b = 4.dG\ max/Li^2$ | $c = (a-b.G0)/(b.G0)$ |
| Exponential | $\alpha = B.\ln(GLi)$ | $B = e.dG\ max/GLi$ | $C = \ln(GLi/G0)$ |

The derived relationships have been experimentally verified on Wistar rats *(Novák and Pípalová, Scripta medica Brno, 69, 1996, 179–190)*, PIC pigs *(Zeman, Novák et al, Symposium TIERERNÄHRUNG BOKU Vienna, 2004, 122–128)* and ROSS chickens *(Novák P., Zeman, Košař et al, Acta Vet. Brno 73, 2004, 17–22)*. Animal growth has a shape of a single exponential function.
Child weight growth however is composed of three components. The adequate constant values of the appropriate dynamic phenotype for the three segments of he ICP growth curve for girls are indicated in Table 3.

*Table 3*

| Component | Age, year | G0, kg | GLi, kg | dGmax, kg/year |
|---|---|---|---|---|
| Infancy | 0–1.5 | 3.2 | 11.0 | 10.1 |
| Childhood | 1.5–10 | 10.69 | 60.0 | 2.68 |
| Puberty | 10–18 | 33.8 | 60.0 | 7.48 |

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*P. Kratochvílová, M. Sikora, L. Zeman* (Department of Animal Nutrition and Forage Production, Faculty of Agronomy, Mendel University of Agriculture and Forestry Brno): **Influence of level *(Vicia faba L.)* in experimental diets on performance of chickens**

The aim of experimental supervision was to detect influence of different level of faba bean (varieties Merkur and Mistral) in chicken nutrition on growth, feed conversion and health condition of chickens.

The study was performed on Prasklice fattening station for chickens. 800 male chickens ROSS 308 aged 2 days were used that were distributed to 8 stalls by 100 idividuals. Average weight of chickens was around 47 g. The dimensions of stalls were computed at final weight of chickens (32 kg live weight/ $m^2$). A brooding source of heat (28–30°C) was provided for the first 2 weeks; thereafter, the birds were maintained at a thermostatically regulated temperature of 25 ± 5°C with continuous lighting. There were installed corresponding numbers of drinker and bunk feeders. Feed and water were available ad libitum. Animals were fed by a standard commercial diet BR1 during first 14 days of the experiment. Feed mixtures with different content of faba bean respectively 0% (group 1, 5), 6% (group 2, 4), 12% (group 3, 7) and 12% plus coarse meal of faba bean available ad libitum in separate bunk feeders (groups 4, 8) were given them starting the 15 day of age. Weighing of chickens was carried out at the 1 and then 14, 28 and 42 day of the experiment by use of digital scales with weighing accuracy 0.1 g. Weight of cockerels, feed consumption and death loss in stalls were noted on a day of weighing. The experiment was finished after 42 days by individual weighing of all animals, which were subsequently slaughtered in company slaughter.

There were selected 6 average weight cockerels from each group (overall 48 pieces), which were subjected to carcass analysis; in the concrete dressing percentage that was carried out in the Prasklice workplace and additional carcass analysis (percent proportion of discrete muscle and tasting) mastered in Mendel University of Agriculture and Forestry in Brno.

Obtained results show that the highest average weight on day 42 achieved cockerels fed by experimental feed mixture with content of faba bean of varieties Merkur 12% (2412.2 g). Groups, which were fed by mixture with 6% of faba bean, had average weight 2289.9 g to 2314.3 g and control groups with 0% of faba bean (both varieties) achieved average weight 2399.3 g.

Standardized biological growth model BIOM N *(Novák, 2000)* has been exploited to visualize differences between experimental data and ideal growth curve of chickens.

*Compiled and revised by S. Čech*