MEETINGS AND ABSTRACTS OF THE CZECHOSLOVAK BIOLOGICAL SOCIETY IN 2008 YEAR

SCHŮZE BRNĚNSKÉ POBOČKY ČESKOSLOVENSKÉ BIOLOGICKÉ SPOLEČNOSTI V ROCE 2008

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B. Fišer (Fyziologický ústav LF MU)*:* **Fyziologický ústav, lidé a baroreflex**
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9. prosince 2008
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(Uspořádala Česká bioklimatologická společnost při ČAV – Sekce bioklimatologie zvířat a Výzkumný ústav živočišné výroby v Praze ve spolupráci s Ústřední komisí pro ochranu zvířat Praha a Brněnskou pobočkou Československé biologické společnosti)

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D. Novotná, P. Okrajek (II. Dětská klinika LF MU a FN Brno a Výzkumné pracoviště preventivní a sociální pediatrie LF MU): **Děti s IUGR v populaci projektu ELSPAC**
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ABSTRACTS

K. Brožková, E. Budínská[1], P. Bouchal, D. Knoflíčková, D. Valík, R. Vyzula, B. Vojtěšek, R. Nenutil
(Masaryk Memorial Cancer Institute, Department of Oncological and Experimental Pathology, Brno, [1]Institute of Biostatistics and Analyses, Masaryk University, Brno): **Proteomic analysis of breast cancer tissue by SELDI-TOF MS**

Microarray-based gene expression profiling provides new point of view on breast cancer classification. Gene expression signatures have been identified to be associated with the presence of hormonal receptors, tumor grade and ability to metastasize. However, cDNA expression profiles cannot detect changes on protein level such as post-translational modification or protein-protein interactions. SELDI-TOF MS offers high throughput protein profiling, leading to extraction of protein array data, which is essential for obtaining biologically and statistically relevant data in medical proteomic research.

Whole tissue lysates of 105 breast carcinomas were analyzed on IMAC 30 ProteinChip Arrays (Bio-Rad, USA). We performed unsupervised clustering of carcinoma cases according to their protein expression profiles and tested distribution of categories of clinical and molecular variables in these groups. Unsupervised hierarchical clustering of 130 peaks detected in spectra from 105 breast cancer tissue lysates provides 6 groups of peaks and 5 groups of patients differing significantly in tumor type, nuclear grade, presence of hormonal receptors, mucin 1 and cytokeratins 5/6 or 14. These tumor groups resembled closely luminal types A and B, basal and HER2 like carcinomas.

The overall aim of expression profiling of human tumors is to provide information that can assist with tumor diagnosis or classification, or can provide prognostic information. Obtained results show that SELDI-TOF MS protein profiling distinguishes between different groups of primary human breast cancers and produces a similar clustering of tumors as cDNA expression profiles.

Supported by IGA MZ ČR grant NR/8338-3/2005.

L. Březinová[1], J. Slanina[1], H. Vlašínová[2], I. Slaninová[3], I. Bohatcová[2], L. Havel[2] ([1]Department of Biochemistry and [3]Department of Biology, Faculty of Medicine, Masaryk University, Brno, [2]Department of Plant Biology, Faculty of Agronomy, Mendel University of Agriculture and Forestry Brno): **Increasing of lignans biosynthesis in embryogenic culture of *Schisandra chinensis* by addition of polymeric adsorbents**

Medicinal herbs are valuable sources of bioactive compounds with diverse chemical structures and are abundantly used in treating human diseases. The fruit of *Schisandra chinensis* has been used for centuries in traditional Chinese medicine as tonic and antitusic. The active principles are lignans with unusual structures derived from dibenzo[a,c]cyclooctadiene. These lignans have been shown to possess a broad range of biological activities. Recently, it has been found that lignan γ-schizandin strongly inhibits P-glycoprotein, the overexpression of which is the most frequent cause for multidrug resistance of cancer cells. Content of lignans in *Schisandra* fruits is relatively low (about 1 %) and amounts of individual lignans considerably vary from plant to plant. Plant cell culture may represent a solution of the supply these lignans.

Schisandra chinensis cultures derived from immature zygotic embryos were developed on Murashige and Skoog and VW5 medium. Embryogenic cultures were established on the medium containing thidiazuron, 2,4- dichlorophenoxyacetic acid and benzylaminopurine. We have explored the possibility of increasing the lignan biosynthesis by addition of two neutral polymeric resins (Amberlite XAD-2 and XAD-7) to medium of five cell cultures.

Both resins enabled significant increases in production of lignans from 2.7 to 130 times dependently on the cell lines with high recovery in the resins. Amberlite XAD-2 and XAD-7 markedly increased portions of extracellular lignans from 2–29 % to 7–99.9 % and 28–99.9 %, respectively. Importantly, Amberlite XAD-2 does not decreased the grow of the cell cultures, the grow of some cell lines was even increased almost 2-fold (80–177 % of the grow of control), whereas Amberlite XAD-7 mostly decresed the grow (58–106 % of control).

Supported by the Grant Agency of the Czech Republic (Project No. 522/07/0995) and Ministry of Education, Youth and Sport of the Czech Republic (Project No. LC06077).

J. Kubešová[1], J. Tallová[1], I. Crha[2], J. Jarkovsky[3] ([1]Department of Biochemistry, [2]Department of Gynecology and Obstetrics and [3]Centre of Biostatistics and Analyses, Faculty of Medicine, Masaryk University, Brno): **Homocysteine and thiols in plasma and follicular fluid during FSH ovarian stimulation**

Elevated plasma homocysteine is an independent risk factor for the development of many pathological states such as atherosclerosis, thromboembolic and neurodegenerative disorders, particularly neural tube defects and late pregnancy complications (pre-eclampsia, intrauterine grow retardation, pre-term birth and intrauterine fetal death and abruptio placentae). The metabolism of homocysteine is closely associated with related aminothiols – cysteine, cysteinylglycine and glutathione.

The aim of the study was to measure and determine the concentrations of homocysteine (Hcy), cysteine (Cys), glutathione (GSH) in plasma and follicular fluid of women undergoing IVF and to analyse possible correlations. Fourteen women (31.4 ± 2.8 years) undergoing IVF/ICSI were enrolled in this study. Plasma samples before and after stimulation and follicular fluid after oocyte retrieval were collected. The analysis of Hcy, Cys and GSH was performed using HPLC with fluorescence detection, the analysis of 17β-estradiol using radioimmunoassay. Statistical analyses were performed using Wilcoxon signed rank test, Mann Whitney test and Spearman's rank correlation.

During the stimulation of recFSH (2300 ± 600 IU) the concentration of Hcy in plasma significantly decreased from 11.2 ± 2.9 μmol/l to 9.2 ± 2.7 μmol/l ($p = 0.001$), the concentration of Cys decreased from 244.1 ± 29.5 μmol/l to 211.1 ± 31.3 μmol/l ($p = 0.001$). The level of GSH (μmol/l) increased insignificantly from 10.9 ± 3.7 to 16.4 ± 14.3. The concentrations of Hcy and Cys in follicular fluid correlated with the concentrations in plasma before stimulation and after oocyte retrieval. Significant differences in the concentrations of Hcy, Cys and GSH in follicular fluid with and without oocytes were not confirmed. The concentrations of Hcy and Cys were significantly lower together with higher 17β-estradiol after stimulation in plasma. A possible correlation between the number of oocytes, embryos, pregnancies and the levels of Hcy, Cys and GSH was not found.

M. Klepárník, J. Tomandl (Department of Biochemistry, Faculty of Medicine, Masaryk University, Brno): **Asymmetric dimethylarginine – risk factor of cardiovascular diseases**

Asymmetric dimethylarginine (ADMA) is a posttranslationally modified form of arginine that is generated in all types of cells during the process of degradation methylated proteins. ADMA is a competitive inhibitor of nitric oxide synthase. The increase of concentration leads to increased blood pressure and reduced blood flow. Elevated plasma ADMA is an independent risk factor for endothelial dysfunction and has been associated with e.g. hypertension, diabetes mellitus, renal failure and atherosclerosis. Physiological ADMA level in plasma is about 0.39–0.69 μmol/l and pathological ranged from 2–15 μmol/l. Today, various methods have been used for quantification of ADMA and other methylated arginines (e.g. ELISA, LC-MS, GC-MS, CE), however, the most aplied method is HPLC with fluorescent detection. As a fluorescence derivatization reagent has been used *ortho*-phthaldialdehyde (OPA). Moreover, OPA derivates of amino acids can be detected electrochemically.

Authors developed a new HPLC method for the determination of ADMA using coulometric detection. After solid-phase extraction procedure on a strong cation exchange column, the samples were derivatived with OPA reagent containing 3-mercaptopropionic acid. Formed derivatives were analyzed on a reversed phase column Hydro-RP using isocratic elution and coulometric detection. The mobile phase consisted of potassium phosphate buffer and acetonitrile. Absolute extraction recoveries measured for three analytes [L-Arginine (L-Arg), ADMA and symmetric dimethylarginine (SDMA)] and internal standard [monomethylarginine] ranged from 86–88 %. Detection limits (*S/N* 1:3) were for ADMA and SDMA 0.013 μmol/l and for L-Arg 0.012 μmol/l. The linear range was at least up to 20 μmol/l (ADMA, SDMA) and to 200 μmol/l (L-Arg). The retention times of all compounds were up to 22 minutes. This method has very good correlation ($R2$–0.97) with HPLC method with fluorescence detection and may be used for the determination of ADMA level in plasma as a cardiovascular risk factor. We used the both methods for the determination of ADMA in plasma samples of patients ($n = 40$) 24 h after acute myocardial infarction. No differences were observed between ADMA level in patients with or without hypertension.

Present results suggest that increased ADMA level could serve as a marker of endothelial dysfunction and early phase of atherosclerosis. Although ADMA levels after acute heart failure are not known yet, the investigation could help with understanding of ADMA role in acute heart failure as well as with monitoring of patients regeneration.

Supported by projects LC06023, MSM 0021622402 and GA203/06/0047.

J. Suchomelová (Department of Biochemistry, Faculty of Medicine, Masaryk University, Brno): **Occurrence of quaternary benzophenanthridine alkaloids in the plant sources**

Quaternary benzophenanthridine alkaloids (QBA) are small group of isoquinoline alkaloids that are biosynthesized from phenylalanine. They occur mainly in the family *Papaveraceae*, *Fumariaceae, Ranunculaceae*. Major QBAs (sanguinarine and chelerythrine) are known by their significant and variable biological effects. Some plants contain in addition to them other QBA (sanguilutine, sanguiribine, chelilutine, chelirubine, and macarpine) that are due to their low content and occurrence named as minor QBA. Information about their biological activities and sources are very sporadic.

The aim of present study was to evaluate QBA content in six species of plants of the family *Papaveraceae*, which are known as main sources of QBA. Methanol extracts obtained from roots of *Dicranostigma lactucoides, Chelidonium majus, Macleaya cordata, Macleaya microcarpa, Sanguinaria canadensis,* and *Stylophorum lasiocarpum* were analysed by HPLC method. The amount of individual alkaloids was determined as percentage of alkaloid content in the dried root. The highest of major QBA- sanguinarine and chelerythrine – was found in root of *Dicranostigma lactucoides* (1.99 % and 3.43 %, respectively). *Sanguinaria canadensis* is supposed for reliable source of all benzophenanthridine alkaloids except macarpine. The only sources of macarpine are plants of species of the *Maclaeya microcarpa* and *Stylophorum lasiocarpum*.

M. Dvořák, M. Matejovičová (Department of Biochemistry, Faculty of Medicine, Masaryk University, Brno): **Comet assay – Studying toxicity and protective effects of natural compounds**

The comet assay is a microelectrophoretic method for evaluating DNA damage expressed by strand breaks. The method can be virtually used for all eukaryotic cells. The examined sample is incubated with studied *agens* that leads to damage of DNA structures resulting in strand breakage. Cell suspension is mixed with low melting point agarose, poured onto agarose coated microscopic slides. Cells are lysed to remove all cell structures except nuclear DNA. Remaining DNA with protein matrix is called the nucleoid. Lysed cells (nucleoids) are denatured with alkali solution so that supercoiled DNA became relaxed. Undamaged DNA is quite tightly aggregated and it is not very mobile in electric field in contrast to fragmented DNA. Slides are put into an electrophoresis chamber and negative charge of DNA molecules causes migration of relaxed and broken strands towards the anode creating a comet-like picture. Comets can be visualized by fluorescent or silver staining. Evaluation can be done by scoring (class sorting according to amount of damage) or by specially designed PC software. In our experiments we used software Lucia. As a marker of DNA damage we use relative tail intensity, normally expressed as % of DNA in tail.

The method was employed to investigate effects of natural compounds on cultured human leukaemia cells (HL-60). Genotoxic effect of benzophenathridine alkaloid chelerythrine (CHEL) was observed in range of concentrations 1–10 μg/ml of growth medium. CHEL in concentration 1 μg/ml caused mild increase of damaged DNA (mean 45% of DNA in tail) whereas 10 μg/ml led to more than 95% DNA in tail. Mechanisms of the alkaloid effect may involve different signalling pathways. Toxicity of CHEL could be partially caused by induction of oxidative stress. Possible DNA integrity protection by compounds with known antioxidative properties was examined. Effects of flavonoid baicaline (BA) and phenolic compound caffeic acid (CA) on HL-60 cells incubated with H_2O_2 (100 μM) in condition with decreased metabolic activity of the cells (0° C, without nutrient solution) were tested. The protective effect of BA (100 μM) was demonstrated (40.6% damaged DNA with antioxidant vs. 50.3 % without BA). Protective effect of CA was found in experiments, in which HL-60 cells in the growth medium were preincubated with antioxidant followed by 60 min incubation with CHE (3 μg/ml). DNA damage was 45.9 % with CA vs. 57.4% without it. Authors conclude that genotoxic effect of CHE could be partially prevented by antioxidants.

L. Kukla (2nd Department of Pediatrics, Faculty of Medicine MU and Faculty Hospital, Brno; Research Institute of Preventive and Social Paediatrics, Faculty of Medicine, Masaryk University, Brno): **European Longitudinal Study of Pregnancy and Childhood – theoretical background and results**

The World Health Organization – its European Office in Copenhagen – evaluated more than 20 years ago the health situation of children and it came to a conclusion that children in Europe are dying only sporadically. This child mortality decrease however is not accompanied by a decrease in child morbidity, especially chronic, and that represents ever more severe health load. The new (child) morbidity also includes these concrete problems: neoplasias, allergies of diverse localizations, metabolic disorders, sensory and motor defects, neurotic and psychological disorders, long-term consequences of various accidents, early and frequent formation of chronic systemic illnesses. The problems in childhood grow over to the adulthood in form of higher chronic morbidity incidence, impaired work ability, increase in disability percentage and in premature death risk which all leads to lower quality of life. The WHO sees the causes in the changed life-style brought on by today's civilization, in the degraded environment and in the change in the perception of health, nature and society. The complex of these causes influences the biological, psychological and social components of the human health. In children it even helps in its formation, in the positive as well as in the negative sense. The possibilities of reinforcing and supporting child health and preventing its disorders, however, have not yet been investigated from the etiological point of view. That is why the project ELSPAC is created as a partial activity within the project "Health for All before the Year 2000".

European Longitudinal Study of Pregnancy and Childhood is a prospective longitudinal study conducted in several European countries and follows selected samples of children and their families from the pregnancy of the mother through all the developmental stages until the end of adolescence (until 19 years of age) of the children included in the sample. In the Czech Republic the project ELSPAC is investigated by the research team at the Research Institute of Preventive and Social Paediatrics (2nd Department of Pediatrics and Faculty Hospital, Brno) Faculty of Medicine MU, Brno. Ass. Prof. Lubomír Kukla, MD, PhD. has been the project's national coordinator since 1990 and has been appointed the project's international coordinator in 2007. The sample of investigated children in each country includes all children born in the course of 1–1.5 years in one or more geographical regions. In the Czech Republic the sample includes all children born between March 1st, 1991 and June 30th, 1992 to mothers with permanent residence in Brno and the rural district of Znojmo. In the beginning the whole Czech sample included cca 7000 children and their families.

The basic research data are obtained with use of questionnaires filled in by parents of the investigated children in exactly defined research dates. At the same time they are completed with data from health documentation from pediatricians and physicians for adolescents. Starting with the age of 8 years the data about studied children are also collected from their school-teachers, the children are continuously subject to a pediatric, anthropometric and psychological examinations and starting with age eleven questionnaires are constructed and administered directly to our child/adolescent sample.

The study aims to uncover the pathogenic and/or sanogenic effect of the factors included in the elements and processes of the closest human and social environment in which the biological, psychological and social components of our young generation's health is formed. From the popular presented areas it would like to name mainly the child growth and development, nutrition, accidentology, mother's smoking and its effects on the child's development in all its phases, personality and temperament characteristics and many others.

Z. Pospíšil[1], *L. Novák*[2] ([1]Department of Mathematics and Statistics, Faculty of Science, Masaryk University, Brno; [2]Research Institute of Preventive and Social Paediatrics, Faculty of Medicine, Masaryk University, Brno): **Mathematical model of child and adolescent growth. Parameters identification from longitudinal data**

The time evolution of body measures (body length or body weight) can be regarded as a phenomenological expression of the genetic determination. That is, a time dependent body size can be expressed as deterministic function subjected to stochastic variations. The deterministic part of the process can be modelled mathematically; the assumption on the stochastic part allows identifying

parameters of the model. The growth of any biological object represents a result of two conflicting actions – anabolism and catabolism. Hence, the growth is a dynamic process with at least two feedbacks, first of them being positive and the second one negative. There are many mathematical models of such processes; the simplest but widely used one is the Verhulst logistic function (*Britton, 2003, Essential Mathematical Biology, 2nd ed. London-Berlin-Heidelberg: Springer)*. It possesses three parameters – initial size, maximal possible size and maximal growth rate.

However, the human growth from birth to maturity is not so simple, it is divided into three separate phases (*Karlberg, 1984, In: Borms et al, eds. Human Growth and Development. New York-London: Plenum Press, 797–802*) – infancy, childhood and puberty. Consequently, a mathematical model of growth might include eleven parameters, three growth parameters for each of the growth phases plus times of childhood and puberty phase beginnings. The empirical growth curves show the smooth connection of growth curves for infancy and childhood phases and the continuous connection for childhood and puberty phase. Moreover, the upper bounds for the childhood and infancy phases coincide; these facts are true both for the body length and for body weight. This observation allows us to reduce the number of parameters to seven – the size at birth, the maximal growth rates and the maximal possible sizes for the infancy and puberty phases, the ages at the start and at the end of childhood phase. Since a body size should be a positive value, one can assume that the stochastic variation from theoretical growth curve is a positive multiplicative noise with unity expected value. An additional technical supposition that the noise comes from lognormal distribution yields a possibility to apply the mean square method to identify the parameters.

The proposed method was implemented to the R-language computational environment (*R Development Core Team, 2005, R: A language and environment for statistical computing. Vienna. http://www.R-project.org*) and it was tested on 13 data sets from the Brno longitudinal (1961–1982) study of child and adolescent growth, cf. (*Bouchalová, 1987, Vývoj během dětství a jeho ovlivnění. Praha: Avicenum)*. Each of the data sets allows to identify parameters (the method converges) and to estimate their statistical characteristics (standard errors). The theoretical growth curves fit all of the data sets both for body length and body weight. That is, the observation does not contradict the proposed method. Subsequently, the two sets of seven parameters (one set for body length, one set for body weight) characterize the human growth. This conclusion may be a starting point for a further research – searching for relations of the growth parameters with genetic characteristic of a person and/or with her/his health status in adult age.

D. Novotná[1], P. Okrajek[2] ([1]2nd Department of Pediatrics, Faculty of Medicine MU and Faculty Hospital, Brno; [2]Research Institute of Preventive and Social Paediatrics, Faculty of Medicine, Masaryk University, Brno): **Children with intrauterine growth retardation in the project ELSPAC population**

The represents a risk factor for newborns (risk of asphyxia, hypoglycaemia, and nutritional disorder) as well as in the long-term development (growth disorder, cognitive disorders, obesity, metabolic syndrome and diabetes mellitus – 2nd type). Children born with low birth-weight and/or low birth-length (≤ -2SD) are labelled as small for gestational age (SGA). The assumed occurrence of these children in the population is 2.3%. About 10–15% of them will not catch up on the height handicap acquired prenatally and their final height remains under -2SD of the given population. To confirm this data we used a solidly defined sample of children form the population study ELSPAC (European Longitudinal Study of Pregnancy and Children). These 7406 children were born in Brno and Znojmo in a 16-month span in the years 1991–1992. We were interested which part of these children were born as SGA and in their further development. After excluding the children who had died before one year of age, severely handicapped children and children with incomplete data we analyzed a sample of 7322 children. There were 3793 boys and 3529 girls.

The SGA criteria were found in 717 children (9.8 %). Within this group, 38.4 % of newborns had low birth-weight only, 26.8 % low birth-length only and 34.8 % had both parameters ≤ -2SD. After excluding children from multiple pregnancies the SGA group comprises 621 children (8.6 %). In the ELSPAC cohort there were 452 (6.17 %) of children born before the 37th week of gestation age. There were 68 SGA children within this group (15 %). We also analyzed the difference in the occurrence

of children with ≤ -2SD height when they were measured at 3, 7, 9 and 11 years of age in the SGA and normal birth parameters children groups. In all of the analyzed phases there were about twice as many very small children in the SGA group than in the group with normal birth parameters. The higher occurrence of SGA in the ELSPAC cohort can be explained by the norm used (Lawrence, 1989), inaccuracy in gestation age determination and in measuring birth parameters, especially birth-length. A higher incidence of SGA in immature children and maximum catch-up growth lasted up to 18 months of age. On the contrary to literature information, more children manifested catch-up growth, only 5.5 % of them had ≤ -2SD height after two years of age. Certainly the analysis of final heights of these children will be interesting.

M. Čuta (Research Institute of Preventive and Social Pediatrics, Faculty of Medicine, Masaryk University, Brno): **Modelling human ontogenesis**

Human ontogenesis consists of a biological and socio-cultural part. There is a strong belief today that the former theory of so-called "Nature versus nurture" has changed into a theory best characterized as "Nature AND nurture", meaning that human ontogenesis is strongly influenced by a biological part as well as the learned, socio-cultural part. The Life History Theory is a currently best accepted theory of speciation, how each species progresses biologically and this theory also deals with the biological part of human ontogenesis. There are two ways species confront evolution and procreation – one type of selection is labeled r-selection, the other K-selection. R-selection species reproduce in a rapid manner, have numerous, less adapted offspring with emphasis on quantity over quality. On the other hand, K-selection species reproduce slowly and less often, their offspring is limited in quantity with emphasis on quality – high level of adaptation.

This biological concept can also be applied on humans. Not only human species as a whole, which is an example of K-selection, but also within (while always having in mind the complementary nature of biological and socio-cultural concepts). Men and women approach reproduction differently, with men seeking having as much offspring as soon as possible (r-selection-like) and women looking for a stable partnership to invest in a quality upbringing of a limited number of children (K-selection-like). Reflections of r- and K-selection can also be seen in individual development regardless of sex. Why some individuals develop and mature faster and earlier than others, follow different auxological growth patterns, these questions can be answered using the following anthropological methods: the method of Dynamic Phenotype allows us to describe and predict the growth of an individual using quite readily available data understandable on the biological level. Methods of shape analysis allow us to record and interpret the changes of the human body shape and use them for predictions on individual development.

L. Novák (Research Institute of Preventive and Social Pediatrics, Faculty of Medicine, Masaryk University, Brno): **Dynamic phenotypes of the growth pattern in boys**

The growth curve of body length in newborns and of posture height in children and adolescents is composed of three components labeled according Karlberg (*1987*) in general as I – Infancy, C – Childhood, and P – Puberty. Growth curve of individual boys is possible to describe by Parameters of Dynamic Phenotype belonging to the Karlbergs three-growth curve components (*Novák et al. 2007, 2008*). Scientific notation of each of the three growth curve components of man represent separate growth curve enclosed by the origin, and by the asymptote determined by the genetics. Asymptote of the I-component Infancy DLi (I) is reached by the sucking infant between the first and third year of its age. It is worth to notice that in the mentioned period the child changes the locomotion from on four limbs to the locomotion on the hind limbs. The value of I – component asymptotes is approximately equal to one half of the posture height at the beginning of pubertal swing up D0 (P) reached in boys in the age of 12 to 13 year.

Average values of Dynamic Phenotype Parameters of (C) and (P) growth curve components, computed by Zimová (*2008*) from individual longitudinal data filed in our institute are presented in *Table I*.

	CHILDHOOD (C)				PUBERTY (P)			
Statistic data	Age [year]	Posture height initial (cm)	Genetic asymptote of posture height [cm]	Peak growth velocity [cm/year]	Age [year]	Posture height initial (cm)	Genetic asymptote of posture height [cm]	Peak growth velocity [cm/year]
	t (C)	D0 (C)	DLi (C)	dDmax (C)	t (P)	D0 (P)	DLi (P)	dDmax (P)
Average	**1**	**77.1**	**181.9**	**8.1**	**12.8**	**155.5**	**181.9**	**27.0**
± SD	0	2.7	7.4	0.7	0.9	7.0	7.4	6.4
Cv %	0	3.4	4.1	9.0	6.9	4.5	4.1	23.5
n	87	87	87	87	87	87	87	87

Posture height pattern in boys are defined by Lebl and Krásničanová (*1996*) by values of posture height in the adult individuals DLi (P) [cm], by the age at which the pubertal swing up occurs t (P) [year] and the dimension of the pubertal swing up which is in Dynamic Phenotype parameters declared as the peak of the growth velocity dDmax (P) [cm/year]. It is evident that to the mentioned criteria's of growth pattern in each individual child may be identified by the corresponding values of Dynamic Phenotype Parameters. Taking in account the statistic values of C- and P- Dynamic Phenotype parameters shown in *Table 1*, the five types of growth pattern in boys were described – see *Table 2*.

	INFANCY (I)				PUBERTY (P)			
Posture height pattern in boys	Age [year]	Posture height initial (cm)	Genetic asymptote of posture height [cm]	Peak growth velocity [cm/year]	Age [year]	Posture height initial (cm)	Genetic asymptote of posture height [cm]	Peak growth velocity [cm/year]
	t (C)	D0 (C)	DLi (C)	dDmax (C)	t (P)	D0 (P)	DLi (P)	dDmax (P)
1	1	77.1	181.9	8.1	12.8	155.5	181.9	27.0
2	1	81.0	174.0	8.8	10.0	163.0	173.0	18.0
3	1	78.0	182.0	8.1	14.5	156.0	182.0	27.0
4	1	70.5	170.0	7.1	12.5	138.0	170.0	18.0
5	1	82.0	192.0	9.0	12.8	164.0	192.0	27.0

The six parameters of Dynamic Phenotypes D0 (C), DLi (C), dDmax (C), D0 (P), DLi (P), dDmax (P), and the age of curves origin t(C) and t(P) presented in Tab. II., uniquely determine the whole trait of corresponding C- and P- components in each of the five growth pattern of boys.

However the main feature of the presented expression of the five growth pattern in boys is the fact that the indicated parameters of Dynamic Phenotypes enable to calculate the trait of the growth velocities and to estimate the age at which the peak velocity of growth is reached (*Novák et al. 2007, 2008*). In this way the relation between the effect of nutrition, hormones secretion and the impacts of various stressing factors on the growth process dynamics may to be investigated.

Compiled and revised by S. Čech