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FROM THE SPHERE OF SCIENCE

XVIIIth GENETIC DAYS – INTERNATIONAL CONFERENCE ON ANIMAL GENETICS

In the issue of the Czech Journal of Animal Science, there is a number of abstracts of scientific papers which were presented at the XVIIIth Genetical Days International Conference held at South Bohemian University in České Budějovice from September 8 to 10, 1998.

The conference of animal genetics is organized biannually by the Commission for Animal Genetics and Breeding of the Czech Academy of Agriculture Sciences in Prague and by the Commission for Animal Genetics and Breeding of the Slovak Academy of Agriculture Sciences in Bratislava. The conference is organized in cooperation with the Faculty of Agriculture of South Bohemian University in České Budějovice.

The abstracts from the plenary session contributions and section sessions which dealt with molecular genetics, cytogenetics, reproductive genetics, health and resistance, genetic diversity, breeding and farm animals and fish genetics, are published in the following text. Subsequent questions regarding the conference itself will be answered by the Chairman of the Organizational and Scientific Committee.

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Plenary session

CONTRIBUTION OF EUROPEAN ASSOCIATION FOR ANIMAL PRODUCTION TO DEVELOPMENT OF GENETICS IN FARM ANIMALS

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European Association for Animal Production (EAAP) entered into the 50th year of it's activities. The meaning and advances of this period could be evaluated from different point of view. EAAP gave under its roof the space for common activities, effective dialogues for researchers, teachers and farmers operating in animal science not only from the territory of Europe, but it could be said from all over the world. EAAP became generally accepted and respectful NGO characterised by high quality of scientific knowledge and searching for solution of hot topics of animal production. We are aware that animal production is being the most complex part of agriculture. Though the research in this sphere is as more and more demanding and expensive by the efficient methods and solutions offered by research ought to assist to overcome the most complex problems of the sector. The main challenges of animal production are as follows: solution of rational nutrition of species and breeds of farm animals, keeping and improvement of reproductive performance of species and breeds of farm animals, improvement of resistance to diseases, and improvement of criteria of longevity in farm animals keeping the present high efficiency of animals. The geneticians and the knowledge from the sphere of genetics contributed significantly to the solution of the given problems in the hitherto history. We are far from the time when it will be possible to put the genetics behind us. The methods of testing and verification of efficiency, elaboration of new methods of efficiency testing and new methods of breeding value estimation are still of great importance. The methods of breeding value estimation will with great probability summarize the contribution of molecular genetics and gene engineering to improve the efficiency of genepool in farm animals in the future as well. The utilization of new knowledge from molecular genetics and biotechnologies could influence the development and exploitation of animal resources during the coming 15 to 20 years in the sphere of nutrition, reproduction, health, and of the qualitative criteria of animal commodities, mainly milk and meat, as well.

METHODS AND PROGRAMS FOR THE ESTIMATION OF BREEDING VALUES AND GENETIC PARAMETERS

E. Groeneveld

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Estimation of (co)variance components and computation of BLUPs are a prereqisite to setting up effective selection programs on the basis of mixed model methodology (MMM). REML, Gibbs sampling and Monte-Carlo EM have been implemented in VCE4 and are readily available to animal breeders around the world. This contribution will describe the relative merits of the procedures in terms of methodology, computing and memory requirements. While optimization on the basis of analytical gradients is the fastest procedure where it can be run, both Gibb's sampling and MC-EM require less RAM at the expense of CPU time. With the rapid development in the area of computer hardware, new avenues open up to tackle large problems in animal breeding. An account of the potential and strategic considerations in regard to operating systems are given in the context of variance component estimation and the computations of BLUPs.

MAPPING FARM ANIMAL GENOMES

S. Čepica

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Fast advances of DNA technology and world-wide assault on mapping and sequencing the human genome resulted in early nineties in initiation of several projects aimed at mapping of farm animal genomes. The aim of this initiative was the construction of partial genetic maps and identification of economic trait loci (ETLs) including quantitative trait loci (QTLs), for subsequent use of these genes in breeding programmes via marker assisted selection (MAS). In principle there are two approaches for finding genes responsible for performance traits: candidate gene approach and genome scan for QTLs. At present cytogenetic and middle density linkage maps suitable for QTL mapping are available in farm animal species. QTL mapping experiments performed on different families in particular farm animal species are under way. It is reasonable to suppose that within short period chromosome regions with mapped ETLs, including QTLs, will be identified in farm animals. For an efficient performance of MAS identification of ETLs is necessary. It is supposed that further progress in identification of particular ETLs will be through comparative mapping and building of integrated map of farm animal genomes. A detailed mapping knowledge of expressed genes in humans and in the mouse will be used for comparative positional candidate gene approach towards the identification of ETLs. For this purpose the human and mouse genome databases will be used.
(Grant GA CR 523/96/0597.)

METHODICAL PROCEDURES FOR MAPPING OF QUANTITATIVE LOCI

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Experiments for detecting quantitative trait loci anywhere in the genome are intensively on the way in most livestock species all over the world. The presence of QTLs is investigated both in specially designed crosses (swine) as well as in outbred population (cattle). Analyzing such data is a demanding task from various statistical points of view and in recent years several procedures were developed. These range from relatively simple LSQ-based analyses (ANOVA, multiple regression) to quite sophisticated methods such as REML-based approaches, ML or Bayesian analysis. The more simple procedures are computationally inexpensive and therefore allow to determine test statistics via simulation or data permutation. However, they less suits for genetic parameter estimation and do not allow the inclusion of relationships among animals. ML and Bayes methods on the other hand exhibit high computational requirements but also take account on the distribution of marker-QTL genotypes on the pedigree. Additionally they permit the investigator to fit different models with respect to the nature of QTLs as well as their number on the same chromosome. Properties of the methods are compared for real and simulated data-sets and strategies for mapping QTLs are proposed.

GENETIC MARKERS AND THEIR ASSOCIATION WITH QTL

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Development of molecular biology technics enable on the molecular level pursuance of DNA mutations and searching or identifying of genes which are responsible for hereditary anomalies or metabolical disorders as well as for hereditary predisposition to create economically important traits. Utilisation of DNA polymorphisms has a great importance, before all, in such traits improvement which are measurable with difficulties, with low heritability, expression in higher age of animal or in such traits they have a negative correlation each to other, where effectiveness of traditional methods of selection is low. The stage of gene mapping in vertebrate species shows that extensive data are available in human and mouse, where over 5000 loci were analysed. Research programmes in farm animals dealing with economically important traits can be used at MAS (marked assisted selection). For example, it is well known that in cattle and most other mammalian species only 6 genes are codying for more then 95% of the whole amount of milk protein. The bovine milk proteins make up roughly 25% of the total animal proteins used for human nutrition. Thus, the corresponding loci may be the main economic trait loci so far known in farm animals. The four gene loci codying the caseins are closed linked within 200 kbp DNA segment. Critical success factors for the effective implementation of genetic linkage maps are maximal flexibility through effective conceptual database modeling and normalization, maintenance of sufficient genotypic and phenotypic data within families to be able to determine transmission of chromosomal fragments between generations, achieving a genetic linkage map with 2 cM resolution, and maintenance of DNA sequence data to aid in standardizing nomenclature. QTL mapping is an idea whose time has come. The number of markers and traits has become so large for many species that joint analysis of all data derived from single experiment is necessary. Application of marker-assisted selection potentially can increase rates of genetic gain by up to 20% but will require significant changes in breeding programs.

GENOME MANIPULATIONS IN FISH

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The development of genome manipulations in freshwater fish within the last 10 years includes wide problems of fundamental research, i.e. laboratory experiments with genetically manipulated organisms (GMOs) and consequent cytogenetical aspects of induced polyploidy (triploidy, tetraploidy or higher ploidy levels), uniparental inheritance (meiotic gynogenesis) and parental genome cloning (mitotic gynogenesis and androgenesis), including radiobiological problems of DNA inactivation, and sex reversal as well. The GMOs induced by some of the methods mentioned or by combination of them are tested and utilized directly for the production [triploids due to the effect of sterility (newly introduced fish species) and thus for stability of marketable products (salmonids) and/or for higher growth given by sterility (salmonids, cyprinids, tilapias), gynogenetic stocks for caviar production (acipenserids), monosex- or triploid monosex stocks of fish of better growing sex (salmonids, cyprinids, tilapias)], in breeding programmes [establishment of highly homozygous lines of fish with uniparental inheritance or of parental clones (salmonids, cyprinids)] and in gene resources conservation (restoration of endangered species by means of gynogenesis or androgenesis). Attention is also paid to the ethical problems of induction and utilization of the GMOs in fish, as well as to possible impacts of stocked or escaped GMOs to autochthonous ichthyocenoses.

Session I: The molecular genetics and cytogenetics

POLISH PROJECT "QTLs MAPPING IN PIGS"

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The Polish pig genome mapping project was started in 1993. The main aim was to identify the QTLs controlling carcass quality in pigs. A population of three generations was founded basing on crossing of Zlotnicka Spotted boars and Polish Large White sows. There were three institutions participating in a project realization: Institute of Genetics and Animal Breeding Jastrzębiec, Institute of Animal Production Balice, Agricultural University Poznań. Investigations were supported by the Committee for Scientific Research (Poland). Ten blood group system, 12 blood proteins, 2 lipoproteins allotype and 18 microsatellites were genotyped. The *RYR1* gene mutation was identified by PCR/RFLP method. The distribution of size variants of positive C-bands (chromosomes 13–18) and silver stained NORs (chromosomes 8 and 10) was analysed. A method of Haley et al. (Genetics, *136*, 1994: 1195–1207) was applied for QTLs mapping. Significant QTLs were identified for fat depth (chr. 2, 4, 7, 13), abdominal fat content (chr. 12), lean meat and fat content in the primal carcass cuts (several regions of genome).

MAPPING OF QTLs ON THE PORCINE CHROMOSOME 4

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Two three-generation F_2 pedigrees (Wild Boar x Piétrain – W x P and Meishan x Piétrain – M x P) were established at the University of Hohenheim for mapping of QTLs. In F_2 animals 43 growth, carcass composition and meat quality traits were measured. In W x P and M x P 5 and 10 markers were typed spanning 127 and 135 cM, respectively. A least square method was used for detection of QTLs and chromosome-wide as well as genome-wide significance thresholds were set by permutation method. Applying 5% chromosomal threshold, 11 traits were mapped in W x P and 18 traits in M x P. They explained 3.3–8.0% and 3.2–7.9% of the F_2 variance, respectively. For 8 traits QTLs were detected in both pedigrees and mapped to the same segment between *SW835* and *Sw2435*. Analyses using models allowing for multiple QTLs on chromosome 4 for these traits detected no QTLs beyond those found with single locus models. In total, 9 QTLs were also significant at the estimated 5% genome-wide thresholds. In contrast to other studies of chromosome 4, no QTL for average backfat was mapped in either of our pedigrees. Animals which inherited both alleles from Piétrain had higher weights of both meat and fat cuts, but not higher lean to fat ratio. This suggests that the QTL controlling growth affects variation in deposition of both lean meat and fat.

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THE COMPARISONS OF THE CHROMOSOME AND DNA LEVELS OF GENETIC VARIABILITY

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Problems of the search of laws in space organization of a genetic material in interphase nucleus are a subject of intensive researches. The appearance of the Robertsonian translocations (RB) in mouse laboratory lines realized throughout the interactions between homologous major satellites near each centromere. Estimation of the interchromosome associations between heterologous chromosomes (for type of RB); the frequencies of the associations between individual chromosomes, identificated by G-bands and mouse line peculiarities, the directions of cytodifferentiation, the stages of cell neoplastic transformation in cell population of a various origin was carried out. The presence of the interrelations between individual chromosome associations and the genetic and cytological cell characteristics with the uses of the different mathematical methods of analysis was revealed. The participation of families of DNA repeats in the overchromosomal level of nucleus organization and in the changes of its are discussed.

THE BREED SPECIFICITY OF KARYOTYPE INSTABILITY IN SOME CATTLE BREEDS

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The distinctions of frequencies of interchromosome associations on the types of Robertsonian translocations (RB) between Holstein, Ukrainian beef and Simmental, that are in accordance to known distinctions between these breeds on frequency of occurrence of Robertsonian translocation are described. The increase of the association between chromosomes on the RB type in experimental cattle group in zone of Chernobyl accident were revealed. It is shown, that Holstein cattle is different from other investigated breeds of the increased frequency of aneuploidy. The positive correlation between aneuploidy in blood cells of cow-embryo donors and the quantity of embryos, receiving from them, were revealed. Data are submitted that the reception of the artificial twins (by transplantation of two embryos to one cow-recipient) is accompanied by expressed karyotype destabilization, certain contribution in which the observed spontaneous somatic hybridization in blood between cells of various origin can introduce.

COMPARATIVE RESTRICTION ANALYSIS OF BOVINE MITOCHONDRIAL DNA

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To date a small number of mitochondrial DNA (mtDNA) studies have done in local bovine breeds. We present the RFLP analysis of non-coding region of mtDNA in Cholmogor cows. The D-loop region and nearest sequences from 15601 to 404 position were amplified using PCR and analysed by 12 enzymes: AluI, ApaI, BamHI, BstXI, Eco47I, EcoRI, HaeIII, HindIII, MspI, PstI, RsaI, TaqI. The number of cleavage sites and molecular length of fragments corresponded well with the values inferred theoretically from the complete sequence of mtDNA reported by Anderson et al (1982). No variations were observed in the cleavage patterns of most of the restriction enzymes except for MspI and RsaI. The polymorphic pattern had one more MspI cleavage site CCGG in the position from 361 to 364. The MsipI (HpaII)-polymorphism was also detected in some maternal lines of Holstein cows (Koehler et al., 1991). The polymorpic RsaI recognition sites localized in L-domen of D-loop were not previously described. The mtDNA polymorphisms can be used as genetic markers to genotype and better use of genetic resources.

CYTOTOXIC EFFECT OF BOVINE SEMINAL RIBONUCLEASE (BS-RNASE) ON HUMAN MALIGNANT NEUROBLASTOMA *IN VITRO* AND *IN VIVO*

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To test *in vitro* the cytotoxic effect of BS-RNase four neuroblastoma cell lines UKF-NB-1 to 4 were used. The cells were cultured in IMDM medium with 20% foetal calf serum. For the cytotoxicity assays cells were seeded in the 96 well tissue culture plates. The highest concentration of BS-RNase was 200 μg/ml. This dose was diluted serially 10 times by factor 2. The cells with BS-RNase, and the controls were incubated in an CO$_2$-incubator at 37 °C for 7 days. To reveal the cell reaction the MTT-test was performed, optical density determined and the results compared with cell control. The assay has shown that the BS-RNase concentrations of 200 to 12.5 μg/ml destroyed cells of the neuroblastoma cell lines. The concentrations of 6.25 to 3.12 μg/ml showed inhibitory effects. In the concentrations of 1.56 g/ml and below the growth of cells was comparable to cell control. Antitumoral activity of BS-RNase *in vivo* was determined in CD-1 nude mice, bearing established s.c. UKF-NB-3 xenografts. The animals were treated daily by the intratumours application of BS-RNase for the time period of 19 days. The experimental group received 250 μg BS-RNase/20 g mouse in 0.2 ml vehicle (saline) and the control animals the equal volume of vehicle. When the treatment was stopped the average size of the treated tumours was 24 mm^3 (SD33) and of the controls 1275 mm^3 (SD 115). The BS-RNase treated mice remained free of tumours for further 20 days. Conclusion:

BS-RNase degenerated neuroblastoma cells and tumors and treated mice remained free of tumors for 20 days after their became extinct.

PRELIMINARY STUDY OF WATERFOWL KARYOTYPE

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Poultry karyotype remains less known in opposite to the progress in mammals cytogenetics. Standardized banding pattern has been established only for eight first pairs from total of 78 chromosomes of *Gallus domesticus*. Only a few papers present investigations run on waterfowl. The work aimed at the analysis of goose and duck karyotype. The investigation covers geese from breeding stocks originated from two species *Anser anser* and *Anser cygnoides* and two ducks strains with different genetic background: *Anas platyrynchos* and *Carina moschata*. The metaphase plates were prepared from lymphocyte culture. RBG and C-banding method were applied for chromosome treatment. First 8 pairs of chromosomes were analyzed for each species. All of them were described morphologically and for heterochromatine regions.

ANALYSIS OF POLYMORPHISM IN THE PORCINE MYOGENIC FACTOR-5 (*MYF5*) GENE

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During the course of skeletal muscle differentiation four myogenic factors, MYF5, MYOG, MYOD1 and MYF6, play important regulatory functions. *MYF5* appears to be the first gene for a myogenic regulatory factor to be expressed in the course of development, and seems to be necessary for the formation of premuscle masses. The gene is considered as one of the candidate genes for lean meat production. The objective of this study was to search for polymorphism in the porcine *MYF5* gene using PCR-RFLP. Primers for PCR were developed from the sequence of the porcine *MYF5 (*forward primer) and human *MYF5* (reverse primer). A 1.2 kb fragment was amplified. The fragment, after cloning in pUC18, was end-sequenced to verify that it was a part of *MYF5* gene. By using restriction enzymes *Hpa*II and *Hae*III biallelic polymorphisms were revealed in Meishan pigs and Duroc. Sizes of alleles were: *Hpa*II *A* – approx. 1 + 0.2 kb; *B* – 0.55 + 0.45 + 0.2 kb; *Hae*III *A* – 1 + 0.2 kb; *B* – 0.75 + 0.25 + 0.2 kb. Codominant inheritance of the alleles at both loci was confirmed in the Hohenheim Meishan x Piétrain and Wild Boar x Meishan pedigrees. There was cosegregation of alleles *Hpa*II *A* with *Hae*III *B*, and *Hpa*II *B* with *Hae*III *A*. Unrelated animals (57 pigs) belonging to different breeds (Large White, Landrace, Czech Meat Pig, Black Pied Přeštice, Piétrain, Hampshire) were monomorphic (*Hpa*II *B*, *Hae*III *A*). The polymorphisms will be used in association studies.

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CONTROL OF FARM ANIMALS AND IN SOME OTHER SERVICE FOR ANIMAL BREEDING

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Parallely with blood typing and protein polymorphisms testing we have used the method of DNA microsatellites in parentage control of farm animal. PCR products were analyzed on automatic DNA analyzer ABI PRISM TM310. 12 microsatellites in horses, 11 microsatellites in cattle, 10 microsatellites in goat, 11 microsatellites in sheep and 6 microsatellites in swine have been routinely used. 2–4 microsatellites were used as a supplement in cause of non informative genotypes. In horses and cattle we are using a set of DNA markers recommended as a standard set of DNA markers for parentage verification by the ISAG (International Society for Animal Genetics). The theoretical cumulated exclusion probabilities of false paternity is 99.9%. We are offering polymerase chain reaction (PCR) based tests in genetic disorders: MHS in swine, BLAD and RED-factor in cattle an also κ-casein gen typing and embryo sexing.

LENGTH VARIATION AND HETEROPLASMY IN WHITEFISH (*COREGONUS* SP.) D-LOOP mtDNA

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Three length variants (S, M, and L) and heteroplasmy of D-loop mitochondrial DNA were observed after amplification with the polymerase chain reaction (PCR) of 113 whitefish (*Coregonus* sp.) representing six populations from Europe and four samples from Lake Baikal. An analysis of the mtDNA variant frequency distribution using a Monte Carlo simulation revealed significant geographic heterogeneity ($\chi^2 = 65.82$; $P = 0.000$) between the samples from Europe and from Lake Baikal. The difference could be attributed to differential population reduction through loss of habitat in the Europe and Lake Baikal during the Pleistocene, followed by the effects of stochastic lineage extinctions. On the basis of nucleotide sequences of this region we propose a model for the origin of length differences.

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THE USE OF NICOTIN ACID AS AN ADDITION TO FEED RATION FOR HOLSTEIN DAIRY COWS

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There was studied the effect of separate feeding versus complete feeding diets on voluntary feed intake, milk yield and health during the first 12 weeks of lactation. The cows were randomly assigned to 4 groups. Two groups were fed by separate rations, two groups by TMR (Total Mixed Ration). The groups number 2 and 4 got 3 g of Nicotin acid per cow daily. Dry matter intake was higher on 1–1.2 kg at the groups Nr. 3 and 4 (TMR). Frequency of metabolic and digestive problems were the highest at the groups without Nicotin acid. Dosage of Nicotin acid in some cases influenced increasing of some essential amino acids in milk protein. The Nicotin acid at 3 g daily dosage per cow positively influenced the number of sick cows and reproductive markers as a service period day and inseminations index, respectively.

GENOTYPING OF GROWTH HORMONE GENE IN CATTLE

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There was a growth hormone gene genotypized in some cattle breeds in the Czech Republic (Czech Pied cattle, Czech Red cattle, Black and White cattle) and in German Black and White cattle. The Czech Red cattle is an original Czech brachycerous cattle and belongs to the endangered genetic resource. There was the polymorphism studied at the amino acid position 127. We used the method of Polymerase Chain Reaction and Restriction Fragment Length Polymorphism (PCR/RFLP). The primers 5'-GCTGCTCCTGAGGGCCCTTCG-3' and 5'-GCGGC GGCACTTCATGACCCT-3' were used to amplify the fragment of 223 bp. The PCR product was split by *AluI*. We found out the frequencies of alleles *L* and *V* and of relevant genotypes, respectively. The frequency of allele *L* was 0.558 in Czech Pied cattle (Simmental), 0.510 in Czech Red cattle, 0.700 in Czech Black and White, and 0.833 in German Black and White. Statistically higher frequency of allele *L* in Black and White population is in accordance with literature. There were also found statistical differences among breeds in genotype frequencies, in German Black and White and Czech Black and White there were stated significant higher frequency of genotype LL and lower frequency of genotype LV compared to the Czech Pied and Czech Red breeds. We found significant differences between empirical and theoretical genotype frequencies in Czech Pied and Czech Red breeds.

THE ANALYSIS OF SOME MICROSATELLITE LOCI IN CATTLE

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There were analysed microsatellite loci BM6438, CSSM004, IDVGA9 and BM6117. The fragments had been amplified in PCR, divided electrophoretically on polyakrylamid gel and stained with ethidium bromid or silver. We found out the allele and genotype frequencies, the heterozygosity and PIC. The study has been carryied out in Czech Pied cattle (C), Czech Red cattle (CC), crossbreds Czech Pied x Czech Red cattle F1 generation (F1), Black and White cattle (N) and German Black and White cattle (NN). There was a higher degree of polymorphism found in four-alelic locus BM6438, there was the heterozygosity in C 0.722, (PIC 0.672), in CC 0.672 (PIC 0.612), in F1 0.626 (PIC 0.561), in N 0.655 (PIC 0.590) and in NN 0.686 (PIC 0.387). The lowest figures of both coefficient were found in two-alelic loci IDVGA9, in C was the heterozygosity 0.375 (PIC 0.305), in CC 0.146 (PIC 0.135), in F1 0.073 (PIC 0.070), in N 0.200 (PIC 0.180) and in NN 0.388 (PIC 0.313). Three-alelic loci CSSM004 and BM6117 had intermediate values. We stated that the Czech Red breed has not lower degree of polymorphism even if its population is several dozens heads only. This breed is an original Czech brachycerous cattle and belongs to the endangered genetic resources. The other analysed locus CSSM015 has shown to be monomorph, also locus BL28 according to the preliminary results does not seem to be polymorphous. The results will be used in the next population studies.

MOLECULAR VARIABILITY OF ESR LOCUS IN PIGS

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Identification polymorphisms of individual genes or anonymous genetic markers associated with litter size in pigs could have a great economic impact on the swine industry. Similar is an estrogen receptor (ESR), which was chosen as a candidate gene to study litter size in pigs. We have detected point mutations in ESR locus by means of PCR amplification followed by restriction endonuclease analysis with *AvaI*, *MspI* and *PvuII* enzymes. Three genotypes in every polymorphism have been established. We have tested total number of 453 animals, all rising from breeding farm. In randomly selected sows of Large White breed the frequency (percentage) of genotypes was: ESR-AvaI: AA = 66.9; AB = 21.6; BB = 11.5 ($N = 227$). ESR-MspI: CC = 61.7; CD = 32.1; DD = 6.2 ($N = 81$). ESR-PvuII: EE = 54.8; ER = 37.7; RR = 13.5 ($N = 135$). In sows of Landrace breed the frequency was: ESR-AvaI: AA = 82.4; AB = 16.9; BB = 0.7 ($N = 142$). ESR-MspI: CC = 80.0; CD = 19.3; DD = 0.7

($N = 130$). ESR-PvuII: EE = 65.0; ER = 30.0; RR = 5.0 ($N = 20$). In sows of Belgian Landrace breed the frequency was detected only in ESR-AvaI polymorphism: AA = 57.7; AB = 34.6; BB = 6.7 ($N = 26$).
(Results were obtained with financial support of FR VŠ MŠMT No. 478/98.)

CHROMOSOME BANDING STUDIES IN BREAM (*ABRAMIS BRAMA*)

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The chromosome complement of bream (*Abramis brama* L.) was investigated using C-banding and replication banding techniques. Diploid chromosome number was $2n = 50$. Karyotype consisted of 16 metacentric, 18 submetacentric and 16 acrocentic chromosomes. C-positive heterochromatin was situated mainly in pericentromeric regions. Three chromosome pairs had heterochromatic blocks on the long arms. The use of *in vivo* 5-bromodioxyuridine (BrdU) treatment for 8-12 hours followed by the FPG technique revealed a mid-late S phase replication pattern. In the present study, BrdU incorporation method was applied to chromosomes of bream for the first time, and the replication banding was consistent in all metaphases analyzed. Segments that incorporated BrdU were pale after FPG treatment and corresponded to late replicating DNA, while those that have not incorporated BrdU were darkly stained and corresponded to early replicating DNA. Replication pattern technigue revealed that C-positive heterochromatin was late replicating. The studies of fish chromosomes is a promising research area in terms of taxonomy, evolutionary studies, and genetic control in fish breeding.

HETEROCHROMATIN LOCATION ON CHROMOSOMES OF *THYMALLUS ARCTICUS*

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The karyotype of *Thymallus arcticus* from Siberia was analysed using C-banding technique. The chromosome number was $2n = 98–100$. The presence of C-positive heterochromatin was observed at the pricentomeric regions af almost all chromosomes. Three chromosome pairs were very easy to identify because they possessed heterochromatic blocks: on the short arm of metacentric pair, on the long arm of submetacentic pair at the pericentromeric region, and at the same region on the big acrocentic chromosome pair. Family *Thymallinae* is very little examined cytogenetically. This is preliminary study of karyotype organization of Arctic grayling.

HUMAN ANGIOGENIN IN HUMAN AND IN ANIMAL SERA

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Angiogenesis is the process leading to the development of a vascular network in normal as well as in malignant tissues. It occurs under various physiological and pathological conditions including wound healing, embryonic development and progressive tumor growth. The human angiogenin was prepared from the synthetic gen in the Biochemical Department of Wisconsin University, Madison, U.S.A. IgG from immunized rabbit sera was isolated, conjugated with peroxidase and used as the reveal antibody. For the capture antibody, the mice IgG against angiogenin was prepared by the immunization of mice. ELISA method was used for the quantitative determination of angiogenin in human, and animal sera. The IgG of rabbits against human angiogenin reacted serologically with the boar spermadhesin isolated from the seminal vesicle fluid. The eventual angiogenic activity of this seminal vesicle fluid protein will be studied by neovascularization of the cornea method in rabbits. We can conclude that antibodies against human recombinant angiogenin are able to detect quantitatively this protein in human sera (around 200 ng/ml). However, ELISA reaction with animal sera was almost negative.

POLYMORPHISM OF PORCINE CANDIDATE GENE *CYP21* AND ITS ALLELIC FREQUENCIES IN LARGE WHITE AND LANDRACE

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The *CYP21* (steroid 21-hydroxylase) gene influences conversion of 17-hydroxy progesterone and progesterone into 11-deoxycortisol and deoxycorticosterone, respectively. For this reason *CYP21* could be considered as a candidate gene for fecundity. It is important that the gene is located in the SLA complex which was described that significantly influences reproductive and productive traits in laboratory animals and in pigs. In man deficiency of this enzyme results in congenital adrenal hyperplasia (CAP) caused by higher level of androgens. Recently we described five PCR-RFLPs in the porcine *CYP21* gene. Using restriction endonuclease *Bcn*I (*Nci*I) two polymorphic loci (*NciI1676* and *NciI2480*) were detected. In total 213 sows of Landrace and Large White breeds were randomly selected from three herds in the Czech Republic. The following allele frequencies were found in Large White for *NciI1676* ($A = 0.62$, $B = 0.38$) and *NciI2480* ($A = 0.25$, $B = 0.75$) and in Landrace for *NciI1676* ($A = 0.47$, $B = 0.53$) and *NciI2480* ($A = 0.22$, $B = 0.78$). At present associations with economical traits are being studied. (This work was supported by a grant from MŠMT FRVŠ 473/98.)

IDENTIFICATION OF GENES AFFECTING CARCASS MEATINESS AND FATNESS IN PIGS

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Population of three generations was founded based on crossing of the contrasting genetic stocks: Zlotnicka Spotted (boars) and Polish Large White (sows). The evaluation of carcass meatiness and fatness was performed for 136 and 130 F_2 castrated males fattened individually and in groups, respectively. For both types of fattening twenty seven carcass traits were determined by dissecting the right carcass side after 24 h of cooling. The ryanodine receptor gene (*RYR1*) mutation was identified by PCR/RFLP method. The genotypes of 18 microsatellites, distributed on chromosomes 2–9, 12 and 13, were defined using an ABI 310 automated sequencer (Perkin-Elmer). A method of Haley et al. (Genetics, *136*, 1994: 1195–1207) was applied for QTLs mapping. Significant QTLs for fat depth were identified on chromosomes 2, 4 and 13. The locus located between microsatellites S0083 and S0090 explained 4.48% of the total phenotypic variance of abdominal fat content in the F_2 population. The QTLs for lean meat percentage in carcass were identified on chromosomes 4 and 12.

IDENTIFICATION OF GENES AFFECTING GROWTH RATE IN PIGS

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Population of three generations was founded based on crossing of the contrasting genetic stocks: Zlotnicka Spotted (boars) and Polish Large White (sows). The evaluation of growth rate was performed for 136 F_2 castrated males fattened individually. The growth rate of porkers was determined in following periods of time: 90–150 days of age, 150 days of age-slaughter, from birth to slaughter. The ryanodine receptor gene (*RYR1*) mutation was identified by PCR/RFLP method. The genotypes of 18 microsatellites, distributed on chromosomes 2–9, 12 and 13, were defined using an ABI 310 automated sequencer (Perkin Elmer). A method of Haley et al. (Genetics, *136*, 1994: 1195–1207) was applied for QTLs mapping. Significant QTLs for growth rate were found on following chromosomes: 2, 5, 7, 12 and 13.

CHROMOSOMAL ANALYSIS OF BULL CALVES WITH ABNORMALITIES OF CHEST LIMBS

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It was the objective of this study to examine bull calves with the abnormalities of chest limbs diagnosed as arthrogryposis using cytogenetic analyses. Since it is possible to mistake arthrogryposis with rachitis, the macromineral profile as well as vitamin E have been determined. As the measured values did not exceed the reference indices, rachitis was excluded. Additionally, their mothers were also cytogenetically examined, they were phenotypically normal. Semen of bull calve father has not been analysed. Lymphocytes from peripheral blood for chromosomal analysis were processed by the method of Moorhead et al. (1960. The identification of centromeric heterochromatin was carried out according to Sumner (1972). Karyotypes were set up according to the recommendation of ISCNDA nomenclature (Anonymous, 1989). From the results it follows that centric fusions occurred in both bull calves and their mothers. Centric fusions were mono- and dicentric type in heterozygous as well as homozygous states from 5.35 to 27.3%. They occurred probably between autosomes of the pair 10/23, 3/11 and 12/13. The percentage of chromatide and chromosome breaks ranged from 6 to 25% in both bull calves and their mothers. Using the biological-molecular methods, it is possible to find the solution to the above mentioned problems in veterinary medicine.

CYTOGENETIC STUDIES IN HYPOTHYROID DOGS

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Hypothyroidism is a rather frequent endocrine disorder in dogs. However, overall there is a paucity of reported cytogenetic analyses of diseases states of the dog. Cytogenetic analyses have been carried out on a hypothyroid German shepherd bitch and its two offspring – sibling pair. The clinical picture testified to hypothyroidism which was confirmed by laboratory diagnosis as well as by the examination of the concentration of thyroid hormones T_4 and T_3 (RIA-kits, RIA-test-T_3 and RIA-test-T_4, Huma-lab., Slovak Republic). Lymphocytes from the peripheral blood were processed by the method of Moorhead et al. (1960). The changes of karyotypes were evaluated according to Langford et al. (1996) and Switonski et al. (1996). From structure aberrations, Robertson's fusions were detected in all three animals (in mother 11%, in offspring 9 and 8%, respectively). Robertson's fusions were between the 1st and 21st pair of chromosomes. Furthemore, chromatid breaks, chromosome breaks, gaps and fragments were determined. Concentrations T_3 and T_4 in the mother at the time of collection were 0,81 nmol/l and T_4 17,5 nmol/l, respectively in daughter No. 1 $T_3 = 0{,}5$ nmol/l and $T_4 = 6{,}0$ nmol/l, in daughter No. 2 $T_3 = 0{,}5$ nmol/l and $T_4 = 0$ nmol/l. From the above results it follows that in dog keeping there is also a need of close cooperation between, associations of breeders and research laboratories.

A SIMPLE METHOD FOR MITOCHONDRIAL GENOTYPE STUDIES BY PCR AMPLIFICATION FROM SINGLE FISH OOCYTES

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We report on a method suitable for analyzing mtDNA sequence variation in single fish oocytes by the polymerase chain reaction (PCR). A detailed protocol for the isolation, lysis, amplification, and detection of D-loop mtDNA haplotypes in single eggs from rainbow trout (*Oncorhynchus mykiss*) and whitefish (*Coregonus lavaretus*) is given.
(The study was supported by KBN Project No. 5P06D 010 13.)

Session II: Biotechnological methods in breeding and reproduction

METHODICAL AND REALISATION ASPECTS OF THE TRASGENESIS IN THE FARM ANIMALS

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Several reviews have been published over the last decade discussing the potential application of transgenic technology. A transgenic animal is one carrying in its genome foreign recombinant DNA molecules that were introduced at the laboratory instead of by traditional genetic selection and animal breeding. The transgene is a recombinant DNA molecule that includes, at a minimum, two parts: a regulatory element (e.g. an enhancer element or a promoter) which confers tissue specificity, controls when the gene will be expressed during development, and modulates the amount of gene expression; and a structural element composed of DNA sequences that encode the genetic information needed to synthesize the protein desired. The efficiency of producing transgenic farm animals (pronuclear microinjection is the only method used successfully to make domestic livestock) is still low due to gene integration rate, embryo survival and transgene behavior.

DNA TECHNOLOGIES IN ANIMAL BREEDING

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The modern stage of agriculture development is characterized by the increased importance of variation of animal breeding ecological conditions in relation of the wide exchanges of genetic materials between different countries. For the investigation of the population-genetical consequences of animal adaptations the cattle intrabred differentiation under influences of the biotic (infection by the bovine leukose virus – BLV) and some abiotic factors of ecological stresses with the uses of protein and DNA markers were investigated. The methods for revealing the DNA provirus BLV integration in cattle genomes with the uses of PCR were worked out. The locus-specific involving in inter- and intrabred differentiations were observed. The comparisons of the genetic variability in domestic and close related wild species were carried out. The "genetic breed portrait" creation is important not only for preservation of genofunds, investigation of breed evolution, but also for the search of genetic markers of major gene of quantitative traits.

BIOLOGICAL CHARACTERISTICS OF INTERRACIAL TROUT HYBRIDS

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Triploidized crosses of rainbow trout (*Oncorhynchus mykiss* – OM), brook trout (*Salvelinus fontinalis* – SF) and sea trout (*Salmo trutta morpha trutta* – ST) were produced using the heat shock method. Karyological tests proved that hybrids OM x ST, OM x SF, ST x SF and SF x ST were triploid with chromosomes numbers 98–11, 100–102, 122 and 124, respectively. The examination of electrophoretic GPI phenotypes confirmed genetic identity of hybrids. The survival and growth rate of hybrids during two years of its life were analysed. The results among crosses varied and between experiments however the hybrids survival was lower (with two exceptions) and growth intermediate (with one exception) comparing with parental species. The rainbow trout hybrids had a more compact body shape and were more similar to rainbow trout. Reciprocal brook/sea trout crosses had a body shape and coloration more or less intermediate between parental species. The OM x SF hybrids and rainbow, brown and brook trout as game fish has been evaluated.

GROWTH FACTOR AS A REGULATOR OF RABBIT OVARIAN CELL FUNCTIONS

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We have studied the effects of insulin-like growth factor I (IGF-I) on secretory, proliferative ovarian functions and early embryogenesis, as well as possible mechanisms of IGF-I action in rabbit. IGF-I significantly increased cAMP, cGMP and progesterone (P) release, but it was inhibitory or had no effect on estradiol (E) output. Tyrosine kinase (TK) blockers, genistein and lavendustin, both prevented IGF-I effects on P but not on E secretion. A protein kinase A (PKA) blocker Rp-cAMPS prevented the influence of IGF-I on E and P. IGF-I increased rabbit embryo cleavage and the percentage of morula/blastocyst stage embryos. PKA blockers eliminated, whereas TK blockers did not modify the effect of IGF-I on embryo development. The addition of IGF-I to the cultured granulosa cells caused an increase in the number of cells expressing proliferating cell nuclear antigen (PCNA, marker of cell proliferation). PKA blockers inhibited IGF-I- induced effect, whereas TK blockers did not modify stimulating influence of IGF-I on cell proliferation. These results suggest some diversity in the mechanisms of IGF-I action on ovarian steroidogenese, including both TK- and cAMP/PKA- dependent mechanisms. The effects of IGF-I on proliferation and generative functions may be mediated through the cAMP/PKA- rather than through the TK-dependent pathway.

METHODS OF ARTIFICIAL REPRODUCTION OF COMMERCIAL AND GAME FISH SPECIES IN THE CZECH REPUBLIC

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Natural changes of water temperature and photoperiod are general factors stimulating a spawning of both all salmonid species (brown trout, rainbow trout, brook trout, Danubian salmon, grayling, European whitefish and northern whitefish) and some riverine cyprinid species (barbel, chub, asp, nase and vimba bream). Immersed aquatic vegetation stimulates spawning of pike. A hormonal induction of ovulation by means of carp pituitary gland is used in spawning of commercial fish species (carp, grass carp, silver carp, bighead, African catfish, tench and European catfish). Recently, in two last-mentioned species and partly in grayling as well, a synthetic analogue GnRH starts to be used. In several other species, methods of hormonally induced spawning are under testing.

RESULTS OF LAPAROSCOPIC TECHNIQUES OF EMBRYO RECOVERY AND TRANSFER IN TSIGAI AND IMPROVED VALACHIAN BREED

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We performed laparoscopic embryo transfer in sheep of Tsigai (T) and Improved Valachian (IV) breed. We prepared 10 donor females (5 of IV and 5 of T) and 30 recipient females (15 of IV, 15 of T). The scheme of synchronization and superovulation treatment was elaborated for 19 days with the use of top preparations (EAZI-BREED CIDR G, OVAGEN, CHRONO-GEST, SERGON). 94 embryos were rinsed, 38 of them were capable of transferring. These rinsed and treated embryos were transferred to 19 recipient females. With the use of sonography in early diagnostics of pregnancy we found that embryotransfer had resulted in the establishment of pregnancies of 6 recipient females after 2 months. Five ewes gave birth to singles and a Tsigai recipient female gave birth to triplets after the transfer of 3 embryos of IV donor female. Among donor females 11 years old Valachian ewe surpassed because of 23 rinsed embryos, 21 of which capable of transferring.

SUBSTANCES OTHER THAN GONADOTROPINS THAT REGULATE PORCINE OVARIAN FUNCTIONS

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We have studied the effects of LH, FSH, LH-RH, oxytocin (OT), growth hormone (GH), insulin-like growth factor (IGF-I) and regulators of protein kinase A (PKA) and tyrosine kinase (TK) on secretory activity, proliferation and apoptosis of ovarian cells, as well as on oocyte maturation *in vitro*. It was observed that LH-RH, OT and IGF-I, as well as gonadotropins, stimulate the production of progesterone, estradiol, OT, vasopressin, prostaglandin F, IGF-I, IGF-binding protein 3 (IGFBP-3), cAMP, cGMP and PKA by cultured ovarian follicles and granulosa cells. These substances prevented apoptosis and in some cases stimulated proliferation of ovarian cells and oocyte nuclear maturation. GH also stimulated steroid, IGF-I and cyclic nucleotide release and blocked apoptosis, but inhibited OT and IGFBP-3 output by these cells. Antisera to OT or IGF-I, inhibitors of PKA RpcAMP or KT5720, and, to a less extent, inhibitors of TK (genistein or lavendustin) prevented most of the effects of gonadotropins, GH, IGF-I and OT. Stimulators of PKA dbcAMP and forskolin mimicked the effects of these peptides. Our observations suggest that porcine ovarian functions are regulated not only by gonadotropins, but also by other peptides including LH-RH, GH, OT and IGF-I. The effects of gonadotropins and GH can be mediated by local OT and/or IGF-I, as well as by cAMP/protein kinase A-dependent intracellular mechanisms.

THE INFLUENCE OF EMBRYOTRANSFER ON HIGHER OF MILK PERFORMANCE IN DAIRY COWS HERD

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The aim of this work was to verify an influence of the use of embryo transfer (ET) method on the increase of milk performance of dairy cows in production herd. The investigation was carried out in 1st to 3rd lactations using the method of contemporaries in a herd of Czech Pied cattle with the blood proportion of A, R, H breeds up to 50%. The rearing and breeding conditions, incl. nutrition level were the same in the compared groups. Studied animals were divided into 4 groups: the 1st group consists of pairs of sisters, one of them was born after ET and the other after insemination (A.I.), the 2nd group consists of half-sister pairs having the same father PR-408, the 3rd group consists of half-sister pairs having different fathers, and the 4th group consists of all evaluated ET and contemporaries. Significant differences in production were revealed in following cases: in group 1 in kg of milk and kg of fat ($P < 0.01$) in 1st lactation in favour of contemporaries - true born sisters and in group 2 in kg of milk ($P < 0.05$) in 1st lactation in favour of contemporaries – half-sisters. In general it can be stated that in group 1, 2 and 3 there was a trend towards heigher milk performance in contemporaries, while in group 4 in ET. These results do not confirm the effectiveness of improvement in milk performance of a herd with method ET under the examined conditions.

EMBRYO TRANSFER AND ABORTIONS IN RECIPIENTS

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The objective of this work was to summarize the level observed abortions during our own and published experiments. In a dairy herd (Holstein x Simental crossbreed) the most yielded cows were superovulated, 7-day embryos were flushed and evaluated. Of suitable one or two fresh embryos were non-surgically transferred into the uterine horn synchronized nulliparous heifers the same breed ipsilateral to the ovary bearing corpus luteum. Diagnosis of pregnancy was confirmed by rectal palpation 6 to 7 weeks later in 35 heifers. Of these animals, 31 continued pregnancy to the term and four (11.43%) of them aborted až two heifers bearing twins in 5 and 7 months and two in 8 months of pregnancy. The same approach except the use of in vitro fertilized and cultivated embryo was used in another experiment. Of four pregnant heifers, all continued their pregnancy to the term without abortion. It was found out (in 22 published papers during last 10 years) the abortion rate 0 to 50% with mean value about 17%. Except of 4 works due to small number of pregnant animals after ET, the abortion rate was between 1.23 to 28.57%, mean 13.78%. Stratification of abortion rates into 5% parts was as follows: 5 to 10% (6 times), 20 to 25% (4 times), 10 to 15% (3 times), 1 to 5% (twice), 15 to 20% (twice) and 25 to 30% (once). We conclude that abortion rates among farms or experiments are very different with the whole level > 10% and require the appropriate attention of the researchers and breeders.

INDUCTION OF FERTILE ESTRUS IN THE BITCH USING FSH-P

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The purpose of the study was to induce estrus and ovulation in normal bitches using original Russian follicule stimulating hormone of porcine pituitary origin (FSH-P). Fourteen mature different breed female dogs (3 to 4 years of age) were divided into 2 groups of 7 animals each. Bitches first group were injected intramusculary with 2 IU (Armour Standart) of FSH-P daily in during 5 days of late anestrus and the second group injected with 4 IU of FSH-P daily in during 5 days. All bitches with observed estrus were subjected to natural breeding on 11–13 day after the beginning of proestrus. Five of seven (1st group) and four of seven (2nd group) bitches came into standing estrus, respectively. After having last injection of FSH-P, proestrus was beginning in first group on 10.5 ± 0.3 days and second group – on 9.2 ± 0.6 days. Of the bitches that came into estrus three conceived in the first group and two in the second group. The average induced litter size was 6.7 and 6.5 for first and second group, respectively versus 7.6 for the colony (spontaneous estrus cycle, $n = 15$). These data suggest that modest result of estrus induction were obtained with using FSH-P, but the litter sizes were normal.

BIOTECHNOLOGY OF REPRODUCTION AND BREEDING OF IDE (*LEUCISCUS IDUS* L.)

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Ide (*Leuciscus idus* L.) is a species that is used in pond aquaculture, as well as in river management, especially by anglers. For this reason, good quality stocking material is necessary. Mass production of ide offspring is possible to do in hatchery controlled conditions with artificial spawning using hormonal treatment. The artificial propagation of ide was tested using different doses of human chorionic gonadotropin (hCG), carp pituitary extract (CPE) and ovopel (GnRH and metoclopramide containing pellets). The best results were obtained when injections from hCG and CPE were combined together, as well as, in ovopel. Ide larvae were reared for 21 days at constant temperature (25 °C), but in different food regimes (*Artemia* sp. naupli, different kind of dry food and mixed food) in density 40 specimens per litre. All experiments (in duplicate) were carried out in 50litre glass aquaria working in recirculated system. The best result were obtained when ide larvae were fed with *Artemia* sp. naupli.

BIOTECHNOLOGY OF REPRODUCTION AND BREEDING OF ASP (*ASPIUS ASPIUS* L.)

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Asp (*Aspius aspius* L.) is a piscivorous cyprinid fish. In Poland, especially in its north part, asp are becoming endangered and asp catches have steadily decreased. To reverse this trend is necessary to produce stocking material of this species in controlled conditions with artificial spawning using hormonal treatment. The artificial propagation of asp was tested using different doses of human chorionic gonadotropin (hCG) and carp pituitary extract (CPE). The best results were obtained when these both hormonal treatment were combined together. Asp larvae were reared for 21 days at constant temperature (25 °C), but in different food (*Artemia* sp. naupli, dry food – Crystal 3600 and mixed food) and density regimes (from 25 to 75 specimens per litre). All experiments (in duplicate) were carried out in 50litre glass aquaria working in recirculated system. The best result were obtained when asp larvae were fed with only *Artemia* sp. naupli in highest stocking density.

INFLUENCE OF TEMPERATURE ON ASP (*ASPIUS ASPIUS* L.) LARVAL DEVELOPMENT

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Influence of water temperature on larval development of asp (*Aspius aspius* L.) was studied. Larvae were reared for 21 days at eight constant temperatures ranging from 10.5 to 31.0 °C, and in constant photoperiod (18 hrs light and 6 hrs dark). Fish were fed *ad libitum* with *Artemia* sp. naupli. All experiments were carried out in duplicate. The instantaneous growth rate in wet weight increased with increasing test temperature from 10.5 to 31.0 °C. Individual growth of fish and biomass gain production rate were observed at the highest test temperature 31.0 °C; mean wet weight 135 mg, in contrast to fish from the lowest temperature – mean weight below 15 mg per specimen. Total observed mortality was low in all tested temperatures; the highest value (about 14%) was noted in fish groups reared in temperatures below 22 °C. In higher test temperatures survival was over 95%. Water temperature 31 °C is recommended as optimal when food availability and photoperiod are not limiting factors. The influence of temperature on asp early development also was studied. Fish reared in the lowest temperatures showed faster development in order to their total length.

REPRODUCTIVE PARAMETERS OF DAIRY COWS BORN FROM EMBRYO TRANSFER

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The aim of this work was to verify an influence of the use of the embryo transfer (ET) method on reproductive parameters of dairy cows in a production herd. The study was carried out in Ist to IIIrd lactations using the method of contemporaries in a herd of the Czech Pied cattle with the blood proportion of A, R, H breeds up to 50%. The rearing and breeding conditions, incl. nutrition level and management technology were the same in the compared groups. The studied animals were divided into 4 groups, their reproductive parameters were evaluated with standard statistical methods and tests. The first group consists of pairs of sisters, one of which was born after ET and the other after insemination (A.I.), the second group consists of half-sister pairs having the same father PR-408, the third group consists of half-sister pairs having different fathers, and fourth consists of all evaluated ET and contemporaries. Significant differences were found in the following cases: in group No. 1 in second lactation at A.I. index ($P < 0.05$) and at calving interval ($P < 0.05$) in favour of ET, in group No. 2 in first lactation the pregnancy was longer in ET ($P < 0.05$) and in second lactation the interval of mating was shorter ($P < 0.05$) in ET. In the remaining cases the results were insignificant. No practical significant influence of ET on reproductive parameters of dairy cows was detected under the examined conditions.

FEDERAL GENOFOND EMBRYOBANK IN RUSSIA

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The federal bank of embryos of Russian breeds cattle was founded at All-Russian Institute of Animal Breeding. There was developed a unique marking system of straws and of their placing. Necessary material may be found by means of the hierarchical principle of placing. The special containers with marking elements for straws and the containers for storage of straws in liquid nitrogen allow to identify any straw. This system is reliable for low temperatures (–196 °C) and expels the possibility of losses. The system of informational provision has a computer-controlled database. Up to now there are 1653 embryos being stored in the embryobank. These embryos have been recovered from 225 high milk productions donors of

15 cattle breeds. The local Russian breeds as Kalmyzkaya beef breed and Yaroslavskaya dairy breed require special consideration. Cattle of Kalmyzkaya breed are highly resistant and adaptable to unfavourable environmental conditions, high rate of live weight gain. Cattle of Yaroslavskaya breed are highly resistant to infectious diseases, free from leukosis virus. Milk of Yaroslavskaya cows contents 4.7–5.3% of fat and 3.8% of protein. The broad use of the embryobank is proposed to maintain gene resources of the local cattle breed.

REPEATED SUPEROVULATION IN BOVINE EMBRYO DONORS

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Efficiency of repeated superovulation and its use in cattle improvement process were studied. Repeated superovulation was classified in high-producing donors (6th–13th lactation) and in high-producing bulls'dams and elite dams (cow and heifers) used as embryo donors in an experimental MOET program. Donor sexual cycle was synchronized with 2 doses of PGF_{2alpha} analogue (Oestrophan, Léčiva, Prague) administered within 11-day interval. FSH (Folicotropin, Spofa, Prague) was administered i.m. (since Day 9–Day 11 of the cycle) twice daily for 4 days (total dose: 560 I.U. – cows, 400 I.U. – heifers). On Day 3 (a.m.) 500–750 µg PGF_{2alpha} analogue were applied. On Day 5 and Day 6 insemination and repeated insemination were performed. The highest recovery rates of ova (14.25 ± 10.05) and of transferable embryos (10.50 ± 11.28) were found in 10 and 8 donors treated 5 and 6 times. There were no significant increases ($P > 0.05$) of mean rates recorded in the 3rd–8th treatment cycle. Non-significant differences were found in number of ova recovered from bulls'dams stimulated repeatedly during the same calving period and during successive calving intervals (8.30 ± 7.05, 8.60 ± 6.38, $P > 0.05$). Rate of transferable embryos was higher in donors stimulated repeatedly in one lactation (62.6%) than donors stimulated in successive lactations (51.2%, $P > 0.05$).

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BIOTECHNOLOGICAL METHODS IN SMALL RUMINANT PRODUCTION – SUPEROVULATION AND EMBRYO SURVIVAL

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Biotechnological methods are in sheep and goat less frequent because of reduced population of breeding animals. Stimulation regimen utilizing CIDR or sponges (Intervet pFSH or Ovagen) was applied in 37 ewes during three reproductive cycles. On average, 11.45 CL were found 9.79 ± 20.71 ova (73.0%) were recovered laparoscopically 8.38 ± 17.53 of them (86.0%) were transferable embryos. Pregnancy rate after laparoscopic transfer of 1–3 embryos amounted to 70.4% (57/81), embryo survival amounted to 61.7% (74/120). Pregnancy rate and lambing rate increased proportionally to the number of transferred embryos (1, 2 or 3) total embryo survival, however, decreased (70.8%, 63.0%, 33.3 %, respectively). Positive results were found after transfer of vitrified embryos. The identical stimulation regimen was used in 30 mohair goats. On average, there were 9.4 ± 10.3 Cl, 8.8 (96.3%) ova, and 7.5/85.3%) transferable embryos recovered. Pregnancy rate after laparoscopic transfer realized during the reproductive season and out of season amounted to 71.4% and to 10.0%, respectively. Similar results were found in white short-hair goat. Transfer of frozen Cashmere embryos imported from Scotland resulted in 70% overall pregnancy rate (35/50) (79.4% in reproductive season, 50.0% off season). Positive results were also obtained in cryopreservation of goat embryos.

SUPEROVULATION OF BOVINE EMBRYO DONORS WITH PROTRACTED FORM OF pFSH

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Reduction of laboriousness and stress impact on embryo donors were the principal objectives of the study. Application of a suitable vehicle resulted in reduction of eight FSH doses to two doses applied as follows: Day 1 (7.00 h): 320 I.U. pFSH – Folicotropin Spofa, Prague (cows) and 240 I.U. pFSH (heifers); Day 2 (7.00): 240 I.U. pFSH (cows), 160 I.U. pFSH (heifers). Prostaglandin F_{2alpha} (Oestrophan, Léčiva, Prague) was administered on Day 3 (7.00 h). Insemination and repeated insemination were done on Day 5 and Day 6, respectively. The total FSH dose amounted to 560 I.U. (cows) and to 300 I.U. (heifers). Embryos were recovered on Day 7 post the first insemination (Říha, 1995). In total, there were 59 cows and 122 heifers treated in the experimental group (vehicle application). In cows, there were 7.58 ± 7.1 ova and 5.04 ± 5.49 (66%) transferable embryos recovered; in heifers, there were 6.11 ± 4,25 ova and 3.26 ± 3,65 (54%) transferable embryos collected. Survival rate after transfer amounted to 54%. In control group (classic aqueous form), there were 60 cows and 233 heifers classified; 10.22 ± 6.6 (cows) and 5.95 ± 4.32 (heifers) ova and 3.63 ± 3.76 i.e. 36% (cows) and 3.15 ± 3.08 i.e. 53% (heifers) transferable embryos were recovered. Survival rate after transfer amounted to 54%.

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A NEW BREEDING TECHNIQUE OF PIKEPERCH (*STIZOSTEDION LUCIOPERCA*) IN NET CAGES

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A new breeding technique of pikeperch (*Stizostedion lucioperca*) was studied during rearing of larvae in cylindrical net cages. In the first step of rearing pikeperch larvae were kept in cages (0.5 m^3 volume) with net mesh 0.2 mm. The initial density was 5500 larvae per cage. All experiments were done in duplicates. Fish were fed by zooplankton collected using light in the additional cage during night and transferred using floating pump. After 20 days of rearing fish were transferred to illuminated cages (mesh size of 1.2 mm, volume 1.6 m^3). Fish were fed by zooplankton collected during the night by light placed over the cages. The second step of rearing ended after 14 days. The larvae survival in the end of experiment was 1,9%. Fish obtained mean body length 21.1 mm together with mean body weight 82.5 mg. The first food of pikeperch larvae in lake cages were *nauplii* (*Cyclopidae* and *Calanoida*) and small cladocerans. In the end of rearing period larvae fed mainly on *Calanoida* (*Eudiaptomus* spp.) and copepodites of *Cyclopidae*.

BIOTECHNOLOGY OF REPRODUCTION AND BREEDING OF PERCH (*PERCA FLUVIATILIS* L.) UNDER CONTROLLED CONDITIONS

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The induction spermiation and ovulation of Eurasian perch (*Perca fluviatilis* L.) using ovopel – GnRh containing pellets was tested, as well as, rearing perch larvae fed with *Artemia* sp. naupli (two kinds of body size), *Paramecium aurelia* and dry food. A volume of milt produced by males from control group was significantly smaller (average 17 ml/kg BW) than those from hormonally treated groups (over 24 ml/kg BW). Significant differences in fertilization ability of sperm collected from individual males was noted. The percentage of ovulated females from treated groups was over 90%. Ovulation in from control group was noted in a limited number of females. The mean embryos survival to the eyed-egg-stage was over 50% in treated groups, in contrast to control group (7.5%). The biological quality of eggs, expressed as a survival to the eyed-egg-stage decreased with time after last injection. The total spawners mortality in all groups was lower than 10%. The highest survival in reared perch larvae (over 70%) was noted in groups fed with mixed food (small *Artemia naupli* + *Protozoa* and small *Artemia* naupli + dry food), especially in contrast to groups fed only with *Artemia* naupli, where observed survival was between 0 to 7%.

PRELIMINARY OBSERVATIONS ON ARTIFICIAL SPAWNING OF EUROPEAN PERCH (*PERCA FLUVIATILIS* L.)

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The methods of inducing spawning of perch (*Perca fluviatilis* L.) were studied using human chorionic gonadotropin (hCG) and ovopel (GnRh containing pellets). Fish (wet weight ranged from 314 to 667 g) were divided into 4 groups (five female in each group): 1 – control; 2 – two injections from hCG: 500 and 2000 IU/kg (time between injections was 24 hrs); 3 – single injection from ovopel (2 pellets/kg). During experiment water temperature was constant (13.5 °C). The percentage of ovulated females from all groups was very high (over 80%). The differences were observed in latency. The shortest time of ovulation was noted in group 3 (2–3 days after injection), in group 2 – 3–5 days and group 4 – 5–6 days. Fish from control group ovulated two days later after last female from treated group. The biological quality of eggs, expressed as the survival of the embryos up to the eyed egg stage was the highest in control groups (85.3 ± 0.3%), and in treated fish – in group 4 (78.0 ± 0.4%). The lowest quality of eggs was observed in group 3 (23.0 ± 0.7% eyed eggs).

SPAWNING OF IDE (*LEUCISCUS IDUS* L.) INDUCED BY MEANS OF CARP PITUITARY GLAND

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Up to the end of April 1997 and 1998, experiments in spawning of ide induced by means of intramuscular injection of carp pituitary gland extract were carried out; a physiological solution was applied to the control groups of fish. An average water temperature reached 13.7 ± 0.5 °C in 1997. Carp pituitary gland was applied in both single dose of 6 mg/kg and two separate doses of 1 + 5 mg/kg (with interval of 12 h). Ovulation was reached after 36.7 ± 0.4 h (503 ± 5 h°) and 26.5 ± 0.3h (363 ± 4 h°), respectively. Ovulation was not reached in control group. In 1998, carp pituitary gland in a single dose of 4 mg/kg was injected to three groups of females kept at three different temperature levels. At water temperature of 11.6 ± 0.5, 13.5 ± 0.7 and 15.5 ± 0.5 °C, ovulation was reached after 49.1 ± 2.8 h (570 ± 32 h°), 37.8 ±1.7 h (510 ± 23 h°) and 33.4 ± 2.0 h (518 ± 31 h°), respectively. A relative weight of spawned eggs oscillated between 10.53 ± 3.92 and 21.1 ± 5.9% in individual groups. An average weight of 1.79 ± 0.07 mg was registered for one spawned unswelled egg.

Session III: Genetics of health and resistance

A COMPARISON OF THE INCIDENCE OF INHERITED ABNORMALITIES IN THE DOMESTIC RUMINANT SPECIES

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Inherited abnormalities recorded in cattle (176), sheep (38) and goats (44) are listed, and standardised symbols for loci and alleles, complying with the COGNOSAG guidelines, are suggested. The detailed information on groups of inherited abnormalities in farm animals will be given at the conference.

GENETIC ASPECTS OF LYSOZYME DIFFERENTIATION IN BLACK-AND-WHITE CATTLE REARED IN THE NORTH REGION OF POLAND

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Lysozymes (E.C. 3.2.1.17) are 1,4-beta-N-acetyl-muramidases cleaving the glycosidic bond between the C-1 of N-acetylmuramic acid (Mur-Nac) and the C-4 of N-acetylglucosamine (Glc-NAc) in the bacterial peptidoglycan. In mammary gland, increased concentration of lysozyme plays a significant role in natural non-specific immunity towards mammary gland infection. In past 10 years, Polish Black-and-White cattle population reared in the north region were analyzed for lysozyme activity in serum, milk and colostrum. In more than 10,000 analyzed animals, the frequency of hypothetical high lysozyme activity (LZM^+) was found very low ($P < 0.01$). However, we have identified two heterozygote bulls for LZM^+ (Walawski et al., 1998). Using lys-mic genotyping technique (for detail, see abstract: Pareek et al.: Genetic association of lysozyme variant with serum lysozyme activity in Polish Black-and-White cattle) in half-sib families from these two bulls, we found a genetic association between macrophage expressed lys-mic alleles and serum lysozyme activity (Pareek et al., 1998, submitted). In this paper presentation, we are summarizing our both recent publications with more emphasis on its genetic aspects and future applicability in Polish Black-and-White cattle population.

ANTIGENIC SPECTRUM OF ANIMALS EVALUATED BY MEANS ANTI HIV-1 TESTS

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Blood serum 802 sheep and 80 pigs was tested by means of anti HIV-1 test (Imuna, Šarišské Michaľany) on the level of natural antibodies presence. In tested collection was found variability of natural antibodies according to tested species, which has binomial segregation. Evaluation of the level of antibodies by the level of absorbance as proposed producer of test, several individuals belong near the limit of immunodeficiency. Relation of the level of absorbance and phenogroups according to a genetic polymorphic systems was not significant. As well we did not find significant differences in tested parameters of economically traits.

ACID PHOSPHATASE POLYMORPHISM OF BLOOD LEUCOCYTES AND IMMUNOLOGICAL AND HAEMATOLOGICAL INDICES

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Occurrence of leucocyte acid phosphatase (AcP) polymorphism appeared as phenotypes A and AB was determined by two autosomal alleles. Existence of phenotype A is more frequent in cows and calves than in bulls. Activity of this enzyme was registered in granulocytes and lymphocytes but not observed in monocytes. Localization of AcP in cells, which plays a significant role in immunological function as well as a little on acquainted biological function of animals suggest that defining an association between leucocyte AcP polymorphism and indices characterizing functional state of immunological system. In these studies, there were 128 cows reared in two herds analysed. The records were estimated 5 times for duration of first lactation and irregular differentiation of analysed indices level was observed at tested terms. Correlent and statistically significant differences were proved in first month after calving. Cows with phenotype A showed lower activity of AcP in leucocytes as well as in immature granulocytes, however, higher activity of AcP in lymphocytes and higher level of lysozyme in serum blood higher values of NBT reduction test. Cows with phenotype A are also characterized by low number of leucocytes, low percentage of neutrophils and immature granulocytes and higher percentage of lymphocytes.

COMPARISON OF NON-SPECIFIC DEFENSE INDICES OF SIBERIAN STURGEON AND A HYBRID SIBERIAN STURGEON x SAKHALIN STURGEON

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Studies were performed for the first time to compare defense indices in the fry of Siberian sturgeon (*Acipenser baeri* Brandt) and its hybrid with Sakhalin sturgeon (*A. baeri* Brandt x *A. medirostris* Ayres) aged 1+ and reared in a recirculation system. Lysosyme activity was similar in both groups and amounted to about 10 mg/l. Ceruloplasmine activity and the content of γ-globulin and total protein in blood serum were at the levels of: 22.4 ± 5.4 and 14.2 ± 2.8 g%; 9.98 ± 3.05 and 7.9 ± 2.87 g/l; and 35.5 ± 1.9 and 28.7 ± 2.3 g/l, respectively, being higher in the hybrid than in Siberian sturgeon. The hybrid was characterised by lower phagocytar activity of the neurocytes: NBT test yielded average values for the hybrid and Siberian sturgeon of 1.2 ± 0.4 and 1.8 ± 0.4 mg/ml, while phagocytar index amounted to 7.4 ± 2.2 and 10.4 ± 3.4, respectively. Also neutrocyte numbers in a unit of blood volume was lower for the hybrid than for Siberian sturgeon, amounting respectively to 1945 ± 270 and 3464 ± 1074 in one millilitre. The results state that in the case of fish rearing in a recirculation system, non-specific defense responses are higher in the pure species compared to its hybrid, and the level of humoral response – lower.

REACTIVITY OF MONOCLONAL ANTIBODIES DETERMINING THE BOVINE CD ANTIGENS IN THE BULL REPRODUCTIVE TRACT

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The objective of this study was to test the reactivity of monoclonal antibodies (mabs) determining some cell surface molecules of bovine cells (CD antigens) on spermatozoa and the fluids of the bull reproductive tract. Indirect fluorescence technique has been used to detect the reactivity of 21 monoclonal antibodies with frozen, fresh and epididymal spermatozoa. The detection of reactivity of the mabs in fluids was performed by dot-blot method. The experiments revealed the presence of WC9, fibrinogen and IgM in the epididymal and seminal vesicle fluids. The same molecules have also been found on ejaculated spermatozoa, but not on epididymal spermatozoa. We suppose that these substances are bound to spermatozoa from the body fluids.

BIOCHEMICAL PARAMETERS IN COMBINED BREEDS AND IN GALLOWAY BREED IN MOUNTAIN CONDITIONS

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Within the research of the prosperity of combined and beef cattle breeds in conditions of Šumava Mountains blood parameters (packet cell volume, hemoglobin, leukocytes, glucose, urea, carotens, alkaline phosphatase, Ca, P, Mg, total lipids and proteins) were studied in calves-crossbreds of Czech Pied cattle (C) with Galloway (G) or Fleckvieh (F) breed. Calves were born freely in shelter in a pasture district (1025 m above sea level) during February 1994, and stayed permanently with their mothers. At the age of 4 months the weight of C x G calves reached 111 kg and the daily weight gain 680 g, while C x F calves weighted 103 kg and weight gain was 570 g. These results demonstrated an excellent prosperity both in calves C x G and in animals C x F. The level of blood parameters accomplished at the calves without the difference of breed the high level of erythropoesis and good saturation of animals with nutriments. An increased content of carotens in blood connected with the reception of pasture growth in early age already. Calves C x G showed statistically significant higher content of total amount of proteins in blood plasma in comparison with C x F calves. This founding and higher growth of breed C x G can give evidence for ability of better nutriment utilization in comparison with the calves C x F.

GENETIC ASSOCIATION OF LYS-MIC MICROSATELLITE MARKER WITH SERUM LYSOZYME ACTIVITY IN POLISH BLACK-AND-WHITE CATTLE

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Widely distributed in nature, lysozyme is known for its remarkable bacteriolytic activity observed in almost all mammalian blood and body tissues. In this poster presentation, we are elaborating the methodology involved in the determination of lysozyme activity in serum, new molecular approach for lysozyme genotyping using lys-mic microsatellite markers and its future applicability in dairy cattle breeding. With the use of polymorphic microsatellite within the immuno-relevant bovine lysozyme encoding gene, a total of 5 different lys-mic variants were observed in Polish Black-and-White cattle population. Out of these 5 variants, polymorphic lys-mic allele 7 showed a complete association with hypothetical gene for high serum lysozyme activity (LZM$^+$). Further, statistical analysis revealed a highly significant effect of lys-mic polymorphism on serum lysozyme activity. From this result, we can conclude that an evaluation of Polish Black-and-White population for high performance lys-mic variants is the essential pre-requisite to establish the rarely existing LZM^+ families.

IMMUNOLOGICAL VALUES OF BLAD-HETEROZYGOUS COWS

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Animals heterozygous for adhesion deficiency (BLAD) represent genetic risk keeping the BLAD allele in the population of cattle. Carrier status, however, has shown to have an effect on some performance and morphological traits. The objective of this study was to examine some immunological parameters related to neutrophile functions of normal as compared to BLAD-heterozygous animals. In all animals the expression of CD11/18 molecule, phagocyte ability, adhering properties of neutrophiles and the leukocyte counts were determined. No significant differences have been found between the leukogram of the two groups of animals. The percentage of the adherent cells of carrier cows was similar to that observed in normal animals. The expression of CD11/18 and the phagocyte activity have been decreased in the carriers.

A PIG MODEL IN THE STUDY OF PROGRAMMED CELL DEATH ACTIVATION IN THE COURSE OF A CARDIOPULMONARY BYPASS

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Programmed cell death (apoptosis) is a genetically controlled type of death. In contrast to pathological necrosis it represents an active process which can be modified. The goal of this work was to show whether apoptosis would be activated in pigs in the course of cardiopulmonary bypass (CPB), and whether the results obtained on a pig exemplar could be used for the investigation of protection of the human myocardium. CPB was carried out by the usual procedure on 10 minipigs with homozygote dominant alleles for the ryanodine receptor gene (*N/N*). Apoptotic cell death was monitored by identifying of specific DNA cleavage patterns using agarose gel electrophoresis. It was shown that apoptosis of myocardial tissues was principally proved at the end of the operation. However, it was not detected in pulmonary tissues. Apoptosis was also proved in bone marrow cells and in cells of peripheral blood (granulocytes, lymphocytes). Depressions of the number of leucocytes in peripheral blood (up to 25 % of initial value) were found together with the discovery of apoptosis. The techniques used for the estimation of apoptosis in pig myocardia were successfully applied to analogical studies of human myocardia.

GENETIC ANALYSIS OF SOME SKELETAL ANOMALIES

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Genetic parameters of embryo spinal column deformations were estimated in six generations consisting of 1498 chicken embryos – offspring of 153 sires and 735 dames. Genetic values and trends were also estimated. The following traits were considered: asymetry of the last pair of ribs (UR); deformation of thoracic region of scoliosis or lordosis type (ESC) and abnormality of synsacral vertebrae (DSC). Up to the third generation was observed an increase both in the mean frequency of the traits examined and the mean (additive) genetic value of the deformations. In the further generations, on the other hand, a considerable decrease was observed in the frequency of skeletal deformation occurrence and a drop in the mean genetic value. Heritability of the skeletal deformations was medium and low ($h^2 < 0.48$). Genetic and phenotypic correlations between the examined traits proved positive and of medium or low value, the highest ones between UR and DSC ($r_G = 0.49$, $r_P = 0.40$) and ESC and DSC ($r_G = 0.52$, $r_P = 0.13$). An increase in the level of the mean frequency and additive value of the traits examined in the first part of the experiment may by related to the introduction of selection both for ESC and DSC. However, the drop in the values of the deformation indicators estimated in the second part of the experiment may be due to the occurrence of acute virus inflammation of bursa fabricii (IBA) in the flock and resulting elimination of the carriers.

Session IV: Theoretical basis of animal breeding and selection

RELATIONSHIP OF CASEIN LOCI USED AS MARKERS TO MILK PRODUCTION TRAITS

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This paper presents some aspects of the relationship of casein loci (CN) used as genetic markers to five milk production traits. The estimated direct effects of markers and also the results of linkage analysis are considered in this connection. The results point out that the casein genes are associated with the performance differing in milk production traits. There are clear suggestions to different directions of casein genotypic effects to milk yield, fat yield and protein yield and fat and protein content according to the results from estimated direct marker effects. These effects may be due to genetic linkage as suggested by the results of linkage analyses. An evidence for medium linkage of a QTL for fat content to κ-casein was gained. The estimated effects show a superiority of $\beta\text{-CN}^{A2A2}$ of 208 kg of milk and 11.5 kg fat and protein compared with the opposite homozygous genotype $\beta\text{-CN}^{A1A1}$. A simultaneous negative influence on fat content and protein content is estimated. The difference between the effects of κ-CN genotypes on content traits is much higher in favour of $\kappa\text{-CN}^{BB}$. The heterozygous genotype $\kappa\text{-CN}^{AB}$ shows desirable effects on yield traits within the κ–CN genotypes.

TEST DAY ANIMAL MODEL IN THE SELECTION ON MILK PRODUCTION

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The perspectives and practical experience of the use of Test Day Models for milk yields were described. The aim of this study was to provide information about genetic evaluation in Slovak Republic with focus in selection on milk production and the future development due to real research, breeding and computation needs. The use of Test Day Models for milk production traits is the next upgraded method in the genetic evaluation methodologies in cattle on the base animal models. Within a few years Test Day Models should be used to improve the accuracy of evaluations and used to allow milk recording changes. Improved accuracy of evaluations, better modeling of milk production on the base test day information and the occasion of the change of the interval between tests with reduction of milk recording costs are the main reason to adopt this method in Slovakian conditions. The genetic evaluation started in 1997 with 700,000 test day records on 100,000 cows. Expected annual growth is 210,000 test day records on 30,000 cows. The relative small cattle population allows to use the Test Day Model without extra computer demands and the new genetic evaluation provide the progressive tool in selection and cattle breeding.

SIMULTANEOUS AFFECTING OF ADDITIVE AND NON-ADDITIVE AND DIRECT AND MATERNAL EFFECTS

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The aim of this review is to present some models and algorithms to estimate the direct additive, non-additive and maternal variance components. In the first part, there are the general questions on intra and interlocus interactions shown. Sources of specific maternal (indirect) and cytoplasmic variability are shortly characterized. The next section contains a literature review on obtained estimates of these genetic variance in different livestock species. The so-called unitrait total merit model (including all known genetic effects, excluding genomic imprinting) with its variance-covariance structure as well as currently applied approaches to estimate genetic parameters are described. In the final section there are some practical implications of estimation of non-additive and maternal variances discussed.

BASIC ASPECTS OF BIOMETRICO-GENETICAL EVALUATION OF ANIMAL POPULATIONS

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Biometrical methods and their applications to the genetic evaluation of animal populations have a important role in genetic improvement of livestock, have gained momentum during past 30 years. Biometrico-genetical evaluation of animal population are dependent on good knowledge of sources of genetic information, postulating adequate theoretical genetic models and their biometric versions by linear models, using modern biometrico-genetical analyses and computers. Basic genetic and statistical methods are associated with the linear models, in animals population mainly with the mixed linear models, in particularly best linear unbiased prediction, restricted maximum likelihood method and various kinds of least square methods, are now considered to be standard procedures for identifying genetically superior animals and estimating genetic trends in breeding programs. The reviewed biometrico-genetical methods for genetic evaluation of pure and hybrid animal population or simultaneously for both type of animals, e.i. mixed population, will serve for orientation of scientific workers in presented area.

LINEAR TYPE TRAIT ANALYSIS IN THE SIRE LINES OF THE OLD KLADRUB HORSE

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Linear type evaluations for 32 traits on 214 individuals in the genetic resource of the "Old Kladrub Horse" were used to analyse the effect of the sire line (10 lines), sex (stallions and mares) and age on these traits. The linear model included fixed effects for the mentioned factors. The analysis was concentrated on sire lines. The effects of sex and age class were analysed in a preceding paper (Jakubec et al., 1998). In this paper both varieties of the Old Kladrub horse (gray and black) were analysed too. The traits were grouped into four body regions: Front, body, rear and limbs. For most traits of all body regions significant and highly significant differences were found between the sire lines. The lines are very typical in the traits. In the withers the lines of SOLO and ROMKE are higher while the line of GENERALISSIMUS is lower. The origin and older lines have a conspicuous concave head profile compared to the lines of RUDOLFO and ROMKE. As a rule the black lines show shorter neck and withers than the gray ones. The lines of gray have a broader and deaper chest than the black lines. The gray lines have also a straight back and a longer and more sloped shoulder. The line of ROMKE is longer in the croup than the other ones. The stance of forelimbs and hind limbs is in the gray lines more correct than in the black ones.

CHOICE OF NEW SELECTION CRITERIA FOR FATTENING EFFICIENCY BY USING EXPERIMENTAL MODEL

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This report describes our selection experiments in Japanese quail during three last years. The aim of this study was to choose a simple selection traits for a change of the shape of the growth curve and to analyse correlated response in feed conversion. The results of selection showed that a relatively gain from 11 to 28 days of age (RG 11–28) is one from suitable selection criteria for this change. Only two generations of a divergent selection for RG 11–28 were sufficient for the reaching of a relative high interline difference in the ratio of the inflection and asymptotic weights ($y^*/A = 0.425$ vs. 0.380 for HG and LG lines, respectively). The correlated response in feed conversion confirmed a significant association between shape of the growth curve and feed utilisation. Line HG selected on the high RG 11–28 exhibited a better feed conversion (FCR) from 14 to 35 days of age than LG line selected on the low gain (FCR from 14 to 17, 18 to 21, 22 to 28, 29 to 35 days of age were 2.37, 2.32, 3.93, 5.99 vs. 2.61, 2.33, 4.55, 6.40 for HG and LG lines, respectively). The test after the fifth generation of selection confirmed these results, too. In addition, the shape of the growth curve seems to be connected with some traits of reproduction (sexual maturity).

INDIRECT EFFECTS OF SELECTION FOR BODY WEIGHT IN MICE FOR 90 GENERATIONS

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Criterion of selection performed throughout 90 generations was body weight of mice in 21st day of life. Effects of the selection in two obtained lines, light (L) and heavy (C) were analyzed. The body weight determination was performed even in time periods from day of birth until the 600th day of life in both lines. In each analyzed life periods there were found significant differences in body weight between the lines. From cross-feeding experiment it can be concluded that the body weight of mice was influenced mainly genetically. In addition the survival time of mice in those two lines was determined. In the heavy line there was found highest mortality in the age about 500 days in males and 600 days in females – in the light line mortality was the highest at the age of about 700 days. The maximal survival time in the both lines was 3 months longer in males than in females.

DERIVATION OF ECONOMIC WEIGHTS FROM PROFIT EQUATIONS

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Sensitivity of economic weights of milk production traits in cattle breeding to production circumstances are considered in situations without output limitations at the farm level. Selection based on economic indices for milk, fat and protein yield was insensitive to a large range of real or expected proportions of prices for carrier, fat and protein. Genetic responses by use of net economic weights at different price ratios for carrier : fat : protein (1 : 10 : 25; 0 : 1 : 1; 0 : 1 : 2; 0 : 1 : 3) was high in all cases (228.9–256.8 kg carrier, 10.7–11.5 kg fat and 8.4–8.8 kg protein per generation). The correlation between index and aggregate genotype was 0.84–0.85. By changing the price of different milk components, (+20% and –20%, respectively) the economic weight of above milk components was quite different. Economic weights were less sensitive to the change of feed cost. However, genetic progress per trait per generation was not sensitive to the change of milk component price and feed cost.

QUEENS – THE DATABASE PROGRAM FOR DATA PROCESSING ON HONEY BEE QUEENS AND COMPUTING OF BREEDING VALUES

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The program QUEENS was developed in the environment of data base system FoxPro 2.5. It runs under Windows on personal computers 386 or better. The program allows data processing on queens and their colonies and of their traits measured. It contents module for generating pedigree of a queen with five generations of ancestors and for computing the inbreeding coefficients of bees and relationship coefficients between two queens as well as printing reports. Generated pedigrees and computed genetic parameters are saved in a separate data base. Using results of evaluating the traits it is possible to compute the breeding values of six traits and the selection indices which combine breeding values of the traits. Supported functions are called from menu or using buttons in working or dialog windows for example data filtering, creating relations among data bases, searching some concrete record, erasing records, data import and export in a few formates, editing and printing reports and so on, it allows the effective work with data bases.

Session V: Breeding and genetics of cattle

INTERLOCI ASSOCIATION AS A NEW CHARACTERISTIC OF GENETIC STRUCTURE OF CATTLE BREEDS

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The results of interloci association analysis between two pairs of syntenic loci (transferrin and ceruloplasmin, receptor for vitamin D and κ-casein) and two not syntenic ones (amylase-I and post-transferrin) in some cattle breeds and intrabred groups, distinguished by origin, inbreeding level (intrabred lines) and environmental conditions of breeding, in particular, Red Steppe, infected by bovine leukose virus and uninfected; Holstein from relatively "pure" zones and from zone of Chernobyl accident; Grey Ukrainian, breeding in Russia (Altai) and Ukraine (Askania Nowa); Pinzgauer, breeding in different mountain zones were presented. The variability and independence of "linkage disequilibrium" revealing between loci from their synteny was observed. The obtained data allowed to suppose, that the interloci associations are controled in more extent by different factors of artificial and natural selection, than by the genetic linkages between genes.

RELATIONSHIPS BETWEEN κ-CASEIN GENOTYPE AND MILK YIELD IN BROWN SWISS CATTLE

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The import of Braunvieh cattle has started after 1990. We have imported about 600 pregnant heifers during the period 1990–1997. Many pregnant heifers were imported from Bavaria, smaller numbers from Austria and Switzerland. Effects of κ-casein genotypes on milk, protein, fat and lactose yields and protein, fat and lactose percentages were estimated from a data set of 218 lactations in imported generation of Brown Swiss cattle in Slovakia. Genotyping of κ-casein alleles was identified by the PCR method. Genomic DNA was isolated from white blood cells. LSM method was used for statistical analysis. The model included herd, parity and genotype of κ-casein as a fixed effects and number of lactation days and age at calving as a covariates. The frequency of *B* allele was 53.39%, *A* allele 46.19 and *C* allele 0.042%. The best milk production was obtained in cows with BB genotype of κ-casein (4503.52 kg). Dairy cows with AA genotype achieved only 4168.97 kg milk per lactation. BB genotypes were associated with high fat percentage, as well. Genotype of κ-casein was not associated with protein and lactose percentage.

GENETIC POLYMORPHISM AND SELECTION INDEXES OF MILK YIELD

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In the selected groups of Slovak spotted breed cows on the base of criteria sufficient variability of the character and overaverage value in the characteristics of body and type evaluation there were analysed differences in the level of protein index (GIBM) and frequency of lactoproteins alleles. In the group of dairy cows ($N = 195$) with overaverage value in the characteristics of type and body was GIBM 100.5% and frequency of allele κCn^B 0.4822. In the group of dairy cows ($N = 102$) having criteria of sufficient variability of the character was protein index GIBM higher 101,13% and at once was found higher frequency of the allele κCn^B 0.4929. The highest frequency at the allele κCn^B 0.5102 and protein index 104.55% was found in the group of dairy cows filling both criteria ($N = 61$). In this group was observed higher appearance of cows with homozygote genotype κCn BB (24.5%) in comparison with the other groups (19.9% and 21.4%, resp.).

INFLUENCE OF BODY MEASURES TO MILK PRODUCTION OF DAIRY COWS

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We compare an influence of body measures to the level of milk production in corresponding lactations of 565 dairy cows of Slovak Pied breed. The values of body measures classified according to 0.5 of standard deviation from average show unambiguous positive influence of height in whithers and lenght of body to raising of milk in kg per lactation ($P \leq 0.01$). A tendency linked with increasing of body measures and at the same time with raising of milk yield was found at measures of chest girth behind the crops, width behind the crops and depth on last rib. The positive influence to milk yield has a lenght of udder base ($P \leq 0.01$) and width of udder ($P \leq 0.01$) as well. The correlation coefficients were low till zero. These results did not confirm the results which we obtained earlier, beside of negative correlation between girth of shin bone and lactation yield ($r = -0.35$).

COMPARISON OF MILK PRODUCTION AND DRY MATTER INTAKE FOR DIFFERENT BREEDS OF DAIRY COWS

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High pregnant heifer (48), calved in the same stable and in the same seasons, were involved in the experiment. An exact individual feeding during the first three lactations and milk production were compared in the years 1992–1995. Two feeding techniques (divided and total mixed) of domestic breeds Czech Pied (C) and Black Pied (N) and imported Holstein (H) were compared. A composition of feed rations was the same for all breeds. An evaluation was carried out with proc. GLM/SAS considering calving season, order of lactation, type of feeding, individuality of the cow, and age at calving. Imported heifers were older at first calving and better prepared for lactation. Differences between breeds decreased with order of lactations. Differences between (H) and (C) were in milk production and as well feed intake approximately 10% in the average of all three lactations (after age correction at calving).

Breed	FCM (kg)	Milk protein (kg)	Dry Matter intake (kg)
H	7.039	213	5.727
N	6.748	206	5.182
C	6.195	193	5.185

IMPLEMENTATION OF BREEDING PROGRAM FOR BLACK-AND-WHITE CATTLE IN THE CZECH REPUBLIC

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Black-and-White cattle is bred in the amount of about 250,000 cows, i.e. 45% of total amount of cows, bred in the Czech Republic. In the Herd-Book there are almost 140,000 cows with various share of Black-and-White blood registered. The Black-and-White Breeders Association is an authorized Herd-Book organization and determines the national breeding program. Potential bull dams are selected out of the active part of pure population. The basic selection traits are as fellows: breeding value for protein yield, conformation and quality of pedigree. The average performance of bull dams in 1997 was 10,084 kg milk, 3.29% and 332 kg protein in first-calvers, 11,271 kg milk, 3.21% and 374 kg protein in older what represents the increase of 89 resp 94 kg protein compared with 1993. Bull sires are selected out of top bulls in the world Holstein population. About 70 to 80 young bulls are tested annually, about 10% of best of them are selected for repeated use. In the population also, the imported semen is used in the volume of about 50% of first inseminations. The average performance recorded cows was 5587 kg milk, 4.27% fat and 3.21 protein in 1997, which represents the increase of 1170 kg milk, resp. 38 kg protein since 1993.

ANALYSIS OF PEDIGREE RECORDS IN RELATIONSHIP TO MILK PRODUCTION IN SLOVAK PIED COWS

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There were the pedigree and results of breeding value evaluation of 94 Slovak Pied sires selected according to relative breeding value of fat production analysed. Total 37 sires with relative breeding value of fat production more than 105% was classed in the first group and 57 sires with relative breeding value of fat production lower than 95% was classed in the second group. Milk yield of mothers of sires was expressively above the average breed population. Sires springed from 57 fathers, from which 18 fathers were improvers, 7 fathers were deteriorators and 28 fathers were indifferent. Calculated correlations were low, statistically not significant, in general. The middle dependences between sires' breeding value of milk production and daughters' milk production in both groups were found. In the first group of sires there was found middle dependence between sires' mothers average milk production and sires' daughters milk production, this dependence was not found in the second group. Dependence between breeding value of fat contents in fathers and sons was similar. Correlation between sires' breeding value of milk production and their daughters' milk production was middle in the second group and low in the first group.

THE INFLUENCE OF MONTH OF CALVING ON THE MILK PRODUCTION AS THE BASE FOR DEFINITION OF THE EFFECT HERD YEAR SEASON

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The aim of this work was to compare milk performance of animals calved in different month of a year. Computations were carried out for a part of the Czech Red Pied (CRP) population with genotype of 50% and more of CRP, i.e. females calving within the period of 1991–1993. The study involved 376,067 cows on the first, second and third lactation. Result of the analysis showed a tendency towards higher milk production in cows that calved in winter months then in summer months. On the first lactation, the performance ranged in dependence on the month of parturition from $\bar{x}$ = 3,483 kg, $s_{\bar{x}}$ = 788.9 kg (August) to $\bar{x}$ = 3,746 kg, $s_{\bar{x}}$ = 813.9 kg of milk (January). Performances on the second and the third lactation corroborated the trends observed in animals on the first lactation. The lowest milk production was observed in May ($\bar{x}$ = 3.905 kg), the maximum was recorded in November ($\bar{x}$ = 4.263 kg). If the year is divided into seasons, it is necessary to consider the results of analyses and trends in production of milk and its components in dependence on the season or month of calving. It is necessary to carry out detailed analyses and genetic evaluations.

LEVEL OF RELATIONSHIPS BETWEEN BODY MEASUREMENTS AND CARCASS VALUE OF BEEF CATTLE BULLS

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The aim of this experiment was to verify the relationship between body measurements of bulls of beef breeds and chosen parameters of meat performance. Basic body measurements were found out before slaughtering and measurements of carcass in 27 Charolais, Simental, Limousine and Angus bulls. High correlation coefficients (from $r_{xy} = 0.493^{++}$ to $r_{xy} = 0.802^{++}$), found between the body size and weight of dressed carcass, certify direct dependence between body measurements before slaughtering, their fleshing and amount of meat on bone. Significant positive relationships were found between body measurements and weights of meat and bones (from $r_{xy} = 0.424^{++}$ to $r_{xy} = 0.878^{++}$). Positive relationships were found between body measurements (except height at the withers) and weight of kidney fat, but they were not statistically significant (from $r_{xy} = 0.151$ to $r_{xy} = 0.242$). It has not been proved that with increasing of body size, the total fat of half-carcass yield is higher (from $r_{xy} = 0.302$ to $r_{xy} = 0.151$) as this is also it confirmed by the low correlation relations between measurements of carcass body and the fat amount of half-carcass yield (from $r_{xy} = 0.368$ to $r_{xy} = 0.208$).

RISK OF DIFFERENT WAYS OF SIRE USING ON A HERD LEVEL

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Expected asset from breeding programme of Slovak Pied breed in Slovakia was evaluated. Based on breeding programme scheme and genetic parameters in the population genetic gain 2369.15 kg of milk per generation interval was estimated. Accuracy of breeding values were estimated by genetic groups of the programme. Accuracy estimated in the group of bull mothers was 0.29 (29%), young bulls 0.77 (77%), proven bulls 0.99 (99%) and bull fathers 0.99 (99%). There were investigated some impacts actuating on reliability of breeding value estimates as well. Effective number of daughters was the most significant source which varied according to the size of population. Its significant influence was observed especially in the group of proven bulls. Based on these findings there were investigated risk related to sire exploitations in the population and influence of their use in herds.

APPLICATION OF BIOTECHNOLOGICAL METHODS IN BOVINE FEMALES WITH REPRODUCTIVE DISORDERS

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Reproductive disorders are frequently found in top, high-producing bovine females. That's why their return into the reproductive process and production of the progeny are desirable and necessary. These females can be used e.g. as embryo donors and recipients. Nineteen dairy cows with reproductive disorders were superovulated with pFSH-PGF_{2alpha} regimen – superovulation response was evident in twelve females. The following mean values were recorded: 6.71 Cl, 5.14 (76,6%) ova, 3.57 (69%) transferable and transferred embryos. Mean calving rate amounted to 2.43 pregnancy rate amounted to 68%.

Twelve cows were used as embryo recipients two of them were pregnant. It is evident that utilization of these females as embryo donors is more effective. In beef breeds, Limousine and Hereford females (*a* = 15, *a* = 7) naturally mated and nonpregnant for 2 years were used as embryo donors. The following data illustrate their superovulation response: 7.36 (Limousine) and 2.33 (Hereford) ova, 1.82 (Limousine) and 0.0 (Hereford) embryos, 5.09 (Limousine) and 2.17 (Hereford) degenerated embryos, 0.45 (Limousine) and 0.16 (Hereford) unfertilized oocytes. Utilization of these females for embryo production is ineffective and unadvisable.
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SECONDARY-FUNCTIONAL TRAITS IN CATTLE SELECTION

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The selection of dual purpose cattle according to the selection of indices includes milk (amount of milk, milk protein) and beef production (daily gain, valuable meat cut, growth capacity, feed conversion) and secondary traits (fertility, longevity, mastitis, calving difficulty). Partial breeding values for traits are combined into selection indexes. Values of 1, 1,5, 2 and 4 multiple of results of the profit function are alternatively used as economic values of secondary traits in a indices. In case of basic variant, the genetic gain of milk production is 58 kg and effects of selection on milk and beef production and secondary traits are in the proportion 81 : 20 : 1. Most important traits in indices are an amount of milk, feed conversion, milk protein contents and daily gain. Most of secondary traits are deteriorated. In case of 1,5 multiple overvaluation of secondary traits the genetic gain is 51 kg of milk and proportions of selection are 72 : 19 : 9. In case of 2 multiple over valuation the genetic gain of milk is 43 kg and proportions of effects for groups of traits are 59 : 18 : 23. In case of 4 multiple overvaluation the genetic gain is 15 kg and proportions 17 : 10 : 73. With overvaluation of secondary traits the proportion between effect of selection on milk and beef production is decreased.

DIFFERENCES IN ECONOMY OF CZECH PIED AND HOLSTEIN CATTLE HUSBANDRY

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This study compared differences in economy of the closed herd with all cattle categories of Czech Pied (Simmental) and Holstein cattle husbandry. Data for both breeds are from identical conditions of the same herd in experimental farm of the Research Institute of Animal Production in Prague from years 1990 to 1997. The data file covers two hundred and thirty-seven cows of Czech Pied and two hundred and ninety-one cows of Holstein cattle and their progeny. Individual recording is for the traits of milk production – number of lactation, milk quantity, fat and protein content and payment for the milk; for meat production – number of bulls and live weight at slaughter, number of negatively selected animals from all categories and live weight at slaughter; for the reproduction - number of inseminations and natality; veterinary - number and price of veterinary treatments and the cost of feeding.

THE EFFECT OF BREED ON INTERIOR MILIEU IN DAIRY COWS

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In the experiment involving 10 Holstein dairy cows and 10 cows of Pinzgau breed the dynamics of the changes of selected parameters in nitrogen and energetic metabolism were observed at the beginning of lactation and 3 to 4 weeks before calving. The cows of the both breeds were clinically healthy in the state of the 3-rd lactation, kept and bred in equal conditions. The parameters stated in blood serum and urine: urea, total proteins, glucose and AST were determined using the Bio-La-chema test. Comparing the values of the selected parameters before and after calving the higher concentrations of urea and AST was stated in the both breeds before calving. On the contrary, the levels of total proteins, glucose and urea were higher in the observed cows of the both breeds after calving. The results of this experiment have proved significant variability of urea depending upon breed descent that corresponds with the statements of several authors. The average level of urea in blood of the Holstein cows before calving was 3,86 mmol/l and in the Pinzgau cows only 1,82 mmol/l. After calving the level of urea in the Pinzgau breed has raised to 1,90 mmol/l and dropped to 2,61 mmol/l in the Holstein breed.

THE BREED PROGRAMME OF BEEF CATTLE IN THE CZECH REPUBLIC

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Central filing register 100% of purebreds animals of 12 beef breeds breed in the Czech Republic. The performance recording of beef cattle watches for age at 1st calving, calving difficulty, calving interval and live weight of calves by born, in 120, 210 and 365 days of age. The data of 11,000 cows and 6,000 heifers are processed by special programme PC-FAND. In the herdbook of beef cattle there are written about 70% of all controled animals. Herdbook has 5 chapters by beef breed proportions of breed. Most of breeding bulls are used in natural service. Breeding bulls are tested in stations (growth, development, exterior, qualified for reproduction). Growth ability of bulls is valuated by 120-days test and bulls are compared to an average of contemporary in station by average of daily gain form birth and in test, height in hips. Bulls exterior is valuated too (using type, body size, body structure, limbs and back). In 1996 there were selected 79.9%, i.e. 275 bulls. In 1997 first 10 bulls were valuated by heredity control (first stage – bulls fertility, calves health and exterior, second stage – fattening control and carcass quality on station, minimum is 15 sons by bull, BLUP – ANIMAL MODEL) and breeding values determined.

BREEDING OF BLACK-AND-WHITE x HOLSTEIN CROSSBREDS F_1 x F_1

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There were productive traits of Black-and-White x Holstein crossbreds (F_1, F_1 x F_1, F_2) and Black-and-White (BW) animals of the same age studied in Middle Povolgie. The analyse of the data demonstrated, that crossbreds heifers F_1 x F_1 had higher growth of live weight compared to BW heifers of the same age. The absolute weight gain was 336.4, 340.6 and 326.8 kg in groups of heifers F_1, F_1 x F_1 and BW, respectively, during growth period. First lactation milk yield was higher in crossbreds F_2 compared to this in F_1, F_1 x F_1 and BW animals. For third and more advanced lactation cows F_1 x F_1 had milk yield 4409 kg that was higher 34, 10 and 719 kg compared to cows F_1, F_2 and BW, respectively. No statistically significant differences among groups of young bulls F_1, F_1 x F_1, F_2 and BW were detected on slaughter meat yield. The use of crossbreds F_1 x F_1 did not decrease milk yield, slaughter meat yield and quality of meat.

THE FREQUENCY OF BLAD-CARRIERS IN BLACK-AND-WHITE CATTLE OF NORTH REGION OF POLAND

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Prevalence of lethal recessive D128G mutation in *ITGB2* gene is the most outstanding break-through in genetic disorder of dairy cattle. High frequency of BLAD-carriers is observed in extremely high valuable HF sires and cows herds. The subject of our present investigation was to detect occurrence of BL animals in relation to milk traits selection procedure. There were AI sires, young bulls, bulls' mothers and cows from large herds tested in the north region of Poland. Obtained results showed three HF sires actually influenced BL frequency in mass population scale. High BL frequency was stated in the group of young bulls (12%) in comparison to cows (6%). Additionally, there were the progeny groups of BL sires examined. There were no regularities in reproduction ability and weight gain of BL and TL young bulls that belong to BL sires observed. The relationship between BLAD and milk traits was not consistently expressed. In some cases of BL sire progeny groups, BL cows were distinguished by high fat and milk protein contents, whereas in remaining cases the differences between BL and TL half-sib cows were not significant.

ADAPTABILITY OF ANIMALS WITH DIFFERENT GENOTYPES FOR κ-CASEIN

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The genetic structure of Black-and-White cattle herd (n = 1051) for κ-casein locus was examined. The frequencies of κ-casein genotypes A/A, A/B and B/B were 0.341, 0.590 and 0.069, respectively. The frequencies of *A* and *B* alleles were 0.636 and 0.364, respectively. There were significant surplus of heterozygous and the unsufficiency of homozygous B/B genotypes were observed in this population. This fact may be explained by differences in adaptability of animals with different genotypes for κ-casein. We analyzed the number of offsprings for the whole reproductive period, the number of deadborn calves and the number of heifers achieved reproductive age. All examined cows were called. These data were presented as accounted on 100 cows. The numbers of calves from homozygous (A/A and B/B) and heterozygous animals were 552, 519 and 546, respectively. The number of deadborn calves was not differed. Bulls were realized in young age therefore their viability were not analyzed. The numbers of heifers from homozygous (A/A and B/B) and heterozygous animals were 244, 246 and 251, respectively. The numbers of sexually mature heifers were 187, 178 and 199, respectively.

THE RELATIONSHIP BETWEEN SOME MILK PRODUCTION TRAITS IN CZECH PIED CATTLE DURING CONSECUTIVE LACTATIONS

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A group of living cows of Czech Pied cattle used for efficiency testing in North Moravia region was used for the analyses of correlation between indicators of milk efficiency (milk, protein and fat production in kg, percentage of fat and protein). Only cows which complied with the conditions for entry in the main section of the breeding book (C1 – minimal proportion of Czech Pied cattle 75%) were analyzed. Cows in the 1st–5th lactation were used.

The results obtained from the studies of dairy cows revealed following facts:

- average amount of milk per lactation: 5398 kg (1st lactation) to 4850 kg (5th lactation)
- average amount of protein per lactation: 133 kg (1st lactation) to 162 kg (5th lactation)
- average content of protein per lactation: 3.34% (1st lactation) to 3.37% (2nd lactation)
- average content of fat per lactation: 4.37% (1st lactation) to 4.38% (2nd, 3rd lactation)

The coefficient of correlation ranged on different lactations:

- $r = -0.107$ (5th lactation) to 0.003 (1st lactation) [milk kg x % protein]
- $r = 0.963$ (4th lactation) to 0.968 (5th lactation) [milk kg x kg protein]
- $r = 0.341$ (5th lactation) to 0.356 (2nd lactation) [% fat x % protein]
- $r = 0.136$ (5th lactation) to 0.251 (1st lactation) [kg protein x % protein]

MILK PRODUCTION OF COWS WITH DIFFERENT PROPORTION OF CZECH PIED BREED AND VARIOUS DAIRY BREEDS

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The data on milk production of 38,536 cows-crossbreds of Czech Pied breed with Ayrshire (A), Red Holstein (R) and Holstein (H) were analysed. The cows were in the third and further lactation and they were kept on farms in East Bohemian region. The most frequent (63.7% of the overall population of cows) is the genotype consisting of Czech Pied cattle and 12–49% of A and R. This group produced 4979 kg of milk, 215 kg of fat (fat content 4.39%) and 165 kg of milk protein (protein content 3.31%). These results are not significantly different from those of group of Czech Pied cows with 12–49% of breed H in their genotypes. The milk production of crossbreds with 50–88% of A, R and H in genotype was higher by 502 kg of milk, 23 kg of fat, 12 kg of protein and fat content 0.03%. On the contrary, the protein content was lower by 0.07%. The girth of chest was the smallest (196) in group with 12–49% of A and R, the biggest (199 cm) in group with 50–88% of H. Calving interval was longer in a group with 50–88% of A, R, H (398 days) then the in group with 12–49% of A, R, H (393 days). There is no significant difference in number of cows culled due to low milk production between groups (9.56–11.41%). The culling due to health problems is lowest in the group with 12–49% of A and R (32.78%) and highest in the group with 50–88% of H (38.60%).

GROWTH OF THE HOLSTEIN BULLS BORN AFTER EMBRYOTRANSFER

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The experimental group consisted of 11 sires born to heifers after embryo transfer. The control group consisted of 28 sires born to cows on the second and further lactation after AI. Both groups were housed in identical conditions. The measurements of live weight were carried out monthly over the period of 10 months (at the age 15–24 months). The growth of the sires at the age of 25 months and older was estimated using Gompertz function. The live weight of bulls at the age of 15 months was 500.909 kg in the experimental group and 524.107 kg in the control group ($d = 23.198$ kg, $P < 0.05$), at the age of 18 months 559.091 kg and 588.393 kg, respectively ($d = 29.302$ kg, $P < 0.01$). No significant difference was found between the groups at the age of 22 months and more. The daily live weight gain of bulls at the age of 15 months was 1011 g in the experimental group and 1062 g in the control group ($d = 51$ g, $P < 0.05$), at the age of 15–18 months the daily live-weight gain was lower in experimental group but this difference was not significant ($d = 68$ g, $P > 0.05$). On the contrary, the live weight gain at the age of 18–21 months and 21–24 months was higher in experimental group ($d = 37$ g, resp. $d = 71$ g, $P > 0.05$). There was no significant difference in the live weight estimation between experimental and control group at 30 months of age.

THE PROGRAM AND RESULTS OF BREEDING OF GENE RESOURCE OF BOHEMIAN RED CATTLE BREEDS

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Bohemian Red Cattle Breed (BRCB) belongs to high endanger cattle breeds. The Department of Animal Breeding and Nutrition, University of South Bohemia, České Budějovice, has been solving the problem of regeneration of Bohemian Red Cattle Breed since year 1991. This project and it's solution is in accordance with international initiatives of FAO and it is supported by Ministry of Agriculture of the Czech Republic. The program is realized by three ways: first is pure breeding, second is accumulation of crossbreeding (F_1, F_{11}...), third is purchase of breeding animals from other breeders. Total number of live BRCB and their crossbreeds was 64 animals by April 27th 1998: 14 dairy cows (5 BRCB, 9 crossbreds F_1), 16 heifers (4 BRCB, 9 F_1, 3 F_{11}), 19 bulls (1 BRCB, 15 F_1, 2 F_{11}, 1 F_{10}), 15 calves-heifers (4 BRCB, 10 F_1, 1 F_{11}). Two dairy cows BRCB were discarded and 14 bulls F1 were killed at slaughter house before April 27th 1998. We observe genetic, physiological and morphological features at the animals with genotype BRCB. Our aim is breed BRCB in Šumava. 16 dams were moved for a farm Nový Svět and Kvilda. The other animals are bred at Faculty of Agriculture Enterprise Hluboká nad Vltavou, Agriculture Co-operative Ločenice and Control Station of Fattening Želeč. To be able to continue with this project we need male breeding material of good quality and finances.

USING BIOCHEMICAL AND IMMUNOLOGICAL MARKERS IN CATTLE BREEDING FOR HIGHER DAIRY PRODUCTIVITY

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We studied possible using biochemical and immunological markers for White-and-Black and Hkolmogor cattle and their hybrids with Holstein bulls for higher dairy productivity. The best rates of growth were proved by low concentrations of lysine, arginine, glutaminic in blood as well as bactericidal blood activity in 4-months heifers. There is high correlation relationship revealed between these rates and productive features of animals. A method of an early prediction for diary cow productivity was based on measuring initial glucose concentration in animal blood and its change in response to adrenaline load. The predicted precision is 72–78%.

DETECTION OF ALLELE *E* OF THE κ-CASEIN IN CATTLE IN THE CZECH REPUBLIC AND POLAND

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Gene for κ-casein (κ-CN) is in cattle localised on chromosome 6. There are 4 alleles – *A*, *B*, *C* and *E* described in this locus. Frequency of allele *E* is in cultural breed very small and in the Czech Republic it occurs rarely. Genotyping was detected by polymerase chain reaction (PCR) and restriction fragment lengh polymorphism (RFLP) method (Schlee et al., 1992). DNA was isolated from blood of tested animals. In this investigation there were 108 bulls of Czech Pied cattle (C), 17 bulls of Holstein cattle (H), 22 cows Czech Red cattle (CC), 65 cows of Polish Red cattle (PR) and 80 cows of Polish cattle (P) tested. In observed animals there was an allele (κ-CN) detected in heterozygous condition with frequent alleles *A* and *B*. Animals with homozygous genotype E/E was not detected. Allele frequencies *A*, *B*, *E* were following: in C bulls: 0.620, 0.338, 0.042; in H bulls 0.677, 0.235, 0.088; in cows of CC 0.636, 0.364, 0; in cows of PR 0.685, 0.315, 0 and in P breed 0.631, 0.356, 0.013, respectively.

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EFFECT OF GENOTYPE (Li, C, C x Li) ON GROWTH AND BEEF UTILITY

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In bull calves of Limousin breed (44 head), Czech Pied cattle (57 head) and their crosses (41 head) live weight and mean daily weight gains at the age 120, 210 and 365 days was observed. At the age of 120 days the highest live weight was found out in crossbreeds (168.0 kg) and the lowest value in Czech Pied cattle (160.3 kg). To this finding the highest mean daily weight gain up to the age 120 days in crossbreeds (1.11 kg) and the lowest value in Czech Pied cattle (1.05 kg) correspond. At the age of 210 days the highest live weight was in crossbreeds (273.0 kg) and the lowest value in Limousin Breed (257.0 kg). The highest mean daily weight gain from the age 120 days up to the age of 210 days was found out in crossbreeds (1.17 kg) and the lowest value in Limousin breed (1.01 kg). At the age of 365 days the crossbreeds reached again the highest live weight (384.6 kg) and Limousin breed reached the lowest value (343.8 kg). The highest daily weight gain was found out in crossbreeds at the age from 210 days to 365 days (0.72 kg) and the lowest value in Limousin breed (0.56 kg). After slaughter (mean live weight before slaughter was 550 kg) the highest carcass weight was found out in Limousin breed (320.8 kg), lower value in crossbreeds (312.3 kg) and the lowest value in Czech Pied breed (307.8 kg). The highest dressing percentage was found out in Limousin breed 62.3%, in crossbreeds 59.8% and in Czech Pied breed 58.6%.

DIRECT TRANSFER OF BOVINE CRYOPRESERVED EMBRYOS

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In conventional cryopreservation and vitrification protocols, cryoprotectants are removed either on the dish under the microscope or by one-step shaking in the straw loaded with freezing and washing media. Transfer of embryos preserved by the mentioned one-step method was associated with 60% (conventional method) and 56% (vitrification method) pregnancy rates. In the second experiment, there were embryos frozen by the conventional regimen (in the freezer) treated with 1.5 M (9%) ethylene glycol for 10 min at max. before seeding (–7 °C); seeding (5 min) was followed by cooling to –32 °C (cooling rate: 0.3–0.5 °C/min) and plunge in LN$_2$. Embryos were thawed in warm water (30 °C) without shaking and transferred immediately into the ipsilateral uterine horn. Direct transfer of frozen embryos produced by top Holstein parents was associated with 57.1% (8/14) pregnancy rate; bilateral transfer of Aberdeen-Angus embryos produced by IVM-IVF-IVC method was characterized with 100.0% (15/15) pregnancy rate; twins were produced by 7 recipients. In a control group, conventionally frozen embryos (Říha, 1990) were thawed in warm water (30 °C) and exposured to glycerol and sucrose (3-step procedure). Pregnancy rate amounted to 52.1% (123/236). Transfer of fresh (unfrozen) embryos was successful in 59.7% (46/77) recipients.

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EFFECT OF FATHER'S BREEDING VALUES TO CONTENTS OF SOLID COMPONENTS IN COWS MILK

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The indicators of production in the herd of 395 heads of Holstein-Friesian breed primipars after fathers from France were evaluated. The common factors of evaluations were the months of calving, age at the first calving and the group of daughters by the quality of breeding value and the height of indices INEL and ISU of father from the years 1992 and 1997. The production indicators observed – milk kg, protein kg, fat kg – were further evaluated in dependence on the length of service period. The evaluation was performed using the least squares method of the SAS programme/STAT 6.03. The higher explained variability and the lower standard deviation showed the breeding value of the father from the year 1997. When evaluating by the breeding value from the year 1997 there was the statistical significance of all factors used. The higher breeding value of the father predicts a higher utility of the daughter. Only by differences between the groups of daughters evaluated by breeding value of father for protein kg this relation was not confirmed. The differences between the groups of daughters were more pronounced and the higher level of significance when evaluating by the breeding value from the year 1997 than at the evaluation by the older breeding value. The effect of month of calving on the production indicators showed up as significant.

CARCASS VALUE OF BEEF CATTLE BULLS

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The investigation involved 27 bulls of beef cattle breeds Charolais (Ch), Limousine (Li), Aberdeen-Angus (AA) and Simental (Si). Bulls were reared in a suckler cows' production system, they were taken from 220.8 days of age (AA) to 257.8 days of age (Li) to the fattening station. The average daily gain in times of fattening was from 820 g (Li) to 970 g (Ch). Bulls were slaughtered from 561.8 days of age (Li) to 607.4 days of age (SI). Statistically significant breed differences (from $P \leq 0.05$ to $P \leq 0.01$) were found out in almost all parameters of investigation of carcass value, except total meat yield and total bones yield. The highest dressing percentage was discovered in groups Li (61.61%) and AA (61.31%) which is connected to lower skeleton on, significantly lower weight of hide and weight of head in these groups. The highest weight of dressed carcass (402.8 kg) in group SI are connected with the highest weight of right half (201.6 kg) and subsequently weight of meat (160.1 g) and bones (39.1 kg). More early maturing of the cattle breed Angus resulted in a high production of kidney fat (4.2 kg) and the highest weight of separable fat from half-carcass (4.4 kg). The relative expression of total separable fat yield was also significantly higher in this group (2.68% in comparison with group Li with the lowest total separable fat yield 0.88%).

GENETIC TRENDS OF MILK TRAITS IN HOLSTEIN, PINZGAUER AND SLOVAK PIED POPULATIONS IN SLOVAKIA

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Genetic trends in milk, fat and protein production were estimated in pure breed population of 12,538 Holstein, 2,898 Pinzgauer and 15,576 Slovak Pied cows. Genetic trends were expressed in average cow breeding values by it's year of birth. Cow breeding values were estimated by Test Day Model with random regression. Positive genetic trends 23.55–56.44 milk yield, 0.26–1.38 fat and 0.86–1.14 protein production were find out in population of Holstein cows born in 1991–1994 year. The genetic trends, expressed by the regression coefficients of individual breeding values of Holstein cows on year of birth were 18.7 kg of milk per year, 0.30 kg of fat per year and 0.42 kg of protein per year. The positive genetic trends in observed milk traits were not find out in Pinzgauer and Slovak Pied cow population.

EVALUATION OF REPRODUCTION PARAMETERS ACCORDING TO A LEVEL OF DAIRY COWS MILK PRODUCTION

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The relations among dairy parameters (yield per lactation in kg, fat in kg and %, proteins in kg and %, lactose in kg and %) and parameters of reproduction (days open, servis period and calving interval) was evaluated in the group of 423 dairy cows with 1876 of 305 days records. According to the analyse of results the dairy yield follow the groups: > 50% HF, $\bar{x}$ = 3736 (average of herds $\bar{x}$ = 3699), 100% HF, > 50% SS, Miscelandous, 100% SS ($\bar{x}$ = 3210) in absolute values. Similar trend was found in the other tested characteristics. The most yielding cows showed the longest calving interval. Similar tendency was found in days open and service period. The correlations among all tested characteristics among dairy character and reproduction were positive but near zero, r = 0,1375 for SP, r = 0,0896 for days open, r = 0,0575 for calving interval.

CHOLESTEROL LEVELS AND FATTY ACIDS COMPOSITION IN MEAT OF BLACK-AND-WHITE COWS AND THEIR CROSSBREDS WITH ITALIAN BEEF BREED BULLS

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Cholesterol content and fatty acid composition were determined in beef samples from the *longissimus dorsi* muscle of Black-and-White cows and their crossbreeds with three different Italian beef breed bulls (Piemontese, Marchigiana and Chianina). Significant differences between breed groups were found mostly in the mono- and polyunsaturated acids in the muscle fatty tissue. Highly significant differences were found in $C_{18:3}$ levels between crossbreeds from Black-and-White x Piemontese and crossbreeds x Marchigiana, Chianina and control group. Based on the ratio of unsaturated to saturated fatty acids it can be found that the fatty tissue of the *longissimus dorsi* muscle of crossbreeds from Black-and-White x Piemontese contained a greater amount of exogenic acids while the cholesterol level in the studied samples was 51–57 mg/100 g meat. No statistically significant differences between the genetic groups studied were found. It is of interest that the intramuscular fat of crossbreeds by Piemontese bulls contained the lowest percentage of saturated fatty acids. The PUFA/SFA ratio in the meat of crossbreeds by Piemontese bulls may indicate the highest proportion of exogenic fatty acids in that breed group compared to the remaining ones.

GENETIC IMPROVEMENT OF RED POLISH CATTLE USING ANGLER BREED

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The Red Polish breed of cattle has a rich, over a hundred years old tradition but its population has been constantly decreasing. Before the second World War it presented 1/3 of the total cattle population of Poland. After this war it decreased substantially making in 1965 but 18% of the total cattle population. Recently it was estimated that in the South of Poland, where it is still kept in larger number, there are only 45 thousands of cows of this breed. A further decrease of the Red Polish population can be checked only by improvement of its dairy traits. At present the main way of such an improvement is the use of Angler bulls semen. The milk yield was recorded in the years 1980–1991 in 3 groups of cows (total 1033 animals) with a different level of Angler genes in their genotype. The yield of Red Polish in the third lactation was 3574 kg milk, 147 kg milk fat, 121 kg protein and 3631 kg FCM milk. The crossbreeds Red Polish Angler (37.5–50% of Angler) produced 3881 kg milk, 166 kg milk fat, 132 kg protein and 4047 kg FCM milk. The Red Polish Angler crosses with inferior percentage of Angler genes gave only 8.6% more milk than the Red Polish cows. The crosses had a higher milk fat content (by average 0.16–0.18%). The crosses were about 2.9 cm higher at withers.

EVALUATION OF FATTENING CAPACITY AND DRESSING PERCENTAGE OF TWO-WAY AND TRIPLE CROSSES OF CATTLE

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The fattening capacity, quality of beef and dressing percentage were evaluated in bull carcasses of crosses of Italian beef breeds (Piemontese, Marchigiana, Chianina) with the Polish Black-and-White cattle, sons of the F_1 sisters of the mentioned bulls and Aberdeen-Angus sires (triple crosses) and two-way crosses (Polish Black-and-White x Aberdeen-Angus, Polish Black-and-White x Simmental). They were fed with broken barley, extracted rape meal, hay and grass silage. The inferiour quality of feedstuffs caused low daily gains (837–978 g). The dressing percentage was 53.73 to 57.05%. The triple crosses had the highest (57%) dressing percentage, 3% more than the remaining groups of bulls. The lowest dressing percentage and daily gains was observed in the control group (Polish Black-and-White). Two-way crosses and especially triple crosses gave better results than Polish Black-and-White and Simmentals (preliminary results).

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GENETIC TREND OF PRODUCTION TRAITS OF PIG POPULATION IN THE SLOVAK REPUBLIC

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The data from a field and a station test of pigs were used to analyse the genetic trend of White Improved (WI) and White Meaty (WM) breed in Slovakia. The data records since 1992 (n = 108,370 and n = 54,961 for WI and WM breed) were available from computing centre of State Breeding Institute of the SR. There were analyzed the field test traits (measured on boars and gilts at farms) – ultrasonic backfat (BFFT), average daily gain (ADGFT) and station test carcass traits – average daily gain at station (ADGST), percentage of valuable cuts (VC) and backfat thickness (BFST). The five traits animal model was used to predict breeding values with different models for different traits simultaneously. Genetic trend for both breeds were computed as averages of BLUPs within birth years. Cumulative genetic trends the in period 1992–1997 for WI breed were –0.08 cm (BFFT), 11.1 g (ADGFT), 23.7 g (ADGST), 1.02% (VC) and –0.13 cm (BFST) for traits studied. Similar values of cumulative genetic trend (–0.09 cm, 11.9 g, 25.9 g, 0.97%, –0.10 cm for BFFT, ADGFT, ADGST, VC, BFST) were found for WM breed. While the percentage of valuable cuts improved, low genetic improvement was achieved in other traits. Comparison with other countries was discussed.

GENETIC TREND OF PRODUCTION TRAITS IN DAM BREEDS OF PIGS IN THE CZECH REPUBLIC

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Herdbook data of pigs born from 1989 to 1996 were analyzed for the Czech population of the breeds Landrace and Large White. There were analyzed following traits: Lifetime average daily gain (ADGF) and lean meat content measured by PIGLOG (LMF) from the field test, average daily gain from 30 kg to 100 kg life weight (ADGS) and valuable cuts in carcass-half at a live weight at slaughter of approximately 100 kg (VCS) from station test. Breeding values were predicted by a four-trait animal model with different models for different traits. In the genetic trend a stagnation was observed till 1992 followed by clear increase from 1992/1993. For the time period 1992–1996 the genetic gain per year was in Landrace: ADGF 2.95 g/day, ADGS 9.29 g/day, LMF 0.29%, VCS 0.15 kg; in Large White: ADGF 1.42 g/day, ADGS 5.54 g/day, LMF 0.39%, VCS 0.14 kg.

THE APPROVAL OF NUCLEUS HERDS OF PIGS AS A COMPONENT PART OF A SELECTION PROGRAMME MODERNISATION IN THE CZECH REPUBLIC

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The selection programme base in the Czech Republic consists of three qualitatively different categories of breeding farms: nucleus selection programme herds, breeding herds of sire breed and reserve herds for pig selection programmes. These breeding herds represent a unified selection base in the Czech Republic. Breeding aims have been stipulated for the individual population. The main objective of newly approved nucleus breeding herds is to secure genetic progress based on the selection within domestic population. Import shall be implemented only in substantiated cases (input of specifically desirable genes, enlargement of lines of descent). Exclusively pure breeding is applied. The aim of these herds consists in the production of breeding boars and sows for selection programmes of the appropriate population and for the regeneration of lower level breeds. This category of herds is usually set up only for large population (above 500 sows).

THE PRACTICAL USE OF ANIMAL MODEL FOR PIG BREEDING

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The multivariate animal model is used to estimate breeding values of purebred pigs. The traits are: lifetime average daily gain and lean meat content from field test, average daily gain and the weight of valuable cuts in carcass-half from station test. The base of population consists of the animals born in 1995. The breeding values for daily gain from field test (BVDG) and valuable cuts (BVVC) multiplied by the economic weights result in aggregate breeding value (ABV) of the animal. ABV expresses the change in profit in crowns for one pen in the fattening station compared to the base population over the period of one year. The economic weights were selected as follows: 8 for BVDG, 270 for BVVC of mother lines and 600 for BVVC of father lines. For better orientation of breeders, there were tables prepared. These tables show limits of BVDG, BVVC and ABV for 1%, 5%, 10%... 50% of top animals of the population tested in last 24 months. Breeding values are computed weekly. Based on these values, the computer programme determines the file of top boars and sows. These animals are then used for the production of breeding boars. Additionally, each week the breeders get list of top young boars that will be available for purchase in auctions in the following period.

STABILITY OF BREEDING VALUE ESTIMATES FOR PRODUCTION TRAITS IN PIGS IN THE CZECH REPUBLIC

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Breeding values were predicted from herdbook data of Czech Landrace pigs born from 1988 to 1997 by a four-trait animal model with different models for different traits. The traits were: lifetime average daily gain (ADGF) and lean meat content measured by PIGLOG (LMF) from field test, average daily gain from 30 kg to 100 kg life weight (ADGS) and the weight of valuable cuts in carcass-half at a life weight at slaughter of approximately 100 kg (VCS) from station test. The calculation was carried out for the full data set (DS10) and for further nine data sets (DS09... DS01) which were formed by successively omitting test data from September 1997 till January 1997. The stability of the breeding value estimates was investigated for a subset of animals (field tested sows born in 1995, $n = 8537$). Spearman's rank correlations coefficient for ADGF (first number), LMF (second number), VCS (third number) and ADGS (fourth number) were: DS10–DS07: 0.995, 0.996, 0.996, 0.994; DS10–S04: 0.989, 0.992, 0.990, 0.988; DS10–S01: 0.971, 0.987, 0.982, 0.974. There were investigated distribution of differences in breeding value estimates among different solutions. Rank changes of the best animals were considered more in detail.

THE EVALUATION OF PIG BREEDING HERDS BY MEANS OF BIOECONOMIC MODEL

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Fifteen productive traits and 10 selection and breeding characteristics in breeding herds of mother breeds Large White (Czech Improved) and Landrace and sire breed Czech Meat were evaluated from the point of view of economic efficiency. For this purpose there were used data from 36 Large White (Czech Improved), 34 Landrace and 16 Czech Meat herds. Profit/sow/year was used as a criterion of economic efficiency of the breeding herd. There were found only small differences in costs/sow/year between herds. Much higher variability among individual herds and breeds was found in the case of output, that is the highest in Czech Meat herds and smaller in the herds producing Large White animals. Profit/sow/year varied from 4,706 to 23,676 Czech crowns in Large White while average reached 12,795 Cc. Corresponding values were from 5,036 to 36,026, with average of 14,839 Cc in Landrace and from 6,208 to 63,694 with average of 21,671 Cc in Czech Meat. Profit amount in the herd is prevalently determined by position of the breed in the schema of crossbreeding and by intensity of selection of young breeding animals, especially of young boars. Intensity of selection depends on different demands for young breeding animals and supply of it in every particular region.

BREEDING PIGS AND ECONOMICS OF PORK PRODUCTION IN THE SLOVAK REPUBLIC

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The research was conducted in 84 enterprises with total number of 293,000 pigs and concentration between 1000 and 10,000 pigs per enterprise. Despite the fact that in the process of breeding, there are used Landrace, Duroc, Yorkshire, Hampshire, Piétrain breeds, 43 per cent of producers expressed their dissatisfaction with biological material and the level of breeding. This stagnation is a result of low economic motivation of producers in quality of slaughtered pigs because 90 per cent of them are sold as alive animals and the evaluation system EUROP is used only in a small scale. With a view to maximization of sale vale under current market mechanism the following combinations of hybrids are recommended: Biele ušľachtilé x Biele mäsové, Biele ušľachtilé x Biele mäsové x Yorshire, Biele mäsové x Biele ušľachtilé x Piétrain. There are own costs of 39 Sk and revenues of 40 Sk per 1 kg of life weight, under current market conditions and assures satisfactory rentability rate while satisfying quality criteria for pig meat.

DEVELOPMENT OF THE SHARE OF LEAN TISSUE IN THE SLAUGHTER PIGS IN THE CZECH REPUBLIC CONDITIONS

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Three separate sets of animals have been evaluated with regard to the changes in the share of lean tissue in pigs during a six-year period. The A collection involved animals from the beginning of the first ideas to evaluate carcass bodies according to this criterion. The other two sets were evaluated at the end of this period. The B set represented final hybrids after the boars of ordinary male breeds and the C set represented the final hybrids sired by boars from the specialized lines marked by a high meatiness. The share of lean tissue at A, B and C sets was 47.26 ± 0.352%, 50.80 ± 0.330%, and 53.53 ± 0.154%, resp. It is possible to say that a substantial raise of the share of muscles was mainly influenced by breeding characteristics. The agricultural primary production was thus orientated in advance on so far unintroduced apparatus way of the slaughter pigs evaluation in the Czech Republic which is already common in the EU countries.

LEAN MEAT DETERMINATION IN PIGS BY INSTRUMENTAL ESTIMATION

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The level of meatiness was studied in 137 pigs of various genotypes *in vivo* by the Piglog, Sonomark and Aloka sets. The Uniform set and two points (TP) method were used for *post mortem* evaluation. The estimated lean meat content (LMC) was statistically compared with results of detailed dissection of carcass side. The average weight of carcass side was 42.12 kg, average backfat thickness 23.4 mm and proportion of valuable meaty cuts 49.72%. LMC determined by dissection achieved 53.72 %. LMC estimated by Piglog 105, Sonomark SM-100 and Aloka 500 were 52.78%, 56.79% and 55.79%, respectively. LMC 51.53%, 53.71%, 52.87% and 52.76% was found by the Unifom S-89 instrument, TP method (our regression equation proposed), TP (Czech equation) and TP (German equation). The non-significant differences were found (*t*-test) between LMC (by dissection), and Piglog, TP (our equation) and TP (Czech equation). High correlation coefficients $r = 0.845$, 0.873 and 0.872 proved reliability of the methods and procedures applied.

VARIABILITY IN PARAMETERS OF FATTENING AND CARCASS TRAITS DAM AND SIRE POPULATIONS PIGS

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The breeding work has an important position at the qualitative production of pork meat. We can positively influence quantity and quality of pork meat production by breeding. The breeding and selection in pigs follow a systematic decreasing of production costs by improving of fattening and slaughtering parameters. The results were processed from all test stations in the Slovak Republic from 1991 to 1997. The variation and statistical analyse was processed on single parameters of fattening and slaughtering value – by average daily increase of weight from 30 to 100 kg, for percentage of meat parts CMC. The best value of daily gain had LD 845 g, BM 835 g, ČS 783 g. The breed BU had at the valuation of percentage of CMC the highest portion in slaughtery 49.8%, LD 48.9%, BM 48.7%, ČS 48.3%. At the valuation of sire breeds very good results in the average daily increase of weight had the DU – 865 g, SM 836 g, PN 832 g, LB 826 g. In the slaughtering parameters the best results reached breeds PN 56.0 %, LB 53.1%, SM 52.0%, DU 50.2%.

REPRODUCTION PERFORMANCE EVALUATION IN PIGS RELATED TO THEIR WEIGHT GAIN CAPACITY

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The set of 3,837 litters of Large White Pig (LW) and 1,722 litters of Landrace (L) was distributed into five groups in compliance with the achieved daily average gain (up to 500 g, ranging between 500–530 g, 530–560 g, 560–590 g and above 590 g). The fertility parameters (the number of all and live-born pigs per litter) in the LW breed did not show any statistically significant differences in the first up to the fifth litters. Statistically relevant differences in the number of all produced pigs per litter up to 21 days of age were found as late as in the fifth and sixth litters between the groups of sows with the highest, and on the other hand, the lowest achieved growth intensity. The limit not exceeding the daily average gain of 560 g was found to be an acceptable growth intensity level in the rearing of young LW sows. Among the individual L-groups no statistically significant differences in the studied reproduction parameters were found in the second to sixth litters. It is obvious that groups with the average daily gain ranging between 500 and 590 g showed a slightly higher level than both fringe groups with the highest and lowest gains within the rearing. The analysis results have proved that the use of the average daily gains in the breed, based on performance tests, can be considered only as an orientation selection criterion.

DIFFERENT SELECTION OF PARENTS ON THEIR PROGENY PERFORMANCE IN PIGS

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In the White Meaty breed pigs there were evaluated results of chosen performance traits according to different selection of their parents. Father of pigs in experimental group achieved in the test of own performance backfat thickness (BF) 1.21 cm, lean meat *in vivo* (Piglog set) 54.1% and its progeny in the progeny testing station (PTS) achieved BF 2.25 cm and valuable meaty cuts (VMC) 50.25%. The own performance of mothers in the experimental group was BF 1.44 cm and Piglog 53.2%. Father of pigs in control group had in the own performance test BF 1.31 cm, Piglog 53.0% and its parameters in PTS were BF 2.36 cm and VMC 48.25%. Mothers in the control group achieved the determined selection criteria of own performance neither for BF (max. 1.5 cm) nor for the lean meat *in vivo* (Piglog min. 52%). The experimental group (n = 33) achieved in all parameters of fattening capacity and quantitative values of meat performance better results compared with the control group (n = 30). The greatest statistically significant differences ($P \leq 0.001$) were in VMC (45.75% the control and 47.92% the experimental group), and in *musculus longissimus dorsi* (MLD) area (33.74 cm^2 and 38.86 cm^2). The experimental group achieved significantly worse results of meat quality compared with the control group (pH_1 in MLD 6.41 : 6.12, electric conductivity of MLD meat 24 hrs after killing 2.19 µS : 2.42 µS).

THE ANALYSIS OF IMPROVING PROCESS OF CZECH MEAT PIG BREED

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Czech Meat Pig breed was admitted in 1991 as a new breed according to the Act No. 132/1989 Coll. concerning "Protection of laws about new plant varieties and animal breeds". Since 1991 the improving process of this breed has been realized by "inter se" method within the scope of pure breeding. We have used Pietrain breed since ca. 1993 in respect of increasing selection pressure on faster growth of meatiness. Pietrain contributed simultaneously to the spreading a number of expansion of genealogical lines. In filling of breeding aim determined for Czech Meat Pig breed in a lean meat content 57–62%, there have already been reached lower boundary of this limit and his next selection progress should be guaranteed by using data about total breeding value within the scope of asserted "BLUP-AM" method. And this is aiming especially at the problems of choice of the most suitable couples of parents and their intentional mating. The share of Czech Meat Pig sires in the structure of father's breeds of using sires for needs of commercional farms, introduces ca 50% in a long-term time and we count on this share in the outlook conception for the future.

APPLICATION OF BIOTECHNICAL PROCEDURES IN PORCINE REPRODUCTION SYSTEM – ACTUAL SITUATION

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Nowadays, effective methods of estrus stimulation in anestrous puberal gilts and anestrous sows after weaning utilizing combination of PMSG and HCG are disposable. Improvement of fertilization rate and reduction of early embryonic mortality are the principal objectives of experiments studying and testing applicability of the protracted form of lecirelin (LHRH). The recommended PMSG dose for superovulation stimulation has been experimentally determined (1.500–2.000 I.U.). Methods of surgical recovery and laparoscopic transfer of porcine embryos guaranting an adequate embryo survival rate were studied as well. Available results do not indicate any negative impact of experimental methods on reproductive parameters of tested donors and recipients. Expanded blastocysts (5-day to 6-day embryos) have been cryopreserved by the vitrification procedure mentioned by Říha (1990). Autoradiographic control of embryos and examining their ultrastructure revealed an adequate embryo development under *in vitro* conditions. Three piglets were born after transfer of vitrified porcine embryos.

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BLOOD SERUM PROTEIN ALLOTYPES AS GENETIC MARKERS IN PIG BREEDING

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There was genetic polymorphism of pig blood proteins regarding immune system studied. There were possibility and the efficiency of the use of this polymorphism in pig breeding examined. The possibility of the use of protein allotypes as genetic markers for individual, group or breed identification was determined. The markers of pig viability and stress resistance were found. The relationship between some protein allotypes and productive traits of pig was established. The data of the linkage and interrelation between protein allotypes alleles and blood groups were presented. The best production traits were found in animals with complex genotypes of α_2-macroglobuline and A-system of blood groups.

ANALYSIS OF THE BASIC HERD OF SOWS RELATED TO FERTILITY

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In order to acquire data, there was a set of Large White and Landrace sows (LW and L) selected out of the reproduction herd. LW-sows achieved the maximum growth in their reproductive performance in the 3rd and 4th litters. The maximum levels in the reproduction performance in L-sows were recorded in the 4th and 5th litters. In both breeds the levels of reproductive performance, after reaching its peak, stagnated with a slightly decreasing trend down to the 8th litter. At the moment of their first parturition, LW-sows, on the average, achieved the age 10 days earlier as compared with L-sows. Similar results were recorded in the values of daily average gains and backfat thickness. There was also studied impact of the age of gilts at the first parturition on selected performance and reproduction parameters. In all examined cases there were calculated only low correlation coefficients, predominantly statistically probably significant or significant. The only exception is represented by a low, statistically non-significant correlation coefficient between the age and backfat thickness determined by ultrasound testing.

ANALYSIS OF INFLUENCE OF ESR GENOTYPES ON LITTER SIZE IN LARGE WHITE BREED

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The aim of this study was to find out an influence of estrogen receptor (ESR) gene on litter size (a number of piglets born all) in population of 50 head sows of breed Large White (LW) from pure breed Frahelž, s. r. o. Gen *ESR* is a candidate gene for fertility in pigs (Rotschild et al., 1996). In ESR locus two polymorphisms based on PCR-RFLP method using restriction enzymes *Ava*I and *Msp*I were detected. In population of 50 females frequencies of ESR genotypes *Ava*I were following: A/A = 74%, A/B = 20%, B/B = 6%. Frequencies of ESR genotypes *Msp*I were found out in 38 sows: C/C = 65.8%, C/D = 23.7%, D/D = 10.5%. Evaluation of numbers of piglets born alive at 2nd and 3rd parity showed the highest value for genotype AvaI B/B. Difference against genotypes A/A and A/B was 0,81–0,94 piglets for litter. The biggest influence of ESR genotypes *Msp*I on a number of piglets born alive was observed in homozygous combination in genotype D/D (0,34–0,39 piglets more than for genotypes C/C and C/D). Number of females with homozygotes condition was the lowest in genotypes B/B and D/D (6 and 10,5%), but a specific trend – bigger number of piglets born alive is shown (in heterozygotes genotypes), too. Differences are not significant. Since the number of investigated females is not to high, this work is considered to be a preliminary study.
(Results were obtained with financial support of FR VŠ MŠMT No. 476/98.)

THE ANALYSIS OF INFLUENCE OF BACKFAT THICKNESS ON FERTILITY IN SOWS

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Breeding and improving work on pedigree and multiplicate farms is characterized especially by increasing selection pressure on a reduction of backfat thickness and an increasment of carcass lean percent. Not least, there are some questions about reproductive characteristics of sows which have been getting ahead now. We evaluated 192 Large White sows which were divided into 7 groups according to backfat thickness in range of 10 mm (80, 90 and so on). The measurement of backfat thickness was done during determination of their own efficiency. The highest number of live-born piglets was in sows with backfat thickness under 80 mm (13.5). The second and third highest number of live-born piglets was recorded in groups with 141 mm and more (11.3) and 101–110 mm (10.2). We also determined the fact that the number of reached litters increased with rising backfat thickness. There was recorded a significant influence ($P < 0.001$) of backfat thickness on fertility in sows with backfat thickness in range between 11 and 140 mm. We determined the correlation between backfat thickness and number of live-born piglets on first litter $r = -0.0695$. There was also determined the correlation of backfat thickness to the lifetime efficiency in number of live-born piglets $r = 0.0919$. We also determined a higher number of litters per life in sows with higher backfat thickness.

THE EFFECT OF THE PIGS BREEDS AND PRODUCTION TYPE OF THE BLOOD PLASMA CHOLESTEROL VARIABILITY

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Cholesterol in blood plasma was analysed in different breeds and production type (White Meat, $n = 30$; Large White, $n = 25$; Large White x Landrace, $n = 15$; Large White x White Meat x Pietrain x Hampshire, $n = 10$; Seghers, $n = 20$). Blood samples were taken from *vena cara* before killing. The average values of the blood plasma cholesterol concentration was higher in the hybrids LW x WM x P x H (2.12 mmol/l), Seghers (1.90 mmol/l) and LW x L (1.733 mmol/l), too. The pure breeds (LW and WM) had lower blood plasma cholesterol concentration (0.96 mmol/l, 1.09 mmol/l, respectively). Breeds and inter breeds differences were significant.

MARKER GENES FOR THE PRODUCTION TRAITS AND MEAT QUALITY IN PIGS

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The genotypes of the porcine *RYR1* gene, growth hormone gene (*GH-Hae*II and *GH-Msp*I) and *PIT1* gene were determined by PCR-RFLP technique in 71 commercial pigs born to (LW x L) sows x sired by hybrid boar. We have studied associations between these genotypes and carcass traits in pigs (PIGLOG) at ca. 80 kg of live weight and *post mortem*. To analyse the associations we used a generalised linear model (Procedure GLM/SAS) to compute the least-squares estimates of marginal means of the effects of *RYR1*, *GH-Hae*II, *GH-Msp*I and *PIT1* genotypes. From all tested candidate genes *GH-Msp*I did not show any association to the considered traits. In *RYR1* genotypes *Nn* pigs were always significantly different ($P \leq 0.0001$) in values pH_1 and EC_{50} values with better meat quality from *nn* pigs, in the *longissimus muscle* area and lean meat content

($P \leq 0.05$) were superior *nn* genotypes. The associations were found between genotypes of the *GH-Hae*II for the average daily gain ($P \leq 0.05$) and the lean meat content ($P \leq 0.01$). The polymorphism in the *PIT1* gene was significantly associated ($P \leq 0.05$) to back fat (T2) and to left half carcass weight warm. The sex has affected all traits under study.

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DIFFERENCE OF FREQUENCY DISTRIBUTION OF RYANODINE RECEPTOR (*RYR1*) GENE IN PIGS IN THE CZECH REPUBLIC

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The *RYR1* gene (ryanodine receptor gene) – formally *HAL* – is located on the sixth chromosome, actuates skeletal muscle cells. Its point mutation is found on the 1843 nukleotid from the genes' beginning. It is a change of cytosin in the *N* allele for thymin which is in the *n* allele. *RYR1* gene participates on the animals resistance towards stress, has connection to the percentage of thin muscles, content of intramuscular fat and with occurrence of PSE meat. The work consists in defining of *n* alleles frequency in breed Large White (LW) and Duroc (D) with same of sow and boar breeds in 1993 till 1997. The allele frequency *n* in LW sows in 1993 was 0.02, in 1994 was 0.05, in 1995 was 0.04, in 1996 was 0.07 and in 1997 was 0.07. The allele frequency *n* in LW boars in 1993 was 0, in 1994 was 0.1, in 1995 was 0.03, in 1996 was 0.06 and in 1997 was 0.06. The allele frequency *n* in Duroc sows in 1994 was 0.5, in 1995 was 0.2, in 1996 was 0.16 and in 1997 was not identified. The allele frequency *n* in Duroc boars in 1994 was 0.5, in 1995 was 0.29, in 1996 was 0.12, and 1997 was 0.04.

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ALLOMETRY OF CARCASS TRAITS OF PIGS FATTENED TO THE HIGHER LIVE WEIGHT CATEGORIES

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Two experiments with fattening pigs to the higher live body weights were done. Slovhyb 1 (White Improved x Landrace) x Synthetic Line 1 pigs were fattened in seven experimental groups to the final live weights from 100 to 220 kg with interval of 20 kg (first experiment). White Meaty pigs were fattened with two feeding mixtures A or B up to ca. 120 kg of final live weight (second experiment). Allometric ratios *a* of basic carcass traits to the right half carcass weight in first experiment were: valuable meaty parts 0.7939, shoulder 0.7502, neck 0.8795, loin 0.8010 and thigh 0.7834. Corresponding allometric ratios in second experiment for A or B feeding mixtures to the killing weight were as a follows: valuable meaty parts 0.3567 or 0.8693, shoulder 0.4782 or 0.8238, neck 0.1209 or 0.5194, loin 0.5955 or 1.3200 and thigh 0.2470 or 0.7577. Except of loin in 2 second experiments with B feed mixture, all allometric ratios were showed on the negative growth allometry of basic carcass meaty parts. Difference between results in both experiments can be explained by genetic and nongenetic factors.

THE EVALUATION OF INFLUENCE OF GENOTYPE ON PUTTING OF PROTEIN IN FOUR DIFFERENT HYBRID COMBINATIONS OF PIGS

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Within the province of the problems mentioned above, there were done 4 balance experiments on growing pigs of 4 defined hybrid combinations: (WI x L) x line 85 (CMP x Pn) (WI x L) x LW (WI x L) x DD (WI x L) x CMP. We put 8 hogs – half-sib progeny in liveweight ca. 30 kg on each balance experiment. The main aim was to determine the limit of effective putting of nitrogen substances (NS) in these animals, with average liveweight 45–48 kg during experiment as a quantitative criterium of meat efficiency. On the basis of that there were pursued following synoptic traits: the fattening capability, the carcass value and the meat quality. Our results show partially a high quality of some combinations (WI x L x L85 or WI x L x DD), partially considerable differences among combinations: WI x L x L85 160–165 g input NS; WI x L x DD min. 150 g NS (in this combination we can not determine the limit of putting of NS because the increasing in NS input has constantly linear progress in this case) WI x L x LW 147–148 g NS and WI x L x CMP 118–120 g NS. There were also determined significant differences among 4 levels of nutrition, f.e. in combination WI x L x DD (152 g NS in level I vs. 209 g NS in level IV, $P < 0.01$) or in combination WI x L x CMP (88 g NS in level I vs. 118 g NS in level II and 121 g NS in level II, $P < 0.05$).

RELATIONSHIP BETWEEN GENETIC MARKERS AND EFFICIENCY IN PIGS

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Advance of laboratory techniques applied in molecular genetics still brings about better condition for marker use (by means of MAS) for farm animal selection. One of the best known marker in pigs at present is halothane gene, known as a gene of ryanodine receptor (*RYR1*). It is localised on chromosome 6 and his recessive allele causes porcine stress syndrome (PSS),

negative meat quality (PSE – pale, soft, exudative) and is tightly linked to carcass and reproduction traits. Candidate gene for growth seems to be a growth hormone gene (*GH*), localised on chromosome 12 and myogenin (*Myf-4*) on chromosome 9. The main aim of this study was to detect genotypes of *RYR1* (using *Hha*I enzyme), *GH* (*Dde*I) and *Myf-4* (*Msp*I) genes using PCR-RFLP method in pure-bred population of sows from farm Martinice and investigation of associations of these genes with growth (daily gain, backfat thickness and lean meat content) and litter size. The *RYR1*, *GH* and *Myf-4* genotypes were determined in 74 sows. Frequencies of alleles were: *RYR1*: $N = 0.87$, $n = 0.13$; *GH*: $D = 0.88$ and $d = 0.12$; *Myf-4*: $A = 0.76$; $B = 0.24$. Significant associations ($P \leq 0.05$) with efficiency (using procedure GLM/SAS) were found only for influence of *RYR1* gene on litter size.
(This work was supported by Grant FR VŠ MŠMT No. 476/98.)

CHANGES IN THE COMPOSITION OF LEAN PARTS IN PIGS FROM THE POINT OF VIEW OF THEIR CARCASS WEIGHT

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The aim of the work was to more precisely define the possibility of evaluating pig meatiness using the percentage of lean cuts. There was shown a rather big influence of the carcass weight on this carcass value characteristics. The increase of carcass weight caused not only decreasing percentage of lean cuts, but determination of their composition with regard to the shares of muscles and fat, too. For the above mentioned changes there were settled, with regard to the carcass weight, these equation curves:

– for the lean cuts percentage (y_5):

$$y_5 = 66.24 - 0.2111x + 0.000349x^2$$

– for the share of lean tissue in the lean cuts (y_6):

$$y_6 = 76.84 + 0.0187x - 0.000394x^2$$

Gained results show that evaluation of pig meatiness according to lean cuts percentage should be restricted to the cases in which the carcass weight does not differ too much.

VARIATION OF THE GROWTH HORMONE IN HYBRID PIGS IN THE CZECH REPUBLIC AND POLAND

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The growth hormone is peptid, which is synthesized and released from the anterior pituitary gland. There are 4 point mutations, described in different localisation. They are detected by PCR-RFLP. Individual alleles can be detected by the restriction enzymes: *Apa*I, *Hae*II, *Msp*I, *Dde*I. Variation of the growth hormone was investigated on group of 44 abattoir pigs of hybrid combination LW x L in one the slaughterhouse in the South of Moravia and on 86 final hybrids from Szczetin in Poland. From results is apparent, that the highest frequency (according to restriction enzymes) $A = 0.829$ and $B = 0.171$, was found at genotypes *GH-Msp*I hybrids from CR (Poland: $A = 0.635$ and $B = 0.365$). In *GH-Hae*II frequency of alleles was in Czech hybrid pigs $A = 0.779$ and $B = 0.221$ and in pigs in Poland *GH-Hae*II $A = 0.477$ and $B = 0.523$. For *GH-Apa*I the frequency of alleles was $A = 0.816$ and $B = 0.184$ in CR. At hybrids from Poland discovered frequency of *GH-Apa*II was $A = 0.333$ and $B = 0.667$. Lower frequency of *GH-Dde*I was observed in hybrids from Poland than in hybrids in CR ($A = 0.798$ and $B = 0.202$). Determined frequency n hybrids from Poland was $A = 0.465$ and $B = 0.535$.
(Results were supported by FR VŠ No. 476/1998.)

THE ANALYSIS OF CARCASS VALUE AND QUALITY OF MEAT BY CROSSING POPULATIONS OF PIG

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Our objective was investigated with a carcass value and a quality of meat of chosen groups of crossing pigs. The fattening of these groups took place in the experimental station for test of crossing pigs Líšiná. The experiment of crossing pigs was made according to Czech regulation (CSN 46 6150). Our experiment consists of 8 breed combinations. The best results of carcass value were took at breed combination (LW x L) x Pn: percentage of valuable lean cats was 52.57%, percentage of meat from ham was 21.97%, average backfat thickness was 22 mm and eye muscle area 4995 mm^2. The second highest values were took at breed combination (LW x L) x (Pn x LW) – 51.34%, 20.87%, 21.5 mm and 4698 mm^2. We had four indices for each object: pH_1, pH_{24}, loss of water and colour of meat. The best results of pH_1 and pH_{24} were at breed combination (Pc x LW) x SL – 6.04 and 5.62. The smallest percentage of loss of water was at breed combination (Pc x LW) x CVM 3.23%. Very good values were at breed combinations (LW x L) x Pn 3.89% and (Pc x L) x LW 5.1%, too. The breed combination (Pc x LW) x BL (62.8%) was the best at an index of colour of meat.

DIFFERENCES IN SELECTED GRADE INDICATORS OF BARROW AND GILT MEAT

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A feeding test was carried out on a (BU x L) x ČVM hybrid combination of pigs to determine possible differences in grade indicators of pork meat. The feeding mode used for the evaluation of two categories (100 and 120 kg) of barrows and gilts. The analysis of slaughter value indicators has repeatedly shown a higher quality of slaughter bodies for the 100 kg category as opposed to the higher weight stated above without considering an evaluation of differences between sexes. The higher fat content in the 120 kg category established relatively favourable values of one of the important technological indicators – the dripping losses of cellular fluids. An evaluation of the entire sensor profile does not provide significant differences during the meat assessment in specified slaughter weights. The critical and important matter to consider is the worsening mark during the evaluation of juiciness and tenderness of sow meat as opposed to barrow meat. This circumstance is apparently caused by significantly low intramuscular fat content ($P \le 0.05$) for the slaughter weight of 100 kg, when the gilts have shown a decrease in the muscle tissue fat content (index of 65.8%) as compared to the barrows in comparison to the 120 kg category (index of 81.6%).

THE PRINCIPAL DIRECTION OF THE DEVELOPMENTS OF THE INFORMATION INQUIRIES FOR PIG BREEDING IN RUSSIA

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The informative-calculational system was developed by authors of this article for the first time. This system corresponds with the purpose and the problems of current pig breeding in Russia. The system carries out the informative, scientific and methodological provision of selectional work in pig breeding.The system includes:

- the development and the calculation of selectional programmes for pig breeds to increase qualitative level of selectional work;
- realizing systematic analyzes of selectional-genetical processes into pig population and pig breeds;
- the coordination and the development of informational technologies in pig breeding on all selectional levels.

This system is based on a data base of different levels (of farms, of districts, of regions, of federation) and allows to achieve an optimum effect in pig selection, to decrease the period of production traits evaluation in animals.

ASSOCIATIONS BETWEEN α-ACTIN GENOTYPES AND GROWTH, CARCASS COMPOSITION AND MEAT QUALITY TRAITS IN THREE PIG F_2 FAMILIES

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The segregation of the porcine α-actin gene was investigated in 970 F_2 animals of the crosses Meishan x Piétrain (M x P), Wild boar x Piétrain (W x P) and Wild boar x Meishan (W x M). α-actin is a muscle specific isoform of actin with a potencial role for meat quality. For the analysis of associations between α-actin gene variants and quantitative traits we examined a *XhoI/HinfI* α-actin PCR-RFLP. In family M x P 4.2% of the animals showed α-actin genotype AA, 60.9% of the animals had genotype BB and 34.9% of the F_2 animals showed genotype AB. In family W x M we found 24% of the animals with AA genotype, 52% of the animals with AB genotype and 24% had genotype BB. 49, respectively 51 perfomance criterions for growth, carcass composition and meat quality were available in the families M x P and W x M. The data were analysed using a general linear model. Taking as a basis a significance level of $\alpha = 5\%$ four traits (liveweight after five weeks, backfat depth, lean to fat ratio and weight of heart) showed significant associations to the α-actin genotypes ($\alpha = 0.05$) in family M x P. In family W x M it were two traits (liveweight after five weeks and conductivity 1 *M. long. dorsi*). The influence of the α-actin genotypes on the explored features could not be shown at a genome-wide significance level ($\alpha = 0.00001$). These results suggest, that there are no contributions of the α-actin gene to the variations in the analysed performance traits in pigs.

Session VII: Breeding and genetics of horses, sheep and goats

THE COMPARISON OF THE GENETIC STRUCTURE OF PRZEWALSKI HORSE AND SOME DOMESTIC HORSE BREEDS (ORLOV'S TROTTER, GUZUL, YACUTIAN HORSE)

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Analysis of albumin (AlB), transferrin (TF), receptor to vitamin D (GC), esterase (ES), alpha$_1$-beta glycoprotein (A1B) polymorphisms in Przewalski horse, Orlov's and Russian trotters, Guzul and Yakutian domestic horse breeds was carried out. The similarities of genetic variability, intraspecies genetic differentiation in wild (populations of a Przewalski horse) and domestic species were revealed. The genetic distances between some breeds are close to revealed between populations of Przewalski horse. The Przewalski horse differs from domestic breeds by reduced polymorphism of AlB and GC, however saves a rather high level of polymorphism on other markers. On the average heterozygosity of the Przewalski horse's populations did not differ from some local domestic horse breeds. The interpopulation distinguishes in Przewalski horse at ES and TF loci is found out. That means, the high inbreeding frequency in populations of Przewalski horse is compatible to preservation of genetical variability, however this process is locus-specific.

THE IMPACT OF ENVIRONMENTAL FACTORS AND SIRES ON PERFORMANCE TRAITS IN THE OLD KLADRUB HORSE

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Performance traits of individuals and sires from stationary performance tests of stallions and mares were analysed in the Old Kladrub breed from 1988 to 1997. Information of 183 progeny from 29 sires were used. These traits were judged by means of a 10 scores scale: total score, type and sex expression, conformation, performance, training, rideability, locomotion mechanism, marathon, span control, test of pulling reability. The linear model considered mixed effects (fixed effects – year, sex; random effects – sire). In the most of traits with the exception of type and sex expression and rideability there were found significant and highly significant differences. The stallions showed higher scores in all traits. The year of test had a highly significant impact on all traits with the exception of total score and pulling reability. There were no significant differences between sires in almost all traits with the exception of rideability. The non-significance was caused by the small number of progeny in sire groups. A BLUP-SIRE MODEL procedure for the estimation of breeding values from information of own and progeny performance was developed and verified. The procedure can be extended to another horse breeds.

USING OF BODY CONFORMATION'S DESCRIPTION IN BREEDING OF CZECH WARMBLOOD

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Five grade system of performance test start to use in Czech Warmblood breeding. Linear description and evaluation of body conformation of horses include this system too. 569 Czech Warmblood mares 3 years old were described for registration to Breeding Book in 1997. Linear description had 15 traits of body conformation (from 1 to 9 points). Four comprehensive characteristics (utility type, stature, legs, movement's traits) were evaluated ten points scale. Defects of body conformation were registered, too. Breeding values of individual traits of body conformation were calculated in stallions with more than 7 daughters (15 stallions) by BLUP (Animal Model). Also exterior index were stated. Models equation included effect of sires (including reciprocal relationship), effect of inspector and effect of mare age. Reliability of calculation was 20–30%, because stallions had little number of daughters.

SYSTEM OF EVALUATION OF SPORT HORSES IN THE CZECH REPUBLIC INCLUDING AN ESTIMATE OF THE BREEDING VALUE OF STALLIONS

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The objective of this project is to carry out an evaluation of performing the population of Czech sport horses after the elimination of effects of all external factors influencing their sports performance and to suggest the method of estimation of stallions breeding value. For that reason a database of Czech sport horses was created for years 1985–1997. The entry of each horse involved following: name, origin and sex, year of birth, year of start(s), type of stud, number of starts in each sports season, rider's category according to results, category of horses according to performance, type of sport discipline and performance of horses as defined by the PPB method (number of ancillary points per each start). Obtained data were analysed according to three principal riding disciplines. Using an Animal model, the genetic value of the population of sport horses in the Czech Republic was estimated together with the breeding value of stallions. Obtained results will be used for the evaluation of the population of sport horses in the Czech Republic with the aim to increase their performance.

GENETIC ASPECTS IN BREEDING OF SPORT HORSE

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Theoretical knowledge from genetics are practically used in breeding process based on selective effect. The aim of our study was to determine genetic correlation between the values of heritability coefficient of selected external marks and the values of performance parameters accomplished in performance tests of mares in breeding of VFU ŠZP Nový Jičín. Total 271 mares have been evaluated by method BLUP-Animal model in a period of years 1985–1996. The values of heritability coefficient for selected marks (WH, head, neck, the length of back) were evaluated in correlation of step, trot, gallop, possibility to ride a horse, jump in freedom and achieved AJV (absolute jump value) received in 2 years of sport jump testing. We have found positive correlation between basic gait and possibility to ride a horse (0.65–0.71). The relationship between trot, possibility to ride a horse and the frame is also important. Middle important correlation (0.41–0.58) has been found between jump in freedom, possibility to ride a horse and AJV. Attention will be paid on evaluation of trot, jump in freedom, possibility to ride a horse, physical conditions and achieved results in sport testation in breeding program of sport horse VFU ŠZP Nový Jičín.

PRELIMINARY ANALYSIS OF THE MATERNAL EFFECTS ON EXTERIOR AND REPRODUCTIVE TRAITS IN HORSES

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The aim of this study was to estimate maternal additive genetic variances and the covariances between maternal additive and direct effects for some performance traits in half-blood horses. There were 2750 recorded mares (883 base individuals) from four Mazury study farms (1932–1994) included into the analyse. The following traits were analysed: height of withers (HH) (in cm), circumference of chest (CC) (in cm), circumference of cannon (CCA) (in cm) and the so called reproduction index (RI) (as total offspring value of mare). The derivative-free REML algorithm under a unitrait animal model was employed. Following fixed effects were included in the model: place of birth, breed and year of birth. Individuals were divided into 49 breed groups. The maternal heritabilities (0.0004 for HH, 0.0005 for CC, 0.0048 for CCA, 0.0021 for RI) were low compared to the direct heritabilities (0.32, 0.35, 0.34, 0.12, respectively). The direct-maternal correlations (r_{AM}) were negligibly negative.

GENETIC POLYMORPHISM OF PROTEINS IN THE BLOOD OF HORSES REARED IN SLOVAKIA

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In the blood samples from Arabian horses (36), English halfblood (50), line Nonius (24) by means of electrophoresis there was identified a genetic polymorphism of hemoglobin, transferrin, albumin, amylase and carbonic anhydrase.

Analyse of results was utilised to establishment of genetic variability in those horse breeds. The highest heterogenity was found in polymorphic system of transferrins (alleles Tf^D, Tf^F, Tf^H, Tf^M, Tf^O, Tf^R) and carbonic anhydrase (alleles Ca^F, Ca^L, Ca^I, Ca^O, Ca^S). A small heterogenity is typical for amylase systems, where appearance of alele Am^B was in the samples of English halfblood horses very low (0,0495). Level of polymorphism at the locus Am as well at the other breeds (Arabian horse 1,28; Nonius 1,43) was low. According to the system of hemoglobin there was found a high heterozygosity degree of tested breeds and equalized frequency of alleles Hb^{A1} and Hb^{A2}.

COMPARISON OF FATTENING AND CARCASS CHARACTERISTICS OF CIGAJA LAMBS FOR PERIOD 1995–1997

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New period for sheep breeding in Slovak Republic started in 1990 when meat production became the most important product. We pay more attention to improve meat production of our sheep breeds. We test rams through their sons for meat production at the test station of Department of Animal Husbandry, Slovak University of Agriculture in Nitra. Every ram has six sons in the test station. The period of test fasts 60 days when there are fattening characteristics observed. After this period three lambs from every group are slaughtered for carcass value. During the period 1995–1997 47 lambs were tested in the test station. The results showed that Cigaja lambs achieved high fattening and carcass value in good condition. The average daily gain was 390 grams, the feed consumption per 1 kg of live weight gain 4.34 kg, the consumption of NEV 0.25 MJ, consumption of PDIN 4.1 grams, the percentage of thigh 31.63, area of MLD 16.16 cm^2, percentage of kidney fat 1.18 and the dressing percentage 51.26. There were differences among animals.

PRODUCTION AND COMPOSITION OF MILK OF MERINO AND MILKING BREED CROSSES

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Milk production and composition of Merino sheep (M), crosses of F_1 generation Merino x East Friesian (M x EF) and Merino x Lacaune (M x Lc) during 113 days lasting milking period were evaluated in the experiment. Official milk recording was performed in conformity with the international rules (ICAR). M sheep were in third and higher lactation, crosses M x EF in second and M x Lc in first lactation. Average day milk production during milking period was 283.5 ml in M, 955.9 ml in M x EF and 668.9 ml in M x La. Milk production during milking period was 31.9 l in M, 107.7 l in M x EF and 74.5 l in M x La ($P < 0.01$). Fat production was 2.35 kg in M, 6.94 kg in M x EF, 4.99 kg in M x La, protein production 1.99 kg in M, 5.90 kg in M x EF, 4.19 kg in M x La and dry matter production 6.01 kg in M, 19.11 kg in M x VF, 13.45 kg in M x La ($P < 0.001$). Content of fat, proteins, lactose and dry matter was 7.38%, 6.34%, 4.51% and 19.13% in M, 6.49%, 5.54%, 4.90% and 17.82% in M x EF, 6.75%, 5.68%, 4.86% and 18.19% in M x La ($P < 0.001$).

EVALUTION OF BODY MEASUREMENTS OF ŠUMAVA SHEEP

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The Šumava Sheep was selected in the years 1953–1987 and based on the original Bohemian Land Sheep. These sheep was of a middle-sized body shape and white colour. Our studies were carried out in three breeding herds in Šumava region. The live weight and selected dimensions in accordance with age were examined. The average live weight in one-year sheep amounted to 40.3 kg. This value is comparable with data stated by Macháček (1991) and by 11.5 kg higher than data stated by Čumlivski (1963) and by 1.9 higher than specified by Čumlivski (1988). The average values of the individual dimensions can be compared only with the data delivered by Čumlivski (1963). The average height at withers was 586 mm, which is by 14 mm less that measured by Čumlivski (1963). On the other hand, the present-day sheep is by 83 mm broader in the chest, the girth of chest shows values that are higher by 195 mm and the depth of chest id being different by 55 mm. The average live weight of sheep older than 3 years amounts to 58.6 kg, ranging between 39 and 78 kg. Mašek (1988) states the standard live weight of adult sheep amounting to 55 kg. Čumlivski (1988) states the live weight of adult sheep being on the average 60 kg, ranging between 55 and 65.5 kg. Based on the results mentioned above, it can be concluded that the Šumava sheep differs from the original Bohemian Land sheep. The live weight has grown considerably and the chest dimensions have increased.

EFFECT OF GENETIC AND NON-GENETIC PARAMETERS ON GROWTH INTENSITY OF LAMBS

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Average daily gains (ADG) and body weight at weaning (BWW) were analysed in 12230 Valachian and 9699 Tsigai lambs. We used data of Efficiency Control collected in the State Breeding Institute in Žilina. The analyses of genetic factor (fixed effect father – FA) and non-genetic factors (fixed effects month of lambing – ML, control year – CY, sex – S, number of weaned lambs – N, flock – FL, age at weaning – AW, age of the mother – AM, litter size – LS) were performed by the least-squares method with the use of linear model (GLM-SAS method). Average values of ADG and BWW were 16.49 kg and 0.227 kg, respectively, in IV breed and 17.57 kg and 0.226 kg, respectively, in T breed. We found that in Tsigai lambs ML, CY, S, N, FL, FA, AW, AM had statistically significant effect ($P < 0.001$ or $P < 0.01$) on ADG. Effect of LS on ADG was not significant. All examined factors had statistically significant effect on BWW ($P < 0.001$) in this breed. In Valachian lambs ML, CY, S, N, FL, FA, had statistically significant effect on ADG ($P < 0.001$), LS, AW, AM were not significant. On BWW of Valachian lambs all examined parameters had statistically significant effect ($P < 0.001$).

EFFECT OF GENETIC AND NON-GENETIC PARAMETERS ON MILK EFFICIENCY OF EWES

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Using centrally collected data of Milk Performance Control of Improved Valachian (IV) and Tsigai (T) ewes raised in Slovakia in 1995 and 1996 ($n = 4021$ for IV and 1247 for C) we evaluated effect of several genetic and non-genetic factors (program SAS, ver. 6.1 on real and standardized milk production (RMP and SMP), content of proteins (% P), fat (% F) and lactosis (% L). After taking genetic and non-genetic factors into consideration in IV ewes RMP was 80.8 l, SMP 84.5 l, % P 5.73, % F 8.15 and % L 4.98 and in T ewes RMP 73.4 l, SMP 79.9 l, % P 5.71, % F 8.49, and % L 4.92. In IV ewes the most significant effect (method SAS-GLM) on RMP, SMP and milk composition had factor of flock ($P < 0.001$), age of ewes and father of ewes ($P < 0.01$ and 0.001, respectively). Interval between lambing and 1st control measure and parameter length of milking period had also significant effect on RMP, SMP and % F. In T ewes factor flock and age of ewes had also significant effect on RMP and SMP ($P < 0.001$), % F ($P < 0.01$) and % L ($P < 0.001$). As distinct from IV breed, there was nonsignificant (ns) effect of number of suckling lambs on milk production and composition in T breed. Effect of father within the flock on RMP and SMP in T breed was less outstanding (ns and/or $P < 0.05$); as well as the effect of this factor on milk composition (% P – ns; % P and % L – $P < 0.01$).

THE PROJECT OF THE BREEDING SYSTEM FOR THE ŠUMAVKA BREED OF SHEEP

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The main breeding objective in the Šumavka breed of sheep is to maintain this breed as a gene reserve if possible in purebred status without influence of the other breeds and at the same time to preserve a sufficient unrelativeness and genetic variability within the breed. At the same time the selection will be aimed at the increasing of the economic ability of the Šumavka breed. Attention will be devoted mainly at increasing of the prolificacy and the growth intensity of the lambs under pasture conditions. In males there will be also provided more intensive selection according to the carcass quality. The planned number of ewes included in the gene reserve of the Šumavka breed of sheep is around of 2000 of heads. This population will be divided into the nucleus and the multiplicative flocks. Roughly 25% of the ewes in the nucleus will be included in a group of dam of rams every year. Approximately 3.7% of the best lamb rams born in the nucleus will be used in nucleus flocks, next approximately 1.6% of lamb rams will be included in multiplicative flocks. The Animal Model will be utilized in the breeding program as a method for estimation the breeding values of the individuals. Aggregated breeding values will be determined by the use of selection indexes. Breeding program will be also managed in such a way that the ratio of the Kent genes in Šumavka breed will decrease.

USING SELECTED SHEEP BREEDS WITH A SPECIAL VIEW TO THEIR SUITABILITY FOR MIXED GRAZING WITH CATTLE

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In a 3-year experiment (1995–1997) in lowland semi-arid conditions a semi-intensive method of rearing was applied and preconditions for an enclosure-pasturing system for mixed grazing of various breeds of cattle with sheep bred for meat production was evaluated. The production of the pasture herbage ranged between 6.33 and 12.14 t/ha and pasture loading was between 3.58 and 4.06 DJ (livestock unit) /ha. The proportion of sheep in the total pasture loading was 20.3% and in the production of live weight it was 31% for the grazing season. Average daily increments for the grazing season were the highest in a group of 55 Charollais lambs (Ch100), i.e. 0.256 ± 0.009 kg. For Merino crosses (Booroola) Bo12.5Ch (9 head) it was 0.198 ± 0.017 kg, for Bo25Ch (30 head) 0.229 ± 0.010 kg, and the significantly lowest value was for Bo50Ch (30 head), i.e. 0.191 ± 0.015 kg, Kent (12 head) 0.192 ± 0.009 kg, crosses of the Improved Wallachian and East Friesian from Bergschaf rams (9 head) 0.250 ± 0.021 kg. The suitability of genotype Ch100 for mixed grazing was also confirmed by the favourable indicators of carcass value.

EVALUATION OF GROWTH CAPACITY AND CARCASS QUALITY OF LAMBS OF THE KENT BREED

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Fattening of male lambs of genotypes Kent (K 100), crosses F_{111} of Booroolo and Charollais (Bo12.5Ch) and Charollais (Ch100) was carried out within the framework of mixed grazing of sheep and cattle on a lucerne-grass stand. Within the interval from birth to the end of fattening period, the highest average daily gain was recorded in lambs of Ch100, i.e. 0.267 kg. As compared with remaining two groups (K100 and Bo12.5Ch), the difference in gains was statistically highly significant ($P \leq 0.01$). The highest dressing percentage of lambs selected for control slaughters was recorded in Ch100, i.e. 49.18%. The corresponding values of Bo12.5Ch lambs were a little lower (48.73%); this difference was statistically insignificant. In K100, the average dressing percentage was 41.36% and the difference from groups mentioned above were statistically highly significant ($P \leq 0.01$). When evaluating the percentage of leg in the total carcass weight, no significant differences were found among experimental groups; in K100 this parameter was 33.20%, while in Bo12.5Ch and Ch100 32.94 and 33.65%, respectively. The lowest and the highest proportions of musculature in the right rack were recorded in K100 and Ch100 (61.28 and 68.79%, resp.). This difference was statistically highly significant ($P \leq 0.01$).

MILK EFFICIENCY OF CROSSES OF IMPROVED VALACHIAN AND LACAUNE BREED

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In Improved Valachian breed (IV), Lacaune (Lc) and crosses of F_1 generation ZV x Lc in 1996 and 1997 daily milk production during suckling of lambs counted on the basis of production for 4 hours period after application of oxytocin (5 I.U.) and average milk production during milking period according to Milk Recording Standard elaborated in conformity with international rules (ICAR) were evaluated. We also evaluated content and production of basic milk components. Average milk production during lamb suckling was significantly influenced by genotype and was dependent on the lactation stage. We found these values: IV – 1274 ml, Lc – 2186 ml, IV x Lc – 1420 ml ($P < 0.001$). Average milk production to weaning was 46.3 l in IV, 97.4 l in Lc and 39.1 l in IV x La; average milk production for milking period was 71.9 l, 157.8 l and 86.2 l, respectively; average production for lactation was 118.2 l, 255.2 l and 125.3 l, respectively. Content of basic milk components was: fat: IV – 9.0%, Lc – 7.7%, IV x Lc – 7.8%; proteins: 5.9%, 5.5% and 5.3%, respectively, lactosis: 4.7%, 4.9% and 4.9%, respectively.

EVALUATION OF SOME CHARACTERISTICS OF CASHMERE

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During the years 1994 and 1995 we followed some characteristics of cashmere as production of cashmere, fibre diameter, true and real length of cashmere. We followed 18 goats cashmere breed in Šošůvka farm which is situated in reservation Moravský Kras. Rearing of goats were in the building during winter then in the pasture. The goats we combing for obtaining the cashmere. Average production of cashmere was 0.225 kg in 1994 and 0.230 kg per goat in 1995 and between years there was no statistical difference. Average diameter of true fibre was 15.94 µm in 1994 and 17.17 µm in 1995. The difference in average production of cashmere between years were statistically significant ($P \leq 0.01$). Average length was 4.79 cm in 1994 and the same in 1995. Average real length of cashmere fibre was 7.45 cm in 1994 and 7.25 in 1995 and between years there was no statistical difference. With the growing age of goats average production of cashmere as well as an average diameter of true fibre increased.

ANALYSIS OF VARIABILITY OF SOME TRAITS IN PURE BREED ENGLISH HORSES FROM ONE STUD

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The studies of variability and changes of the traits were performed on a basis of the results from one stud of pure breed English horses in Poland. During a period of 20 years the height at withers, chest circumference, cannon circumference, boniness (proportional relation of cannon circumference to height at withers), chest index (proportional relation of chest and cannon circumferences) were studied. There was found statistically significant effect of the birth year on all of the traits. Sex significantly influenced cannon circumference, boniness and chest index. In the studied period there was observed a slight increase of chest and cannon circumferences and decrease of height at withers, while boniness and chest index did not changed. The variability coefficients of the traits were 2–3% for height at withers, 2.4–4.3% for chest circumference, 3–4% for cannon, 1.7–3.3% for chest index and 2–4% for boniness.

EFFECT OF LIVE WEIGHT OF CHAROLLAIS SHEEP ON THEIR FERTILITY

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The aim of the research was an observation of the effect of live weight of gimmers and ewes on select reproduction indicator. 241 gimmers were included in the experiment in the first year of observation, 220 ewes (age 2 years) in the second year. All animals were weighed before commencment of the mating period (November) and in the course of the reproduction period basic fertility indicators were observed. For evaluation usual statistical methods were used. The highest percentage of conception, fertility percentage per ewe (gimmer) of the basic herd and fertility percentage per ewe (gimmer) lambed was found in gimmers whose live weight was from 45.1 to 50.0 kg (81.37, 107.80, 132.50). In 2-year ewes the best results were reached at the group with live weight 65.1 to 75.0 kg (95.20, 153.60, 161.30).

BEHAVIOURAL CHARACTERISTICS OF GOATS BREED ONLY IN THE BUILDING DURING

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Observation of animal behaviour is important for finding the best condition for their breeding. During the last eight years the number of goats increased in the Slovak Republic. The goats were bred by small holders in the past but the situation has changed. We have more as 70 big farms in our republic but we have very limited experience with the breeding of goats in such condition. The observation was conducted on a private farm that is situated in the south part of Slovak Republic. We observed 18 goats (three groups of six goats with different milk production) of Slovak white short hair breed on second lactation during three months in 1996. The animals were milked twice per day. During the whole day they were in the stable just after milking they were in the outlet for one hour. These activities were followed during 24 hours period : standing, standing and ruminating, walking, eating, laying and ruminating, laying and sleeping and aggression. The most active animals were in the second group (middle level of milk production) then the third group (the highest milk production) and the first group of goats. We found differences among groups but nonsignificant.

THE GENOTYPING OF SILESIAN NORIC HORSE USING MICROSATELLITES

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There was studied the population of gene resource Silesian Noric (n = 39), compared to the similar Noric population "Lánský" (n = 16). This population has been characterised using polymorphisms of some microsatellites (VHL$_{20}$, HTG$_4$, AHT$_4$, HMS$_7$, HTG$_6$) from the international test panel ISAG. The genotyping has been carry out by automatic DNA sequencer ABI-PRISM Perkin Elmer and software GeneScan Analysis. There were stated allelic and genotype frequencies, heterozygosity, and genetic distance between groups in the study. The heterozygosity was 0,63, the genetic distance 0,2657.
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Session VIII: Breeding and genetics of poultry

GENETICALLY DEFINED LINES OF CHICKENS

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Investigations carried our at out Institute over the past decades resulted in the creation of a unique model system for avian immunogenetics, a group of inbred and congenic lines of chickens. At present, model system consists of 12 congenic lines on the genetic background of C line, differing in MHC haplotypes (5 of them are recombinant – congenic) and 2 another congenic lines on the same background but differing in endogenous ALV loci. Model system is supplemented by 5 other inbred lines and 3 genetically defined outbred lines of chickens. The development of the model system is directed towards studying the interaction of the genom's components, especially MHC genes, endogenous retroviral structures and exogenous viral infections.

THE MAPPING OF CHICKEN GENOME

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There were at least 1100 genetic markers have been mapped on the chicken genome. This provides an important tool for the localisation of genes regulating spontaneous autoimmune thyroiditis in obese strain chicken. A technique of quantitative locus mapping has already been successfully used for the dissection of other complex genetic interactions. At present, this approach is considered to be the best method of identifying loci involved in pathogenic processes. The role of markers fulfill optimal microsatellites regarding their high degree of polymorphism and presence in every 10 kb. Now that many genes have been mapped in the chicken, comparisons may be made between the linkage maps of chicken and man. It will suggest gene assignments to specific chromosomes. Besides that, it will contribute to better understanding of vertebrates evolution, because the extent of genome conservation, in particular that of gene order, is of great practical as well as evolutionary interest. The degree of conservation between man and chicken is much greater than e.g. between man and rodents. Therefore, the comparative gene mapping between chicken and man employing biometrical methods is the next step after revealing of respective genes codying for SAT in chicken. This enables the identification of genes regulating Hashimoto thyroiditis in man. The final goal is the identification of patients endangered by HT.

DIALLEL ANALYSIS OF A LAY AND AN EGG WEIGHT IN JAPANESE QUAIL

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A complete diallel cross was carried out among four outbred lines of Japanese quail of different body weights to analyse the effects influencing the reproduction traits. The number of egg, egg weight and feed consumption was measured from 45 to 300 days of age. The rate of lay and feed efficiency was calculated. At first week of lay the direct genetic effect for egg weight was low in line 1 and high in two high body weight lines. The similar values of that effect were found at the end of lay period. The overall heterosis was positive for the whole lay period and its values increased in the last part of lay period. The line heterosis was negative and non-significant except the positive estimate (0.05) for line 3. Reciprocal effects were positive and low at the beginning of lay and increased with continued lay period. The positive maternal effect for the egg weight occurred in the low body weight line, the negative estimate was found in the highest body weight line. The direct and maternal effects for the rate of lay showed no association with the body weight of line. The highest heterotic effects occurred in the lines with the lowest rate of lay. The feed efficiency for the egg mass showed the positive overall heterosis. The maternal effect was significant in line 3 with the highest body weight.

SELECTION FOR LOWER YOLK CHOLESTEROL CONCENTRATION IN JAPANESE QUAIL

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The outbred egg type stock of Japanese quail was the base population for this divergent selection experiment. In each generation there were approximately 20 females from 60 ones in each lines selected to form the further generation. The yolk cholesterol content continuously but irregularly decreased in line selected for low yolk cholesterol concentration (LCH line) and raised in the line selected for high yolk cholesterol concentration (HCH line). The content of yolk cholesterol concentration F_{10} selected generation was in LCH line 1508, in HCH line 2092 and in control 1694 mg yolk cholesterol/100 g wet yolk. Realized heritability h^2 estimated from 10 selected generation was 0.233 for LCH line and 0.208 for HCH line. The h^2c values corrected according control line results were 0.226 for LCH and 0.211 for HCH lines. Concerning inbreeding depression in selected generations blood refreshment should be done from foreign population in the next F_{11} generation.

THE DIVERSE REACTIVITY PERFORMANCE OF GENETICALLY DIFFERENT LAYING HYBRIDS ON THE SOME ADDITIVES AND THE BIOSTIMULATORS

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In the trials with four gene combinations of laying hybrids of hens (LW x LW, RIR x RIW, LW x RIR and PB x LC) during 252 days lay, egg weight and a feed consumption were observed. For the feeding we used a basic feed mixture with ca. 17% crude protein and the feed mixture was added (0.1 and 0.2% methionine, 3% Ecovit, 2.5% and 5% *Rhaponticum* hay, 1.00 and 2.00% *Rhaponticum* seed). We observed different effects of the same addition for the different genotypes of layers. The addition of 0.1% methionine had a depressive effect for the intensity of lay by LW x LW by 1.7% compared to the test however by the other combinations it was stimulant. The addition had also a slightly depressive effect by the combination LW x LW for the egg weight (by 0.5 g), by the combination PB x LC even by 0.8 g. By the combination RIR x RIW it meant a higher average egg weight by 0.2 g. The addition of methionine however has effected for a lower feed consumption per unit of production. Various additions effected the different reaction of performance primarily in according to the genotypes of laying hens.

THE POLYMORPHISM OF MICROSATELLITES IN CHICKEN AND THE PROSPECTS OF EXPLORATION IN SAT ANALYSIS

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Chicken is an important experimental organism for study of many problems in experimental biology including the study of genetic regulation of diseases. Better understanding of spontaneous autoimmune thyroiditis (SAT) on the chicken model enables better comprehension of the genetic regulation of human Hashimoto thyroiditis, which is a serious autoimmune disease. A chicken model is for the study of HT advantageous. There has been prepared obese strain (OS), in which massive infiltration of thyroid gland and other symptoms of SAT occurs in a few days after hatching. The OS is homogeneous, for more than 40 generations it has been reared as a close-bred and selected for SAT. The disease begins in age about 6–10 days, thus, it is possible to study the initiating mechanisms. The extent of offspring of one couple comparing to the low number of children of handicapped people enables the analysis of genetic regulation in detail. What's more, in man the study of HT is complicated because the peak of incidence is in women between 40 and 60. So far known great number of microsatellites and their extent polymorphism make them an optimal tool for the study of linkage between marker loci and disease in chicken affected SAT. This method has already been successfully used when solving similar problems.

ACTUAL PRODUCTION WAYS OF TRANSGENIC CHICKEN

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Production of transgenic chicken appears to be the major goal in future in the poultry industry. There have been several different methods developed including the direct injection of DNA into the oocytes, the use of retroviruses or lately *in vitro* transfection of chicken pluripotent cells. Transfection of PGCs cells and their reintroduction into the blood of recipient seems to be a promising way. Transfection of blastodermal cells and their introduction into the recipient embryos seem to be promising as well. For this purpose and for sex identification there has been colour model for production of chicken chimeras using in vitro cultivated blastodermal cell developed. In our model as a donor of blastodermal cells are used chicken pluripotent cells from the embryo which origin is crossing the male Black Minor – ii, EE, b/b and the femal Barred Leghorn – ii, ee, B/–. Barred gene *B* is sex linked gene located on the non-homologous segment of Z-chromosome. Recipient embryo originated from crossing male and female of White Leghorn breed. In our experiments we could construct chicken chimera from 24 hours *in vitro* cultured cells. During this time it is possible to transfect the cells and identify the sex of transmitted blastodermal cells by PCR.

ON TRANSFORMATION OF THE HATCHABILITY TRAITS IN LAYING FOWL

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Hatchability traits are usually non-normally distributed. This can lead to underestimating genetic parameters, which in turn reduces the efficiency of genetic evaluations. The objective of this study was to analyse the variance component estimates obtained by use of different transformation approaches (untransformed data, the Box-Cox transformation – denoted as BC, square root transformation – SQRT, and transformation of arcsin square root – ASSQRT). The analysis comprised percentage of fertilized eggs (PFE), percentage of hatched chicks (PHC), percentage of healthy chicks hatched (PH) of two lines. Derivative-free REML was used for estimation of variance components. It was concluded that the SQRT and ASSQRT transformations (for all traits) yield the dosest approximation to non-normality. Generally, the use of the BC transformation induced a significant increase of both additive genetic and error variance estimates, whereas other transformations led to opposite results.

THE ONTOGENESIS OF CHICKEN IMMUNE SYSTEM

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The bursa of Fabricius itself develops from the cloacal entoderm while the duct is derivative of anal invagination of the ectoderm. The proctodeal lymphatic tissues – histologically peripheral lymphoid tissue – is continuous those of the bursal duct and the distinct flat-shaped fold of the bursa, which may be developed on ectodermal site. The bursal follicles are of entodermal origin.The bursal tissue consists of stromal and lymphoid cells. The stromal cells are the epithelial, secretory dendritic cells (SDC), and macrophages. The lymphoid and macrophage precursors are blood-borne cells as it was brilliantly proved by Le Douarin et al. It was suggested that the precursors of the the SDC differentiate from the bursal mesenchyme during the 8–9 days of embryogenesis. These precursor cells are released from the mesenchymal network and migrate to the surface epithelium of the folds where they form small groups underneath the epithelium. Between 11 and 13 days of incubations the cells enter the epithelium which responding by an extensive cell proliferation, producing an epithelial bud. The bud receives the blood-borne B cell precursors. Inside the bud the precursors of the SDC differentiate to dendritic shaped cells and elaborates vimentin intermediate filaments and cytoplasmic granules. The SDC, locating exclusively in the medulla of the follicles, becomes surface IgG positive around hatch. Their number increases up to 4 weeks of age and afterwards remains unchanged. Embryonic testosteron treatment inhibits the differentiation of SDC precursors from the bursal mesenchyme, therefore the bud formation is impaired due to which the hatched chickens are bursaless.

THE ROLE OF CYTOKINES IN IMMUNITY

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Cytokines are important regulators of the immune system. In mammals, a large number of cytokines has been characterized and is now widely used to study their role in resistance and susceptibility to diseases. In chickens, however, very little information on cytokines was available until recently. Using functional expression cloning a number of chicken cytokines was characterized during the last few years, including the interferons, IL-1, IL-2 and IL-8. Interestingly, the avian interferon system turned out to be very similar to the mammalian system with several IFNα genes and a single gene for IFNβ and IFNγ, respectively. Antiviral activity was demonstrated *in vitro* for all of them. *In vivo* antiviral activity of IFNα was shown in a Rous Sarcoma model in congenic birds of the CC and CB line. This cytokine inhibits the replication of RSV thus leading to a delay in tumor growth and mortality of infected birds of the progressor line. By contrast, tumor growth was enhanced and regression was delayed if chickens of the regressor line were treated with anti-IFNα. These experiments demonstrate that valuable information on the *in vivo* function of avian cytokines can be obtained if recombinant cytokines are used in well established disease models and selected chicken lines.

THE ROLE OF MACROPHAGES IN IMMUNITY

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Macrofages play a key role in many aspects of immunity. Their phagocytic activity is an important component of nonspecific defence mechanisms. Through their ability to process and present antigen to lymfocytes in the context of class I and II cell surface products of the major histocompatibilty complex (MHC), macrofages play a pivotal role in specific immune responses. Furthermore, they secrete an array of cytokines and other immunologically important effector molecules that amplify the immunoresponse. In addition, activated macrofages perform effector functions such as bacterial and tumor cell killing. In chickens, several studies have shown that phagocytosis, bacterial killing, chemotaxis, respiratory burst and nitric oxide synthase activity are influenced significantly by the allelic differences in the MHC. The influence of this complex on the adherence potencial of monocyte-derived macrofages was examined using congenic chicken lines CB and CC and recombinant congenic lines. From the obtained results we conclude that the gene regulating adherence potential is localised within the B–F/L region of the chicken MHC.

GENETIC CONTROL OF IMMUNE RESPONSE TO AVIAN RNA TUMOR VIRUS INFECTION

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Exogenous avian leukosis sarcoma viruses (ALSV) can induce lymphomas or other tumors in chickens. Some of these viruses are of economic importance. It is well documented that subclinical exogenous ALSV infection results economical losses to the poultry industry. Rous sarcoma virus (RSV), which contains the complete replicative genome of leukosis viruses and the oncogene *v-src*, serves as a model for the study of virus-host interaction in this system. Genetic studies with different inbred lines of chickens have established that MHC (B) genotype is by far the largest influence on the regression of RSV-induced tumors. The immune based mechanism of tumor progression resistance has been studied in detail using this immunogenetic model.

GENETIC RESISTANCE AND NEW VACCINES TO CHICKEN VIRUSES

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It is known that there are genetic differences in the response of chickens to certain economically important viral diseases like infectious bursal disease and Marek's disease. A well studied system for MHC gene control of antiviral immunity is the MHC congenic CB and CC chicken strains with the RSV Prague strain C. Both chicken strains become infected and develop tumors. These tumors progress unchecked in CC chickens causing nearly complete mortality, but regress in CB chickens. Tumor regression is due to cytotoxic T cells, which recognise MHC class I molecules bearing RSV-derived peptides. Sequence analysis of the peptides bound to the class I molecules from CB and CC chickens has identified peptide motives for these strains, which have been used to predict antigenic peptides from the *src* gene of RSV. With the help of a simple and rapid *in vitro* assay it was possible to identify those peptides which actually bind with sufficient affinity to class I molecules of CB chickens. None of the predicted peptides fitted the motif of the susceptible CC strain. In first *in vivo* studies CB chickens were inoculated with the appropriate RSV peptides together with Freund's incomplete adjuvans in order to investigate the influence of peptide vaccination on tumor growth after challenge with RSV.

INFLUENCE OF 1-DAY LIVE WEIGHT ON GROWTH AND CARCASS CHARACTERISTICS OF CHICKENS

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The aim of our study was to analyze if the compensation growth of chickens having the lower hatching weight is present in comparison with the heavier ones and also to analyze the influence of various genotypes to this phenomena. Analysis of fattening test showed a very strong effect of 1-day live weight of chickens on their following growth and we have not found the compensation of this factor during the growth period. There was not sexual effect on the embryonic growth because the difference between 1-day live weight of males and females was very small and non significant. The influence of 1-day live weight and also of the sex increased during the growth and the 21-day old cockerels were significantly heavier than 21-days pullets. In the 42-day final slaughtery age chickens with heavier 1-day live weight were much heavier (+364 g, i.e. 22%) than the chickens with smaller 1-day live weight. Also the differences between cockerels and pullets were large and statistically very high significant in the age of 42 days. The influence of genotyp was significant in all age categories. In final slaughtery 42 day the chickens of pure male line Slovgal O3C (2019 g) and combinations O3A x 03C (2018 g) and 06A x 03C (1742 g) were the heaviest.

EFFICIENCY PARAMETERS OF THE DWARF TYPE OF HENS

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The objective was to evaluate parameters of growth and egg production of the parent population of dwarf hens (ISA VEDETTE 215) and to compare them with a control population of hens of standard growth (ROSS 208). The investigations involved 300 hens housed on deep litter. We studied the parameters of body weight during rearing and during egg laying. In the test of egg production up to the 64th week of age the following indicators were studied – total number of laid eggs, egg weight, feed conversion and longevity. The body weight of males of the parent ISA VEDETTE (DW/DW) at 22 weeks of age was 3.37 kg, for ROSS (DW/DW) it was 2.96 kg. The young ISA VEDETTE (dw/–) pullets of the same age weighed 1.95 kg, ROSS (DW/–) 2.4 kg. In terms of the number of laid eggs, this value was slightly higher for the ISA VEDETTE pullets (182 eggs), for ROSS it was 180 eggs with a considerably better feed conversion per 1 settable egg for the ISA VEDETTE combination. In addition, the ISA VEDETTE hens showed during the egg laying period a significantly lower ($P < 0.01$) mortality (4.64%) than the ROSS hens (7%).

EFFECT OF BIOACTIVATED SODIUM AZIDE ON THE HATCHABILITY INDICES OF HENS

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For this investigation there were used the hatchability eggs of R.I.R breed. Before incubation the hatchability eggs were intraovally treated with bioactivated sodium azide (bioactivation through the barley germs affected with 0.001 M sodium azide). There were control groups: homogenate from barley germs without sodium azide treatment, physiological saline and intact eggs. Total amount of vehiculum was 0.1 ml per egg. The basic hatchability indices – infertile eggs, died embryos, hatchability and sex ratio – were evaluated. The results revealed that the intraoval application of bioactivated sodium azide and a single homogenate without sodium azide treatment markedly lowered the hatchability indices mainly embryonal mortality and hatchability. The unaffected homogenate group had 72.0% mortality, group with bioactivated sodium azide 70.8% mortality whereas the intact control only 8.8% mortality. There was the same tendency at hatchability. The differences between groups were highly significant ($P < 0.01$) in both indices. The infertile eggs and the sex ratio were slightly influenced however they were also highly significant ($P < 0.01$) at infertile eggs. The differences between groups at sex ratio were not significant. The highest dying of embryos was up to the 5th day of incubation.

THE COMPARISON OF PERFORMANCE OF ANY GENOTYPES OF LAYING HYBRIDS

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We used four different production genetically defined laying hybrids from the firm DPB Dobřenice. The hybrids LW x LW, RIR x RIW, LW x RIR and PB x LC were placed for the basic judgement of the utility qualities at the central stage of 3-tier cages. The layers were fed by a commercial feed mixture "N" with the analysed contents 16.9–17.1% crude proteins. The test has lasted 252 days, i.e. 9 cycles per 28 days. The results of the performance of four genotypes under the feeding by feed mixture "N" are seen in the Table:

Combination	Egg production (pcs)	Feeding days	Intensity of lay (%)	Average egg weight (g)	Feeding per 1 kg eggmass (kg)	Feeding per feeding day (kg)	Feeding per 1 egg (kg)
LW x LW	4 819	5 851	82.4	59.9	2.595	0.128	0.155
RIR x RIW	4 370	6 091	85.8	63.9	2.324	0.127	0.149
LW x RIR	5 808	6 701	86.7	60.2	2.454	0.128	0.148
PB x LC	4 673	5 943	76.9	57.6	2.884	0.128	0.166
Average	19 570	23 586	83.0	60.4	2.561	0.128	0.154

TIME TRENDS OF REPRODUCTIVE TRAITS IN EIGHT GENERATIONS OF PEKING TYPE DUCK FROM SIX CONSERVATIVE GROUPS

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The mean value of reproductive traits was determined in the conservative groups of ducks of Danish (P8), French (P9), English (A1, A2, A3) and Polish (P33) origin, each maintained over eight generations in the first and second performance period in comparable environmental and feeding conditions and without selection. Linear regression equations illustrating the time trends of changes were also calculated. In the first performance period, downward trends over 8 generations were found: in egg number within all groups (except P33); in egg weight (A2) and in egg fertilization (P9 and A3) groups. In the second performance period many downward trends in the studied traits (except hatchability from fertilized eggs) were observed, among them: egg number (P8, A1, A3); egg weight (P8, P9, A1, A2); egg fertilization (P8, P9, A1); hatchability from the eggs set (P8, P9, A1, A3).

INTERLINE DIFFERENCES IN EGG PRODUCTION OF THE JAPANESE QUAIL (*COTURNIX JAPONICA*)

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The Japanese quail is the smallest poultry species with meat of good quality as well as a high egg production which is, however, very variable. The objective of our study in laying test No. 2 was to evaluate the parameters of egg production of

3 different lines (03, 07, 20) kept at the Mendel University of Agriculture and Forestry in Brno. We evaluated the parameters of egg laying until the end of the 6th month of the laying period, i.e. the following indicators: number of laid eggs, egg weight, production of egg mass, including qualitative egg indicators. The eggs were laid within the system of individual efficiency test, each line had 90 hens. Line 03 showed the highest egg production in number of laid eggs (156.9 eggs), the values were lower in lines 20 and 07 (i.e. 155.8 and 153.9 eggs, respectively). The heaviest eggs were produced by line 03 (11.20 g), followed by lines 07 and 20 (i.e. 11.16 and 10.92 g, respectively). The differences between lines 03 and 20 were significant ($P < 0.5$). The tendency was similar for the total egg mass, line 03 achieved the best results (1756 g), followed by lines 07 and 20 (i.e. 1719 and 1701 g, respectively).
(Investigations were carried out within the GA CR, Grant No. 235/1021/6GA 0676.)

INFLUENCE OF DEPHENURONE HERBICIDE ON JAPANESE QUAIL

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In this work the influence of dephenurone herbicide on the hatchability indices, growth intensity and body development of Japanese quails was investigated. In praxis defenurone is used against monocotyledonous grass weeds. It is dilutable by water and has a repellent effect too. Hatching eggs of Japanese quails were intraovally treated with two concentrations: 0.05 and 0.01%. Control group was influenced with aqua *pro injectione*. Total amount of vehiculum was 0.1 ml per egg. The basic indices of reproduction and production during 3 generations, growth allometry and correlations between body weight, pelvis width and thigh length were investigated. The results revealed that the dephenurone herbicide lowered values of basic indices of reproduction. It did not influence the body weight and the growth allometry. It did not induce any malformations.

SOME OF THE REPRODUCTIVE TRAITS IN JAPANESE QUAIL ANALYSED BY THE LOGISTIC REGRESSION METHOD

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The paper presents analysis of reproductive performance in three lines of Japanese quail as follows: P1 – the proportion of fertilised eggs to set eggs as an indicator of fertility and early mortality; P2 – the number of hatched eggs to set eggs and P3 – the number of hatched eggs to fertilised eggs. The data were collected in two generations, which were different regarding to incubation conditions. To develop a proper statistical approach there were used two regression methods in analysis of lines' reproduction parameters: GLM and logistic regression, which is more suitable in the case of all-or-none traits. Several models were constructed including combinations of effects observed in this experiment. In the final model the effects showing a strong collinearity were excluded. The relative impact of different effects on variation of reproductive traits was compared. In the final analysis the generation, line and interaction effects were statistically significant regardless to the method. P1 parameter showed a significant line effect; no differences between generations were observed while the interaction between both effects was also significant. In one line only, an increase in P1 was observed in the second generation. Generally, in the second generation hatching results improved. When expressed as P2 they were better in two lines (with an exception of one line with the highest inbreeding level) while expressed as P3 they were higher in all lines observed. It indicates an improvement of incubation conditions during final incubation period.

BURSAL SECRETORY DENDRITIC CELLS IN THE BIRDS SURVIVED IBDV INFECTION

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In immunosuppressed chickens the repopulation of bursal follicles by B cells is preceded by the normal appearance of surface IgG on the bursal secretory dendritic cells (SDC). After infectious bursal disease virus (IBDV) infection the bursa of Fabricius rapidly involuted (4–6 days postinfection) and the number of follicles drastically reduced. We have studied the BSDC in animals survived the IBDV infection by light- and transmission electron microscopes and immunocytochemistry. Four week old SPF SPAFAS chickens were infected with IBDV particles (strain CVL 52/70) by eyedrops and they were sacrified between 2 and 7 week postinfection. By two week postinfection the number of follicles is low and their size is small. Some of them seems to be detached from the surface epithelium and embedded in the connective tissue of the bursal fold. In the connective tissue remarkable number of plasma cells accumulated which produced neither IgM nor IgG immunoglobulins. The highest number of plasma cells appeared around 3 weeks postinfection and afterwards their number was reduced. By two weeks postinfection IgG negative or weakly positive BSDC reappeared in several follicles. These follicles contained significant number of B cells.The epithelial arcades of these follicles were loaded with "blast-like cells" while follicles with absence of these arcade and blast-like cells did not show any sign of follicular regeneration. It can be concluded that the corticomedullary arcades have significant role in the follicular regeneration.

Session IX: Breeding and genetics of fish

CONSERVATION PROGRAMME FOR FISH GENE RESOURCES IN THE CZECH REPUBLIC

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"The National Programme for Conservation and Utilization of Gene Resources of Commercial and Utility Animals" comprises above all *in situ* conservation by keeping live fish gene banks of original breeds of the following species: common carp (*Cyprinus carpio*), tench (*Tinca tinca*), brown trout (*Salmo trutta* m. *fario*), rainbow trout (*Oncorhynchus mykiss*), wels (*Silurus glanis*) and of pure species of European whitefish (*Coregonus lavaretus maraena*), sterlet (*Acipenser ruthenus*) and beluga (*Huso huso*). The programme includes fish tagging (P.I.T. tags), broodstock data recording, mass reproduction by means of artificial propagation with an effective population size (N_e) maintained at 120 in each broodstock, and periodic genetic characterization of both the broodstock and its progeny in order to prevent loss of genetic variability. The latter is performed by means of biochemical genetic analyses of polymorphic protein systems in low-risk tissues (common carp: 6 systems, 12 loci; tench: 9 systems, 15 loci; brown trout: 16 systems, 38 loci; rainbow trout: 9 systems, 22 loci; wels: 17 systems, 31 loci; European whitefish: 14 systems, 19 loci), while mitochondrial DNA and microsatellite nuclear DNA studies are made on wels and they will be applied also on common carp and tench, especially in cases of low differentiation ability of polymorphic protein electrophoresis. Both acipenserid species are next objects of study.

ARTIFICIAL SELECTION FOR BODY LENGTH AND GROWTH RATE IN GUPPY FISH (*POECILIA RETICULATA*)

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There was a two-way selection for body length at 70 days performed on laboratory populations of guppy fish (*Poecilia reticulata*). A significant divergence between the "up" and "down" selected lines was observed and regression between the divergence and the number of generation from 1 to 6 was 0.426 ± 0.045 for the first replicate and 0.525 ± 0.141 for the second replicate. A positive correlating response to selection was detectable on the growth rate up to the age at which the selection was performed so that the "up" and "down" selected lines showed different growth curves. The mean age of the initiation of maturation the male progeny was about 60 days for both selected lines but the percentage of males beginning the process of maturation up to this age was greater in the "up" line than in the "down" line. The "up" and "down" selected lines showed a different reaction norm detectable on the first period of the growth process when the fish were fed with two different diets. In particular, the greater growth rate up to 40 days observed in the "down" selected line fed with live diet also produced an increase of a percentage of male fish beginning the maturation process at an early age.

PRELIMINARY OBSERVATIONS ABOUT ARTIFICIAL ANDROGENESIS OF BREAM (*ABRAMIS BRAMA* L.)

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Androgenetic offspring of bream (*Abramis brama* L.) were produced using oocytes which had been genetically inactivated by ultraviolet light, to which a high temperature (38.5 °C lasted 2 minutes) and pressure shocks (600–900 ATM lasted for 1 to 3 minutes) were applied. The first step to produce androgenetic fish was test of some artificial ovarian fluids for keeping oocytes during genetic inactivation. Than conditions of semi-lethal shocks and genetic inactivation of oocytes were optimalized. Bream spawners used in these experiments were individually marked and fin epithelium was taken to biochemical recognize. Genetically inactivated oocytes were fertilized and shocked between 30 and 60 minutes after fertilization. Larvae were reared viable and without any development abnormalities. After few weeks of rearing a small part from tail fin epithelium of each young bream was cut. The results of androgenesis procedure was tested by electrophoretic method (GPI-1). In the end the results of efficiency of both kinds of shock procedure were compiled and discussed.

RAINBOW TROUT SELECTIVE BREEDING IN DEPARTMENT OF SALMONID RESEARCH RUTKI

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As basis for rainbow trout selective breeding an incomplete diallel cross of 5 lines (4 maternal and 5 paternal) was done in April 1988. 15 groups of fish were tagged with Carlin tags. As very low heterosis was observed all fish were treated thereafter as one outbred stock and family selection was chosen as the propriety method of stock amelioration. In 1991, 87 families of the generation called hereafter F1 were produced – each consisting of full sibs within paternal half sibs (2 females mated with one male treated as one mixed unit). The families were reared separately until the first Autumn and then the fish were measured, weighted and tagged with PIT tags (individually) and with Carlin tags according to family numbers. Next measurements were done during the following Spring and Autumn in two different sites. Analysis of F1 did not show any regression of parental body weight on the progeny growth. After evaluation the 10 best families were selected and from each of them 10 biggest females and 5 medium males were chosen (within family selection) to start next (F2) generation consisting of 100 full sibs families. These families were evaluated on four traits basis (survival in two embryos stages, market body size and percentage of PM males). The 10 top families were chosen to start in 1993 the F3 generation. As each generation was reproduced and reared differently the different ANOVA models were used to evaluate the genetical parameters. Heritability value for market body weight amounted to 0.1–0.22 depending on model used in F1 and to 0.05 or 0.21 depending on model and component in F2, showing somehow diminishing tendency. The correlation coefficients between sizes (weight and length) in different age amounted to 0.2 when evaluated on half sibs sire component.

TENCH (*TINCA TINCA* L.) BREEDING PROGRAM IN THE CZECH REPUBLIC

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Breeding work in tench culture has been developing since 1979. The Research Institute of Fish Culture and Hydrobiology at Vodňany has collected tench populations from several localities of Czech Republic, Hungary, Romania and France and established initial lines for the breeding programme using a method of group artificial spawning within populations. Method of brother-sister mating and meiotic gynogenesis are utilized to reach higher homozygosity of basic lines. At present time, there are 9 Czech strains and 3 foreign strains in the gene bank. The bank was enlarged by increasing the number of different line hybrids for human consumption and of different color lines. Experimental work has been carried out, including value of performance tests of their progenies, a systematic crossing programme by diallele crossing and the performance of their F1 progeny was evaluated. The best results for commercial stocking are reached by line hybrids with the Mariánské Lázně strain (either in maternal or paternal position). For practical use is it advisable to use all-female triploid population (mean weight differences of triploids 11.7–45.7% to diploids) or just all-female population after gynogenesis and sex reversal.

PREVIOUS IMMUNOGENETIC STUDY IN COMMON CARP (*CYPRINUS CARPIO* L.)

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Unless one is dealing with inbred animals, host populations will show a various response to the infection with a pathogen, owing to the genetic heterogeneity. The response will reflect in variability within parameters for the natural resistance. In our study, three lines of Zator origin, two lines from Hungary and Yugoslavia, one line of Japanese origin (orange) and their hybrids were used. We analysed the relationship among the effect of the production and the survival in first and second year, nonspecific defence mechanisms and the protection against diseases in natural environment of ponds. Blood from 30 fish of all lines and hybrids were separated to study immunological parameters and polymorphism. We analysed the lysozyme and ceruloplasmin activities, total protein and immunoglobulin (Ig) levels in serum. The specific cellular and humoral immune response of O-antigen *A. salmonicida* was tested. The challenge test 14 days after application of the antigen was used in order to study the resistance against furunculosis in carp. The results suggested the relationship between effects of production and nonspecific humoral defence mechanisms and disease resistance. The highest relation in the Ig levels was observed in the first and second year of the culture. The best immunological parameters were observed in triplicate hybrids with orange Japanese carp and a positive influence of heterosis probably determined our preliminary immunogenetic results.

BREEDING PROGRAMME OF COMMON CARP IN THE CZECH REPUBLIC

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The breeding work is focused on gene resources conservation, testing programme, selective breeding programme and genome manipulations. Gene resources conservation is performed on autochthonous Czech breeds/strains both *in situ*, i.e. in live gene banks and *ex situ*, i.e. in a bank of cryopreserved sperm. Genetic characterization of 40 breeds/lines was performed by polymorphic protein markers and morphometric traits, in total of 900 individually tagged brood carps with breed/strain – specific software-recording. Breeds/strains with the highest genetic distance (up to 0.19 according to Roger's test) with anticipated heterosis effect of crossbreds are included in a testing programme by means of topcrossing: during the first year, tests are performed in triplicate, during the second and third year, tests are performed with nine replicates. The selective breeding programme is carried out on two established synthetic lines with the level of genetic similarity at 0.97–0.96 and 0.91–0.88, and with selection pressure 99.9% (0.999). The genome manipulation programme is focused to production of all-female line of common carp by means of meiotic gynogenesis and sex reversal. Masculinized gynogenotes will be used for production of all-female lines with anticipated 5–10% higher growth rate against normal lines.

PERFORMANCE TEST OF COMMON CARP UNDER FISH FARM CONDITIONS

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The breeding goal of the Breeding Station of RIFCH USB Vodňany, along with the testing stations (Rybářství Tábor, a. s., Rybníkářství Hluboká, a. s., and České rybářství Mariánské Lázně, s. r. o.) was to test weight gain and survival in low, medium and high altitudes. The breeding programme is focused to search for heterosis effect of hybrids by means of topcrossing. A newly established Hungarian synthetic mirror carp line (HSM), composed of M2, HVM, 215, M2M-I and M x A lines, was chosen for testing as a maternal line. The HSM, as well as wild Amur carp (AC), Ropsha carp (ROP) and Tata carp (TAT) were used as paternal lines. The genetic distance between the maternal line and the paternal ones according to the Roger's test is 0.19 for AC, 0.15 for ROP and 0.12 for TAT. The first season of the topcrossing test was performed by means of separate rearing of each group of fry with controls, both the second and third seasons are performed by means of communal rearing with controls. The best survival was gained by HSM x ROP crossbred. The highest production was gained by HSM x AC crossbred in one case, reaching 1857 kg/ha. The mean values of production for all testing stations are 781 kg/ha for HSM x TAT, 934 kg/ha for HSM x ROP and 885 kg/ha for both HSM x AC and HSM.

CONTRIBUTION TO THE CHARACTERISTICS OF CARP LINES OF THE ŽĎÁR REGION

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To precise the condition and exterior parameters, 226 individuals of carp lines Žď-Š (scale carp) and Žď-L (mirror carp) and the hybrid between Žď-Š and Ropsha carp were analysed and processed statistically To determine the variability level of 12 protein loci, blood samples were taken and analysed in 11 hybrids and 219 individuals of both pure lines. Following results were achieved:

- both pure lines belong to the forms with high body depth as regards the external parameters
- the index of body depth in the line Žď-Š ranged between 2.49 and 2.61; and the index of body width was 22.10–24.73
- the external parameters in Žď-L and the hybrid Žď-Š x Rop were more variable
- the hybrid showed better body yield traits
- the genetic variability was proved in six loci; the basic genetic parameters of Žď-L and Žď-Š lines were: percentage of polymorphic loci was 33.3 and 41.7, resp.; mean number of alleles per locus was 1.8 in both lines; and mean heterozygosity was 0.136 and 0.099, resp. (the line Žď-Š showed the moderate deficiency of heterozygotes)
- in the hybrid Žď-Š x Rop we could not find any alleles characteristic for the Ropsha carp (probably due to a low number of individuals analysed).

IMPROVED METHOD OF CRYOPRESERVATION OF NORTHERN PIKE SEMEN

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The aim of this study was to develop an efficient technique for cryopreservation of sperm of northern pike. A special attention was given to thawing process. Milt was pooled from 5 males, diluted 1 : 3 with extender and cryopreserved in pellets on dry ice within 1 min. Pellets were stored in liquid nitrogen. The extender contained 0.6 M sucrose + 15% DMSO (found as the most effective in our previous studies), supplemented (or not) with egg yolk or LDL fractions. Fertilization with cryopreserved samples was carried out in two independent trials. The beneficial effect of sperm motility activating factors (caffeine or theophylline), and several fertilization diluents for insemination with cryopreserved sperm was tested. The most effective was an extender without the addition of egg yolk or LDL, and the use of Billard's fertilization diluent for thawing (78.8% of eyed eggs vs 72.4% in control fertilization). Also, fertilization success of cryopreserved sperm in comparison to control inseminated with intact milt was ensured with use of an extender containing egg yolk or LDL, and with the use of Billard's fertilization diluent for thawing of pellets. Developed procedure is a complete technique for efficient cryopreservation of northern pike semen.

THE USE OF PROGRAMMABLE FREEZER FOR CRYOPRESERVATION OF RAINBOW TROUT SEMEN FOR GENE BANKING

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Cryopreservation of rainbow trout sperm was attempted to develop a repeatable procedure for gene banking purposes. Milt was pooled from 5 males and kept in a refrigerator at 1 °C for 2 days until treatment. For cryopreservation, samples of milt were diluted 1 : 3 with extenders, and frozen in 0.5 ml straws using computer programmable ultrafreezer. Three extenders and freezing rates were tested. Frozen straws were stored in liquid nitrogen for 4 month until insemination. Fertilization success was evaluated at the eyed-egg stage of embryos. There were found very significant first-order interactions between freezing rate and the type of extender; these effects were also very significant when considered separately. The highest fertilization success was obtained with the use of sperm cryopreserved in 0.3 M glucose + 10% DMA with freezing rate –45 °C/min and –35 °C/min (74.8% and 72.2% of eyed eggs, respectively). All tested factors gave high fertilization success; 7 of 8 experimental variants did not differ significantly, resulting in a range of 62.3–74.8% of eyed eggs. The use of programmable freezer ensures repetition of the method in each laboratory, and it is necessary for gene banking purposes. This procedure is successful even for samples obtained and stored in field conditions for 2 days.

CRYOPRESERVATION OF COMMON CARP (*CYPRINUS CARPIO*) SPERMATOZOA FOR GENE RESOURCES

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Two cryopreservation methods were elaborated for gene resources of Bohemian common carp strains sperm. A first is a stepwise cryopreservation method where sperm is equilibrated for 1 h by dilution in 200 mM KCl, then adding 10% glycerol followed by transfer into 0.5 ml straws. Then after cooling for 10 min in liquid N_2 vapors at –85 °C, straws were transferred into liquid N_2. The second method was the progressive cryopreservation of sperm diluted as described in the first one. Ten percent of DMSO was added in 2 ml cryotubes and cooled from +4 °C to –7 °C at a rate of 4 °C/min, then from –7 °C to –80 °C at a rate of 11 °C/min and finally transferred into liquid N_2. The spermatozoa were thawed in a water bath (35 or 40 °C for 5–10 s) and checked for sperm motility rate at 10 s after activation of spermatozoa (% age and velocity) or for fertilization rate. In the first method, a 275 mM NaCl, 30 mM Tris HCl pH 7, solution for incubation of thawed spermatozoa was found best, leading to sperm motility of 80% and velocity of 96 μm/s with $P < 0.05$ when comparing to undiluted thawed sperm (28% and 58 μm/s , respectively). Native sperm showed 100% motility and 188 μm/s velocity. Using the second method, we observed 80% motility, and 112 μm/s velocity.

COMPLETE DIALLELE CROSS BETWEEN FIVE STRAINS OF COMMON CARP

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A complete diallel cross among five strains of common carp (Polish 3, 6, Hungarian W, 8 and French F) was used to estimate general and specific combining abilities in respect of weight gain and the following traits of body shape: the condition factor and the dorsal index. The average hatching rate of the all mating groups was 28.2%, the hatching rate of the crossbreds was 1.5% higher. Each group was reared in separate small ponds, 670 m^2 each, under the same environmental conditions. The carp were caught, weighed and measured after 3 months. The average survival rate of purebreds was 25.6% and crossbreds was 28.3%. Significant differences ($P < 0.001$) in general combining ability between strains were found for all studied traits. Strains F and W showed the highest positive GCA effect for weight gain. Negative GCA value was found for strain 6. Differences in the specific combining ability for all the traits were also significant ($P < 0.001$). The highest positive SCA effect for body weight was found in 8 x F crossbred. The proportion of the non-additive variance in the total genetic variance of weight gain was 53.3%. This result suggests a great role of SCA in the improvement of weight gain of hybrid carp.

DIFFERENCES BETWEEN THE PROPAGATION EFFECTS IN POLISH AND HUNGARIAN CARP FEMALES TREATED WITH KOBARELIN

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The aim of the study was to evidence the effects of Kobarelin compared with these of pituitary gland in carp females of Polish (Family 2) and Hungarian (Family W) provenance. For estimating the effects of the substance stimulating ovulation and of the provenance, analysis of variance was carried out using the least squares method. It was found that the stimulating substance, provenance, and interaction of these factors did not significantly effect the weight of obtained eggs. On the other hand, the stimulating substance, provenance, and interaction had a highly significant effect on the percentages of fertilization and live embryos. Females of Hungarian provenance treated with Kobarelin yielded eggs of a much better quality but of smaller weight than after the pituitary treatment. In the case of carp females of Polish provenance the yield of eggs of smaller weight and very poor quality was noted as compared with weight and quality of eggs obtained after hypophysation.

ALLOZYME VARIATION IN ZATOR CULTURED COMMON CARP (*CIPRINUS CARPIO* L.)

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Experimental Fish Culture in Zator has been occupied in selection breeding in common carp (*Cyprinus carpio* L.) and the aim of these works is breeding of homozygous lines of a common carp. Progeny of these lines were put into interline crossing which gave us a heterosis effect. Study of enzymatic protein polymorphism was done with a method of electrophoretic distribution and specific histochemical stains. Investigations were carried out for 13 enzyme products of 35 genetic loci. White muscle, liver and eye tissue were used to prepare tissue extracts. Four homozygous lines of common carp cultured in Experimental Fish Cultures in Zator were: (1) Starzawski carp, (2) Hungarian carp, (3) Israelite carp Dor-70 and (4) Japanese orange subspecies of carp. Among 35 genetic loci there were 24 identically monomorphic. Japanese carp had the following polymorphic loci: GPI-2*, GPI-4*, sIDHP-3*, sIDHP-4*, LDH-4*, PGM-1*, mMEP-2, mMEP-1*, for Israelite carp Dor-70 it was GPI-2*, LDH-4*, sMDH-A2*, PGM-1* and for Hungarian carp it was CK-1*, sIDHP-3*, sIDHP-4*, LDH-4*. Starzawski carp had only one polymorphic loci sAAT-3*. In general, from two to three variant alleles were present at each of the polymorphic loci. Mean heterozygosity values varied from 0.0286 (1), 0.052 (2), 0.095 (3) to 0.144 (4). The values of mean number of alleles per locus showed a range among 1.08 (1), 1.20 (2), 1.25 (3) to 1.37 (4). The percentage of polymorphic loci varied from 3% (1), 11.5% (2), 14% (3) to 27% (4). Japanese orange subspecies of carp showed a much higher proportion of polymorphic loci, heterozygosity mean value and mean numbers of alleles per locus in comparison with the other cultured lines, indicating the more genetic variation in an ornamental carp. Japanese orange subspecies of carp was recognized as line required exact selection for attaining higher homozygosity. Lines as Starzawski carp, Israelite carp Dor-70 and Hungarian carp were estimated as lines which have high degree of homozygosity.

GENETIC CHARACTERIZATION AND PERFORMANCE TESTING OF TENCH (*TINCA TINCA*) STRAINS: PRELIMINARY RESULTS

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Four tench populations (two cultured strains from Czech Republic, one cultured and one wild strain from Germany) were genetically characterized by their polymorphisms in 11 enzymatic systems representing 23 loci. The mean number of alleles per locus (1.3) was equal for all populations. Both German strains showed a higher percentage of polymorphic loci (30.4% each) than the Czech strains (26.1% each). Observed heterozygosities were highest in the Czech populations (0.092 each) followed by the German wild (0.081) and cultured (0.071) strains. The unbiased genetic distance (Nei, 1978) was very small between the two German strains (0.007) but remarkably higher between the German and Czech (0.017 to 0.035) as well as between the two Czech strains (0.023). The four populations clustered into two groups according to the country of origin. All three cultured strains were used to carry out a first performance test under warm water conditions in a closed recirculating system. Starting from fry the tench reached mean body weights of 48.07 g (Vodňany pure strain), 41.32 g (Vodňany hybrid strain), and 21.00 g (German pure strain) after 446 days. These differences were statistically significant to each other. An identical ranking of populations was observed for food conversion efficiency (2.41, 2.62, and 3.56 kg feed/kg weight gain) and mortality rates (19.0, 22.6, and 35.6%), too. Our preliminary results indicate a great potential of tench for genetic improvement by classical breeding methods (intra- and interpopulational selection, intraspecific hybridization).

COMPARISON OF THE BREEDING INDEXES OF SIBERIAN STURGEON (*A. BAERI* BR.) AND ITS HYBRID WITH GREEN STURGEON (*A. MEDIROSTRIS* AYRES)

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An experiment was conducted aimed at fattening heavy fry aged 2+ of Siberian sturgeon and its hybrid with green sturgeon in tanks included in a recirculation system, with fresh and saline (7–8‰ salinity) water, for the period of 50 days. The fish were fed trout grower feeds (Aller-Safir) in both variants, and there were used the same feeding curves (Kolman, 1997). Water temperature in the recirculation system was maintained at a similar level (22–23 °C). Average individual weight of Siberian sturgeon cultured in fresh water increased by 63% i.e. from 705 to 1153 g, and of the hybrid – by 66%, from 807 to 1341 g. Rate of growth was higher in saline water, in which body weights increased by 84% (from 504 to 932 g) and 67% (from 688 to 1159 g), respectively. The differences in the growth between fresh and salt water were even more noticeable in the case of standard growth rate (SGR); their average values were 1.06 (fresh water) and 1.50 (salt water) for Siberian sturgeon, and 1.02 (fresh water) and 1.42 (salt water) for the hybrid. Water salinity also affected the condition coefficients, which increased in salt water from 0.58 to 0.68 for Siberian sturgeon, and from 0.51 to 0.58 for the hybrid, while their values in fresh water increased respectively from 0.58 to 0.61 and from 0.51 to 0.54.
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A METHOD OF PLOIDY LEVEL DETERMINATION IN GENETICALLY MANIPULATED BREAM (*ABRAMIS BRAMA*) AND PIKE (*ESOX LUCIUS*)

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Silver-staining of cell preparations followed by counting the mean number of active nucleoli per cell enabled determination of the ploidy level in genetically manipulated bream (*Abramis brama* L.) and northern pike (*Esox lucius* L.). Haploid bream and pike resulted from activation of eggs with UV-irradiated sperm, and triploid specimens were obtained by applying cold- and high-temperature shock, respectively. Cells of haploid individuals from both species had one (almost 100% of cells examined) or sporadically, two nucleoli (depending on the specimen, mean number of nucleoli per nucleus ranged from 1.0 to 1.06). In diploid fish the mean number of active nucleoli per cell ranged from 1.58 to 1.81. In triploids the mean number ranged from 2.08 to 2.46. Positive identification of ploidy level in bream and northern pike required examination of up to 40 cells per individual, as determined by the regression analysis. The method required a very small amount of any kind of tissue (i.e. fin epithelium), enabling determination of ploidy level in juvenile fish without sacrificing them.

THE INFLUENCE OF EGG SOURCE ON THE EFFICIENCY OF HEAT SHOCK INDUCING GYNOGENESIS AND TRIPLOIDIZATION IN BREAM

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Our preliminary observations about gynogenesis and triploidization in bream showed very different results in egg survival and heat shock efficiency. For this reason we individually tested egg obtained from several times during three spawning seasons. Although all parameters were the same: the method of obtaining gametes, the dose of ultraviolet light applied to genetic inactivation of spermatozoa, incubation temperature was 20 °C, temperature of heat shock was 38.5 °C, shock duration 2 minutes and shock was applied at 4, 6 and 8 minutes after fertilization, high variable in results were observed in all seasons. In conclusion, the improvement of efficiency of heat shock applied to induction gynogenesis and triploidization in bream might be resulted by using eggs from several females.

TRIPLOIDIZATION OF EUROPEAN CATFISH (*SILURUS GLANIS* L.) WITH HEAT-, COLD- AND HYDROSTATIC PRESSURE SHOCKS

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Firstly, heat shock of 41 °C lasting for 30, 45 and/or 60 seconds, starting 5, 7 and/or 9 minutes after gamete activation and cold shock of 6 °C, lasting for 10, 15 and/or 20 minutes, starting 5,7, and/or 9 minutes was used. Later on, cold shocks of 0.3, 3.2 and 6.2 °C, starting 7, 8, 10 and/or 12 minutes were investigated. Hydrostatic pressure shocks of 600 bar with a duration of 4 minutes starting 3, 4.5, 6, 7.5 and/or 9 minutes and later ones starting 3, 4, 5 and/or 6 minutes after gamete activation were investigated also. A cold shock of 6 °C lasting for 20 minutes and starting 9 minutes after gamete activation gave the best result with 100% of triploids yielding in 33.37 ± 3.77% triploid yield. Ploidy level was investigated by karyotyping, quantification of Ag-stained nucleoli per cell, flow cytometry and erythrocyte nuclear sizing. Induction of triploidy under mass conditions in experiments 1, 2 and 3 the triploid yield gained 11.47%, 7.42% and 8.12%, respectively, directly after hatching. Five months later the percentage of triploids significantly decreased to 12.4%, 8.15% and 21.4% in experiment 1, 2 and 3, respectively. ANOVA showed influence of ploidy ($P < 0.0001$) on growth rate and multiple range analysis (LSD) assessed difference between total diploids (12.55 g) and total triploids (9.47 g) on $P < 0.01$ level.

THE INFLUENCE OF EGG SOURCE ON THE INDUCTION OF GYNOGENESIS AND TRIPLOIDY IN NORTHERN PIKE (*ESOX LUCIUS*) WITH A HEAT SHOCK

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Activation of northern pike eggs with intact or UV irradiated sperm and subjecting those eggs shortly after activation to heat shock enables obtaining relatively high percentage of triploid or gynogenetic larvae, respectively. The survival in experimental groups and percentage of triploid or gynogenetic larvae in different experiments significantly depended on the source (maternal effect) and quality of eggs. High variability of survival and heat shock efficiency was observed, although all parameters were the same, including the method of collecting and storing gametes, UV irradiation of spermatozoa, spermatozoa:egg ratio, temperature of incubation between gametes activation and application of heat shock, parameters of the heat shock (temperature, time of application, duration). Thus, there is need of further increase of the efficiency of these manipulations, especially in relation to mass production of triploid and gynogenetic offspring of northern pike.

INDUCED GYNOGENESIS OF SHOVELNOSE STURGEON (*SCAPHINRYNCHUS PLATORYNCHUS*) AND PADDLEFISH (*POLYODON SPATHULA*)

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Gynogenesis was induced in paddlefish (*Polyodon spathula*) and shovelnose sturgeon (*Scaphirhynchus platorynchus*) with heat shock after activation with UV-treated shovelnose sturgeon and paddlefish spermatozoa, respectively. Without irradiation treatment, shovelnose sturgeon spermatozoa used for paddlefish eggs and paddlefish spermatozoa used for shovelnose eggs appeared to activate the eggs (up to gastrulation), but no viable hybrids were produced. For sturgeon gynogenesis, activated eggs of shovelnose sturgeon were incubated at 18 °C until shocking at 35 °C for a 2-min duration. Shock was applied at 0.05 τ_0 intervals (duration of one mitotic cycle of synchronous cell division related to water temperature) from 0.15 to 0.40 τ_0 (8.25 to 22 min post fertilization; τ_0 at 18 °C 55 min). The highest calculated percentage (11%) of shovelnose sturgeon gynogenotes was obtained from eggs shocked at 30 τ_0 (i.e. at 18.15 min post activation). For paddlefish gynogenesis, the best yields (12–19%) of gynogenotes were obtained when eggs incubated at 18 °C were heat-shocked (35 °C at 2 min duration) at 16.5, 18.5, 20.5 min after activation. When these times were expressed in terms of o units, the optimal activations for paddlefish gynogenotes were 0.26, 0.29 and 0.32 τ_0 (τ_0 at 18 °C 63.5 min).

IMMUNOLOGICAL RESPONSE OF DIFFERENT CARP LINES TO STANDARD ANTIGENS

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Observed differences in the survival of carp stocks of diverse genotypes may results from the genetically conditioned different efficiency of resistance mechanisms. In order to confirm the above thesis the immunological response of carp of four breeding lines and of one interlinear crossbreed to intramuscular immunization with cellular (SRBC) and soluble (O-antigen *Yersinia ruckeri*) antigens was investigated in different conditions. Using the PFC test, the number of lymphocytes of the head kidney producing specific antibodies and specific antibody titres was determined. A fairly great individual variability of the carp was observed in the investigated resistance reactions. Interlinear differences were evidenced in the immunological response expressed by the number of lymphocytes producing specific antibodies. The titres of antibodies were similar in the carp population compared. Differences in the number of lymphocytes were more distinct after the repeated contact with the antigen. The results suggest the occurrence of differences in the rate of formation of the immunological response between genetically differentiated carp lines. Changes, observed in peled and whitefish hybrids gonads during the annual cycle point to certain regularity, reflected in the succession of stages of germ cells development. Both the course of gonads development and values of previtellogenetic oocytes were similar in both lakes. Previtellogenetic oocytes were observed throughout years, but they were most numerous (83% Leginskie Lake, 84% Mutek Lake) in the post-spawning period. Increase in number of oocytes was caused by supplementation of germ cells reserve. The lowest values of resting oocytes (about 60–66%) were recorded in July (Leginskie Lake) and in August (Mutek Lake).

GENETIC STRUCTURE OF CZECH TENCH (*TINCA TINCA*) POPULATIONS AS REVEALED BY PROTEIN VARIABILITY STUDIES

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More than 900 individuals (mostly brood fishes) pertaining mostly to 16 defined breeding strains/lines were analysed to determine the genetic structure of individual lines. Method of starch gel electrophoresis of proteins was utilised for this purpose. As the fishes were stated for future breeding, the analysis was restricted to the "low-risk" tissues (blood in this case). Hence, analysis of products of 20 structural loci out of 29 possible was carried out. From this, variability was found in 10 loci with two or three alleles in each. Basic genetic parameters varied in individual lines – mean percentage of polymorphic loci is 25 to 45%; mean number of alleles per locus is 1.3 to 1.5; and mean observed heterozygosity is 0,133 to 0,279. Considering the first results of the analysis of protein variability we can establish that the tench strains/lines reared in the region are genetically very similar. For the deeper description the more sophisticated methods as a DNA analysis should be used.

PRELIMINARY RESULTS OF THE GENETIC STRUCTURE STUDIES IN SELECTED POPULATIONS OF BROWN TROUT (*SALMO TRUTTA*) IN BOHEMIA

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In the years 1993–1997, brown trout from the selected populations were sampled for the genetic analysis in total amount of 680 individuals. Moreover, 103 individuals from Italy, Poland, Slovakia and Moravia were sampled and analysed as the comparative material. This group also comprised also the artificially reared strains originated form the eggs imported from Italy. The starch gel electrophoretic separation of products of 38 protein/enzyme loci representing 16 systems was the method of choice. The genetic variability was found in 25 loci that possessed two to four alleles. The found genetic variability was rather high in all samples studied. The basic genetic population parameters were stated as follows: mean percentage of polymorphic loci = 16.7 to 30.6%; mean number of alleles per locus = 1.2 to 1.5; and mean observed heterozygosity = 0.052 to 0.137. Nevertheless, the inter-population genetic differences were found rather small which could be caused by the extensive exchanges of the eggs, fry and adult fishes among different localities and regions in the past. Fishes from the comparative sample sets (constituted mainly from the "Italian" trout strains) differed markedly and constituted the discrete cluster in the phenetic tree. As concerns the Bohemian trout populations, the application of methods able of more detailed genetic description of this organism is needed as is the DNA analysis.

BREEDING OF WILD EUROPEAN PIKEPERCH (*STIZOSTEDION LUCIOPERCA* L.) IN CONTROLLED CONDITIONS

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The pikeperch (*Stizostedion lucioperca* L.) is one of the most important commercial fish species in Poland. For commercial pikeperch aquaculture to develop, methods are needed for maturing and spawning pikeperch in controlled conditions. We used fyke-nets to catch the spawners just before or during the spawning season (April–May). The fish were transported in plastic bags (one fish per bag) within 60 min to the Dgal Experimental Hatchery near Gizycko (Northern Poland), and held in fibreglass tanks – water temperature 12.0–15.5 °C. Broodfish were sorted by sex and ripeness. Stages of final oocyte maturation were determined using a four-division scale. Eight females were randomly assigned to each of the following treatment group: (1) saline-injected control, (2) hCG injected (700 IU/kg), (3) carp pituitary injected (0.8 mg/kg), and (4) carp pituitary injected (2.4 mg/kg) – two injections at 24-hour interval. Males were not injected. Spawning success was highest in fish treated with hCG (2). Over 70% of females treated with hCG spawned 44–52 h after injection. The control group (1) had the lowest percentage (30) of the ovulating females, indicating that the hCG and carp pituitary definitely increased spawning capability. There were no apparent differences in egg quality between groups (75.2 to 82.3% survival to eyed-stage embryos).

SEX DIFFERENTIATION OF ASP (*ASPIUS ASPIUS* L.)

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Sex differentiation appear in fishes at different stages of the ontogenesis. The process of gonadal development depending on the fish species and on several environmental factors. The objective of this study was to follow up gonad differentiation in the asp (*Aspius aspius*) reared under intensive culture conditions (water temperature 17–20 °C). Histological observations of asp gonads were carried out since 12 June 1995 till 13 February 1996. Every 7 days of the course of the experiment 10 fish were individually measured, weighed, preserved in Bouin's solution and immersed in parrafin. Serial cross-sections (4–6 μm) were cleared, stained with Mayer's haematoxylin and eosin, and examined by light microscopy. Our studies suggest that the sexualization period of asp depends on fish age. Appearance of primordial germ cells and their migration to the forming gonads is observed until the 80th day after hatching. Anatomical differentiation proceeded a cytological one – presumptive ovaries were spindle like, whereas the males were of circular shape. Oogonia appear about 170 days after hatching, when the spermatogonia were observed since the 265th day after hatching.

THE RESERVE OF OOCYTES OF PELED (*C. PELED*) AND WHITEFISH (*C. LAVARETUS*) HYBRIDS FROM TWO MASURIAN LAKES

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Oocytes of polycyclic fish species developed periodically. Previtellogenetic oocytes in the ovaries of mature fish females represent a group of reproductive cells which give raise to eggs that are to be spawned in the next years. In this study we examined annual cycles and reserve of oocytes of peled and whitefish hybrids from two Masurian lakes: Leginskie and Mutek; they were differed in morphological and trophical conditions. For histological study fish were measured, gonads were dissected and fixed. Sections were examined by light microscopy, developmental stages of the ovaries were defined and reserves of oocytes were calculated.

SEX CONTROL IN NORTHERN PIKE (*ESOX LUCIUS*) USING GYNOGENESIS AND HORMONES

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Gynogenetic, all-female northern pike were produced using UV irradiation of sperm and heat shock applied to inseminated eggs shortly after gametes activation. Milt was diluted in immobilizing solution (1 : 9) and UV irradiated (6.4 W/m^2) for 2–20 min, with dosage in the range 768–7680 J/m^2. Genetic inactivation of spermatozoa was most efficient when milt was irradiated for 8 min (3072 J/m^2). After insemination with irradiated sperm eggs were exposed to a thermal shock of 34 °C or 34.5 °C, lasting 3 or 5 min, applied 11–16 min after gametes activation. Gynogenetic larvae were obtained in all experimental groups, with hatching rate up to 24%. Gynogenetic juveniles were fed with dry diet supplemented with 17-methyltestosterone (MT) in order to reverse their phenotypic sex (masculinization). Successful hormonal sex reversal, up to 87% of gynogenetic fingerlings, required that the fish of the total length 26.0–30.0 mm were reared for two weeks at 22.0 °C temperature and fed with the diet supplemented with 20 or 30 ppm MT. Oral administration, lasting for two weeks, of diet supplemented with 11-hydroxyandrostenedione (OHA) (30 ppm) to fish (28.0–32.0 mm t.l.) obtained from natural spawning resulted in obtaining the stock comprised of 83% of males and 17% of bisexual animals.

Session X: Breeding and genetics of other species

HYBRIDIZATION AND CROSSBREEDING OF MEAT BREED AND RABBIT BROILERS

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Since 1991 the production of rabbit broilers in the Czech Republic is rapidly growing up. Great part of this production is exported to EU market, 10% of the whole production is sold on the domestic market. The role of large scale farm producers is more substantial from year to year – in 1991 it was fattened on large scale farms approx. 7.7% of all rabbits killed on abbatoirs, for 1998 according to the prediction it could be roughly 65–70% – in 1991 there was killed 1,950,000 rabbits on abbatoirs, in 1997 it was 2,150,000 animals. Large scale farmers are fattening so called "rabbit broilers", which are bred using parental and grandparental lines imported from commercial producers from France, Germany, Italy. Performance tests of these hybrids were carried out during the period 1992–1997 at the Czech University of Agriculture with following results of fattening at the age of 35–82 days of life: average daily gains 32–38 g, food consumption 3.2–4 kg per 1 kg of gain, final weight 2.3–2.8 kg at the age of 82 days. The appropriate of genotypes for different fattening schemes were also studied. We have registered some defects in application of hybridization scheme – eg. exploatation of final hybrids in breeding scheme. The traditional systems of rabbit keeping, if their production have to be comparable, should breed specialized meat breeds – white breeds namely Californian and Newzealander. Nowadays, breeding to improve these breeds is partly aimed towards traits which are nonimportant for meat production.

GENETIC DETERMINATION OF MOTION ACTIVITY IN RABBITS

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In our study of motion activity in rabbits we recorded the number of crossings the line in the tested area by rabbits in "open field" during interval of 10 minutes. There were two lines of broiler rabbits (M91, P91) tested. Following the statistical evaluation of the number of crossings it is clear that the between-groups variability of genotypes and sex was very significantly influenced by the time factor and by animals. From the regression and correlation coefficients follows that the linear regressions of the crossing of squares by descendants from crossings by ancestors were not statistically significant. The non-significance of linear regression coefficients and the correlations as well show practically the independence of the descentants' behaviour from the parents' behaviour in the reaction to the test conditions in open field. This indicates that the behaviour of animals evaluated by motility is practically determined by the production environment. It is impossible to generalise that there is no heritability of the studied characteristic, however, there is the aditivity probably covered by the non-additive effects of genes in our experiment. It is influenced also by small sets. There may also exist some clusters of animals which should be evaluated separately from the viewpoint of genetic determination of the studied trait.

GROWTH, FEED CONSUMPTION AND CARCASS VALUE

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The paper presents a comparative study of growth, feed consumption and carcass quality of 9 rabbit broiler lines. The study involved 240 rabbits. The individual body weight and feed consumption was measured weekly through the fattening period. Traits analysed were: the body weight, average daily gain, daily feed consumption, feed conversion and relative growth. The carcass quality was assessed by final body weight (82–87 days of age), carcass weight and carcass yield. The analysis showed the significant differences in the parameters describing the growth performance, only carcass yield was similar for almost analysed broiler lines. The highest final weight (at 82 days of age) showed the broiler line HYLA (2808 g, average daily gain 37 g, feed efficiency 3.16). The broiler line ZIKA seems to be the least suitable for fattening (carcass weight at 82 days of age 2270 g, average daily gain 30.18 g, feed efficiency 3.61 and carcass yield 53%).

GENETIC PARAMETERS OF REPRODUCTION TRAITS IN FOX POPULATION

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There were analyzed records of 933 males and 2072 females of silver fox (*Vulpes vulpes*) used in years 1988–1994 in Śniaty farm in Poznań district. Evaluated reproduction traits were: duration of mating season and number of matings in season – in males group and number of born and weaned pups – in females group. Genetic parameters were estimated by using a model with sire and year (or year–season) effects. Heritabilities of male traits (by REML method) were 0.259 for duration of mating season and 0.755 for number of matings in season. Phenotypic correlation coefficient of these traits was $r_P = -0.299$ and genetic $r_G = -0.671$. Heritabilities of number of born and weaned pups were 0.040 and 0.167, respectively. Phenotypic correlation coefficient of these traits was $r_P = 0.416$ and genetic correlation coefficient $r_G = 0.465$. Slightly lower values of analyzed trait heritabilities were obtained using the model with year–season effect. Because of relatively small number of population standard errors of heritability were high (from 0.066 to 0.137). Therefore, an interpretation of received results should be rather careful.

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VARIATION OF THE EXTERNAL GRADING TRAITS IN CHINCHILLA

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The productive progress expressing as the increase of values of performance features in the following generations may be obtained due to improvement of environmental conditions and the breeding works. One of the important stages is estimation of the performance value. In fur animals, most of valuated traits depend on subjective feelings of each judge, and it results from his skills, biometeorological conditions, illumination and tiredness state of estimating person. Material for studies was collected during the judge exam organized by Central Station of Animal Breeding in 1997. Participants were 20 judges divided into 4 groups. Each was estimating – according to the standard of conformation estimation – 4 animals in 3 repetitions in a different sequence. The animal size, as the only measurable trait whose valuation is the most objective was accepted as the maximum one for all the animals. For the other features, there was a repeatability coefficient in three variants defined: on a ground of three judge's estimations, on a ground of three judge's and board estimations as well as on a ground of deviations between the three following judge's estimations and board's one. The best repeatability was achieved for structure and the worst – for color estimation. In some cases, judge's opinion was different to that of board's which can prove the misguided interpretation of a common standard for chinchilla valuation.

VARIABILITY OF THE REPRODUCTION TRAITS IN FOXES OF DIFFERENT COLOR TYPES

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Variability of breeding animals depends on the hereditary and environmental factors as well as the interactions between them. Animal improvement and breeding progress are possible thanks to genetical variability. The purpose of present research was to evaluate the parameters of phenotypical variability of performance traits in common foxes. Common fox herd (of silver, pastel, gold, platinum, pastel-platinum, and platinum-gold varieties) from The Fur Animals Farm Vera-Rol in Jeziory Wielkie, near Poznań, were material for studies. There have been observed 1700 females of various colored varieties performed in 1995–1997 from which 4640 progenies were obtained. On a base of breeding documentation, there were results of females reproduction and youth rearing collected. It was found that the percentage of females giving birth on the farm gradually increased in the following performance years at simultaneous increase of empty and aborting females number as well as the decrease of females number that damaged litters. The highest mean values of born youth were found in flame variety ($\bar{x} = 4.76$ at SD = 28.98) and in crayon one ($\bar{x} = 4.70$ at SD = 34.42); the lowest ones were in silver variety ($\bar{x} = 4.46$ at SD = 32.78). There were found statistically significant differences as regarding to reproduction and kids rearing at one-year and older females found (more favorable for the latter). Correlations between the kittening term and mean number of born and reared progeny appeared to be statistically insignificant and close to zero.

BLOOD SERUM PROTEIN FRACTIONS IN RACCOON DOGS

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The relative level of protein fractions in blood serum of young raccoon dog females and males during their full maturity of a hair was investigated. Animals were taken from the fur animal farm belonging to Vera-Rol in Jeziory Wielkie, near Poznan. The quantitative analysis of protein fractions separated by means of vertical electrophoresis on polyacryloamide gel was made using a computer program Image Master^{TM} 1-D by Pharmacia. Proteins of blood serum were divided into the following fractions: albumins (Alb), postalbumins (Poa1, Poa2, Poa3, Poa4), pretransferrins (Ptf1, Ptf1a, Ptf2, Ptf3, Ptf3a), transferrins (Tf1, Tf2) as well as post-transferrins (Potf1, Potf2, Potf3, Potf4, Potf4a, Potf5, Potf6). Relative mean fraction level was: albumins – 24.2%, postalbumins – 11.4%, pretransferrins – 17.7%, transferrins – 11.0% and post-transferrins – 35.3%. Percentage of protein fractions in males and females did not significantly differ. Slight differences at both sexes occurred as regarding to the percentage of albumins and post-transferrins. Observed variability of blood serum protein fractions in raccoon dogs population is probably based on genetical ground and may suggest the connections with productive features.

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VARIABILITY OF GENETIC AND PHENOTYPIC PARAMETERS IN WHITE AND SHADOW POLAR FOXES (*ALOPEX LAGOPUS* L.)

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Heritability coefficients and genetic and phenotypic correlation were estimated for body and fur quality traits in white and shadow polar foxes. The parameters were calculated for 7 studied years and separately for each particular year. Heritability coefficients varied for body size from 0.158 to 0.673, colour purity from 0.263 to 0.661, fur density from 0.040 to 0.513, hair's length 0.04 to 0.754, total number of scores 0.296 to 0.719 and fur structure from 0.136 to 0.498. Trait structure comes from summarization of scores points for hair's density and length. A big fluctuation of the correlation coefficients between the analysed traits were also found during the studied period. The correlations were from negative to positive they were as well significant or not significant statistically. On the basis of the results it can be clearly seen, that they were different in particular years. The results also indicate on dynamic changes in the population.

"SPOTTED" BLUE FOX – NEW COAT COLOUR MUTATION?

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In 1995 on the Śniaty Fox Farm in Poland the new mutant called "spotted" blue appeared. This individual was a male in the Arctic fox litter of 10 pups resulting from the parents of a different coat colour: the father was shadow and the mother was blue. Among his siblings (4 males and 5 females) there could be found 5 white and 4 blue coated individuals. The general colour of this mutant is white with a blue mask on the right side of the snout reaching and covers the right ear. Moreover, a broad blue stripe from the back to the belly can be seen. Heterochromy does not occur (both eyes are blue). In order to explain the nature of the new mutation (whether this mutation is somatic or will be inherited) and the new coat colour rules of heredity (whether this mutation is dominant or recessive, lethal in certain conditions or not and in which locus occurred) an investigation has been conducted. So far, 13 matings between the "spotted" blue male and the blue females which gave 83 pups have been analysed. Moreover, inbreeding and matings with the foxes of shadow colour type are planned. Any final conclusions cannot be drawn after first stage of the study.

GENETIC PARAMETERS OF COAT TRAITS IN FOX POPULATION

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Information about coat traits of 2554 silver foxes (*Vulpes vulpes*) kept in years 1988–1994 in Śniaty farm in Poznań district was collected. Genetic parameters were estimated using model with sire and year effects. Heritabilities ranged from 0.027 for skin length to 0.374 for total conformation score. The highest values of phenotypic correlation coefficient were obtained between total conformation score and hair length, silver quality and general appearance (0.593, 0.558 and 0.825, resp.). Hair density was highly phenotypically correlated with hair length (0.688) and also silver quality with hair density and hair length (0.672, 0.675, resp.). Genetic correlations were not always similar. The strongest genetic correlation was observed between total conformation score and general appearance (0.874) and between silver quality and hair length (0.833). Silver quality was also highly genetically correlated with hair density (0.540). Colour type and skin length reached $r_G = 0.579$. Negative genetic correlations of skin length and general appearance, and also size and colour quality ($r_G = --0.7$) were showed. It should be noted, that estimation was made for relatively small number of population. Additional difficulty of interpretation was an evaluation subjectivity of above traits (point scale).

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Session XI: Genetic diversity

INTERNATIONAL COOPERATION IN EFFORT FOR CONSERVATION OF ENDANGERED BREED OF DOMESTIC ANIMALS

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For the Czech Republic an effective international co-operation also includes a support of country people acquaintance with club activity and private initiatives of breeders of endangered breeds in neighbouring states. For example exchange of publications and personal contacts with foundation PSR (Pro Specie Rara), SAVE Organisation (Safequard for Agricultural Varieties in Europe), Austrian breeders of breeds Waldschaf and Rotvieh and with GEH (German Association for the Conservation of old and endangered Farm Animals) thrived to deliminate themes of the next co-operation for Czech breeders. The subject under discussion is a co-ordinate meeting to the topic of the condition and the next breeding of Red Cattle breeds, genetic distance, risk of inbreeding and another practical problems which follow from sheep disease "Maedi Visna". With help of PSR it was possible to extend the number of breeders of Šumava breed sheep in western Bohemia to 30 breeders. In Germany, there was formed the gene – reserve for the Valachian breed (58 rams and 88 ewes at 15 breeders). Annual FOCUS report, which is published by SAVE organisation, contributes to continual acquaintance and contacts of breeders of endangered breeds, registered in the herd books of Switzerland, Germany, Austria, Czech Republic, Slovakia, Hungary and other European countries.

THE GENETIC STRUCTURE OF SOME COMMERCIAL AND LOCAL SHEEP BREEDS

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The comparative analysis of genetic structure of a number of sheep breeds (Clun Forest, Romanov sheep, Carpathian mountain, Tsigai, Askanian sheep and some others), with the use of some polymorphous molecular-genetic markers was carried out. The breeds distinguished on the history of creation, ecologo-geographical conditions of breeding and productivity traits. Each breed had its own specific pattern of the allelic distribution in investigated marker loci. Certain associations between variability of genetic structures investigated breeds and their origins, regions of breeding and fecundity were revealed. However the significances of such associations were locus-specific and varied from breed to breed. The possibilities of allelic associations even on one locus with distinguished traits in different breeds, may be, throughout the allelic involvement in different interloci associations in genetic background of different sheep breeds were discussed.

GENETIC DIVERSITY IN A RESERVE GOOSE POPULATION

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Native and foreign geese in the total number of 13 varieties each consisting of 100 to 200 birds is a task of conservation genetic diversity. Description of the genetic structure involves the comparison of frequency of protein alleles within every variety. Protein polymorphism within and between varieties was used in studies designated to document the genetic structure of the whole population of geese designated as a reserve stock. Direct side-by-side comparisons of single locus electrophoretic protein mobility have been performed on all individuals. Totally 17 different protein were observed on gels during horizontal electrophoresis, from which 7 were proved to heritage according to Mendelian ratio. All heterozygosities (H's) were determined by direct counts of mean proportions of loci heterozygous per individual. Mean genetic distances across loci were estimated by Nei's and Rogers formulas. Nei's D values were employed to develop a phylogenetic tree by the assistance of unweighted pair group method analysis (UPGMA).

POPULATION PURITY CONTROL OF THE HONEY BEE BY MEANS OF CHARACTERS IN WINGS

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The original geografic honey bee races are jeopartized in consequence of the big move of people and hardly controllable import of bee queens of other races. Methods of gene pool conservation need clear taxonomic definition of individual populations and must be quick and cheap. Differences in wing venation of honey bees are applied for taxonomic classification for a long time. But methods used until now are slow or need expensive hardware. The authors introduced a simple digitalization method of characters on wings of the honey bee by means of scanner. They developed very rapid consumers program for resulting procession of bitmap picture. The user finds the bearings of the venation crosses with the mouse pointer and the program saves their coordinates into a file. From the coordinates program computes single characters in wings – angles, lengths of veins, indexes. Discriminant analysis with 28 characters in bee wings of pure races gave the characteristics of four most important bee races. Other work is directed to the possibility to separate the interracial hybrids from pure race individuals.

STUDY OF GENETIC DIVERSITY IN SOME PARAMETERS CHARACTERIZING DAIRY COW LACTATION

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Genetically determined component of biologic variability has been utilized for improving productive parameters in farm animals since the neolitic revolution. Intensive study of exterior and efficiency aspects is followed by actual problems associated with health condition and immunity of animals. Mentioned studies can be realized thanks to adequate physiological experience and good-quality analytical procedures. Genetic diversity of the following milk health parameters (MHP) was tested: somatic cell count (SCC); milk urea (MU), milk acetone (MAC), titric acidity (SH). Parameters were analyzed in individual milk samples for 2 years approx. Milk production (MP) was controlled simultaneously. Minimum analyzable sets of data were determined for female progenies of individual sires. The total sets of specific parameters included 3.516–19.364 data. A similar data base is not available in CR. Significant differences between the Black Pied and Red Pied population were found in: log SCC, $P < 0.001$; MU, $P < 0.001$; MAC, $P < 0.05$; log MAC, $P < 0.05$; SH, $P < 0.01$; MP, $P < 0.001$. Significant differences within a couple of combinations of individual female progeny groups were established for: SCC 52%, log SCC 68%, MU 59%, MAC 6%, log MAC 14%, SH 69%, MP 62%. Some of the mentioned parameters of genetic diversity of MHP indicate their potential utilization in breed health programs.

GENETIC DISTANCES AMONG ANALYSED CATTLE BREEDS

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Czech Red cattle belongs to the oldest original cattle breeds in Bohemia and Moravia, the requirements of quick improvement especially in the 19th century led to the crossing with imported breeds, so that it became almost extinct. At this time it belongs to the most endangered genetic resources. That is why the resuscitation program was started in 1992 at the University of South Bohemia, České Budějovice. We want to enlarge the number of animals and to introduce them to mountainous and sub-mountainous regions of Šumava. These results are the component of the project. There were studied the genetic distances among Czech Red cattle (breed 1), Czech Pied cattle (breed 2) and their crossbreds of F1 generation (breed 3). There were stated the allele frequencies in some microsatellite loci and in locus for milk κ-casein and for growth hormone. The greatest genetic distance as measured by method Manhattan matric was found between population 2 and 3 ($D_{CM\,i} = 1.750$), the middle one between population 1 and 3 ($D_{CM\,i} = 1.382$) and the lowest between population 1 and 2 ($D_{CM\,i} = 1.154$). In the following studies there will be included next breeds kept in the Czech Republic and some fylogenetic related external breeds like Polish Red cattle and other Middle-European red breeds.

MORPHOLOGICAL AND GROWTH DIVERSITY OF JAPANESE QUAIL

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Concerning morphological variability of Japanese quail, there are 27 mutations of plumage color and pattern, 6 mutations of feather growth and structure, 3 mutations of egg shell color and 4 mutations of muscles and skeleton contemporary known from the literature. Considerable variability exist also in the growth of body weight. The heavy type quails are 2 times heavier than the light egg type. Our various morphological and research varieties are important to preserve the genetic variability of Japanese quail. In our gene resource pool of Japanese quail we rear 7 different plumage color varieties and 6 different wild type plumage color lines for research and for economical purposes. Contemporary 4 of them are registered in the "World watch list for domestic animal diversity", FAO, Rome. A preserve of various mutant alleles of Japanese quail in our gene resource stocks should be also important by their utilization in transgenesis in chicken.

THE POLYMORPHISM OF SOME LOCI IN CATTLE POPULATION IN THE CZECH REPUBLIC

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There were studied allele and genotype frequencies of milk protein genes in Czech Pied cattle, Czech Red cattle, Black-and-White cattle and in crossbreds F1 generation Czech Red x Czech Pied cattle. There were genotypised κ-casein and α-lactalbumin loci using the method Polymerase Chain Reaction and Restriction Fragment Length Polymorphism (PCR/RFLP). We found significant higher frequency of allele *B* (0.414) and of genotype BB (0.171) on the κ-casein locus in the Czech Pied cattle comparing to Black-and-White cattle (0.220 and 0.024, respectively). The frequencies in Czech Red cattle were similar to Czech Pied cattle – allele *B* 0.481, genotype BB 0.192. The frequencies of allele *E* were low – 0.071 in Czech Pied cattle, 0.024 in Black-and-White cattle and 0.058 in Czech Red cattle. In crossbreds F1 generation of Czech Red x Czech Pied was the frequency of allele *B* 0.386, we did not find any allele *E* in this breed. The occurrence of allele *C* were found out in the Czech Pied cattle, Czech Red cattle and Black-and-White cattle, we found one heterozygous animal in Czech Pied cattle. Theoretically expected and empiric frequencies of genotypes did not differ statistically. There was acknowledged the monomorphism of α-lactalbumin locus in European cattle breeds.

ELECTROPHORETIC HETEROGENEITY OF PLASMA PROTEINASE INHIBITORS IN SHEEP

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After one-dimensional and two-dimensional electrophoresis on polyacrylamide gel (PAG) – (agarose-PAG), fractions of proteinase inhibitors (PI, trypsin (T) and α-chymotrypsin (α-AchT) have been evaluated from the blood plasma of Merino sheep. The detection of PI was done by a modified method of Uriel and Berges (1968). Unlike the common method, we determined the higher number of PI trypsin fractions in PAG. Evaluating the positions according to Engliš (1992), higher number of fractions has been found in particular in the region of postalbumins, α_1-antitrypsin, immunoglobulins, and post-γ-globulin. The positions of majority PI fractions against α-AchT were the same as those of T. The intensity of other PI fractions of α-AchT was weaker and the number of minority ones was lower following the isoelectric focusing (IEF) on PAG, a total of 7–12 fractions inhibiting T were determined in individual animals. 2 to 4 of these fractions occurred most frequently. 5–7 fractions detected after IEF inhibited α-AchT, of these 1–3 fractions occurred most frequently. PI fractions of the both proteinases occurred within the range of isoelectric points 4.55–5.85 and had identical positions. According to some literary data, PI fractions α-AchT were not detected by charge or IEF electrophoresis (Juneja, Gahne, 1980; Estomba et al., 1993 etc.).

VARIABILITY OF LACTATE DEHYDROGENASE ISOENZYMES IN BLOOD SERUM OF SOME BREEDS OF HORSES

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Horses of the breeds of Slovakian Warm-blood ($n = 30$), Cold-blood ($n = 13$), Czech Warm-blood ($n = 5$), and English half-bred ($n = 3$) were analysed electrophoretically on 5.5% PAGE gel by the method of Dietz and Lubrano (1967). Statistical evaluation of the results was done using the program of Sigma Stat® version 2.0. The total activity of LD in Slovakian breeds of horses ranged from 3.7 ± 2.2 μkat/l to 5.11 ± 1.65 μkat/l. There were, however, no significant changes. The isoenzyme LD spectrum in Slovakian Warm-blood horse was as follows: LD1 = 25.7 ± 11.5 %; LD2 = 27.5 ± 18.2%; LD3 = 35.4 ± 11.2%; LD4 = 7.5 ± 6.5%, and LD5 = 3.0 ± 3.8%. Significant differences ($P < 0.05$) were recorded only in the case of isoenzyme LD2 activity between Slovak Warm-blood and Czech Warm-blood horses. There were, on the other hand, significant differences between gelding and mare in the activity of LD1 isoenzyme and between gelding and stud in the activity of LD1 and

LD3 isoenzymes. In horses, the highest activity was observed with isoenzymes LD2 and LD3. The minority fractions were also observed with some isoenzymes.

ELECTROPHORETIC CHARACTERISTICS OF LACTATE DEHYDROGENASE ISOENZYMES IN SHEEP ERYTROCYTES

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There has been polymorphic isoenzyme system of LD in erythrocytes of 2 month-old Merino sheep studied. LD isoenzymes were separated on 5.5% PAGE gel by the method of Dietz and Lubran (1967. IEF of hemolysates was done with Pharmalyts (pH 4.2–4.9; 4.5–5.4 and 3.5–9.5) on polyacrylamide gels (0.5 x 230 x 160 mm, T = 7.5, C = 3%). Statistical evaluation of the results was done using the program of Sigma Stat® version 2.0 (Descriptive statistics-test). At the age of 2 months, ewe lambs showed the highest activity in erythrocytes with isoenzyme LD1 = 86.5 ± 8.9%, then LD2 = 4.99 ± 2.85%, LD3 = 4.06 ± 2.68%, LD4 = 2.79 ± 3.5% and LD5 = 1.8 ± 2.24%. Based on the determined activities of LD isoenzymes in erythrocytes we suppose that this is the genotype of LD-LL. Using IEF hemolysates of ewe lambs, the heterogeneity of LD isoenzymes was recorded ranging within pH 3.5–9.5. Three majority LD fractions were focused in a zone of LD1 with pH 4.0–4.6, except for two animals. In a zone of LD2 with pH 5.2–5.4, only one intensive fraction (4–5 minority fractions) was observed in the same position in all animals. Two fractions were in the zone of LD3. In alkaline region with pH above 8.0, 3 lower-intensity fractions were recorded, namely in zones of LD4 and LD5 that were more difficult to differentiate.

Language corrections of the published abstracts were made by the conference organizers.

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