

**Анотации**  
**на материалите по чл. 76. от ПРАСПУ**  
**на Евгения Нешова Иванова**

**Научни публикации извън представените за научната и образователна степен „доктор” и за академичната длъжност „доцент”**

1. Ivanova, E., Staykova, T., Bouga, M. Allozyme variability in honey bee populations from some mountainous regions in southwest of Bulgaria. // Journal of Apicultural Research, 2007, 46, (1), 3-8. **Impact factor: 0.743**

Honey bee populations from different mountainous regions in southwest Bulgaria have been studied on four enzymatic systems (MDH, EST, PGM and HK) corresponding to 4 genetic loci. All loci were found to be polymorphic in almost all populations. The observed heterozygosity ranged from 0.172 to 0.262. Allele frequencies of all loci were used to estimate Nei's (1972) genetic distance, which was found to range between 0.009 and to 0.052 among the populations studied. A Neighbour-Joining phylogenetic tree was obtained by genetic distance matrix methods.

2. Ivanova, E., Staykova, T. Stage specificity in the expression of proteins of honey bee fat body (*Apis mellifera* L.) in the course of ontogenesis. // Journal of Cell and Molecular Biology, 2007, 6, 2, 129-135. **SJR – 0.03.**

The aim of this study was to investigate and analyze some peculiarities in the age specificity of protein expression in the fat body of *A. mellifera* during the ontogenesis of the individuals. By using 7.5% polyacrylamide gel electrophoresis, 189 individual samples of fat body extracts were investigated in the course of their development in the following stages and ages: larvae-third, fourth and fifth larval age (L3, L4, L5); prepupae (PP) and pupae-white-eyed and dark-eyed pupae (WP, DP). A total of 25 protein fractions were expressed in the fat body of male and female individuals during their development. Some sex-differences in studied fat body proteins were noticed. The age and stage specific dynamics in the expression of established proteins of the fat body spectrum were analyzed and commented.

3. Ivanova, E., Petrov, P. Regional differences in honey bee winter losses in Bulgaria during the period 2006-9. // Journal of Apicultural Research, 2010, 49 (1), 102-103. DOI: 10.3896/IBRA.1.49.1.17. **Impact factor: 1.028**

Here information about Bulgarian honey bees and their vitality, as well as Bulgarian Ministry of Agriculture and National Veterinary Service concerning local honey bees' health and conservation is presented. Local honey bees are with high queen fertility, high honey productivity, good winter resistance, low aggressiveness, good hygienic behaviour. The genetic structure of Bulgarian honeybees is studied now through the usage of morpho-ethological, biochemical and molecular-genetic approaches. According to the survey, the colony losses were considerable in the Rila–Pirin Mountains massif, the Danubian Plain and the region of Dobrudzha during the winter of 2008-9 with 30%, 20% and 15%, respectively.

Throughout the period studied (2006-2009), lower levels of colony losses (3%-7%) were noticed in the Sredna gora and Strandzha mountainous regions and in the Thrace valley.

4. Meixner, M., Costa, C., Kryger, P., Hatjina, F., Bouga, M., Ivanova, E., Büchler, R. Conserving diversity and vitality for honey bee breeding. // Journal of Apicultural Research, 2010, 49 (1), 85-92. DOI 10.3896/IBRA.1.49.1.12. **Impact factor: 1.028**

This is a review article conserving importance of diversity and vitality of honey bees for breeding. Beekeepers in Europe, North America and other parts of the world have repeatedly been afflicted by elevated and sometimes unexplained colony losses. Multiple factors have been considered in connection with increased winter losses. In addition to national programmes investigating possible causes for increased honey bee mortality, scientists collaborate at an international level on different aspects of bee health within the COLOSS network. Within this network, Working Group 4 explores aspects of genetic diversity in relation to the vitality and health of honey bee populations. In this paper, briefly review the genetic diversity of honey bees in Europe is presented, the effects of beekeeping and selective breeding on honey bee populations under the aspect of genetic diversity and bee health and review the current status of EU legislation with respect to protection of native bee populations is discussed. Recent approaches in honey bee selective breeding to improve disease resistance by introducing traits related to colony vitality are introduced and discussed also. The aims of WG4 within the COLOSS network and its experimental approach are we presented.

5. Ivanova, E., Petrov, P., Bouga, M., Emmanouel, N., Ivgin-Tunka, R., Kence M. Genetic Variation In Honey Bee (*Apis mellifera* L.) Populations From Bulgaria. // Journal of Apicultural Science, 2010, 54 ( 2), 49-60. **Impact factor: 0.489**

Genetic variation of honey bee populations from 9 different locations of Bulgaria was studied using 4 enzymic systems (MDH, ME, EST and ALP) corresponding to 4 genetic loci and PCR- RFLP's analysis of 16s rDNA, COI, and ND5 gene segments of mtDNA. Allozyme analysis revealed that all loci were polymorphic in almost all studied populations. The observed heterozygosity was found to range from 0.146 to 0.258, and Nei's genetic distance between 0.006 and 0.057 among the populations. Bulgarian honey bees are clustered into three groups in neighbor-joining and UPGMA dendrograms. The Pomorie and Slivovik populations are in a separate clade while all other populations are grouped together. The mtDNA analyses revealed no variation in the Bulgarian honey bees. A comparison was made of the results of similar analyses on honey bees from the neighboring countries of Greece and Turkey. The results showed that honey bee populations from Bulgaria and Greece considered to belong to *A. m. macedonica* subspecies are discriminating, which means the bees show differences.

6. Bouga, M., Alaux, C., Bienkowska, M., Büchler, R., Carreck, N., Cauia, E., Chlebo, R., Dahle, B., Dall'Olio, R., De la Rúa, P., Gregorc, A., Ivanova, E., Kence, A., Kence, M., Kezic, N., Kiprijanovska, H., Kozmus, P., Kryger, P., Le Conte, Y., Lodesani, M., Murilhas, A., M., Siceanu, A., Soland, G., Uzunov, A., Wilde, J. A review of methods for discrimination of honey bee populations as applied to European beekeeping (Review article). // Journal of Apicultural Research, 2011, 50(1), 51-84. DOI 10.3896/IBRA.1.50.1.06. **Impact factor: 1.028**

This is a review of methods for discrimination of honey bee populations as applied to European beekeeping. Here, scientists from 19 European countries, most of them

collaborating in Working Group 4: “Diversity and Vitality” of COST Action FA 0803 “Prevention of honey bee COLony LOSSes” (COLOSS), review the methodology applied in each country for discriminating between honey bee populations. Morphometric analyses (classical and geometric) and different molecular markers have been applied. Even if the approach has been similar, however, different methodologies regarding measurements, landmarks or molecular markers may have been used, as well as different statistical procedures. There is therefore the necessity to establish common methods in all countries in order to have results that can be directly compared. This is one of the goals of WG4 of the COLOSS project.

7. Ivanova, E. N., Bienkowska, M., Petrov, P. P. Allozyme Polymorphism and Phylogenetic Relationships in *Apis mellifera* Subspecies Selectively Reared in Poland and Bulgaria. // Folia biologica (Kraków), 2011, 59 (3-4). doi:10.3409/fb59\_3-4.09-13. **Impact factor: 0.761.**

The genetic variability of honey bee populations of three subspecies selectively reared in Poland (*A. m. carnica* and *A. m. caucasica*) and Bulgaria (*A. m. macedonica* – type *rodopica*) was studied using isoenzyme analysis of six enzyme systems (MDH-1, ME, EST-3, ALP, PGM and HK) corresponding to 6 loci. All loci were found to be polymorphic in the studied populations. The observed and expected heterozygosities ( $H_o$  and  $H_e$ ) ranged from 0.196 (*A. m. macedonica* SM) to 0.265 (*A. m. carnica* MV) and from 0.224 (*A. m. macedonica* SM) to 0.273 (*A. m. carnica* GR), respectively. Allele frequencies of all loci were used to estimate Nei's (1972) genetic distance, which was found to range from 0.003 (between *A. m. macedonica* TR and SM and between *A. m. carnica* GR and MV populations) to 0.057 (between *A. m. macedonica* SM and *A. m. caucasica* populations). The estimated mean  $F_{ST}$  value from allozyme data was 0.0364. A UPGMA dendrogram was obtained by genetic distance matrix methods; *A. m. macedonica* (type *rodopica*), *A. m. carnica* and *A. m. caucasica* populations represented different clades.

8. Nikolova, S.N., Ivanova, E.N. Genetic variability in a local Bulgarian honey bee population. // Acta Zoologica Bulgarica, 2012, 64 (1), 199 – 204. **Impact factor: 0.269**

Local Bulgarian honey bee *Apis mellifera rodopica* from Selective Center Plovdiv has been studied for genetic variability using analysis of six enzymic systems (MDH, ME, EST, ALP, PGM and HK) corresponding to six loci (Mdh 1, Me, Est 3, Alp, Pgm and Hk) and DNA analysis of 9 microsatellite loci (Ac011; A024; A043; A088; Ap226; Ap238; Ap243; Ap249 and Ap256). All of the studied loci were found to be polymorphic. Two to five alleles were detected with allozymic analysis: two alleles – at Mdh-1 and Pgm loci; three alleles – at Me, Alp and Hk loci. Est-3 locus was polymorphic with five alleles. It was calculated that the average number of alleles per locus is 3; the percent of polymorphic loci ( $P=0.95$ ) is 83.3 and the observed and expected heterozygosity – 0.24 and 0.259, respectively. Three to seven alleles were detected using microsatellite DNA analysis: three alleles – at Ap243 and Ap249 loci; four alleles – at Ac011, A043, A088, Ap226 and Ap238; six alleles – at A024 and seven alleles – at Ap256. It was found that the observed heterozygosity varies between 0.444 and 0.567 and the expected heterozygosity – between 0.435 and 0.548. This research provides new information regarding the genetic variability in selected local Bulgarian honey bees and will be useful for selection and conservation purposes.

9. Иванова, Е., Стайкова, Т. Възрастова специфичност в експресията на протеините от мастното тяло на медоносната пчела (*Apis mellifera* L.) в хода на ларвното развитие. // Аграрен Университет - Пловдив, Научни трудове, 2005, L, 3, 35 – 40.

Чрез електрофореза в ПААГ е изследвана динамиката в експресията на протеините от мастното тяло на медоносната пчела в хода на ларвното развитие. Констатирано е наличие на общо 19 фракции в спектъра на изследваните индивиди от двата пола и е установена и коментирана възрастовата специфичност в експресията им. Не е установен полиморфизъм, както и зависими от пола различия в експресията на анализирани протеини.

10. Стайкова, Т., Иванова, Е. Онтогенетични проучвания на протеините от мастното тяло на черничевата копринена пеперуда (*Bombyx mori* L.) в хода на ларвното развитие. Аграрен Университет - Пловдив, Научни трудове, 2005, L, 3, 47 – 52.

Изследвани са промените в протеиновия спектър на мастното тяло в хода на онтогенезата на черничевата копринена пеперуда (*Bombyx mori* L.) при шестнайсет породи и осем междупородни хибриди отглеждани в България. Използвана е PAGE. В хода на ларвното развитие са установени общо 25 протеинови фракции със стадийно специфична експресия. Идентифицирани са резервните белтъци SP1, и SP2 и основните MHPs протеини. Установен е вътрепороден и междупороден полиморфизъм по един от протеиновите локуси. Не са констатирани полови различия.

11. Ivanova, E., Staykova, T., Petrov, P. Some preliminary data about genetic variability in local Bulgarian honeybee *Apis mellifera*. Proceedings of International Apimondia Symposium "Selection and Queen Breeding". Bulgaria, 1-3 September 2006, 1-11. (цитирана в списание с ИФ)

Different honeybee colonies from two regions - Gornotrakijska nizina (locations near Plovdiv) and Ihtimanska Sredna gora - were investigated in this study. The queens of the local *A. mellifera* race were inseminated in the Scientific Center of Agricultural University in Plovdiv and their colonies (marked as "controlled colonies") were studied in order to be compared with others free crossed colonies. Four enzyme systems were studied by using starch-gel electrophoresis (MDH – malatedehydrogenase, EC 1.1.1.37; EST - esterase, EC 3.1.1; PGM – phosphoglucomutase, EC 5.4.2.2 and HK – hexokinase, EC 2.7.1.1). There were found two alleles of Mdh-1 locus (Mdh 65, Mdh 100), two alleles of Est-3 locus (Est 70, Est 100), two alleles of Pgm locus (Pgm 75 and Pgm 100) and three alleles - of Hk locus (Hk 87, Hk 100 and Hk 110). There was found that Est 100 and Hk 100 were fixed for the studied colonies of the local in Bulgaria *Apis mellifera* race. Genotype and allele frequencies and enzyme heterozygosities were calculated.

12. Staykova, T., Ivanova E. Ontogenetic studies of fat body proteins mulberry silkworm (*Bombyx mori* L.) from spinning stage to imago. // Genetics and Breeding, 2006, 35, 3-4, 51-57.

The ontogenetic dynamics in the expression of fat body proteins of mulberry silkworm (*Bombyx mori* L.) has been analyzed by means of electrophoresis in polyacrylamide gel (PAGE). Sixteen breeds and eight inter-breed F<sub>1</sub> hybrids have been studied. Total 24 protein bands have been ascertained from spinning period to imago. A stage-specific expression has

been established. A stronger expression of proteins has been observed during the first half of pupal period. An inter-breed and intra-breed polymorphism had been established. Strongly expressed sex specificity has been ascertained.

13. Tunka, R., Staykova, T., Ivanova, E., Kence, M., Grekov, D. Differentiation of silkworm, *Bombyx mori* strains measured by RAPD analyses. // Proceedings of the International conference “Sericulture challenges in the 21<sup>st</sup> Century & the 3<sup>rd</sup> BACSA meeting, 18-21 september, 2007, Vratza, Bulgaria, 247 – 251.

The patterns of random amplified polymorphic DNA (RAPD) variation among six silkworm (*Bombyx mori*) strains with different origins are examined. A total of ten RAPD primers were used and all of the loci are polymorphic. The genotypic diversity ( $H'$ ) inferred from Shannon's index (0.4459 for all populations) is higher than gene diversity ( $H_i$ ) (0.2896 for all populations), which suggests that diversity is distributed among lineages. Estimates of gene diversity in populations are higher in total ( $H_t$ ) as compared to within population diversity ( $H_s$ ). Highest genetic differentiation is obtained between China 23 and the other five strains. The highest genetic distance is determined between China 23 and Shova (0.1713). The highest gene flow (6.8048) is obtained between Asahi and Gindga 8 strains, whereas the lowest - between China 23 and Shova. The highest  $G_{st}$  value corresponds well with the lowest  $N_m$  value which designates that there is a small amount of gene flow. The dendrogram is constructed by using the UPGMA method based on Nei's (1978) genetic distance and separated the China 23 strain from all the others that formed together a large cluster. The genetic diversity in the studied strains is moderately low.

14. Ivanova, E., Staykova, T., Velcheva, I. Cytotoxicity and genotoxicity of heavy metal- and cyanide-contaminated waters in some regions for production and processing of ore in Bulgaria. Bulgarian Journal of Agricultural Science, 2008, 14 (2), 262-268.

This study generalizes the data of investigations on cytotoxic and genotoxic effect of heavy metal- and cyanide-contaminated waters in 2001, 2003 and 2005. The water samples were collected from different water sources in the region of “Assarel-Medet” Copper Refinery Works. The contents of copper, arsenic, cadmium, lead, and cyanides (mg.dm<sup>-3</sup>) were determined using the method of automatic photometry. The *Allium cepa* and *Pisum sativum* plant systems were used for testing of the cytotoxicity and genotoxicity of heavy metals and cyanides. A lower mitotic index and a higher frequency of chromosome aberrations were established in all test samples than in the control ones. Chromosome fragments, anaphase and telophase bridges, micronuclei, lagging chromosomes and C-mitotic effect in cells were observed. It was concluded that the pollution found in the regions for production and processing of ore has cytotoxic and genotoxic effect on cells and it could be a potential threat to water ecosystems and human health.

15. Ivanova, E., Petrov, P. La Bulgarie La diversite, l'apiculture et la vitalite – la situation actuelle des abeilles bulgares. // Bulletin Technique Apicole, 2009, 146, 36 (2), 67. ISSN 0335 3710.

General information about local Bulgarian honey bees, the principals of their selection and the activities for their conservation health services is presented in this article. It was mentioned that the genetic structure of Bulgarian honey bees is studied recently through the usage of morpho-ethological, biochemical and molecular-genetic approaches. According to the survey

done, the colony losses were considerable in the south-west and north-east part, the Danubian Plain and the north-east regions of Bulgaria during the winter of 2008-9. Throughout the period studied lower levels of colony losses (3%-7%) were noticed in the south-central and south-east of Bulgaria.

16. Ivanova, E., Bouga, M. Genetic variability in honey bee population from Northern Bulgaria. // Proceedings of the 41<sup>st</sup> Congress Apimondia, 15-20 September, 2009, Montpellier – France. (цитирана в списание с ИФ)

The aim of this research is to investigate the genetic variability and phylogenetic relationships of honey bee populations from various regions of North part of Bulgaria using molecular markers such as isoenzymes and mtDNA. All enzymic systems were polymorphic in most of the populations studied, at the 95% level. The mean number of alleles per locus, percentage of polymorphic loci, observed and expected heterozygosities are calculated. In UPGMA dendrogram two branches are formed. The sizes of PCR-amplified mtDNA segments for all populations examined were found to be about 964bp, 1028bp, and 822bp for 16s rDNA, COI, and ND5 gene segments respectively. No variability was detected among the honey bee populations studied.

17. Staykova, T., Ivanova, E., Tzenov, P., Vasileva, Y., Arkova-Pantaleeva, D. Differentiation of silkworm (*Bombyx mori* L.) strains by isoenzyme markers. // Genetics and Breeding, 2009, 38 (1), 47-55.

This study included 12 strains of various origin, grown at the Sericulture Experiment Station of Yratza, Bulgaria. The nonspecific esterases from the haemolymph, phosphoglucosyltransferase and aspartate aminotransferase from the silk glands of V instar larvae were analyzed by 7.5% PAGE. Polymorphism was found in the nonspecific esterases and the phosphoglucosyltransferase. The allele frequencies, the average number of alleles per locus, the percentage of polymorphic loci, the observed and expected heterozygosity, genetic distance (Q'le, 1972) and the fixation index (F<sub>st</sub>) were calculated through the BIOSYS-1 program. In the constructed UPGMA dendrogram the studied strains were grouped in two main clusters. It was found that nonspecific esterases are very suitable markers for analyzing inter-strain polymorphism and strain differentiation, while phosphoglucosyltransferase is more suitable for studying intra-strain polymorphism and determining the degree of intra-strain genetic variability.

18. Ivanova, E., Staykova, T., Dzhambazov, B. Cytotoxicity and genotoxicity of the cyanoprokaryote *Nostoc microscopium*. // Genetics and Breeding, 2009, 38 (1), 13-19.

*Allium root* meristem was used as an in vivo test system to evaluate the toxicity of cyanoprokaryote *Nostoc microscopium*. Extracts in water-Dimethyl sulfoxide (9:1, v:v), water-methanol (1:9, v:v) and water-acetic acid (9.5:0.5, v:v) solutions were used for testing. To studying the cyto- and genotoxicity of *Nostoc microscopium* temporary squash preparations were prepared from *Allium cepa* root meristem tissue. Seeds germinated in dechlorinated tap water were analyzed as a control sample. Seeds germinated in the extracts mentioned above but diluted 50 and 100 times were used as test samples. Two thousand cells per sample were examined. Comparing the test samples with the control, a lower mitotic index after treatment with water-methanol extracts and higher mitotic index after treatment with water-dimethyl sulfoxide extracts was established. In most of the samples tested, the



total frequency of chromosome aberrations was higher than in the control. It was found that different extracts of cyanoprokaryote *Nostoc microscopium induce* damages such as C-mitosis, fragments, laggards, anaphasic and telophasic bridges, disturbed anaphase and micronuclei.

19. Staykova, T., Ivanova, E., Tzenov, P., Vasileva, Y., Arkova-Pantaleeva, D., Petkov, Z. Acid phosphatase as a marker for differentiation of silkworm (*Bombyx mori*) strains. // Biotechnology & Biotechnological Equipment, 2010, 24 (2), 379 – 384.

This study was carried out on twelve silkworm strains maintained by the Sericulture and Agriculture Experiment Station germplasm bank, located in Vratza, Bulgaria. The polymorphism of acid phosphatase from larval haemolymph was investigated by method of electrophoresis in polyacrylamide gel. Five fundamental types of this enzyme were found in the studied strains of various origins. The acid phosphatase isozymes were considered to be controlled by five codominant alleles. It was found out that the acid phosphatase is very suitable marker for analyzing the inter- and intra-strain diversity and the strain differentiation.

20. Ivanova, E. Investigation on genetic variability in honeybee populations from Bulgaria, Greece and Serbia. // Biotechnology & Biotechnological Equipment, 2010, 24 (2), 385–389. (цитирана в списание с ИФ)

Genetic variation of honey bee populations from Bulgaria (local type *A. m. rodopica*), Greece (*A. m. macedonica*) and Serbia (*A. m. carnica*) was studied on 6 enzymic systems (MDH, ME, EST, ALP, PGM and HK) corresponding to 6 genetic loci. Allozyme analysis revealed that all loci studied were polymorphic in most of the populations studied. Four alleles were detected at MDH-1 locus, three – at ME, five – at EST-3, three – at ALP, two – at PGM and three – at HK. The observed and expected heterozygosities ranged from 0.163 (Serbia) to 0.236 (Bulgaria) and from 0.248 (Greece) to 0.263 (Serbia), respectively. Nei's genetic distances range from 0.012 (between Greece and Bulgaria) to 0.157 (between Serbia and Bulgaria). In UPGMA dendrogram there are two clusters formed. Bulgarian and Greek populations are clustered together in first branch and Serbian population is grouped in the second cluster.

21. Staykova, S., Ivanova, E., Panayotova, G., Cvetkova, I., Dzhoglov, S., Dzhambazov, B. General toxicity and genotoxicity of *Nodularia moravica* (Cyanoprokaryota, Nostocales). // Biotechnology & Biotechnological Equipment, 2010, 24 (2), 397 – 400.

General toxicity and genotoxicity of cyanoprokaryote *Nodularia moravica* was investigated on the base of *Allium* root meristem in vivo test system. Seeds sprouted in dechlorinated tap water were analyzed as a control sample. Seeds sprouted in the water-Dimethyl sulfoxide (9:1, v:v) extract, diluted 50 and 100 times (D1-797 and D2-797, respectively) were used as test samples. It was found that different concentrations of dilutions of the initial extract of cyanoprokaryote *Nodularia moravica* induced damages such as micronuclei (MNI), fragments, anaphasic and telophasic bridges and laggards with higher total frequency than in the control. Germination percentage and root length were found to be in positive correlation with percentage of chromosome aberrations and depend on the extract concentration. It was concluded that *Nodularia moravica* extract in water-DMSO solution induces general and genotoxicity in *Allium cepa* root meristem cells. There were not found data about cytotoxicity.

22. Staykova, T., Ivanova, E., Grekov, D., Petrov, P., Tzenov, P., Vasileva, Y., Petkov, Z., Arkova-Pantaleeva, D. Development of a specialized center for scientific, training and diagnostic work for the needs of Apidology and Sericology in Bulgaria. // *Advances in Bulgarian Science – Annual, 2010, 1, 63-67.*

The aim of this project is the establishment and development of a specialized center for scientific, training and diagnostic work for the needs of apidology and sericology in Bulgaria, uniting the scientific-research units of “Pasisii Hilendarski” University of Plovdiv, the Agricultural University – Plovdiv, Sericulture Experimental Station at the Agricultural Academy and the National Breeding Association of Apiculture. The following activities will be carried out in the center: interdisciplinary researches for a complex evaluation of populations *A. mellifera* and *B. mori* through phenotype and genotype characterization at different levels, training of students, master degree students, postgraduate and PhD students, qualification of farmer-beginners and active farmers in the field of apiculture and sericulture and selective-genetic diagnostics through reliable isoenzymic and DNA-markers. The project realization will lead to improving and updating the research facilities of the consortium, as well as the conditions for research and training activity. New opportunities for work at the European university and scientific space will be created through establishing an optimal environment for international cooperation. The complex scientific-research activity of the operating center will be also oriented to creating highly productive breeds, lines and hybrids of silkworm, as well as highly productive queen bees and initial drone families. All this, together with the training of farmer-beginners and active farmers and the promotion of the center activity, will provide opportunities for more intensive development of apiculture and sericulture in regions with suitable climatic conditions and resource. The specialized center will have the necessary intellectual and material-technical potential to continue its scientific-research, training and diagnostic activity for an indefinitely long period of time.

23. Staykova, T., Ivanova, E. Concerning genetic variability and usable isozyme markers for characterization of *A. mellifera* L. populations and *B. mori* L. breeds in Bulgaria. // *Advances in Bulgarian Science, 2011, 20-28.*

Genetic variability in different populations of Bulgarian honey bee *Apis mellifera* from the all six regions in the country have been studied using analysis of six enzymic systems corresponding to six loci (MDH 1, ME, EST 3, ALP, PGM and HK). All of the studied loci were found to be polymorphic. Three to six alleles were detected for the different allozymic systems: three alleles – at MDH-1, ALP and HK loci; four alleles – at ME and PGM loci and six – at EST-3 locus. Genetic markers, usable for discrimination of Bulgarian honey bees were described in this study. A genetic analysis was conducted on 10 breeds of *B. mori*. Suitable isoenzyme markers were specified for evaluation of interbreed and intrabreed polymorphism and breed differentiation for this species. The phylogenetical relationships were studied. It was established that breeds E 27, Japanese 106 and Jena may be used in future breeding programs as donor breeds as they are genetically distant from all others.

24. Иванова, Е, Николова, С. Създаване на банка с ДНК образци от популации *Apis mellifera*, обитаващи територията на България. // Пловдивски университет „Паисий Хилендарски“ Юбилеен сборник, Биологически науки за по-добро бъдеще, 2012, 77 – 88.



Организирането на банка с ДНК образци от български популации *A. mellifera* е етап от научен проект с реална перспектива за обогатяване и доразвитие. Той цели централизирано съхраняване на ДНК материал и информация, която да бъде използвана за бъдещи научни цели и за изследователски схеми с различен мащаб. Съхранената ДНК предоставя информация за генетичната история на вида, популацията, индивида и сложните генетични взаимовръзки. За създаване на ДНК банка на българските медоносни пчели на този етап са използвани 1443 индивидуални ДНК проби от медоносни пчели, обитаващи 26 различни местонахождения (популации) на територията на цялата страна, както и около 350 ДНК проби от европейски популации медоносни пчели на подвидвете *A. m. macedonica*, *A. m. carnica* и *A. m. caucasica*. Банката с ДНК образци предоставя възможности за проучване на генетичната изменчивост сред популациите медоносни пчели на територията на страната при решаване на селекционни и консервационни въпроси, както и за провеждането на проучвания относно филогенетичните зависимости между българските медоносни пчели и други раси и екотипове от различни райони на територията на Европа с цел изясняване и характеризиране на подвидовия статус на отглежданите в България медоносни пчели.

25. Ivanova, E., Mitkovska, V. Organ specificity in the expression of proteins and unspecific esterases in widely spread in Bulgaria *Passer domesticus* and *Passer montanus*. University of Plovdiv „Paisii Hilendarski“, 2012, 147 – 160.

The aim of this study was to investigate and analyze some peculiarities in the organ specificity of the protein and esterase expression in the muscle and liver of *Passer domesticus* and *Passer montanus* individuals, which are inhabitants in South-central part of Bulgaria. Forty six individual samples from muscular and liver extract were studied using starch-gel electrophoresis. Totally 27 protein fractions were found in the electrophoretic spectra of muscular and liver extracts in *P. domesticus* and 12 protein fractions in *P. montanus*. There were 13 esterase fractions established in the electrophoretic spectra of muscular and liver extracts in *P. domesticus* and 6 esterase fractions in *P. montanus*. Organ specificity in the expression of the studied proteins and esterases of both species was found and characterized. Polymorphism with two allele system of the genetic control for some products was admitted.

26. Стайкова, Т., Иванова, Е. Вътрепороден и междупороден генетично детерминиран полиморфизъм по малатдехидрогеназа и хексокиназа и филогенетична диференциация при черничевата копринена пеперуда *Bombux mori* L. // Пловдивски университет „Паисий Хилендарски“ Юбилеен сборник, Биологически науки за по-добро бъдеще, 2012, 253 – 263.

Изследвани са десет породи с различен произход, отглеждани в България. Чрез 7.5% PAGE са анализирани малатдехидрогеназата (MDH - EC 1.1.1.37) от хемолимфата и хексокиназата (HK - EC 2.7.1.1) от копринотделителните жлези на ларви V възраст. Констатиран е вътрепороден и междупороден полиморфизъм по малатдехидрогеназата и междупороден полиморфизъм по хексокиназата. Чрез BIOSYS-1 програмата са изчислени алелните честоти, средният брой алели за локус, процента на полиморфни локуси, установената и очаквана хетерозиготност, генетичната дистанция по Nei и индексът на фиксация на Wright ( $F_{ST}$ ). Построена е дендрограма, в която изследваните породи са групирани в два основни кластера. Установено е, че MDH е подходяща за изследване на вътрепородния полиморфизъм, а HK е подходяща за анализиране на междупородния полиморфизъм и породната диференциация.

27. Staykova, T., Popov, P., Ivanova, E., Breed specific expression of gut silkworm (*Bombyx mori* L.) nonspecific esterases. // Journal of BioScience and Biotechnology, 2012, 1 (1), 27–31.

Nonspecific esterases of silkworm (*Bombyx mori* L.) gut were investigated by means of polyacrilamide gel electrophoresis (PAGE). Stage-specific expression of eleven esterase bands was detected during larval development of breeds and inter-breed hybrids kept in Bulgaria. In two esterase zones, intra- and inter-breed polymorphism was found. The polymorphism in fraction GES II specific for the gut may be used for testing of the breeds raised in our country with reference to determining the degree of genetic heterogeneity. The specific expression in zone GES L1 observed at present study confirmed gene determinate polymorphism in zone BES E1, observed earlier.

28. Ivanova, E., Staykova, T., Stoyanov, I., Petrov, P. Allozyme genetic polymorphism in Bulgarian honey bee (*Apis mellifera* L.) populations from the south-eastern part of the Rhodopes. // Journal of BioScience and Biotechnology, 2012, 1 (1), 45–49.

Allozyme genetic polymorphism in Bulgarian honey bee populations from four different locations in the south-eastern part of the Rhodopes was studied on six enzymic systems (MDH, ME, EST, ALP, PGM and HK) corresponding to six genetic loci. Allozyme analysis revealed that all loci studied were polymorphic in almost all populations studied. The observed heterozygosity was found to range from 0.110 to 0.208 and Nei's genetic distance – between 0.016 and 0.061 among the populations studied. These honey bee populations were clustered in two groups in UPGMA dendrogram. The Tihomir population was in a separate clade while other three populations (Kurdzali, Krumovgrad and Dolni Yurutci) were grouped together.

#### **Учебници:**

1. Иванова, Е., Стайкова, Т., Андреевко, Е. Генетика с биологични основи на поведението и психогенетика. Университетско издателство „Паисий Хилендарски“. Пловдив, 2011, 380.

В настоящия учебник са разгледани основите на общата генетика в комбинация с биологични основи на поведението и с психогенетика. Това комбинирано четиво е подходящо за студенти, както от специалностите „Психология“ и „Специална педагогика“ (Дефектология) на Педагогическия факултет, изучаващи дисциплините Биологични основи на поведението и генетика и Основи на генетиката, така и за студентите от специалностите на Биологическия факултет, изучаващи дисциплините Основи на генетиката, Генетика, Обща и популационна генетика. Учебникът може да се използва успешно и от студентите на специалност Дефектология, изучаващи дисциплината Анатомия и физиология на висшата нервна дейност, както и от всички студенти по биология, които изучават морфологията и физиологията на нервната система като база за изява на човешкото поведение.

Темите, включени в съдържанието на учебника покриват в по-голямата си част програмите на посочените дисциплини в учебните планове на акредитирани специалности в двата факултета на Пловдивския университет „Паисий Хилендарски“.

Учебникът е разработен от специалисти с дългогодишен преподавателски опит в областта на общата и популационна генетика, анатомията и физиологията на висшата нервна дейност и има амбицията да поднесе полезно и интересно учебно съдържание, провокиращо стремеж към познание и творчество. Посочено е участието на всеки от авторите при разработване на тематичното съдържание.

2. Иванова, Е., Стайкова, Т., Андреевко, Е., Василева, П., Калайджиева, В., Стоянов, И., Джоглов, С., Дончева, В., Панайотова, Г., Цветкова, И. Генетични основи на поведението. Университетско издателство „Паисий Хилендарски”. Пловдив, 2011, 237.

Книгата „Генетични основи на поведението” е разработена от голям колектив, включващ преподаватели от три катедри на Биологическия факултет на ПУ „П. Хилендарски” – Биология на развитието, Анатомия и физиология на човека и Зоология, както и магистри и магистранти от магистърската програма по генетика.

Книгата е планирана като учебно пособие за студенти по психология и дефектология, както и за студенти-биолози, интересувани се от (и изучаващи) генетика на поведението. Съдържанието е структурирано в четири части: Основи на генетиката; Биологични основи на поведението; Генетика на поведението (при животните) и Генетика на човешкото поведение. Към всяка част са посочени конкретните автори.

## **Обобщение относно приносите в представените за рецензиране научни трудове**

Научните интереси и разработки на доц. д-р Евгения Н. Иванова са в областта на популационната и селекционна генетика, онтогенетиката и екологичната генетика и включват:

- Отчитане на популационно-генетични параметри при два вида полезни насекоми - *Apis mellifera* и *Bombus mori*;
- Провеждане на генетичен мониторинг на *Apis mellifera* в България във връзка с реализирането на национална селекционна програма;
- Изучаване на връзката между степента на генетично разнообразие и жизнеността в популации медоносни пчели от България и Европа;
- Изследване на филогенетичните връзки между популации *Apis mellifera* и породи *Bombus mori* с различен произход;
- Създаване на банка с ДНК проби от медоносни пчели, обитаващи различни местонахождения на територията на България, както и медоносни пчели от подвидвете *A. m. macedonica*, *A. m. carnica* и *A. m. caucasica*, разпространени в Европа;
- Определяне на подходящи генетични маркери за междупопулационни сравнения на територията на Европейския континент;
- Проучване на различни методи за диференциране на популациите *Apis mellifera*, обитаващи европейския ареал и прилагането им в селекционната и развъдна дейност;
- Изучаване на органната, стадийна и възрастова специфичност в изявата и генетичния контрол на общи протеини и някои изоензими при същите обекти;
- Проучване на цитотоксичния и генотоксичен ефект на замърсени с тежки метали и цианиди питейни и природни води;
- Изучаване на обща токсичност, цито- и генотоксичност на цианокариоти от видовете *Nostoc microscopium induce* и *Nodularia moravica*;
- Проучване на възможности за осъществяване на експресен екологичен мониторинг на базата на цитогенетични методи с използване на растителни тест-обекти.

18.07. 2012 г.

гр. Пловдив

Подпис:

(доц. д-р Е. Н. Иванова)