Table 2 Important traits to include in a breeding goal according to the constraints on fed resources and environmental stress of the production system (after Amer et al., 1998)

	Constrained feed resources	Unconstrained feed resources
High Environmental stress	Adaptability Feed efficiency	Adaptability Productivity
Low Environmental stress	Feed efficiency Product quality	Productivity Product quality

An important consideration when deciding on how to approach problems for sustainable systems in also the probability of solving the problem trough breeding (Francis, 1997). The fewer the number of genes, the less antagonism between various important traits and the less environmental influence, the greater is the probability of success in breeding. Also, other technical and practical solutions should be considered, as genetic change is a long term and complex process. Animal breeding has so far focused on cumulative short term genetic change, because breeding optimisation has to a very large extent been based on market economy. Many examples show that animal breeding has lead to unwanted side effects, which are in conflict with sustainable agriculture.
Sustainable animal breeding is a long term and complex process and therefore we need more focus on long term biological, ecological and sociological solutions.

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ANALYSIS OF BLOOD SERUM POLYMORPHIC PROTEINS IN JAPANESE QUAIL.

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Summary

In three pedigree recorded lines of Japanese quail divergently selected for low and high concentration of yolk cholesterol we analyzed polymorphism of blood serum proteins. The birds of F_{10} and F_{11} generation were used for this analysis. The average number of adult quails were 30 males and 60 females for every lines. for genetical mapping were used blood serum of 7 and 6 birds of LCH line, 8 and 7 birds of HCH line and 10 and 6 birds of CCH line from F_{10} and F_{11} generations respectively. The electrophoretic picture of blood serum albumins showed monomorphic homozygous AA combinations of all selected lines. In the transferrin locus we found in two birds of low cholesterol line genotype B. In all other birds and lines we found only genotype AB. In the albumin system of F_{11} generation we found genotype AB in all blood serum protein samples. We found similar situation also in transferrin locus because of monomorphic combination of BB genotype in all tested samples of all lines.

***Key words*:** Japanese quail, blood serum proteins, polymorphism, yolk cholesterol selected lines

Introduction

The progress of biochemical genetics in the recent years brought many theoretical information. Some of them influence also the practical breeding work of large animals, poultry and Japanese quail which is used not only for poultry and biomedical research, but also for commercial purposes because of their biological and economical value.
The genetic polymorphism of Japanese quail was studied by several authors. Kimura (1989) studied the influence of domestication process on polymorphic proteins of wild Coturnix populations. He found electroforetic variability of 32 protein and enzymatic loci in wild quail population which was after the catching in the wildness, reared in domestic environment without artificial selection during 15 years period. After this period of domestication, the gene frequency of domesticated formerly wild population was very similar to the commercial populations of Japanese quail but significant different from their wild ancestors. Ghosh et al (1992) studied biochemical polymorphism on the Hb locus of three lines of Japanese quail (German, meat and egg lines). All of them had codominant alleles A and B. The frequency of allele A was higher than of allele B in all of three investigated populations. The genotypic frequencies of meat lines were genetically unequal, the frequency of BB genotype was significant higher as supposed ($P < 0,05$). The two other lines were genetically identical. Kuryl (1988) analyzed the frequency of albumin and prealbumin types in blood and egg yolk in 293 Japanese quail. The progeny analysis showed that polymorphism of blood and yolk prealbumin was controlled with two pairs of codominant alleles on the autosomal locus. The electrophoretic analysis of body liquids of three lines of Japanese quail from Canadian Genetic Stock Center was made to ascertain genetic diversity selected lines with larger body weight in comparison with unselected and randomly paired populations (Cheng et al., 1993) .
The aim of this paper was to evaluate the changes of genetic polymorphism of serum proteins in the lines selected to low and high egg – yolk cholesterol concentration and to compare the obtained values with the non – selected control population of Japanese quails reared in Research Institute of Animal Production Nitra – Poultry Breeding Station Ivanka prunaji (RIAP, Nitra).

Materials and methods

Two lines of Japanese quail, divergently selected for low (line LCH) or high (line HCH) and one unselected control population (CCH) of F_{10} and F_{11} generations reared in RIAP Nitra were analyzed in this experiment. All analyzed quails had agouti feather color pigmentation (e^+). The average number of adult quails were 30 males and 60 females for every lines. For genetical mapping were used blood serum of 7 and 6 birds of LCH line, 8 and 7 birds of HCH line and 10 and 6 birds of CCH line from F_{10} and F_{11} generations respectively.
The standard starch gel electrophoresis was used to analyze the samples of blood proteins. We used horizontal electrophoresis with the one – way electric current Multidrive XL – LKB Pharmacy. The starch gels were prepared with application of potato starch , which was hydrolyzed by hydrogen 0,1 N chlorhydrogenic acid (HCL) 40 minutes by the temperature 38 °C. The gels were prepared by heating of starch suspended in puffer by the temperature of 85 °C in water bath. After mixing of few minutes the liquid mass of gel was poured out into electrophoretic bowls and the next was used for application prepared samples. After electrophoretic separation, the gel was cut along into two halves. The interior cut was colored by saturated solution of amidoblack 10 B in the mixture methanol – distilled water – vinegar acid in the 5 : 5 ratio. The gels were colored about 10 minutes and the redundancy of dye was many times washed with solution of equal composition but without the dyes. After the finishing of electrophoretic separation, the proteins fraction results were statistically evaluated.

Results and discussion

The electrophoretic results of blood serum polymorphs proteins and the statistical comparison between the evaluated lines are shown in Tables 1.
The electrophoretic picture of blood serum albumins of F_{10} generation showed monomorpic homozygous genotype AA combinations in all analyzed birds of all analyzed lines. This reality was probably caused by relative high frequency of A allele.
We recorded the identical genotypes AA albumins in all three tested lines of F_{10} generation. Which is in conformity with results of Baumgartner et al (1997).
In blood serum transferrin locus of F_{10} generation we found in low cholesterol line 2 birds BB genotype as results of one allele TfB. In low high cholesterol lines and also control line we found in 71,43 % of analyzed birds the AB genotype, what showed on the existence of two different alleles TfA and TfB in the blood transfferin locus. In the high cholesterol line was separated monomorpic genotype combinations AB in all analyzed blood serum samplles of analyzed birds.
In albumin system of analyzed lines in F_{11} generation we found AB genotype in blood samples, which is caused by presentation of two alleles AlbA and AlbB. our finding closely correspondent with results of Ghosh (1992) who studied polymorphism of three populations (German, meat and egg lines) of Japanese quail. in all tested populations he found two codominant alleles A and B. The frequency A was higher as frequency B in all analyzed lines. Similar results reported Kuryl (1988) who declared that polymorphism of blood serum albumin of Japanese quail is controlled by the pair of codominant

alleles on the autosomal locus. In analyzed samples we did not found the homozygous genotype CC and also its heterozygous combinations, which was probably caused by low frequency of allele C. Our results correspond also with Mazumder and Mazumder (1990) who did not found homozygous CC genotype or their heterozygous combinations and transferrin subunits B_1 C_1.
In the blood transferrin locus of F_{11} generation we recorder in all analyzed lines only one homozygous genotype combinations BB.
Our results are similar to Kosak et al. (1989) and Asala et al. (1993), who did not found in three strains of Japanese quail differences in the transferrin Tf genotype frequency.

Table 1 Polymorphism of blood serum proteins of Japanese quail. LCHL = low cholesterol line, HCH = high cholesterol line, CCH = non selected control line

Line	Bird s number	F_{10}			Bird s number	F_{11}	
		Albumins	Transferrins			Albumins	Transferrins
		AA	AB	BB		AB	BB
LCH	4008	1	-	1	2003	1	1
	4105	1	-	1	2011	1	1
	4107	1	1	-	2013	1	1
	4108	1	1	-	2017	1	1
	4145	1	1	-	2100	1	1
	4013	1	1	-	2028	1	1
	4026	1	1	-		1	1
HCH	4809	1	1	-	2926	1	1
	4810	1	1	-	2937	1	1
	4836	1	1	-	2909	1	1
	4855	1	1	-	2934	1	1
	4859	1	1	-	2935	1	1
	4841	1	1	-	2913	1	1
	4907	1	1	-	2918	1	1
	4888	1	1	-		1	1
CCH	4174	1	1	-	2314	1	1
	4176	1	1	-	2478	1	1
	4180	1	1	-	2487	1	1
	4185	1	1	-	2324	1	1
	4192	1	1	-	2417	1	1
	4197	1	1	-	2418	1	1
	4202	1	1	-			
	4212	1	1	-			
	4216	1	1	-			
	4226	1	1	-			

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