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GENETIC POLYMORPHISM OF SLOW–MIGRATING PREALBUMIN IN GEESE

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ABSTRACT

Blood serum proteins of 36 males and 71 females of parental generation and of 516 progeny of various breeds of geese were separated by means of thin–layer, horizontal, alkaline polyacrylamide gel electrophoresis. In the subregion of slow–migrating prealbumin (PASG) in alkaline gel, ten different phenotypes were found. It was determined, both in the parents and the progeny, that the genes of a single, autosomal locus encoded the proteins of this subregion, and the alleles were named: $PASG^A$, $PASG^B$, $PASG^C$ and $PASG^D$, in order of decreasing speed of migration to anode. The $PASG^B$ allele was commonly found in all the studied geese, $PASG^A$ was found only

in the geese derived from *Anser anser*, whereas the $PASG^C$ and $PASG^D$ alleles were present in the geese originated from *Anser cygnoides*.

Key words: genetic polymorphism, blood serum prealbumins

INTRODUCTION

The studies on the polymorphism of blood serum and egg content proteins of the goose provide evidence of polymorphism in transferrins and conalbumins [6, 11]. Using horizontal starch gel electrophoresis, the polymorphism was confirmed of the proteins that migrate between albumins and transferrins. Namely, it was established that the proteins of this subregion are encoded by a single pair of autosomal alleles [10]. Those results have not been confirmed either with horizontal polyacrylamide gel electrophoresis [1] or with two–dimensional agarose or polyacrylamide gel electrophoresis [7].

Protein polymorphism of blood serum, egg yolk and egg white of geese as well as heredity of the proteins in the transferrin subregion were studied by Brodacki *et al*. [1, 2, 3], who used polyacrylamide gel. Kuznetsov [8, 9], who analysed serum proteins in polyacrylamide gel, carried out highly extensive studies on protein polymorphism in various species of the genera *Anser* and *Branta*.

This study was aimed at an analysis of the polymorphism and genetic determination of slow–migrating prealbumins in blood serum of geese.

MATERIALS AND METHODS

The analyses covered 36 males and 71 females of parental generation and 516 progeny of geese kept in genetic reserve flocks of the Water Poultry Breeding Farm in Dworzyska, Poland. The blood was collected from alar vein and placed in tubes. The morphologic components were centrifuged out, and the serum was taken for horizontal polyacrylamide electrophoresis, carried out according to the method by Gahne *et al*. [4], with modifications by Głuchowski *et al*. [5].

The heredity analysis of the proteins of prealbumin subregion was based on phenotype segregation in the progeny derived from intentional mating of males and females of different breeds. The correspondence of the observed vs. the expected number of prealbumin phenotypes in the flock was compared with the chi–square test.

RESULTS AND DISCUSSION

A fragment of the electrophoregram is presented in Fig. 1, whereas Fig. 2 displays the pattern of slow–migrating prealbumin (PASG) phenotypes in goose blood serum. These proteins were found in goslings as early as the first day of their life, whereas no such equivalents were recorded in hens, turkeys, Japanese quails or ducks [2]. Ten phenotypes are highlighted in the electrophoregram: four phenotypes the have a single, intensively stained band, and six phenotypes, each of which is represented by two bands. The distance between the bands C and D was twice as long as between the bands A and B or between B and C, which may suggest that there is an additional band migrating with intermediate speed in relation to the speed of C and D. However, no geese of such phenotype were found in the studied flocks. Considering the migration speed of band D in relation to the remaining bands, it should have been labelled as “E”, nevertheless, this was not applied, due to the fact that this label was used

in previous reports [1, 2, 3]. The proteins of the subregion probably correspond to the prealbumins marked as Pr–2 in the reports by Kuznetsov [8, 9], who analysed blood serum polymorphism in the geese belonging to various Anser and Branta species. In the former study [8], the author presented five alleles, A, B, C, D and E, which encode the Pr–2 subregion proteins, and in the latter report [9], two additional alleles were introduced, marked as A' and B', which were found in the Branta genus. The author carried out his studies on geese in zoological gardens and did not analyse the heredity of these protein phenotypes in the parents and the progeny. The band denoted as B in this paper probably corresponds to the band C presented by Kuznetsov [8, 9]. This conclusion arises from the comparison of the occurrence frequency of the phenotype in geese. In our study, the band B was commonly found in all the geese, whereas the phenotype A was present only in the birds that originated from *Anser anser*, and the bands C and D – only in the geese that originated from *Anser cygnoides*. Their occurrence frequency in the studied populations was low, below two percent [1]. In the studies by Kuznetsov [8, 9], the occurrence frequency of the particular phenotypes was not presented, however it can by noticed that the band marked as Pr–2C was present in all of the ten studied goose species. In contrast, the remaining phenotypes appeared only in some of the species.

Figure 1. Fragment of electrophoregram of goose blood serum proteins

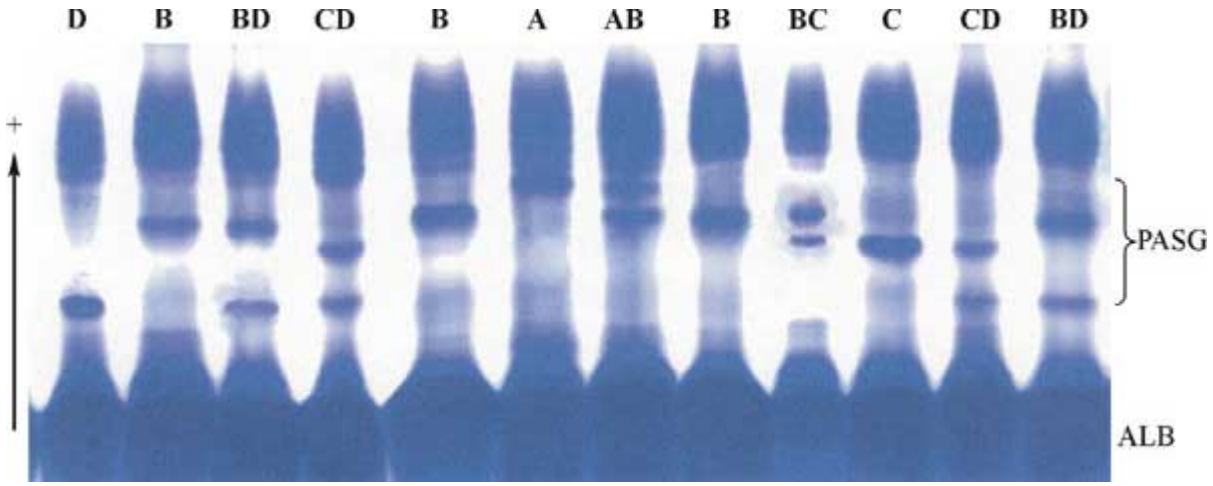
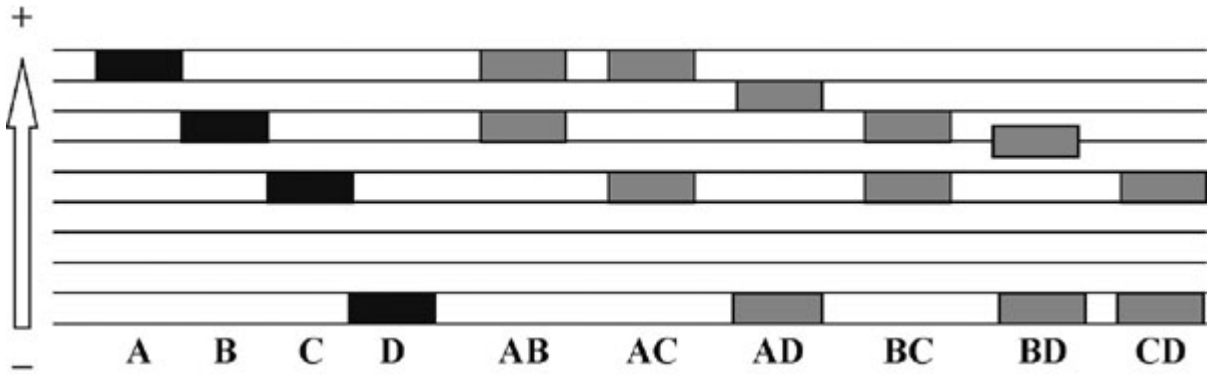


Figure 2. Phenotypes of slow-migrating PASG prealbumin of goose blood serum



The phenotype segregations in progeny, presented in Table 1, correspond to the expected ones. The probabilities $\chi^2 - p(\chi^2) \geq 0.1$ demonstrate that the proteins of the subregion in geese are encoded by a range of autosomal alleles, which are composed of four genes that – in order of decreasing migration speed – were named $PASG^A$, $PASG^B$, $PASG^C$ and $PASG^D$.

These alleles determined four homozygous genotypes that encoded the single–band, intensively stained phenotypes, as well as six heterozygous, double–band phenotypes of lower intensity of band staining. Considering the fact that each of the bands encoded by each of the genes occurred in the heterozygotes, and there were no hybrid bands, it can be assumed that the studied protein is a monomer [1].

Table 1. Frequency distribution of phenotypes of PASG prealbumin subregion proteins of goose blood serum in parents and progeny

Parental phenotypes ♂×♀	Number of matings	Filial phenotypes										P(X^2)
		A	B	C	D	AB	AC	AD	BC	BD	CD	
AB × AB	1×1	3	4			3						0.7–0.5
AB × B	2×6		17			10						0.3–0.2
AB × BD	1×1		2			5		3		7		0.3–0.2
AB × D	1×3							24		14		0.2–0.1
B × B	3×7		77									1.0
B × BD	1×2		13							13		1.0
B × D	1×2									27		1.0
BC × AB	1×1					2	2		1			0.7–0.5
BC × D	3×5									26	25	0.9–0.8
BC × BC	1×2		1	1					2			1.0
BC × BD	1×3		11						7	10	12	0.8–0.7
BD × B	6×10		42							31		0.2–0.1
BD × BD	5×11		10		10					14		0.7–0.5
BD × D	1×1				6					6		1.0
D × B	2×5									45		1.0
D × BD	1×2				8					9		0.8–0.7
D × D	1×1				13							1.0
Total	31×63	3	177	1	37	30	2	27	10	202	37	0.99–0.98

CONCLUSIONS

1. In the subregion of blood serum prealbumin of geese (PASG), slow–migrating in polyacrilamide gel electrophoresis, ten different phenotypes were observed: four single–band phenotypes and six double–band phenotypes.
2. Basing on the analysis of phenotypes in parents and progeny, it has been demonstrated that the proteins of slow–migrating prealbumin subregion (PASG) are encoded by a range of autosomal alleles of a single locus composed of four genes $PASG^A$, $PASG^B$, $PASG^C$ and $PASG^D$.

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