# EGG ALBUMEN POLYMORPHISMS IN SOME FOWL POPULATIONS OF SMALL SIZE

## Polymorphismes génétiques des protéines du blanc d'oeuf dans des groupes de poules à effectif limité

## El polimorfismo genético de las proteínas de la clara de huevo en pequeñas poblaciones de gallinas

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INTRODUCTION

The genetic variation in the proteins of egg albumen, noticed by several authors for the first time at the beginning of the last decade (1, 2, 16, 17, 22) seems to be very usefull as a tool for ellucidating some aspects of the evolution, i.e. with respect to the process of differenciation of species and the origin of different breeds of domestic fowl, or as an aid in taxonomy (3, 4, 5). At the same time, the association of dams'egg-white genotypes with somme characteristics such as eggs fertility (25), embrionic mortality (14, 20, 21) precocity or even intensity of egg production (15, 25) was correlated with the population fitness (14, 20, 21) and seems to offer the opportunity for finding new and more effective solutions for the improvement of the flocks. Several researches attempt to characterise the populations by means of protein polymorphisms (5, 13, 15) or try to ellucidate the tendencies of the genetic structure in the populations, by comparing the observed values of the gentoype frequences with those estimated by the HARDY-WEINBERG equilibrium (13).

In the present paper the attempt was to see whether the analysis of egg-white protein polymorphisms may be usefull in preventing the gene loses in the small nuclei of breeds and strains, maintained as gene pools in order to avoid their disappearance due to the present breeding methods.

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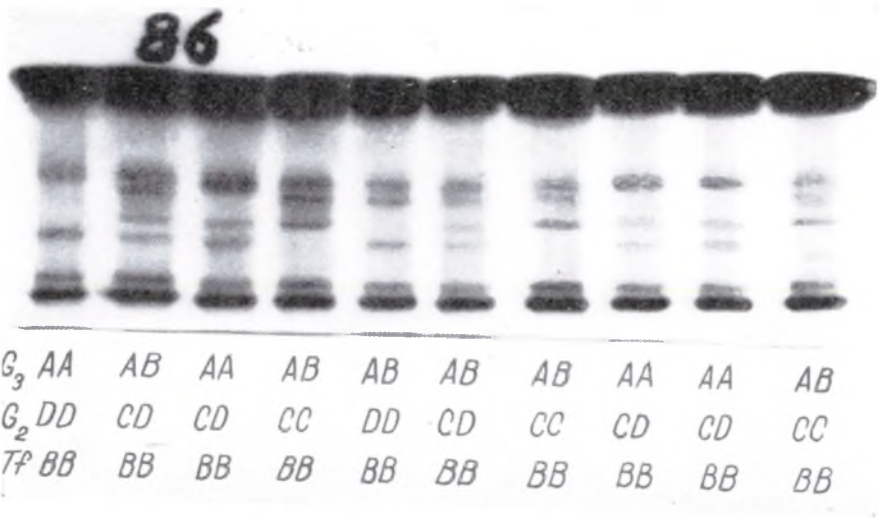
## Materials and methods

The study was carried out on 1560 eggs from hens belonging to 15 strains of 7 breeds. By means of starch gel electrophoresis in tris-EDTA-borate gels, using the method described by Croizier (11), the polymorphisms geneticatly controlled at $G_3$ and $G_2$ globulins *loci* and at the conalbumin *locus* (*Tf*) were examined. The observed genotype frequencies were compared with the Hardy-Weinberg equilibrium state, and the tendency of different alleles to be fixated respectiv elliminated was also revealed.

## Results

1. *$G_3$ globulin.* The $G_3$ fraction of ovoglobulin is controlled by a polyallelic system of genes: $G_3^A$ and $G_3^B$, described by Baker and Manwell in 1962 (1), and $G_3^J$,




1. Electrophoregrams of the proteins controlled at the $G_3$, $G_2$ and Tf *loci.*

detected by Baker in 1964 (2) in the Red Jungle fowl; by Croizier in 1966 in the Marans breed (10), and by Baker in 1968 in the Yokohama. Some other uncertain variants are described by Baker at this *locus* (7).

In our investigations we hawe found only the three genotypes determined by the $G_3^A$ and $G_3^B$ alleles (Fig. 1) with the frequencies shown in Table 1. All the groups are polymorphic with the only exception of group *Mn-A* (Minorca) wich is monomorphic. No group shows neither deviation from Hardy-Weinberg equilibrium nor tendencies for fixation of the genes. It is interesting to see the great differencies in gene frequencies among the groups belonging to the same breeds.

2. *$G_2$ globulin.* The genetic variation of this ovoglobulin fraction is determined by a diallelic system at the *$G_2$ locus.* The alleles $G_2^C$ and $G_2^D$, firstly describes

TABLE 1

GENOTYPE AND GENE FREQUENCIES AT $G_3$ *locus*

| Nr. | Group | *N* | *AA* | *AB* | *BB* | $p^A$ | $\chi^2$ |
|---|---|---|---|---|---|---|---|
| 1 | *It. br. - A* | 120 | 0.758 | 0.242 | — | 0.879 | 2.27 |
| 2 | *Sxh - U* | 180 | 0.439 | 0.433 | 0.128 | 0.655 | 0.60 |
| 3 | *Sxh - Ms* | 120 | 0.342 | 0.492 | 0.166 | 0.588 | 0.03 |
| 4 | *Sxh - T* | 150 | 0.200 | 0.513 | 0.287 | 0.456 | 0.14 |
| 5 | *Sxh - B* | 135 | 0.555 | 0.408 | 0.037 | 0.759 | 1.74 |
| 6 | *Sxh - r* | 135 | 0.400 | 0.444 | 0.156 | 0.622 | 0.15 |
| 7 | *PRb - P* | 100 | 0.460 | 0.440 | 0.100 | 0.680 | 0.06 |
| 8 | *PRb - A* | 80 | 0.262 | 0.488 | 0.250 | 0.506 | 0.05 |
| 9 | *Og - A* | 89 | 0.247 | 0.472 | 0.281 | 0.483 | 0.38 |
| 10 | *Og - B* | 60 | 0.666 | 0.334 | — | 0.833 | 2.41 |
| 11 | *Og - S* | 61 | 0.344 | 0.475 | 0.181 | 0.581 | 0.12 |
| 12 | *Ao - A* | 90 | 0.322 | 0.533 | 0.145 | 0.539 | 2.54 |
| 13 | *Ggn - D* | 60 | 0.383 | 0.467 | 0.150 | 0.617 | 0.08 |
| 14 | *Gga - D* | 89 | 0.742 | 0.224 | 0.034 | 0.854 | 0.87 |
| 15 | *Mn - A* | 91 | 1.000 | — | — | 1.000 | — |

by BAKER and MANWELL in 1962 (1), are responsable for the three corresponding genotypes. Baker supposes that a third allele, which under special conditions is distinguished from $G_2^P$, may occur at this *locus*.

All but one of the groups investigated in our study are polymorphic; (Fig. 1) the Minorca is the only group monomorphic (Table 2). The frequencies of homozigous for $G_2^C$ are very low, but in some group may be observed some very high frequencies, such as in *PRb-A, Og-B, PRb-P* or *Sxh-r*. It is also interesting to see

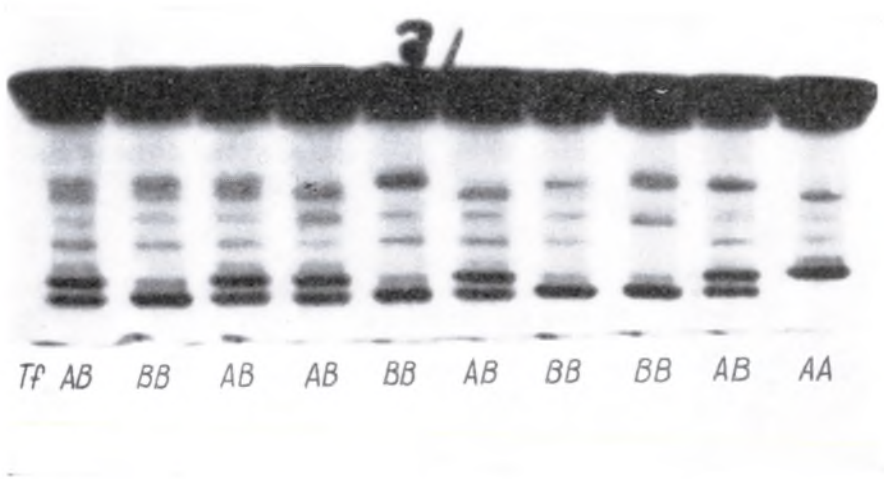
TABLE 2

GENOTYPE AND GENE FREQUENCIES AT $G_2$ *locus*

| Nr. | Group | *N* | *CC* | *CD* | *DD* | $p^C$ | $\chi^2$ |
|---|---|---|---|---|---|---|---|
| 1 | *It. br. - A* | 120 | 0.008 | 0.125 | 0.867 | 0.070 | 0.31 |
| 2 | *Sxh - U* | 180 | 0.011 | 0.156 | 0.135 | 0.089 | 0.31 |
| 3 | *Sxh - Ms* | 120 | 0.017 | 0.050 | 0.933 | 0.042 | 17.60 |
| 4 | *Sxh - T* | 150 | 0.053 | 0.387 | 0.560 | 0.247 | 0.25 |
| 5 | *Sxh - B* | 135 | — | 0.067 | 0.933 | 0.034 | 0.10 |
| 6 | *Sxh - r* | 135 | 0.148 | 0.593 | 0.259 | 0.445 | 4.99 |
| 7 | *PRb - P* | 100 | 0.190 | 0.500 | 0.310 | 0.440 | 0.02 |
| 8 | *PRb - A* | 80 | 0.475 | 0.275 | 0.250 | 0.612 | 8.19 |
| 9 | *Og - A* | 89 | 0.090 | 0.472 | 0.438 | 0.426 | 0.46 |
| 10 | *Og - B* | 60 | 0.217 | 0.518 | 0.266 | 0.476 | 0.08 |
| 11 | *Og - S* | 61 | 0.049 | 0.836 | 0.115 | 0.467 | 28,10 |
| 12 | *Ao - A* | 90 | 0.044 | 0.356 | 0.600 | 0.222 | 0.07 |
| 13 | *Ggn - D* | 60 | 0.100 | 0.500 | 0.400 | 0.350 | 0.59 |
| 14 | *Gga - D* | 89 | 0.034 | 0.450 | 0.516 | 0.259 | 2.64 |
| 15 | *Mn - A* | 91 | — | — | 1.000 | 1.000 | — |

the great variation in gene frequencies, and the high values shown by the $G_2^C$ allele which in several groups is nearly equal to $G_2^D$. It is well known that commonly the $G_2^C$ allele has a very low frequency or is completely absent, at least in the European breeds.

3. *Conalbumin.* This fraction of egg white proteins is controlled at the same *locus* with the serum transferrin: the *Tf locus.* The diallelic system described by OGDEN *et al.* in 1962 (22), with the alleles $Tf^A$ and $Tf^B$, is completed with a third allele, found by CROIZIER in 1966 and designated as $Tf^C$ (10); by STRATIL in the same year and designated as $Tf^C$ (23), and by BAKER in 1967 and designated as $Tf^{SJ}$ (6). The common allele of domestic fowl is the $Tf^B$ and most of the breeds




2. Electrophoregrams with the $Tf^A$ variant.

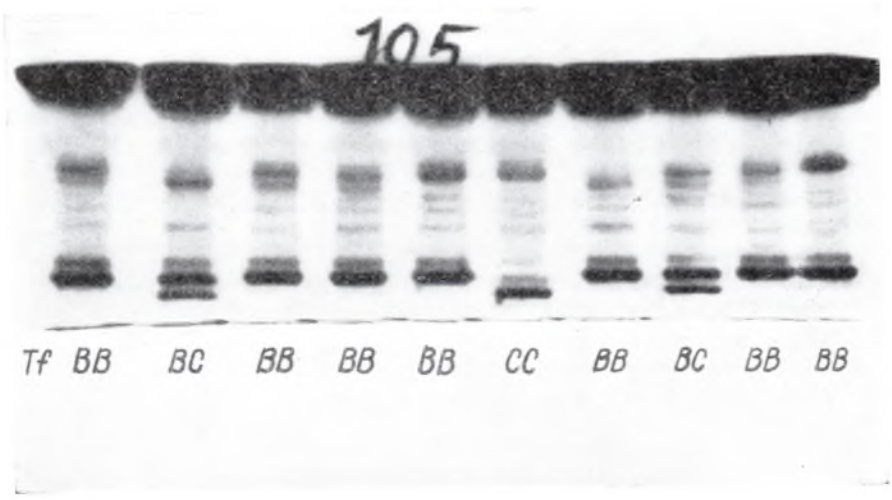
are monomorphic at this *locus.* The $Tf^A$ was found only in some flocks of Light Sussex (7, 17, 20, 22) in Old English Game (7) in Wyandotte (10) and in some indigenous Indian chicken (8). The $Tf^C$ is scarcely found, only as heterozigous, in Marans (6, 7, 10), in Cornish (23), and indigenous Indian chicken (8).

TABLE 3

THE FREQUENCIES OF GENOTYPE AND GENES AT *Tf - locus*

| Group | *N* | *AA* | *AB* | *BB* | *BC* | *CC* | $Tf^A$ | $Tf^B$ | $Tf^C$ | $\chi^2$ |
|---|---|---|---|---|---|---|---|---|---|---|
| *Sxh - Ms* ... ... ... ... ... ... | 120 | 0.042 | 0.375 | 0.583 | — | — | 0.230 | 0.770 | — | 0.461 |
| *Sxh - T* ... ... ... ... ... ... | 150 | — | 0.127 | 0.873 | — | — | 0.064 | 0.936 | — | 0.627 |
| *Sxh - r* ... ... ... ... ... ... ... | 135 | — | 0.037 | 0.933 | — | — | 0.019 | 0.981 | — | 0.451 |
| *Ggn - D* ... ... ... ... ... ... | 60 | — | — | 0.716 | 0.217 | 0,067 | — | 0.825 | 0.175 | 2.124 |
| *Gga - D* ... ... ... ... ... ... | 89 | — | — | 0.989 | 0.011 | — | — | 0.995 | 0.005 | — |

At this *locus*, five of the investigated groups was polymorphic (Table 3). Three of them are Light Sussex strains from different origin, and they are the $Tf^A$ and $Tf^B$ alleles (Fig. 2) but only in the *Sxh-Ms* strain we have found homozygotes for $Tf^A$. In the other two groups (*Ggn-D* and *Gga-D*) we have found the variant $Tf^C$ (Fig. 3); have these groups belong to the indigenous breed from Rumania, named Transylvanian




3. Electrophoregrams with $Tf^C$ variant.

Naked Neck. It is interesting to note the high frequency of $Tf^C$ in the *Ggn-D* group, where there are even some homozygotes for this alleles not found till now in other breeds. The *Gng-D* group deviates a little from HARDY-WEINBERG equilibrium; the deviation is not significative ($P \approx 0.3$) but it is interesting to see that the homozygotes for $Tf^B$ are in excess.

## SUMMARY

The distributions of genotypes of the three *loci* investigated in the present study do not reveal any aspect which could be considered as effect of the small size of the groups. Where a deviation from HARDY-WEINBERG equilibrium is observed, rather the particular genotypic constitutions of sires than the genetic drift are responsable. That means, the original genetic structure at the *loci* studied may be maintened by controlling the mating. In this case, both the $G_3$ and $G_2$ *loci* are to be simultaneously considered; the original distribution of the 9 genotypes possible in each group is to be noted and the pertinent frequencies of the four gametes may be ensured by getting the mates accordingly. The *Tf-locus* has to be considered separately.

As for the presence of the $Tf^C$ variant in Transylvanian Naked Neck, further investigations are necessary in order to ellucidate its origin. We have allready observed one band migrating between $G_2^C$ and $G_3^B$ (Fig. 3) which has to be clarified.

## RESUME

Les polymorphismes de trois fractions protéiques du blanc d'oeuf, à savoir, les ovoglobulines $G_3$ et $G_2$ et la conalbumine, ont été étudiées en but de déceler les possibilités d'éviter les pertes de gènes dans les populations à effectif limité. Les déterminations, executées à l'aide de l'électrophorèse en gel d'amidon, ont été portées sur 1560 poules de 15 noyaux de races et lignées différentes, maintenues en nombre limité, comme réservoir génétique.

En comparant les valeurs observées avec les valeurs théoriques, on ne constate pas des déviations qui pourraient être atribuées à la dérive génétique. Malgré le nombre effectif relativement réduit, le polymorphisme se maintient dans 5 groupes chez tous les trois, et dans 9 groupes chez deux *loci*. Un seule groupe (Minorca) est monomorphe pour tous les trois *loci*.

L'intervention avec des individus à constitution génétique determinée peut être utilisée pour la prévention de pertes des gènes. Les auteurs signalent toutefois l'existence de l'allèle $Tf^C$ chez une autre race aussi: la Cou Nu de Transylvanie; ainsi qu'il est connu, cette allèle n'avait été signalée jusqu'à présent que chez le sraces Marans et Cornish.

## RESUMEN

Con la ayuda de la electroforesis en gelatina de almidón, se ha investigado el polimorfismo genético de los *loci* determinantes de las proteínas de la clara de huevo: las globulinas $G_3$ y $G_2$ y la conalbúmina, en 15 núcleos de gallinas de raza y líneas diferentes, mantenidos en número restringido como reserva genética. Se aprecia la tendencia de desviación de valores observados de los valores esperados, para detectar eventualmente los efectos del *drift* genético, y se evidencian las posibilidades de mantenimiento del polimorfismo característico de cada grupo.

Se recalca el hecho de que, aunque los grupos tienen un número efectivo relativamente pequeño, se mantiene, sin embargo, el polimorfismo por lo menos en dos de los tres *loci* estudiados. Un solo grupo (Minorca) es monomorfo en todos los *loci*.

Con esta ocasión, los autores señalan la presencia de alelos $Tf^C$ aun en la raza Gît Golas de Transilvania; como se sabe, este alelo fue señalado hasta el presente sólo en las razas Marans y Cornish.

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