Study on Correlation between Hb and Tf Locus Genotypes and Some Milk Yield Traits within a Gray Steppe Cattle Population

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Abstract
Having considered the importance of genetic polymorphism of biochemical structures we considered a study of the genetic characterization of a sample in a cattle population, based on the information offered by the genetic polymorphism at hemoglobin and transferrine loci and the analysis of the serum. Single phenotypic category, hemoglobin A, has been identified for hemoglobin locus. Five categories of individuals, homozygous for Tf^D/Tf^D, Tf^E/Tf^E genes and heterozygous for Tf^A/Tf^D, Tf^A/Tf^E, Tf^D/Tf^E have been identified on seric transferine loci.
Another objective of the report was to study whether the protein fractions types, observed in the electrophoresis field, at the loci coding the three types of proteins, influence certain traits of economic importance in the genetic improvement programs in cattle. The targeted traits within this study were: milk yield, milk fat percentage as well as amount of milk fat. Tf^E/Tf^E homozygous individuals recorded the highest milk yield, while Tf^A/Tf^D individuals recorded the lowest average milk production.

Keywords: genetic polymorphism, genetic structure, economic traits, correlations

1. Introduction

Having considered the importance of genetic polymorphism of biochemical structures we considered a study of the genetic characterization of a sample in a cattle population, based on the information offered by the genetic polymorphism at hemoglobin and transferrine loci and the analysis of the serum. Single phenotypic category, hemoglobin A, has been identified for hemoglobin locus.
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2. Materials and methods

In order to determine the types of serum proteins, blood samples were collected from 36 individuals of the breed Gray Steppe Cattle Population.

The technique of vertical electrophoresys was employed in order to determine the types transferine in the analysed samples, using polyacryl amidae as migration support.

For establishing the types of hemoglobin, we used the technique of vertical electrophoresys, using

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polyacryl amidae as a migration support, the same (1992), adapted to the conditions in the biochemistry laboratory the Faculty of Biology of The University of Bucharest [1].

The analysis was performed on ranges of individuals, grouped according to the aggregate genotypes expressed at the loci of proteins and the four targeted traits.

3. Results and discussion

Protein variants were described in order to use them as genetic markers with the purpose of determine the homogenity or heterogenity degree for the Gray Steppe cattle population, as the genetic inheritance (genofound) investigation has cattle breeds (table 1).

technique as used by Meriaux J.C. a special impact over the preservation measures in this breed [2,3].

The locus of haemoglobin

On the basis of electrophoresys interpretation, performed in order to establish the haemoglobin types for the observed population, a single type was observed in the electrophoretic field, corresponding to the A type for haemoglobin [4].

Accordingly, we can not conclude if a certain haemoglobin type is associated with higher performances for the studied production traits.

We may value that this type of cows, belonging to the Gray Steppe breed, is marked by a much lower milk quantity than for the cows that presents the same haemoglobin type from other

Table 1. Average performances according to haemoglobin locus genotype

Genotipul	N	Milk zield $\overline{X} \pm S\overline{X}$	Fat percentage $\overline{X} \pm S\overline{X}$	Fat zield $\overline{X} \pm S\overline{X}$
Hb^A/Hb^A	36	1589.61±133.46	4.47±0.11	81.11±6.71

Regarding the fat percentage, we may say that the established average performance for this trait is strongly to the performance averages mentioned in the literature for the cows presenting the haemoglobin A type.

As for the fat quantity in the milk, the performance average, registered by the cows with A haemoglobin type, is lower than the performance average obtained at the cows having the same haemoglobin type and belonging to other cattle breeds, in our country.

The locus of serum transferines

The interpretation of electrophoresis graphs for the 36 individuals has detected five categories of individuals: homozygous for genes Tf^D, Tf^E, heterozygous Tf^A/Tf^D, Tf^A/Tf^E and Tf^D/Tf^E (figure 1).

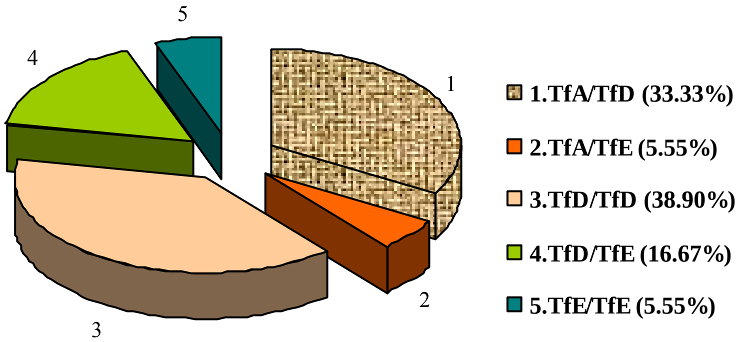

Figure 1. The weight (%) of genotypic categories on seric transferine locus

The presence of five genotype categories in the group demonstrates the presence of three categories of genes, Tf^A, Tf^D and Tf^E, identified with different frequency (figure 2).

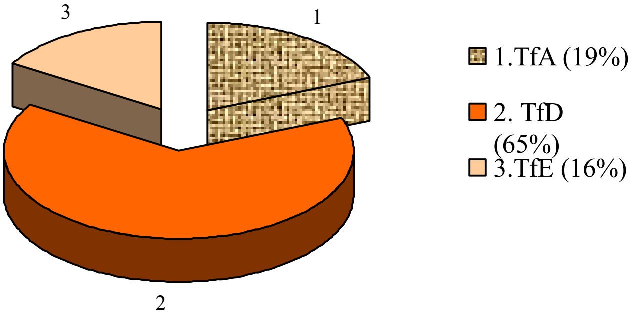

Figure 2. The weight (%) of genic categories on seric transferine locus

As a result of higher share of D type transferine, gene controlling this phenotype presents a 46%higher frequency as compared to Tf^A frequency, and 50% higher than Tf^E.

Determining the ratios of the genotype categories and, as a result, the genetic structure of the sample in this study allowed building an estimate for the status of genetic equilibrium, for locus analyzed. The results are presented in Table 2.

The analysis of genetic equilibrium was made using χ^2 test, and it led to the conclusion that the studied sample express genetic equilibrium for transferine locus [5].

Table 2. The estimate of genetic equilibrium

Genotypes	**Nr. of genotypes observed**	**Nr. of genotypes expected**	**d^2/A**
Serum transferine locus			
Tf^A/ Tf^A	0	1.2996	1.689
Tf^A/ Tf^D	12	8.8920	1.086
Tf^A/ Tf^E	2	2.1888	0.016
Tf^D/ Tf^D	14	15.2100	0.096
Tf^D/ Tf^E	6	7.4880	0.296
Tf^E/ Tf^E	2	0.9216	1.262
Total	36	36	χ^2= 4.44

For the individuals hierarchical system, depending on the performances obtained for the character regarding the milk quantity, fat percentage and fat quantity in the milk, the average performances were determined for each group of individuals, established depending on the genotype on transferrin locus.

The results are presented in Table 3.

Table 3. Average performances according to genotype on transferring locus

Genotypes	**N**	**Milk Yield** $\overline{X} \pm S\overline{X}$	**Fat percentage** $\overline{X} \pm S\overline{X}$	**Fat Yield** $\overline{X} \pm S\overline{X}$
Tf^A/Tf^D	12	1365.33±239.79	4.32±0.24	80.16±15.16
Tf^A/Tf^E	2	1920.00	4.90	94.00
Tf^D/Tf^D	14	1563.57±231.42	4.47±0.17	77.43±11.23
Tf^D/Tf^E	6	1839.66±334.73	4.63±0.26	84.00±14.22
Tf^E/Tf^E	2	2037.00	4.45	91.00

The data presented in table 3 shows that the group of cows presenting Tf^E/Tf^E genotype produced higher milk yield, respectively with 617.7 l of milk more than the Tf^A/Tf^D genotype cows which registered the best performance.

The Tf^A/Tf^E cow group is situated on the second place for this character, with a plus of 554.7 l comparatively with the lowest performance cow group.

By analyzing the performance averages for the five cow categories, it may be observed that the cows who have in the genotype at least a Tf^E gene are characterized by a good milk production.

It is very possible that the gene Tf^E is associated with a great amount of milk, situation valid for cows of Gray Steppe breed.

A great variability degree was observed for the Tf^D/Tf^E cow group, which directed to a sufficient great average error.

The higher fat percentage was found for the genotype Tf^A/Tf^E cow group, respectively with 0.58 percentages more than for the cows which present the genotyp, which gives the lowest fat percentage in the milk.

A second category of cows which realize a good average for this character performance is the one who present the genotype Tf^D/Tf^E, with a difference of only 0.27 percentages less than the group of cows having the best performance.

The groups of cows presenting type D, respectively type E of transferine were placed on the third place, having approximately the same performance average for the fat percentage character.

The best fat quantity was found at cows with AE type of transferine. These cows realize 16,57 kg extra than the cows having type D of transferine, for which was determined the lowest fat quantity in the milk.

It was established that cows with Tf^E gene presents a higher performance for fat quantity in the milk.

If the three studied characters are simultaneously analyzed, it may be observed the superiority of cows with Tf^A/Tf^E genotype, who realize the best performances for two from the three analyzed characters, respectively for fat percentage and fat quantity in the milk. As for the third character, milk quantity, this group of cows is placed on the second place.

The lowest performances were registered for cows with AD type of transferine. This cow category is on the last position for characters regarding milk quantity and fat percentage, and on the last but one place for the third character, respectively fat quantity in the milk.

We may conclude, taking into account the performance averages for three analyzed characters, that Tf^E gene is associated with higher performances.

4. Conclusions

1. At the haemoglobin locus, a single category of individuals was identified, respectively homozygous Hb^A/Hb^A.
2. The polymorphism study from the seric protein locus pointed out five genotypic categories: Tf^D/Tf^D, Tf^E/Tf^E, Tf^A/Tf^D, Tf^A/Tf^E and Tf^D/Tf^E
3. Following the analysis of the genetic balance conditioner seric transferine locus, was concluded that a genetic balance condition already exist for the analyzed population.
4. The highest milk production was registered for the homozygous individuals Tf^E/Tf^E.
5. Following the hierarchical system of the average performances for three studied characters, the individuals heterozygous Tf^A/Tf^D were placed on the last place.

On the basis of the original researches, pointing the main conclusion of the work.

Acknowledgements

"This work was cofinanced from the European Social Fund through Sectoral Operational Programme Human Resources Development 2007-2013, project number POSDRU/89/1.5/S/63258 ”Postdoctoral school for zootechnical biodiversity and food biotehnology based on the eco-economy and the bio-economy required by eco-san-genesys”.

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