# GENETIC STRUCTURE OF ITALIAN CATTLE BREEDS STUDIED BY MEANS OF HAEMATIC POLYMORPHISMS UNDER GENETIC CONTROL

## Das genetische System des hämatischen Polymorphismus beim Studium der genetischen Struktur der Rinderpopulation Italiens

## Les systèmes génétiques des polymorphismes hématiques pour les études de la génétique de populations chez les races bovines italiennes

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### Introduction

The genetic behaviour of haematic polymorphisms in cattle has been studied, making possible to point out the rules of inheritance for nearly all the investigated characters and to apply these knowledges to studies on genetic population (A. B. A., 1969; Bouquet and Grosclaude, 1968; Barbieri *et al.*, 1969; Carenzi C. *et al.*, 1969; Fiorentini *et al.*, 1969; Rognoni *et al.*, 1969; Crimella C., Persiani *et al.*, 1970). The main interest of these studies is due to the possibility of utilizing such genetically controlled biochemical and antigenic polymorphisms for the characterisation of different cattle breeds, for phylogenetic studies and for the planning and control of selection on a genetic bases (Bouquet *et al.*, 1970); Kidd e Zonta Sgaramella, 1970). It is necessary therefore, a deep knowledge of the genetic behaviour of the haematic polymorphisms in the studied breeds. For this purpose since many years our institute is carrying on researches both on the detection of erythrocyte antigens, by means of isoimmune sera, and the detection of protein and enzyme polymorphisms by means of electrophoretic techniques.

Since every year our Istitute is testifying more than 10,000 blood sample from the different Italian breeds, we have at our disposal a good deal of data for the statistical analysis applied to the population genetics.

The purpose of this research is to go deep into knowledge of the genetic structure of the studied breeds, both by means of the genic frequencies and the homozygosity degree; moreover, we utilize these gene frequencies for a philogenetic study of the italian breeds and for a characterisation of populations and strains within the Holstein Friesian and Brown Swiss breeds in Italy.

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MATHERIAL AND METHODS

The blood group formulae have been detected by isoimmune sera, obtained in our laboratory according to the techniques described by FIORENTINI e GALIZZI (1967) (see Table 1). The haemolitic test has been performed as described by ROGNONI (1969) with a slight modification. The techniques utilized in the determination of protein and enzyme polymorphisms were the classic ones of SMITHIES (1955, 1957, 1958), SMITHIES and HICKMAN (1958), slightly modified.

TABLE 1

ISOIMMUNE REAGENTS UTILIZED FOR THE BLOOD GROUPS FORMULA DETERMINATION
(from CARENZI et coll., 1970)

| *Locus* | Reagents |
|---|---|
| *A* | $A_1$, $A_2$, *H* |
| *B* | *B*, *G*, *K*, $I_1$, $I_2$, $O_1$, *O*, $O_3$, $O_4$, *P*, *Q*, $T_1$, $Y_2$, *A'*, *B'*, *D'*, $E'_1$, $E'_3$, *F'*, *G'*, *G''*, *I'*, $I'_2$, *J'*, $J'_2$, *K'*, *O'*, $O'_2$, *P'*, *Q'*, *Y'*, $M_6$ |
| *C* | $C_1$, $C_2$, $R_1$, $R_3$, *W*, $X_1$, $X_2$, *C'*, *L'* |
| *F* | *F*, *V* |
| *J* | *J* |
| *L* | *L* |
| *M* | *M* |
| *S* | *H'*, *S*, *U*, *U'*, *U''* |
| *Z* | *Z* |
| *R'* | *R'*, *S'* |

Not all the subjects have been tested for each *locus*; in the table are indicated the number of subjects utilized for each breed, and the gene frequencies at the considered *locus*.

Where possible, the allelic frequencies have been calculated by the gene counting; while in the case of dominance we calculated the root square of the frequency of the recessive factors.

The homozygosity indexes have been calculated by means of $\Sigma_i q^2_e$ according to FALCONER (1967). Only for the *loci* with non- significant $\chi^2$ the genetic homogeneity has been calculated as the probability of random drawing two equal genotypes, by means of $p^4 + 4p^2 q^2 + q^4$; the genetic likeness of the considered breeds has been calculated with the $\chi^2$ test according to BRANDT and SNEDECOR, utilizing the observed allelic frequencies for *loci* with condominant alleles and the stimated ones for the *loci* with dominant and recessive alleles.

To value the B-system allotypes distribution, in different districts, we utilized the $\chi^2$ test according to SCORY; since the $\chi^2$ values were higly significant, we

utilized the KIMBALL decomposition for the first nine phenogroups more frequent between the zones of maximum and minimum frequency.

## RESULTS

Table 2 reports the allelic frequencies in the most important italian breeds; only in the Piedmont cattle we could find the *Tf H*; in the same breed we did

TABLE 2

ALLELIC FREQUENCIES OF THE DIFFERENT LOCI IN THE VARIOUS BREEDS
(from CARENZI et coll., 1970)

| | | Breed | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Chianina | | Marchigiana | | Piedmont | | Valdostana red pied | | Friulana red pied | | Rendena | |
| *Locus* | Allele | N° of subjects | frequency | N° of subjects | frequency | N° of subjects | frequency | N° of subjects | frequency | N° of subjects | frequency | N° of subjects | frequency |
| *Hb* | *A* | 264 | 0,964 | 112 | 0,987 | 66 | 0,917 | 63 | 0,904 | 94 | 0,894 | 94 | 0,883 |
| | *B* | | 0,036 | | 0,013 | | 0,083 | | 0,095 | | 0,106 | | 0,117 |
| *Ca* | *S* | 264 | 0,928 | 115 | 0,804 | 66 | 0,773 | 62 | 0,968 | 95 | 0,679 | 94 | 0,947 |
| | *F* | | 0,072 | | 0,196 | | 0,227 | | 0,032 | | 0,321 | | 0,053 |
| *Tf* | *A* | 259 | 0,334 | 125 | 0,324 | 64 | 0,351 | 63 | 0,190 | 95 | 0,284 | 94 | 0,250 |
| | $D_1$ | | 0,328 | | 0,192 | | 0,109 | | 0,182 | | 0,216 | | 0,122 |
| | $D_2$ | | 0,313 | | 0,340 | | 0,476 | | 0,603 | | 0,458 | | 0,590 |
| | *E* | | 0,025 | | 0,144 | | 0,016 | | — | | 0,042 | | 0,037 |
| | *H* | | — | | — | | 0,047 | | 0,024 | | — | | — |
| *Alb* | *S* | 264 | 0,114 | 124 | 0,258 | 66 | 0,000 | 56 | 0,018 | 92 | 0,022 | 94 | 0,005 |
| | *F* | | 0,886 | | 0,742 | | 1,000 | | 0,982 | | 0,978 | | 0,995 |
| *Am* | *B* | 256 | 0,801 | 116 | 0,888 | 63 | 0,714 | 63 | 0,849 | 91 | 0,797 | 94 | 0,814 |
| | *C* | | 0,199 | | 0,112 | | 0,286 | | 0,151 | | 0,203 | | 0,186 |
| *FV* | $F^F$ | 378 | 0,857 | 127 | 0,756 | 62 | 0,790 | 137 | 0,774 | 99 | 0,919 | 124 | 0,754 |
| | $F^V$ | | 0,143 | | 0,244 | | 0,210 | | 0,226 | | 0,081 | | 0,246 |
| *R'S'* | $R'^{R'}$ | 378 | 0,196 | 127 | 0,193 | 62 | 0,242 | 137 | 0,146 | 99 | 0,167 | 124 | 0,181 |
| | $R'^{S'}$ | | 0,804 | | 0,807 | | 0,758 | | 0,854 | | 0,833 | | 0,818 |
| *J* | $J^J$ | 378 | 0,161 | 127 | 0,167 | 0 | — | 137 | 0,100 | 99 | 0,062 | 124 | 0,197 |
| | $J^-$ | | 0,839 | | 0,832 | | — | | 0,900 | | 0,937 | | 0,803 |
| *L* | $L^L$ | 378 | 0,289 | 127 | 0,158 | 62 | 0,207 | 137 | 0,167 | 99 | 0,147 | 124 | 0,192 |
| | $L^-$ | | 0,711 | | 0,842 | | 0,793 | | 0,833 | | 0,853 | | 0,808 |
| *M* | $M^M$ | 378 | 0,027 | 127 | 0,016 | 62 | 0,075 | 137 | 0,018 | 99 | 0,015 | 124 | 0,000 |
| | $M^-$ | | 0,973 | | 0,984 | | 0,924 | | 0,981 | | 0,985 | | 1,000 |
| *Z* | $Z^Z$ | 378 | 0,714 | 127 | 0,556 | 62 | 0,579 | 137 | 0,564 | 99 | 0,364 | 124 | 0,322 |
| | $Z^-$ | | 0,286 | | 0,444 | | 0,421 | | 0,436 | | 0,678 | | 0,678 |

TABLE 3

PROBABILITY OF RANDOM DRAWING TWO EQUAL GENES
(from CARENZI et coll., 1970)

| *Locus* | Breed* | | | | | |
|---|---|---|---|---|---|---|
| | Chianina | Marchigiana | Piedmont | Valdostana red pied | Friulana red pied | Rendena |
| *Hb* | 0,931 | 0,974 | 0,847 | 0,828 | 0,810 | 0,793 |
| *Ca* | 0,866 | 0,685 | — | 0,938 | 0,564 | 0,899 |
| *Tf* | 0,318 | 0,278 | 0,365 | 0,434 | 0,339 | 0,427 |
| *Alb* | 0,799 | 0,617 | 1,000 | 0,965 | 0,957 | 0,989 |
| *Am* | 0,681 | 0,801 | 0,592 | 0,744 | 0,676 | 0,697 |
| *FV* | 0,755 | 0,631 | 0,669 | 0,650 | 0,851 | 0,629 |
| *R'S'* | — | 0,689 | 0,633 | 0,751 | 0,722 | 0,703 |
| *J* | 0,730 | 0,721 | — | 0,820 | 0,883 | 0,684 |
| *L* | 0,589 | 0,734 | 0,672 | 0,721 | 0,749 | 0,690 |
| *M* | 0,948 | 0,969 | 0,861 | 0,964 | 0,970 | 1,000 |
| *Z* | 0,591 | 0,506 | 0,512 | 0,508 | 0,537 | 0,563 |

* The values indicate the $\Sigma q^2$.

not find the *S* variant of albumin; the *E* variant of trasferrins and the *M* antigen of blood groups have not been found in the Valdostana red pied and in the Rendena breeds. The agreement with HARDY-WEINBERG model has been calculated for each *locus* and in no case we could find a significant deviation from the expected frequencies.

In the Table 3 are reported the $\Sigma q^2$ values for each *locus*, which express the possibily of random drawing two equal genes from a population (homozygosity

TABLE 4

PROBABILITY OF RANDOM DROWING TWO EQUAL GENOTYPES
(from CARENZI et coll., 1970)

| *Locus* | Breed | | | | | |
|---|---|---|---|---|---|---|
| | Chianina | Marchigiana | Piedmont | Valdostana red pied | Friulana red pied | Rendena |
| *Hb* | 0,868 | 0,948 | 0,729 | 0,670 | 0,674 | 0,651 |
| *Ca* | 0,760 | 0,519 | — | 0,881 | 0,413 | 0,814 |
| *Tf* | 0,168 | 0,129 | 0,200 | 0,242 | 0,178 | 0,240 |
| *Alb* | 0,658 | 0,454 | 1,000 | 0,932 | 0,918 | 0,979 |
| *Am* | 0,515 | 0,661 | 0,434 | 0,586 | 0,510 | 0,532 |
| *FV* | 0,600 | 0,466 | 0,501 | 0,484 | 0,736 | 0,465 |
| *R'S'* | — | 0,522 | 0,468 | 0,595 | 0,560 | 0,538 |
| *J* | 0,569 | 0,559 | — | 0,689 | 0,786 | 0,518 |
| *L* | 0,431 | 0,574 | 0,505 | 0,559 | 0,593 | 0,524 |
| *M* | 0,890 | 0,939 | 0,750 | 0,930 | 0,941 | 1,000 |
| *Z* | 0,433 | 0,378 | 0,381 | 0,379 | 0,395 | 0,413 |

* The values indicate $p^4 + 4\,p^2\,q^2 + q^4$.

degree); in Table 4 the genetic homogeneity of the considered breeds is valued; Table 5 completes the genetic view on th Italian breds, giving a comparison between the real and estimated frequencies in the various breeds.

TABLE 5

ALLELIC FREQUENCIES, REAL AND ESTIMATED, OF ALL THE BREEDS
(from CARENZI et coll., 1970)

| Allele | Comparison between all the breeds |
|---|---|
| | real allelic frequencies |
| $Hb^A$ ... ... ... ... ... | 34,413 *** |
| $Ca^S$ ... ... ... ... ... | 113,098 *** |
| $Tf^A$ ... ... ... ... ... | 13,681 ** |
| $Tf^{D1}$ ... ... ... ... ... | 55,201 *** |
| $Tf^{D2}$ ... ... ... ... ... | 73,711 *** |
| $Tf^E + Tf^H$ ... ... ... | 52,490 *** |
| $Alb^E$ ... ... ... ... ... | 130,599 *** |
| $Am^B$ ... ... ... ... ... | 18,576 *** |
| $F^2$ ... ... ... ... ... | 39,239 *** |
| $R'^{S'}$ ... ... ... ... ... | 6,537 |
| | estimated allelic frequencies |
| $J^-$ ... ... ... ... ... | 23,188 *** |
| $L^-$ ... ... ... ... ... | 38,638 *** |
| $M^-$ ... ... ... ... ... | 23,310 *** |
| $Z^z$ ... ... ... ... ... | 160,396 *** |

(1) ** = $P < 0{,}05$; *** = $P < 0{,}001$.

TABLE 6

OBSERVED FREQUENCIES OF THE MORE COMMON B-SYSTEM PHENOGROUPS IN THE HOLSTEIN FRIESIAN AND BROWN SWISS BREEDS
(from FIORENTINI and coll., 1969)

| Phenogroups | % freq. in H. F. | % freq. in B. S. | Phenogroups | % freq. in B. S. | % freq. in H. F. |
|---|---|---|---|---|---|
| $GY_2E'_1Q'$ ... ... ... ... ... ... ... ... | 12,67 | — | $GO_2O'H_4$ ... ... ... ... ... ... | 9,73 | 0,17 |
| $I_2$ ... ... ... ... ... ... ... ... ... ... | 10,59 | 0,20 | $O_1T_1Y_2E'_3F'H_4$ ... ... ... ... | 6,81 | 0,47 |
| $BO_3Y_2A'E'_3G'P'Q'H_4$ ... ... ... ... | 4,70 | 0,02 | $Y_2$ ... ... ... ... ... ... ... ... | 6,76 | 0,65 |
| $E'_3H_4$ ... ... ... ... ... ... ... ... ... | 4,46 | — | $I_1E'_3G'H_4$ ... ... ... ... ... ... | 6,32 | 0,41 |
| $BO_1Y_2D'H_4$ ... ... ... ... ... ... ... | 4,34 | 0,07 | $O_1O'H_4$ ... ... ... ... ... ... ... | 6,06 | 0,77 |
| $BGKO_2Y_2A'O'H_4$ ... ... ... ... ... | 3,45 | — | $O_3E'_2F'_3J'_2H_4H_{1,2}$ ... ... ... ... | 4,51 | 0,41 |
| $I'H_4$ ... ... ... ... ... ... ... ... ... | 3,15 | 0,28 | $GO_2E'_3F'O'H_4$ ... ... ... ... ... | 4,00 | — |
| $Q'_1H_4$ ... ... ... ... ... ... ... ... ... | 2,91 | 1,31 | $BI'P'H_2$ ... ... ... ... ... ... ... | 3,51 | 0,05 |
| $BO_3A'I'P'Q'H_1$ ... ... ... ... ... ... | 2,44 | 0,02 | $BI_1$ ... ... ... ... ... ... ... ... | 2,35 | 0,17 |
| $Q'$ ... ... ... ... ... ... ... ... ... ... | 1,96 | 1,75 | $OJ'K'O'_2$ ... ... ... ... ... ... ... | 2,29 | 0,83 |

TABLE 7

FRECUENCIES ON THE TOTAL POPULATION AND IN THE SINGLE DISTRICTS FOR THE HOLSTEIN FRIESIAN BREED

| Phenogroups | % on the total | % in the Mantova district | % in the Cremona district | % in the Milano district |
|---|---|---|---|---|
| $GY_2E'_1Q'$ | 12,6786 | 9,1743 | 16,8085 | 19,2139 |
| $I_2$ | 10,5952 | 15,5963 | 2,7659 | 5,2401 |
| $BO_1Y_2A'E'_3G'P'Q'H_2$ | 4,7024 | 6,4220 | 0,8510 | 5,2401 |
| $E'_3H_4$ | 4,4643 | 5,0968 | 3,8297 | 3,0567 |
| $BO_1Y_2D'H_4$ | 4,3452 | 5,1987 | 3,6170 | 2,1834 |
| $BGKO_xY_2A'O'H_4$ | 3,4524 | 4,7910 | 1,0638 | 2,6200 |
| $I'H_1$ | 3,1548 | 3,8735 | 0,8510 | 4,8034 |
| $O'H_1$ | 2,9167 | 2,8542 | 3,6170 | 1,7467 |
| $BO_1A'I'P'Q'H_4$ | 2,4405 | 2,4464 | 3,1914 | 0,8733 |
| $Q'$ | 1,9643 | 1,1213 | 2,9787 | 3,4934 |
| $O_1Y_2A'$ | 1,8452 | 0,3058 | 4,4680 | 3,0967 |
| $O_1A'H_4$ | 1,7957 | 1,1213 | 3,1914 | 1,7467 |
| $BGKO_xE'_2F'O_2H_1H_{1?}$ | 1,7957 | 1,7329 | 2,5531 | 0,4366 |
| $BO_2A'E'_3G'P'Q'$ | 1,6071 | 2,3445 | 0,2127 | 1,3100 |
| $GI_1$ | 1,3690 | 0,6116 | 2,9787 | 1,3100 |
| $BO_1H_1$ | 1,2500 | 0,7135 | 2,7659 | 0,4366 |
| $Y_2D'G'I'Q'H_1$ | 1,2500 | 1,6309 | 0,2127 | 1,7467 |
| $PI'H_4$ | 1,0714 | 1,4271 | 0,6382 | 0,4366 |
| $Y_2E'_2G'Y_2$ | 0,9524 | 1,2232 | 0,6382 | 0,4366 |
| $GO_1Y_2H_1$ | 0,8929 | 1,0193 | 0,8510 | 0,4366 |
| Phenogroups at lower frequency ... | 35,4762 | 31,2946 | 41,9149 | 40,1747 |

TABLE 8

$\chi^2$ VALUES OF THE MOST FREQUENT PHENOGROUPS, ACCORDING TO SKORY AND THE DECOMPOSITION METHOD OF KIMBALL

(from FIORENTINI and coll., 1969)

| | | | |
|---|---|---|---|
| $BGKO_xY_2A'O'H_4$ | Between Mantova and Cremona = 1,3251 | n. s. | (1 g. l.) |
| $BO_3Y_2A'E'_3G'P'Q'H_4$ | Between Mantova and Cremona = 22,0069 | | (1 g. l.) |
| $BO_1A'I'P'Q'H_4$ | Between Cremona and Mantova = 3,4752 | n. s. | (1 g. l.) |
| $BO_1Y_2D'H_4$ | Between Mantova and Milano = 4,0614 | | (1 g. l.) |
| $GY_2E'_1Q'$ | Between Mantova and Milano = 16,9030 | | (1 g. l.) |
| $I'H_2$ | Between Cremona and Milano = 7,8729 | | (1 g. l.) |
| $I_2$ | Between Mantova and Cremona = 55,2213 | | (1 g. l.) |
| $E'_3H_4$ | Between Mantova and Milano = 1,8117 | | (1 g. l.) |
| $Q'H_1$ | Between Cremona and Milano = 1,9021 | n. s. | (1 g. l.) |

$\chi^2$ according to SKORY = 177,65916 (d. f. = 24).
$\chi^2$ decomposition according to KIMBALL.

The B-system, one of the most interesting in the blood group systems owing to its high haplotype number, has been studied only in the Holstein Friesian and Brown Swiss breeds in Italy. To simplify, in Table 6 only the frequencies of the more common B-system haplotypes for the two breeds are reported.

It can easily be seen how the two breeds differ in their genetic structure.

TABLE 9

FREQUENCIES ON THE TOTAL POPULATION AND IN THE SINGLE DISTRICTS FOR THE BROWN SWISS
(from FIORENTINI and coll., 1969)

| Phenogroups | % on the total | % in Valtellina | % in Trentino |
|---|---|---|---|
| $GO_1O'H_1$ | 9,7366 | 10,6189 | 8,9089 |
| $O_1T_1Y_2E'_3F'H_4$ | 6,8182 | 7,2038 | 4,4564 |
| $Y_2$ | 6,7665 | 5,0693 | 8,3593 |
| $I_1E'_3G'H_4$ | 6,3275 | 5,9765 | 6,6566 |
| $O_1O'H_4$ | 6,0692 | 6,1899 | 5,9559 |
| $O_3E'_3F'_2J'_2H_4H_{12}$ | 4,5196 | 2,9348 | 6,0060 |
| $GO_1E'_3F'O'H_4$ | 4,0031 | 5,3361 | 2,7527 |
| $BI'P'H_4$ | 3,5124 | 3,0416 | 3,9539 |
| $BI'$ | 2,5310 | 2,6680 | 2,4024 |
| $OJ'K'O'_2$ | 2,2986 | 2,0811 | 2,5025 |
| $O_1A'$ | 2,2211 | 1,4407 | 2,9529 |
| $Q'$ | 1,7562 | 1,6542 | 1,6016 |
| $BGKO_xA'B'O'H_4$ | 1,6529 | 1,0138 | 2,2522 |
| $BO_3A'P'Q'H_4$ | 1,5496 | 2,4012 | 0,7507 |
| $BGKO_3O'H_4$ | 1,5496 | 2,2945 | 0,8508 |
| $I'Q'H_4$ | 1,4979 | 1,4941 | 1,5015 |
| $I_1Y_2Y'H_4$ | 1.4721 | 1,8676 | 1,1011 |
| $BGKO_xE'_2F'G'O'_2H_{12}$ | 1,4721 | 1,8143 | 1,1511 |
| $Q'H_4$ | 1,3171 | 1,3874 | 1,2512 |
| $O_1E'_1$ | 1,2913 | 2,2411 | 0,4007 |
| Phenogroups at lower frequencies... | 31,6413 | 31,2704 | 31,9821 |

In Tables 7 and 9 it can be seen distribution of the frequencies of the B-system haplotypes in different districts for the same breed; in Tables 8 and 10 the $\chi^2$ values calculated on the most frequencies of the most common phenogroups, both in Holstein Friesian and in Brown Swiss, were reported.

TABLE 10

$\chi^2$ VALUES OF THE MOST FREQUENT PHENOGROUPS, ACCORDING TO SKORY AND THE DECOMPOSITION METHOD OF KIMBALL
(from FIORENTINI and coll., 1969)

| | | | |
|---|---|---|---|
| $BI_1Q$ | $\chi^2 = 1$ n. s. | $Y_2$ | $\chi^2 = 16{,}8510$ *** |
| $BI'P'H_4$ | $\chi^2 = 2{,}3749$ n. s. | $O_1$, $T_1$, $Y_2$, $E'_3$, $F'$, $H_4$ | $\chi^2 = 1$ n. s. |
| $BGKO_xA'B'O'H_4$ | $\chi^2 = 9{,}1760$ ** | $O_3$, $E'_3$, $F'_2$, $J'_2$, $H_4$, $H_{12}$ | $\chi^2 = 21{,}1350$ *** |
| $BO_1$ | $\chi^2 = 7{,}5514$ ** | $O_1$, $E'_1$ | $\chi^2 = 25{,}7069$ *** |
| $BO_3A'P'Q'H_4$ | $\chi^2 = 10{,}827$ ** | $OJ'$, $K'$, $O'_2$ | $\chi^2 = 1$ n. s. |
| $BGKO_xE'_2F'G'O'_2H_{12}$ | $\chi^2 = 2{,}9319$ n.s. | $O_x$, $O'$, $H_4$ | $\chi^2 = 1$ n. s. |
| $BGKO_xO'H_4$ | $\chi^2 = 13{,}2115$ *** | $O_x$, $E'_3$, $F'$, $O'$ | $\chi^2 = 6{,}6837$ ** |
| $GO_1O'H_4$ | $\chi^2 = 3{,}2177$ n. s. | $O_x$, $A'$ | $\chi^2 = 10{,}1819$ ** |
| $GO_1E'_3F'O'H_4$ | $\chi^2 = 16{,}7945$ *** | $Q'$ | $\chi^2 = 1$ n. s. |
| $I_1E'_3G'H_4$ | $\chi^2 = 1$ n. s. | $O'$, $H_4$ | $\chi^2 = 1$ n. s. |
| $I_1Y_2Y'H_4$ | $\chi^2 = 3{,}9176$ * | $H_4$ | $\chi^2 = 3{,}7323$ n. s. |
| $I'Q'H_4$ | $\chi^2 = 1$ n. s. | | |

$\chi^2$ according to SKORY = 170,166230 (d. f. = 26).
$\chi^2$ decomposition according to KIMBALL.

## Conclusions and discussion

From the results here reported we can point out some considerations; through the utilized parameters it has been possible to quantify the differences between the studied breeds as can be seen from the highly significance of the comparison among the allelic frequencies of the various breeds. This was expected since the six considered breeds are quite different in origin and morphological aspect. The genetic variability at the *B locus* has been studied only in the Holstein Friesian and Brown Swiss cattle, owing to the high polymorphism of this *locus* and the difficulty to obtain a sufficiently wide and random sampling; it is interesting to notice how the two breeds are different and moreover how it is possible to differentiate within a breed the different strains. In fact, we know that in the Cremona district the Canadian Holstein Friesian imported strain has been intensively utilized, while in the Mantova district have been overall utilized subjects of European origin and in the Milano district the American ones.

The higly significant $\chi^2$ of the comparison between the districts confirms the usefulness of haematic polymorphisms in the control of the differences between populations within a breed and as a criterion to value the selection degree.

Since the traditional methods for the distinction of different breeds, based only on the morphological aspects, lacks of scientific basis, it is obvious how important is the knowledge of the genetic structure both from a population genetics and a phylogenetic point of view.

Even if it is not actually possible, in the animal breeding practice, to overcome the traditional distinction between breeds, it would be right to tend to a more wide analysis of the genetic situation of the animals breeds studying the genetic variability and utilizing these knowledges to program the selection in the breeds of practical use. We have seen how, by means of the haematic polymorphisms, a complete analysis can be performed in a quite simple way.

The modern zootechnics bases the genetic improvement of quantitative characters on two programs: selection and planning of matings. Selection consists in the use of subjects able to trasmit more favorable characters if compared with the average population; this leads to a reduction of variability, which is necessary for the selection itself. Moreover selection apart from the subsequent matings planning, reducing the number of the utilized subjects increases the homozygosity of polymorphic characters, with the following decrease of genetic variability.

On this bases the study of genic frequencies allows us to control the homozygosity degree and hence the selective pressure on a given population.

The continuous control of the genetic situation in a population is the bases of selection and matings planning, by the use of imbreeding and outbreeding for the maintenance of the genetic variability, which is necessary to the production improvement.

## SUMMARY

The authors point out the usefulness of Mendelian genetic systems, particularly the haematic polymorphisms, in the study of cattle population genetics. The authors report the results of the researches performed on the Italian cattle

breeds and of populations within a breed, and for the evaluation of the homogeneity in the examined populations.


## ZUSAMMENFASSUNG

Die Autoren unterstoeichen die Nutzlichkeit der MENDEL'schen Vererbungssysteme und besonders der des hämatischen Polymorphismus für das Studium der populations Genetie der Rinder. Sie berichten uber Untesuchungsresultate an italienischen Rinderrassen, die einige Kriterien der Rassenunterscheidung der Unterscheidung verschiedener Populationen innerhalb einer Rasse, und der Valutation der Homogenität innerhalb der Populationen stabilieren setten.

## RESUME

Les auteurs discutent l'utilité des systèmes génétiques mendeliennes et surtout celui des polymorphismes hématiques pour les études de la génétique de populations chez les bovins. Tout specialement ils réferént les resultats das recherches sur les races italiennes pour établir des critères de distinction entre les races et entre différent populations à l'intérieur de la même race, et pour evaluer l'homogénéité présente dans les populations en examen.


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