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RIASSUNTO – Analisi di pedigree nelle razze italiane da carne – *Sono state analizzate le informazioni di pedigree di quattro razze da carne italiane (Chianina, Marchigiana, Romagnola e Maremmana) utilizzando il metodo della probabilità di origine genica. La razza Marchigiana ha mostrato i valori più bassi di numero effettivo di fondatori (f$_e$), ancestrali (f$_a$) e di genomi fondatori (N$_g$). La profondità dei pedigree è risultata ridotta ed all'ottava generazione gli ancestrali conosciuti erano meno del 3% per tutte le razze. Nel complesso i valori trovati per le 4 razze non si discostano da quelli incontrati per altre razze da carne confermando la discreta dimensione delle razze indagate dal punto di vista della diversità genetica. Si deve comunque monitorare per conservare al massimo il pool genico iniziale.*

KEY WORDS: beef cattle, pedigree analysis, genetic variability.

INTRODUCTION – Trend in inbreeding is the most frequently used method to quantify the rate of genetic drift but, as pointed out by Maignel *et al.* (1996), it relies on some assumption that could be not fully satisfied in cattle populations. In fact, trend in inbreeding is very sensitive to the quality of the available pedigree information and some beef cattle populations might have a large amount of missing information. An alternative way to quantify the genetic drift is to utilise the method based on probabilities of gene origin (Boichard *et al.*, 1997) with its various measures of genetic contributions of the founders. This approach has been employed in this paper to analyse the pedigree structure of some Italian beef cattle breeds [Chianina (CN), Marchigiana (MC), Romagnola (RM) and Maremmana (MM)] in order to verify the maintenance of the original gene pool.

MATERIAL AND METHODS – Complete pedigree of the four breeds were available for the analysis. For each pedigree the following parameters were calculated: i) generation interval for reproducing progeny, ii) inbreeding parameters, iii) average number of ancestors, iv) effective number of founders (f$_e$), v) effective number of ancestors (f$_a$), vi) effective number of founder genomes (N$_g$).10,000 replications for each population were run using PEDIG software (Boichard, 2002). A detailed description of these measures is reported elsewhere (Boichard *et al.*, 1997; Sölkner *et al.*, 1998).

RESULTS AND CONCLUSIONS – The generation intervals were computed for the four populations and five years was taken as being approximately the equivalent of a generation. The reference population was thus defined as those female animals registered in the herd books from 1992 to 1996 which had been mated at least once.

Table 1 reports the consistencies of the four populations and the inbreeding coefficients. MM is the smallest population whereas MC is the greatest one. Average inbreeding is below 10% for all populations and MC shows the maximum value (47.02). Results of the pedigree analysis for the reference populations are reported in Table 2. The average number of ancestors reflects the time since recording of pedigree data is started and, accordingly, the lowest values has been found in MM breed. Also the equivalent number of known generations shows differences among the populations, with the lowest value reported for MM and the highest for CN. Such different results are strictly related to the depths of the pedigrees

(Table 3), in fact only 18.92% of ancestors are known for MM at generation 4 whereas, at the same generation, CN has 69.83% of known ancestors. It is noteworthy to point out that, already at generation 8, all the analysed populations showed less than 3% of known ancestors. Similar values have been found only in some highly endangered Austrian cattle (Baumung and Sölkner, 2002) or in Abondance breed (Boichard *et al.*, 1997).

Table 1.   Number of individuals and inbreeding parameters.

	CN	MC	MM	RM
No. of individuals	260,441	350,710	29,351	119,489
No. of inbred individuals	95,341	97,359	4,383	55,262
Avg. inbreeding coeff.	0.033	0.040	0.071	0.024
Max. inbreeding coeff.	39.64	47.02	37.50	38.13

Table 2.   Results of the pedigree analysis for the reference populations.

	CN	MC	MM	RM
Size of reference population	20,336	34,884	2,252	11,276
Number of founders	7,182	14,531	1,419	4,557
Average number of ancestors	77.30	36.88	14.08	47.96
Equivalent no. of known generations	4.19	3.46	2.58	3.73
Effective number of founders (f_e)	167.1	83.8	142.3	94.2
Effective number of ancestors (f_a)	81.75	61.73	114.04	62.26
Number of founder genomes (N_g)	44.01	32.73	70.83	40.26

Despite the size of its reference population, the smallest values of f_e, f_a and N_g (Table 2) were found for MC breed whereas the highest values of f_a and N_g were found for MM breed. Probably, the management system has strongly influenced these results. In fact MC breed is characterised by small size of herds and intense use of A.I. whereas in MM breed A.I. is absent and herds are of medium or large size. The other two breeds, namely CN and RM, showed intermediate values and CN presented a strong reduction when moving from f_e to N_g, because of the more intense use of A.I. which might have produced some bottlenecks and loss of genes during segregation, as already observed by Pérez *et al.* (2002). Nevertheless the results for N_g in all the populations were within the range of values for cattle breeds found in the literature (Maignel *et al.*, 1996; Sölkner *et al.*,1998). As shown in Table 4, the contribute of the most important ancestor ranged from 4% (MM) to almost 8% (MC) and the first ten ancestors explain almost 30% of the genes present in the reference populations for CN, MC and RM breeds, whereas for MM they explain only 22% of the diversity. Thus it seems that MM breed could be the most genetically diverse population. However, observing the number of ancestors necessary to explain 50% of the genes in the reference populations it could be noted that the values are quite high for all the investigated breeds even when compared with data in the literature (Baumung and Sölkner, 2002; Maignel *et al.*, 1996; Sölkner *et al.*, 1998).

Table 3.   Percentage of known ancestors.

	CN	MC	MM	RM
Generation 2	85.80	81.43	84.97	92.14
Generation 4	69.83	54.93	18.92	55.37
Generation 6	26.97	8.10	0.33	13.23
Generation 8	2.41	0.14	0.02	1.02

Table 4.   Description of most important ancestors.

	CN	MC	MM	RM
Proportion of genes contributed by:				
First ancestor	0.0573	0.0790	0.0402	0.0643
Second ancestor	0.0469	0.0528	0.0305	0.0498
Third ancestor	0.0390	0.0282	0.0247	0.0488
First 10 ancestors	0.2925	0.3300	0.2228	0.3359
No. ancestors contributing for the first 50%	44	28	45	27

Even with the variable quality of underlying pedigrees, this study highlights that the Italian beef cattle breeds under study are not small with regard to genetic diversity. Nevertheless the maintenance of the variability of their genic pool is highly recommended.

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