WORLD RABBIT SCIENCE 1996, 4(3), 121-126

GENETIC CHARACTERISTICS AND DISTANCES AMONGST SPANISH AND FRENCH RABBIT POPULATIONS

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ABSTRACT : A total of 990 rabbits were tested using 18 blood electrophoretic markers. These animals belong to 6 breed populations presently breed in Spain (Spanish Common, Spanish Giant, Butterfly, Burgandy Fawn, New Zealand White and Californian), one Spanish cross-breed population, three French crossbreed populations originated from the INRA selected lines (1077, 2066 and 9077) and one Wild Spanish population. 12 markers were found to be polymorphic (Dia-2, 6-Pgd, Es-1, Es-2, Es-3, Es-7, Ada, Hp, Tf, Ca-2 and Hb), each one being controlled by one locus and showing autosomal co-dominant Mendelian inheritance. We have found large differences in gene frequencies of Dia-2, 6-Pgd, Ada, Es-1, Es-2 and Es-3 loci in French populations. The genetic variabiliy estimated using the average degree of heterozygosity was lower in French than in Spanish populations. The results obtained from genetic distance analysis showed differences between French and Spanish populations. France 3 was the most divergent population. The genetic distance values obtained revealed that French populations are as different amongst themselves as they are between Spanish populations (the value obtained was corresponding to subspecie, NEI, 1987). These differences could have originated from the high selective pressure applied to parental lines. In the Spanish group, Spanish Giant was the most divergent population.

RÉSUMÉ: Caracteristiques genetiques et distances entre populations espagnoles et françaises de lapins.
Un total de 990 lapins appartenant à 11 populations élevés en France et en Espagne (Commun espagnol, Géant espagnol, Papillon, Fauve de Bourgogne, Néo-Zélandais Blanc et Californien, une lignée hybride espagnole et tros lignées hybrides françaises -obtenues pour croisement d'une lignée mère Néo-Zélandais Blanc et une lignée père Californien , toutes les deux fermées pendants 25 ans- et une population de lapins de garenne espagnole) ont été étudiés pour 11 marqueurs électrophorétiques sannguins polymorphes, avec une hérédité Mendélienne codominante (Dia-2, 6-Pgd, Es-1, Es-2, Es-3, Es-7, Ada, Hp, Tf, Ca-2 et Hb). On a trouvé de grandes différences pour les fréquences alléliques des loci Dia-2, 6-Pgd, Ada, Es-1, Es-2 et Es-3 dans les lignées françaises. La variabilité génétique, estimée par le degré moyen d'hétérozygote, était plus faible dans les lignées françaises que dans les lignées espagnoles. Les résultats des distances génétiques séparent les populations françaises des populations espagnoles. La population France 3 se distingue nettement des autres. Les populations françaises sont aussi éloignées les unes des autres qu' elles le sont des populations espagnoles (la valeur obtenue correspond à la distance entre 2 sous espèces). Ces différences sont peut-être dues à la grande pression de sélection réalisées dans les lignées parentales françaises. Le Géant espagnol étais le plus different des populations espagnoles.

INTRODUCTION

The study of genetically controlled biochemical polymorphisms of blood proteins is at present a useful tool to characterize livestock breeds and populations; hence it contributes to the knowledge of genetic similarities and distances amongst breeds (RICHARDSON *et al.*, 1980; ZARAGOZA *et al.*, 1987; ARANA *et al.*, 1987a,b).

Not only are these studies of genetic and phylogenetic interest but they may also be applied practically in livestock improvement programs. They provide information to the breeder in programs where hybrid vigour is desired and they are also useful to determine the genetic distances amongst the parental breeds.

Electrophoretically detected blood proteins have been studied in rabbits (RICHARDSON *et al.*, 1980; JUNEJA *et al.*, 1981; ZARAGOZA *et al.*, 1990). Given the importance of the conservation of the gene pool in the rabbit species and the increasing use of these animals as livestock, we have studied the genetic characterization and the genetic divergences in order to characterize the Spanish wild rabbit and domestic populations presently breed in France and Spain.

MATERIALS AND METHODS

A total of 990 rabbits were used in this study. They belong to populations of seven breeds: Spanish Common, 102 animals; Spanish Giant, 67; Butterfly, 79; Burgandy Fauve, 64; New Zealand White, 105; Californian, 81; Wild Spanish rabbit, 124; a Spanish crossbreed population, 100 ($F_1$of mating between selected New Zealand females and highly selected Californian males) and three French populations (called in this work as France 1, 2 and 3).

The origin of the last three populations has been described by ROCHAMBEAU (1994). France 1 (108 animals) is a crossbreed population obtained by mating of the 1077 line (originated from a pure-breed New Zealand White population in 1975) and a male selected line (called by the author as "line A"). France 3 (86 animals) or 9077 line is the control line with the same origin than 1077 pure line and France 2 (74 animals) is a different crossbreed population obtained in the same way than France 1, but in this case the female line was 2066 line (originated from a Californian population).

Samples (approx. 4 ml. of heparinized blood; 750 heparin units/tube) were collected from the ear's marginal vein. Samples were processed by the method described by ZARAGOZA *et al.*, (1987).

Eighteen blood proteins were studied by electrophoresis (Cat, Dia-1, Dia-2, 6-Pgd, Es1, Es-2, Es-3, Es-7, Ada, Ak, Sod, Hp, Cp, Alb, Trf, Ca-1 and Ca-2) following the techniques described by ZARAGOZA *et al.*, (1985, 1987) and ARANA and ZARAGOZA (1986).

In order to study genetic variability we estimated: gene frequencies, Hardy-Weinberg equilibrium, Wright Index (F) as a measure of Hardy-Weinberg equilibrium deviation (WRIGHT, 1965), partial and average heterozygosities, proportion of polymorphic loci and the average number of alleles per locus. Genetic distances were estimated by the procedure of NEI (1972). Genetic distance dendograms corresponding to the best solution obtained from distance matrix were elaborated using the UPGMA (Unweighted Pair-Group Method with Arithmetic averaging algorithm (SNEATH

Table 1: Genetic Structure at 11 rabbit populations established with 11 genetic markers.

Pol locus	Alleles and [B]Estimations	[A]N.Z:B.	Cal	S.C.	F1	F2	F3
Pgd	Pgd1	0.93	0.96	0.92	0.57	0.99	0.73
	Pgd2	0.07	0.04	0.08	0.043	0.01	0.27
	X2	N.S.	N.S.	***	N.S.	***	N.S.
	ho(he)	0.10 (0.12)	0.05 (0.07)	0.08 (0.15)	0.56 (0.49)	0 (0.03)	0.37 (0.39)
Es1	Es1A	0.36	0.52	0.38	0.78	0.62	0.08
	Es1B	0.64	0.48	0.62	0.22	0.38	0.92
	X2	N.S.	N.S.	N.S.	N.S.	N.S.	***
	ho(he)	0.40 (0.46)	0.50 (0.44)	0.45 (0.47)	0.37 (0.34)	0.47 (0.43)	0.10 (0.15)
Es2	Es2F	0.31	0.39	0.32	0.22	0.28	0.06
	Es2S	0.69	0.61	0.68	0.78	0.72	0.94
	X2	N.S.	N.S.	N.S.	N.S.	N.S.	N.S.
	ho(he)	0.36 (0.43)	0.42 (0.48)	0.47 (0.43)	0.35 (0.35)	0.41 (0.32)	0.10 (0.11)
Es7	Es7A	0.55	0.60	0.46	0.75	0.70	0.13
	Es7B	0.45	0.40	0.54	0.25	0.30	0.87
	X2	N.S.	N.S.	N.S.	N.S.	*	N.S.
	ho(he)	0.42 (0.50)	0.43 (0.48)	0.41 (0.50)	0.42 (0.37)	0.30 (0.42)	0.18 (0.22)
Hp	Hp1	0.34	0.23	0.43	0.55	0.68	0.60
	Hp2	0.66	0.77	0.57	0.45	0.32	0.40
	X2	N.S.	N.S.	N.S.	***	***	***
	ho(he)	0.36 (0.45)	0.29 (0.36)	0.44 (0.49)	0.11 (0.50)	0.11 (0.43)	0.16 (0.48)
Ca2	Ca2F	0.95	0.96	0.97	1	1	1
	Ca2S	0.05	0.04	0.03	0	0	0
	X2	***	N.S.	N.S.	---	---	---
	ho(he)	0.04 (0.09)	0.05 (0.07)	0.05 (0.05)	---	---	---
Trf	Trf1	1	1	1	1	1	1
	Trf2	0	0	0	0	0	0
	X2	---	---	---	---	---	---
	ho (he)	---	---	---	---	---	---
Hb	Hb1	0	0	0	0	0	0
	Hb2	1	1	1	1	1	1
	X2	---	---	---	---	---	---
	ho (he)	---	---	---	---	---	---
Dia-2	Dia-2A	0.78	0.75	0.87	0.39	0.50	0.50
	Dia-2B	0.14	0.17	0.02	0.47	0.50	0.49
	Dia-2C	0.08	0.08	0.11	0.14	0	0.01
	X2	N.S.	N.S.	N.S.	***	***	***
	ho(he)	0.34 (0.36)	0.37 (0.41)	0.22 (0.23)	1 (0.61)	1 (0.50)	0.99 (0.51)
Es3	Es3A	0.87	0.61	0.72	0.97	0.99	0.89
	Es3B	0.09	0.28	0.18	0.01	0	0.01
	Es3C	0.04	0.11	0.10	0.02	0.01	0.10
	X2	*	N.S.	N.S.	***	N.S.	N.S.
	ho(he)	0.20 (0.23)	0.56 (0.54)	0.35 (0.43)	0.05 (0.06)	0.03 (0.03)	0.22 (0.19)
Ada	Ada1	0.68	0.44	0.66	0.88	0.74	0.81
	Ada2	0.28	0.41	0.25	0.12	0.26	0.19
	Ada3	0.04	0.15	0.09	0	0	0
	Ada4	0	0	0	0	0	0
	X2	N.S.	N.S.	N.S.	N.S.	N.S.	N.S.
	ho(he)	0.40 (0.46)	0.56 (0.61)	0.47 (0.49)	0.21 (0.21)	0.39 (0.39)	0.36 (0.31)
Ho (s.e.)		0.15 (0.06)	0.19 (0.05)	0.17 (0.05)	0.18 (0.07)	0.15 (0.06)	0.14 (0.06)
He (s.e.)		0.18 (0.05)	0.21 (0.06)	0.19 (0.05)	0.17 (0.05)	0.16 (0.05)	0.14 (0.04)
F		0.15	0.10	0.09	-0.05	0.03	-0.04
X2F		2.49 (N.S.)	0.82 (N.S.)	0.88 (N.S.)	0.22 (N.S.)	0.08 (N.S.)	0.16 (N.S.)
Pol 99%		52.94	52.94	52.94	47.06	41.18	47.06
Pol 95%		47.06	41.18	47.06	41.18	35.29	47.06
# al/locus	(s.e.)	1.7 (0.19)	1.7 (0.19)	1.7 (0.19)	1.59 (0.17)	1.47 (0.12)	1.59 (0.17)

[A]Populations: N. Z. B., New Zealand White; Cal., Californian; S.C., Spanish Crossbred; F1, F2, F3, French populations.
[B]estimations: gene frequencies; equilibrium X2 (N.S., Non significant effect, * p 0.05; ** p 0.01; *** p 0.001) partial heterozygosities (ho, he); average heterozygosities (Ho, He); Wright Index (F), percentage polymorphic loci (Pol 99%, Pol 95%) and number of alleles per locus (#al/locus).

Table 1 : Cont.

Pol locus	Alleles and [B]Estimations	[A]W.R.	S.Com.	S. G.	But.	F.B.	Total Pop Av (s.e.)
Pgd	Pgd1	0.89	0.94	0.96	0.96	0.91	
	Pgd2	0.11	0.06	0.04	0.04	0.09	
	X2	***	N.S.	N.S.	N.S.	N.S.	
	ho(he)	0.12 (0.19)	0.09 (0.10)	0.05 (0.07)	0.08 (0.07)	0.11 (0.16)	0.15 (0.14)
Es1	Es1A	0.47	0.64	0.76	0.60	0.57	
	Es1B	0.53	0.36	0.24	0.40	0.43	
	X2	N.S.	N.S.	N.S.	N.S.	N.S.	
	ho(he)	0.43 (0.50)	0.38 (0.46)	0.33 (0.36)	0.42 (0.48)	0.39 (0.49)	0.38 (0.42)
Es2	Es2F	0.38	0.42	0.57	0.28	0.30	
	Es2S	0.62	0.58	0.43	0.72	0.70	
	X2	N.S.	***	N.S.	N.S.	N.S.	
	ho(he)	0.40 (0.47)	0.27 (0.50)	0.45 (0.49)	0.30 (0.40)	0.39 (0.42)	0.36 (0.40)
Es7	Es7A	0.45	0.68	0.80	0.79	0.64	
	Es7B	0.55	0.32	0.20	0.21	0.36	
	X2	**	N.S.	N.S.	N.S.	N.S.	
	ho(he)	0.39 (0.49)	0.38 (0.43)	0.28 (0.32)	0.27 (0.33)	0.34 (0.46)	0.35 (0.41)
Hp	Hp1	0.11	0.62	0.76	0.47	0.38	
	Hp2	0.89	0.38	0.24	0.53	0.62	
	X2	N.S.	N.S.	N.S.	N.S.	N.S.	
	ho(he)	0.18 (0.19	0.51 (0.47)	0.33 (0.36)	0.54 (0.50)	0.55 (0.47)	0.33 (0.43)
Ca2	Ca2F	0.97	0.98	1	0.96	1	
	Ca2S	0.03	0.02	0	0.04	0	
	X2	N.S.	N.S.	---	N.S.	---	
	ho(he)	0.06 (0.06)	0.04 (0.04)	---	0.05 (0.07)	---	????
Trf	Trf1	0.85	1	1	1	1	
	Trf2	0.15	0	0	0	0	
	X2	N.S.	---	---	---	---	
	ho (he)	0.35 (0.25)	---	---	---	---	
Hb	Hb1	0.02	0	0	0	0	
	Hb2	0.98	1	1	1	1	
	X2	**	---	---	---	---	
	ho (he)	0.02 (0.04)	---	---	---	---	???
Dia-2	Dia-2A	0.66	0.90	0.63	0.88	0.63	
	Dia-2B	0.27	0.04	0.28	0.08	0.34	
	Dia-2C	0.07	0.06	0.09	0.04	0.03	
	X2	***	N.S.	N.S.	N.S.	N.S.	
	ho(he)	0.33 (0.48)	0.15 (0.18)	0.60 (0.52)	0.18 (0.22)	0.42 (0.49)	0.51 (0.41)
Es3	Es3A	0.31	0.59	0.38	0.54	0.51	
	Es3B	0.43	0.29	0.22	0.28	0.32	
	Es3C	0.26	0.12	0.40	0.18	0.17	
	X2	***	N.S.	N.S.	N.S.	N.S.	
	ho(he)	0.43 (0.65)	0.46 (0.55)	0.60 (0.65)	0.53 (0.60)	0.53 (0.61)	0.38 (0.44)
Ada	Ada1	0.55	0.46	0.57	0.47	0.47	
	Ada2	0.38	0.42	0.31	0.39	0.33	
	Ada3	0.05	0.14	0.12	0.14	0.20	
	Ada4	0.02	0	0	0	0	
	X2	***	N.S.	N.S.	N.S.	N.S.	
	ho(he)	0.44 (0.55)	0.54 (0.61)	0.40 (0.56)	0.59 (0.61)	0.53 (0.63)	0.44 (0.49)
Ho (s.e.)		0.18 (0.05)	0.17 (0.05)	0.18 (0.05)	0.17 (0.05)	0.19 (0.06)	
He (s.e.)		0.23 (0.06)	0.20 (0.06)	0.20 (0.06)	0.19 (0.06)	0.22 (0.06)	
F		0.22	0.15	0.09	0.10	0.13	
X2F		5.90 *	2.29 (N.S.)	0.56 (N.S.)	0.76 (N.S.)	1.03 (N.S.)	
Pol 99%		64.70	52.94	41.17	52.94	47.06	
Pol 95%		52.94	47.06	47.06	41.18	47.06	
# al/locus	(s.e.)	1.88 (0.21)	1.7 (0.19)	1.65 (0.19)	1.7 (0.19)	1.65 (0.30)	

[A]Populations: W. R., Spanish Wild Rabbit; S. Com., Spanish Common; S. G. Spanish Giant; But. Butterfly; F. B. Fauve de Bourgogne.
[B]estimations: gene frequencies; equilibrium X2 (N.S., Non significant effect, * p 0.05; ** p 0.01; *** p 0.001) partial heterozygosities (ho, he); average heterozygosities (Ho, He); Wright Index (F), percentage polymorphic loci (Pol 99%, Pol 95%) and number of alleles per locus (#al/locus).

and SOKAL, 1973). The BIOSYS-1 program (SWOFFORD and SELANDER, 1981) was used for all variability, genetic distance and dendogram analyses.

RESULTS

Genetic characteristics of the populations

As shown in Table 1, 11 of the 18 proteins analysed were controlled by polymorphic loci. Eight of these were diallelic (6-Pgd, Es-1, Es-2, Es-7, Hp, Trf, Hb and Ca-2) two were triallelic (Dia-2 and Es-3) and one was tetrallelic (Ada). The remaining proteins were monomorphic.

Hb ^{1}, **Trf** ^{2} and **Ada** ^{4} alleles were specific to Wild Rabbit populations. On the other hand, **Ada** ^{3}, **Dia-2** ^{C} and **Es-3** ^{C} alleles were not present in French populations. This fact explains the high level of polymorphisms, average number of alleles per locus and proportion of polymorphic loci found in Wild Rabbits (1.88 and 52.94, respectively) and the low level of polymorphism observed in French populations (France 2).

Considering Hardy-Weinberg genetic equilibrium, an equilibrium situation was not observed for 6 loci in wild rabbits (see Table 1). French populations show more loci in disequilibrium than in Spanish domestic ones.

Heterozygosity (ho) values differed amongst loci, ranging from 0.15 in the case of **6-Pgd** to 0.51 in **Dia-2**. On the contrary, average heterozygosity (Ho) values were similar amongst breeds, ranging from 0.15 (New Zealand White) to 0.19 (Spanish Common).

Wright index (F) were significantly different from zero in Wild Rabbit, we found a fault of the observed heterozygotes respect to the expected ones in this population.

Genetic Distances

Genetic distances between the 11 rabbit populations studied are shown in Table 2. The dendogram obtained is provided in Figure 1.

The smallest distance was noted amongst New Zealand White and the Spanish crossbred population (0.006, Table 2). The distance between French populations and New Zealand White and Californian Spanish breed populations (0.07, Table 2) was found to be larger than the distance observed between these breeds and the Spanish crossbred population (from 0.006 to 0.02, table 2).

The largest distances (0.141 to 0.041) were observed between French populations and the rest of the studied breeds.

As show in Figure 1, one population appeared alone in a unique branch (France 3), the remaining French populations also appeared separate from the rest. Within the Spanish group, Spanish Giant was the most divergent population.

DISCUSSION

Genetic characteristics of the populations

The electrophoretic variation obtained in this work agrees with those found by different authors (RICHARDSON *et al.*, 1980; SALERMO *et al.*, 1982; ROBINSON and OSTERHOFF, 1983; ZARAGOZA *et al.*, 1984, 1985, 1986; ARANA and ZARAGOZA, 1986).

The observed gene frequencies for total loci were different than results reported by the authors cited above. The greatest differences were found in French populations.

Considering the different loci, in the case of **6-Pgd** locus, the bibliography shows that the **6-Pgd**^{1} allele has a gene frequency higher (near 1) than the **6-Pgd**^{2} allele (COGGAN *et al.*, 1974; RICHARDSON *et al.*, 1980; ZARAGOZA *et al.*, 1987). In the present work, France 1 and France 3 populations showed intermediate frequencies for this locus (see Table 1).

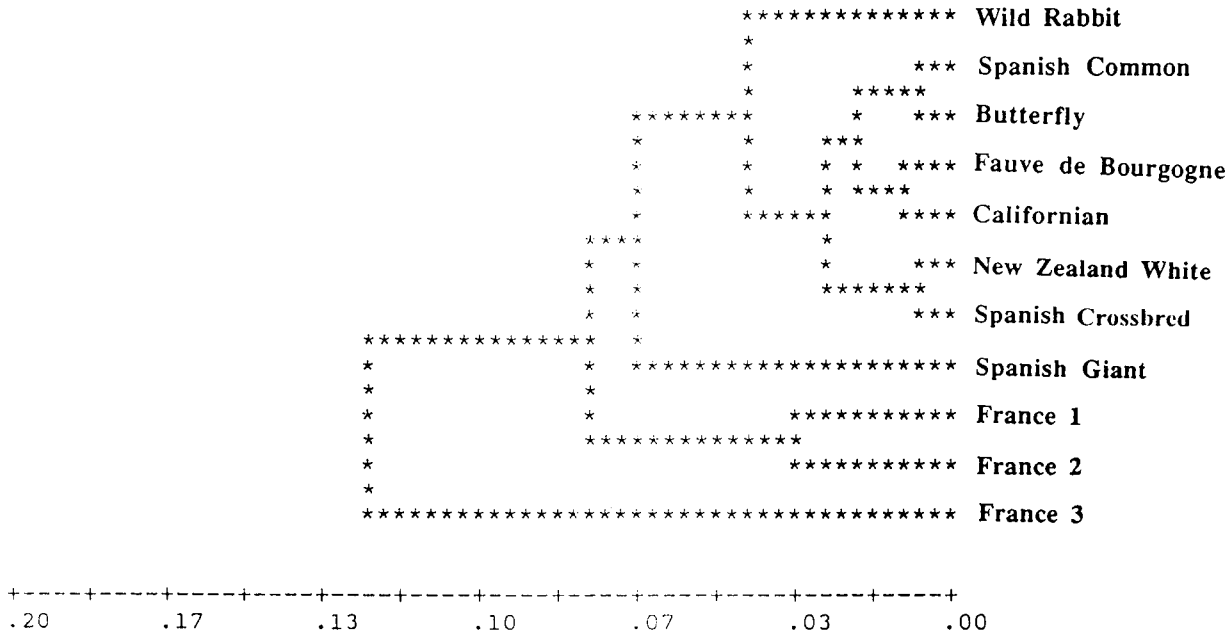
These results do not agree with the theory of GILLESPIE and KOJIMA (1968), who observed that enzymes with significant function in energetic metabolism showed little variation in natural populations. This possible contradiction could be due to the origin of French populations. To produce offspring with intermediate frequencies, both parental lines should have intermediate frequencies (or each one could have high frequencies for the different alleles). This only could be possible if the most frequent allele were **6-Pgd**^{2} in one parental line (the female selected INRA lines or the pure male breed population), due to founder effect and the high selective pressure to which it has been subjected.

Similar results were observed for the **Dia-2** locus. RICHARDSON *et al.*. (1980), ARANA *et al.*, (1987) and ZARAGOZA *et al.*. (1990) reported intermediate frequencies in wild rabbits. In our results, French populations showed more variation than wild rabbits, but we consider that this variation could be "artificial" and it could have originated by two parental lines with low variability. Likely, for this reason we have found high heterozygosity (near 1) and Hardy-Weinberg disequilibrium in the three French populations.

Table 2. Estimated genetic distance matrix for 7 Spanish and 3 French populations (Nei, 1972)

Populations	Wild	S. Common	S. Giant	Butterfly	Fauve B.	N. Z. W.	Califor -nian	Span. Cross.	France 1	France 2	France 3
Wild Rabbit	-----										
Spanish Common	0.068	-----									
Spanish Giant	0.105	0.029	-----								
Butterfly	0.054	0.008	0.039	-----							
Fauve Bourgogne	0.028	0.023	0.045	0.014	-----						
New Zealand White	0.050	0.039	0.093	0.033	0.030	-----					
Californian	0.021	0.025	0.070	0.018	0.010	0.019	-----				
Spanish Crossbred	0.045	0.028	0.082	0.028	0.029	0.006	0.020	-----			
France 1	0.141	0.091	0.093	0.087	0.072	0.075	0.099	0.090	-----		
France 2	0.117	0.051	0.058	0.054	0.045	0.042	0.065	0.055	0.032	-----	
France 3	0.1333	0.152	0.204	0.153	0.113	0.069	0.128	0.070	0.123	0.092	------

Figure 1 : Genetic distance dendogram corresponding to the best solution obtained from distance matrix (Table 2) using the SNEATH and SOKAL method (1973).



Ada, Es-1, Es-2, and **Es-3** loci showed high gene frequencies in French populations and intermediate frequencies in the rest of the populations. Similar results were obtained by SUZUKI and STORMONT (1972); RICHARDSON *et al.*, (1980); ZARAGOZA *et al.*, (1987); ARANA *et al.*, (1987) in Californian and New Zealand White rabbits.

Six of the eleven loci studied were in Hardy Weinberg disequilibrium in French populations, perhaps due to these having originated from two parental pure breeds which had been strongly selected showing in this moment different allelic frequencies. Wild Rabbit also showed disequilibrium, because this population is divided in subpopulations (Whalund effect) . This property in Wild Rabbit population was described by ARANA *et al.*, (1987). Whalund effect could also explain the significant Whright Index found in this population.

Average degree of heterozygosity (Ho) was similar amongst the Spanish breeds and there was no difference between non-selective (Spanish Common, Spanish Giant, Butterfly and Fauve de Bourgogne) and industrial selective systems (New Zealand White, Californian and the crossbred population). This result could be caused by different factors: planned matings by farmers to obtain higher production, small number of animals involved in reproduction, or high frequency of matings between related individuals.

Genetic distances

Results obtained for genetic distances amongst Spanish populations are in agreement with the findings of ARANA *et al.*, (1989), ZARAGOZA *et al.*, (1990). However, in our dendogram the difference found by these authors between breeds under selective and non-selective production systems is not clear. This fact may also indicate signs of pure breed extinction produced by cross-breeding.

The genetic distances of the Spanish breeds correspond to differences between breeds (0.00 - 0.05) (KIMURA, 1983 and NEI, 1987). However the differences between Spanish and French populations correspond to differences amongst subspecies (0.002 - 0.20). French populations were as different amongst themselves as they were between Spanish populations.

Genetic distances found in French populations and Spanish Giant population are not in agreement with the history of these rabbit breeds. The results of the present study suggest that these populations are more divergent than Wild Rabbit with respect to the rest of populations. We have to consider that several factors could have affected gene frequencies contributing to their isolation from the other breeds: the breeding strategy looking for a relatively large size of the Spanish Giant and the selective pressure to which French parental populations have been subjected.

As a result of the high selective pressure applied at the 1077 pure line (ROCHAMBEAU, 1994) , France 1 and France 3 appear more divergent than the expected divergence between two populations with the same maternal origin (1077 and 9077 lines came from a pure breed New Zealand White population). In the present work, France 1 and France 2 appear more similar within themselves than France 3; to explain this result we have to keep in mind that these populations are sharing the same male parental line. In the study realized by Rochambeau (1994) about the genetic improvement of the rabbit in France, we can find that the populations called in this work as France 1 and France 2 show similar selection effects. It is also possible that the selection made in the pure lines 1077 and 2066 in order to get a better female line has changed the allelic frequencies in some of the studied loci. Several genotypes studied in these populations could be associate with the improvement of meat production. In this work, we have detected important differences at protein level, we could consider these loci as candidates for future Molecular Genetics studies in QTL (Quantitative Trait Loci) programs.

The data presented in this work show the selection effect at biochemical polymorphism level and it could also serve as a database for research on the genetic potential, structure and characterization of the wild and domestic rabbit populations. The knowledge of the genetic structure and inter-breed

differentiation could be used in studies of the genetic and productive potential of unselected breeds and in research involving cross-breeding between different populations or breeds. Experimentation on crosses between genetically distant v. close populations to obtain hybrid vigour may involve biochemical polymorphism analyses to be of use for the improvement of the rabbit livestock production.

ACKNOWLEDGEMENTS

We wish to acknowledge the co-operation of Dr. Rouvier (INRA de Toulouse, Station de Recherches Cunicoles) who made the arrangements for providing the French animals, and we also thank the collaboration of Servicio de Experimentacion Animal de la Universidad de Zaragoza.

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