

SIMPLE AUTOSOMIC RECESSIVE INHERITANCE OF CATAPLEXY IN FIGHTING BULLS.

(HERENCIA AUTOSOMICA RECESIVA, SIMPLE, DE LA CATAPLEJIA DE VACUNO BRAVO).

por

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The problem of collapsing in the fighting bull breed was conceived from a scientific point of view beginning in the thirties when different experts (Castejón y Martínez de Arizala, Peralbo, González García, etc. (8)) tried to give a solution based on explanations taken from pathology. Since then numerous investigators, breeders and enthusiasts have expressed their opinion and/or the results of their work and comments in this respect (4, 5, 6, 7, 8, 9, 10). It is common for them to refer directly or indirectly to the genetical component as an influencing factor. However, only recently has experimental data been proposed which tries to explore the possible genetical bases of collapsing.

In a study of Spanish breeds of cattle Kidd et al. (11) initiated from the observation of different polymorphological systems, 0.17 is given as the inbreeding coefficient for fighting bulls. The team which profesor Zarazaga (16) leads also found out the inbreeding coefficients of different populations of fighting bulls using blood markers and morphological characters. The inbreeding coefficient in this case reaches an average mean value of 12.6 per 100. At the same time they studied the structure and the genetical heterogeneity of the different strains.

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García Martín (4) investigated the inbreeding coefficients from a sample of stock farms in the three areas of rearing fighting bulls, and from the total of the sample analyzed he obtained an average mean coefficient of 7 per 100. In his doctoral thesis, not yet published, García Martín (4) analyzes the possible relationship between the value of the inbreeding coefficient and the percentage of collapses, reaching the conclusion that there is no significant association between these two variables.

We estimated that in order to discern the rôle which the genotype of the animals that show the collapse syndrome plays it would be best to carry out a genetic analysis which would not be the one merely made to determine the correlation between the degree in breeding and the frequency of collapses. Two types of analysis were applied: one based on data coming from two generations of animals whose pedigree was known, and which in a number of 73 offspring and 75 parents all belonged to the same breeder. A second type of genetical analysis was made from controls on a single generation relating to 442 individual animal and 77 families, which were distributed over three areas of fighting bull farms. This second group included the results obtained from 13 families from a Portuguese breeder totalling 123 animals.

We thought that we might be finding ourselves facing a case of simple autosomic recessive inheritance. In that case the following conditions ought to be present: 1) All the offspring of two parents affected must also be affected. 2) Both sexes would be equally affected. 3) The risk of having an offspring which collapses is greater in the inbred crosses than in non-related animals. 4) Among the offspring of normal animals crossed with normal animals, offspring affected at a value of $\theta = 1/4$ would appear (θ represents the probability, denominated the probability of segregation, that an offspring affected would be born in a family of parents with given genotypes). Out of the four conditions quoted the first is difficult to detect as it is rare for a breeder to purposely cross animals showing this defect. At any rate this condition is met in the few cases we have been able to study.

With regard to the second condition we carried out a t test between the percentages of both sexes; the t value obtained turned out to be equal to 0.46, which is not significant with a low risk. The third condition is also fulfilled with the data we possess. Lastly we still have to obtain the value of θ in order to infer if this fits the proportion of 1/4.

θ was calculated by two methods: the Li and Mantel method and Weinberg's, bearing in mind in both cases the differences in size of the families, and having a complete knowledge of the members of each family. By the Li and Mantel method the value of θ obtained was 0.226, and by

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Weinberg's, 0.220. The variance inferred as the reverse of the quantity of information $I(\theta)$ has turned out to be equal to 0.0016, and the standard deviation, therefore, equals 0.0404.

It can be inferred that in both methods the differences found between the values of the observed and the theoretical value $= 1/4$ are not significant to a high level of probability, which means that the fourth condition required was fulfilled. The significance of the differences has been proved by the $Z^2 = (\hat{p} - p) / \sqrt{\frac{p}{n}}$ test, which is approximately distributed as χ^2 with one degree of freedom. In this way we obtained a $Z^2 = 1.54$ in the Weinberg test, and $Z^2 = 0.25$ in Li and Mentel's. In both cases, as we have said, they are not significant.

Elandt-Johnson (2) proposed a check by joint Z^2 tests, which enable us to obtain an inference not only about the fitting of data to the proposed hypothesis but also the homogeneity of the family data. We obtained:

$$Z_{\text{total}}^2 = \sum_{s=2}^s \frac{(r_s - n_s A_s)^2}{n_s B_s}; \quad Z_{\text{combined}}^2 = \frac{R - \sum_{s=1}^s n_s A_s)^2}{\sum_{s=a}^s n_s B_s}$$

and Z_{dif}^2 as the difference between both, in which r_s = the number of offspring which show the trait in families of a given size; and n_s = the number of the total of affected animals in the whole sample; A_s = the expected value of r (number of affected animals) in a sample of a size; and B_s = the variance of r .

In our case $Z_{\text{total}}^2 = 6.4356$; $Z_{\text{combined}}^2 = 0.4549$, and $Z_{\text{dif}}^2 = 5.9803$. For $\alpha = 0.05$, Z_{com}^2 is lower than $\chi_{0.91;1}^2 = 3.841$, which suggests that the data fits the hypothesis of recessivity well. In the same way χ_{dif}^2 is lower than $\chi_{0.95;8}^2 = 15.51$, which enables us to accept the hypothesis that the family data is homogeneous.

Other processes which we have applied to prove the hypothesis start from the supposition that we are faced with populations close to the genetical equilibrium, which permits us to find the gene and genotypic frequencies from the data at hand. In these circumstances the frequency of the offspring which show the collapsing trait, descending from heterozygote parents, would be equal to $\frac{1}{2}q + \frac{1}{2}pq$ in the case of recessive inheritance. In our work this has proved to be equal to 0.2325 for the q obtained, whilst the calculated value by direct counting was 0.2361.

Here again there is a good fit between the observed data and the expected one, according to the hypothesis. In the same context we obtain greater accuracy if we use the phenotypical distribution of parents-offspring as exposed by Elandt-Johnson (1).

Father \ Son	A -	aa
A -	$(1-q)(1+q-q^2)$	$q^2(1-q)$
aa	$q^2(1-q)$	q^2

With our data the value of χ^2 to test the accuracy of the fit is equal to 0.227 (non significant), which confirms our hypothesis. We consider that the results obtained being agreement in all the tests, increase the reliability of accepting the hypothesis.

Inconsistency with other results.

In spite of what has already been stated, we wish to mention that on some occasions, according to data provided by breeders, the crossing of a sire which collapsed and females of the same phenotype produced and offspring which, contrary to what was expected, was marked as an animal with the dominating character. This is not unusual if we bear in mind that in the character under consideration its appearance or not is greatly dependent on the animal being placed in conditions which favour this happening in any noticeable measure.

Speaking subjectively, we consider that the expressivity of the character is relatively high although its penetrance is not general, for its rate is estimated at a value of β roughly equal to 0.85; therefore 15 per cent of animals remain which do not show signs of the character for environmental causes.

Another aspect which concerned us and which we have already mentioned refers to the result obtained by García Martín (4) in his doctoral thesis showing the lack of association between the inbreeding coefficients

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and the percentage of animals which collapse.

The genetical determination which we have detected would imply that inbreeding would increase the homozygosis and, consequently, the proportion of animals in which the character is apparent. In this respect the following considerations must be taken into account:

The inbreeding coefficients were obtained with a reduced number of generations when the majority of fighting-bull farms have originated from a small number of strains and by using a low percentage of sires. For that reason when we estimated the inbreeding relationship from blood group data and biochemical polymorphism this has turned out to be higher.

The increase of homozygosis not only depends on the inbreeding in the population but also on the initial gene frequencies. From what we have been able to ascertain these are different from farm to farm, probably due to the size of the population.

We must take into account the genetical drift which may have affected this type of population for their special features. Bearing in mind the average size of the populations on which we have made the calculations this gives us an estimate of the genetical random drift (Falconer (2)) $\theta = 0.0397$ depending and 0.0537 whether we consider 5 or 7 generations. For the same number of generations the increase of the inbreeding coefficient would be $\Delta F = 0.0430$ and $\Delta F = 0.6020$, respectively. Thus we can safely say that the size of the population and the drift factor have played an important part in the inbreeding coefficient found which we recorded as reaching 0.07.

Implications.

Having proved the hypothesis of simple autosomic recessive inheritance, the problem of collapsing in fighting bulls is placed in a much clearer perspective, as much from a practical as an experimental point of view. In theory it would be advisable to investigate all the possible metabolic paths which culminate in the bull's collapse and which might be affected by the enzyme or structural protein resulting from the reading of the genetical information of the mutant allele peculiar to the collapse syndrome. It would also be of great interest to fathom out the natural or artificial processes which have produced a relatively high incidence of the frequency of the aforementioned allele with differences, on the other hand, among some populations.

In the respect it would be revealing to find out the relationship of the collapse with other characters concerning the animals' bravery. Although we have not made an exhaustive enquiry into this matter we have indeed tried to approach it using χ^2 tests carried out on contingency

tables with data proceeding from two sources: on one hand we worked with information provided by different breeders who classified the animals, according to their behaviour in the ring, in "brave" and "not brave", "collapsing" and "non-collapsing" out of a total of 442 animals. On the other hand, we used data obtained by one of our group, about 281 animals, which were listed as "brave", "middling brave" and "not brave", according to one viewpoint, and in "collapsing", "ataxic" and "non-collapsing", according to another. In the first case the value of χ^2 was 1.4672 which, with one degree of freedom, proved not to be significant. In the second case a value of $\chi^2 = 9.4910$ was obtained which with 4 degrees of freedom is significant ($P \ll 0.05$). When we partitioned the degrees of freedom of the contingency table, it only proved to be significant when the not brave animals were placed versus the brave and middling ones ($\chi^2 = 8.0459$).

The proportion of collapsing animals in relation to the total of bulls in each one of the two samples was 0.17 and 0.16, respectively; these figures are extremely close and show us that in the data provided by the breeders, the animals classified by us as "ataxic" and as "non-collapsing" appear clustered. Similarly those bulls we found to be "brave" and "middling" are clustered in the "brave" category.

On the basis of all that we have reported up to now, we venture to suggest that the not brave bulls tend to collapse less than the rest of the animals who are killed in the ring.

From a practical point of view, starting from the study we are presenting, a process of elimination is proposed of reproducing animals which are carriers of one or two recessive alleles either in males or females. If the recessives were easily detected, the pedigree and family data will have to be studied in the heterozygotes in order to, as a last resort, put them through progeny tests, although the number of matings necessary to affirm the heterozygosity of the bull, with a probability level of at least 95 per 100 may be high, (over 25).

Conclusions.

1) By different methods we have proved the supposition expressed of simple autosomic recessive inheritance in the collapsing character of fighting bulls.

2) It has been determined that the character has an incomplete rate of penetrance (85 per 100) and that its expressivity is variable and high.

3) The lack consistency between these results and the finding of García Martín on the independence of inbreeding with the character being considered is justified due to the difficulty of finding out the coefficients of inbreeding and the effects of the genetical drift. As a measure to be taken, we propose a selection via the elimination of carriers of the gene determining the collapse after prior pedigree and family studies and, alternatively, progeni tests.

4) On the other hand from the analyses carried out it is inferred that the animals considered to be "not brave" tend to collapse less than the rest of the bulls killed.

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