

SEVENTH INTERNATIONAL THERIOLOGICAL CONGRESS

Seventh International Theriological Congress

Acapulco, México, 6-12 september, 1997

Abstracts of oral and poster papers

Organized alphabetically by author's last names

A SPATIAL AUTOCORRELATION AND AN ISOLATION BY DISTANCE ANALYSES APPLIED TO FIVE BLOOD ALLOZYMES DEMONSTRATED THAT THERE WAS NOT ANY SPATIAL STRUCTURE IN A RARE CATTLE BREED (PYRENEAN BROWN) IN CATALONIA (SPAIN). INTERESTING DATA FOR MAMMALIAN CONSERVATION

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In the last years, different studies showed that exists an enormous genetic admixture in diverse domestic animal breeds (Baker et al., 1993). The actions of mankind in transporting domestic animals was invoked for it. The Pyrenean Brown cattle is an interesting case. This is a rare cattle breed living in the Catalonian Pyrenees. This breed is characterized by: (1) recent origin (last years of XIXth century), (2) coming from the fusion between Brown Swiss cattle in French populations with local ecotypes of 'Pirenaica' breed, (3) the formation of this rare cattle was in a local point of the Pyrenees (Vall d'Aran), (4) the overall effective population size is probably relatively small. All these points let us to think that could exist a strong spatial genetic structure in this cattle breed. For this, 543 blood samples were obtained from nine populations in Catalonian Pyrenees. Five loci were analyzed using different electrophoretic techniques: Haemoglobin (Hb), albumin (Alb), transferrin (Tf), group-specific component (Gc) and post-transferrin 2 (Ptf-2). The following population genetic analyses were carried out. (A) Hardy-Weinberg equilibrium analysis (H-W.E). All cattle populations were in H-W.E for these five loci using Robertson and Hill (1984)'s statistic with a Bonferroni multiple test. (B) Analysis of the heterogeneity of genotype distributions. Stuart's T, Somer's D, uncertainty coefficient and Cochran-Mantel-Haenszel statistics were used. Only two loci, Tf ($p = 0.025$) and Alb ($p = 0.000$) showed significant heterogeneity. (C) The first spatial analysis used was a spatial autocorrelation analysis using both Moran's I and Geary's c indexes. The correlograms were obtained with different networks (total connections, Gabriel and Sokal network, Delaunay's triangulation, etc.) and were

never significant. Different Mantel's tests were performed contrasting genetic distance matrices with geographical distance matrices. Also multivariate Mantel correlograms, standardized by Hubert (1985)'s method, and Dietz's permutations using Spearman and Kendall non-parametric correlations did not show any spatial trend. The third spatial technique employed was that defined by Slatkin (1993). This test was applied to our data and did not detect any spatial pattern resembling to isolation-by-distance. All these results suggest us two different points. We affirm that, independently, of origin, distribution and small effective sizes, there is not spatial structure in this breed probably because an important gene flow exists. Whatever population analyzed is a good place for obtaining new cattles to develop a reproductive and genetic program. Second, this kind of studies would be applied to different wild mammals for analyzing possible genetic patterns. From a conservation point of view, it should be very important.