GENETIC CHARACTERIZATION OF SOME POPULATIONS OF WILD BOAR (Sus scrofa scrofa) IN PIEDMONT (ITALY)

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Abstract: Electrophoretic data were obtained from 200 wild boars hunted in Piedmont mountains and were compared with those from other feral populations.

Keywords: Wild boar, Sus scrofa scrofa, Suidae, Population genetics, Biochemical genetics, Polymorphism, Europe, GPI, PGD.

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1. Introduction

In Piedmont, following dramatic environmental modifications, the Wild boar diffused rapidly since the early sixties also as a consequence of absence of predators, decrease of cultivation, and transformation of cattle, sheep and goats breeding techniques, particularly in mountain zones. Some role is also due to introduction for hunting purposes of crosses with domestic pig and of wild boars from Eastern Europe. Therefore we have now a well adapted animal which sometimes presents biometrical traits similar to those of domestic pig. However, biometrical traits, being multifactorial, are only in part expression of gene activity, being heavily influenced by environment. Instead biochemical polymorphisms are useful markers to study the genetic structure of a population. because they are controlled by genes on which the environmental influence is almost null.

2. Material and methods

The samples (liver, heart, kidney and diaphragm) come from 197 wild boars hunted during 1990-1992 in different mountain areas of Piedmont and from 26 domestic pigs from a slaughterhouse as a control. By means of horizontal starch gel electrophoresis the loci GPI, PGD, LDHA, LDHB, ADA1, ADA2, ME1, ME2, MDH1, MDH2, IDH1, IDH2, SODA, SODB, HK, ACP were analyzed. The results have been compared with those relative to Sus scrofa scrofa from Austria (Hartl & Csaikl, 1987), from peninsular Italy (Apollonio et al., 1985) and with those of Sus scrofa meridionalis from Sardinia (Apollonio et al., op. cit.).

3. Results

GPI system has been found polymorphic as in Austrian Wild boar (GPI*A .24, GPI*B .76); in domestic pig the frequency of GPI*B varies from .30 to .97.

PGD system showed a single allele (PGD*A) as it has been observed in other Wild boar populations. In domestic pig the system is polymorphic and the frequency of PGD*A varies from 0.30 to 0.83.

ADA1 and ME1 were monomorphic in our sample in contrast with Austrian populations. The remaining systems were monomorphic.

4. Discussion and conclusions

All the wild boars of the Western Europe so far examined are similar, although coming from different zones. The constant trait is the monomorphism of PGD locus wich is polymorphic in domestic pig and in some populations of Asian Wild boar (Kurosawa & Tanaka, 1991). This seems to indicate that the alleles PGD*B and PGD*C arose from mutation when Sus scrofa scrofa was already differentiated. In this case, if in a population of Wild boar one of these two alleles should be present, the occurence of crosses with domestic pig or of individuals of Asian origin could be hypothesized, although conclusions from a single locus can not be absolute. However, karyotype analysis (Macchi et al., in press) evidenced that chromosome polymorphism is absent in individuals from the same mountain zones, where the present material has been collected. It seems reasonable to accept that in the Piedmont mountains is present the typical Western Europe

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Wild boar (Sus scrofa scrofa), on which introduction of crosses or wild boars of other subspecies did not have notable influence. Anyway, it seems to be useful to control all the Wild boar centers existing in Piedmont both with karyotype and biochemical polymorphism examination because, if differences from wild population should be found, it would be possible to detect at least one of the sources of illegal introduction.

References

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