

CYTOGENETIC VARIABILITY IN THE WILD BOAR (*Sus scrofa scrofa*) IN PIEDMONT (ITALY): PRELIMINARY DATA

Macchi E. *, Tarantola M. *, Perrone A. *, Paradiso M.C. **, Ponzio G. ***

* C.R.E.A - Centro Ricerche in Ecologia Applicata - Via Belfiore 61 bis, 10126 Torino, Italy.

** Servizio Universitario di Genetica Medica - USSL VIII, via Santena 19, Torino, Italy.

*** Dipartimento di Genetica, Biologia e Chimica Medica - Facoltà di Medicina - Università di Torino, via Santena 19, Torino, Italy.

Abstract: The authors have carried out a cytogenetic study on the Wild boar (*Sus scrofa* L.) in Piedmont in order to assess the origin of the population. The existence of some polymorphism in the diploid number indicates that Piedmont's animals may have different origins. The modified technique we used proved satisfying.

Keywords: Wild boar, *Sus scrofa*, Suidae, Europe, Population genetics, Karyotype.

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1. Introduction

The cytogenetic studies point out a chromosomal polymorphism in the Wild boar (Bosma *et al.*, 1984; Nombela *et al.*, 1990). The diploid chromosome number of the West European subspecies is $2n=36$, the Eastern European populations have $2n=38$, while in the subspecies of Central and Far East Asia it ranges from 36 to 38. The domestic pig has always $2n=38$ and its karyotype is identical to that of wild boar with $2n=38$.

The aim of this research is to characterize, under the cytogenetic point of view, the populations of *Sus scrofa* living in Piedmont.

2. Material and methods

We analyzed 14 blood samples, drawn from the femoral vein of wild boars trapped and anesthetized in mountainous and plain areas, and 4 blood samples from pigs.

Two methodologies were used: the first is the standard one on whole blood (Moorhead *et al.*, 1960), the second is derived from the standard modified by us and using separated blood.

Here we describe the latter because it gave better results.

- Separate the blood using 1 ml of Emagel for 1 ml of blood, leave it for 30 minutes.
- Centrifuge the supernatant for 10 minutes, at 900 revs per minute (RPM), with the same quantity of RPMI-1640.

- Remove and discard the supernatant with a pipette.
- Add 6 ml of RPMI-1640 Dutch modification, 2 ml of fetal bovine serum, 0.2 ml of phytohaemagglutinin, 0.1 ml of antibiotics and 0.1 ml of heparin (100 U/ml).
- Put the cultures in thermostat for 72 hours (37°C).
- 2 hours before the cell collection add 0.3 ml of Vinblastina sulphate ($0.5\ \mu\text{g/ml}$); wait 1 hour then add 0.5 ml of Actinomycin D ($100\ \mu\text{g/ml}$).
- Centrifuge at 900 RPM for 10 minutes.
- Remove and discard the supernatant with a pipette.
- Add a hypotonic solution (KCL 0.075 M) pre-warmed for 15 minutes at 37°C .
- Centrifuge at 900 RPM for 10 minutes, remove and discard the supernatant with a pipette.
- Add 5 ml of Acetic acid (5%).
- Leave it for 5 minutes at room temperature.
- Centrifuge at 900 RPM for 5 minutes.
- Remove and discard the supernatant with a pipette.
- Add 10 ml of fixative (1 part of glacial acetic acid + 3 parts of methanol).
- After 30 minutes centrifuge at 900 RPM for 10 minutes, remove and discard the supernatant with a pipette, add the fixative, centrifuge again at 900 RPM for 10 minutes, remo-

ve and discard the supernatant with a pipette and prepare the slides.

The classic banding technique of Caspersson *et al.* (1970) and Zech (1973) for the Q bands was used.

3. Results

Karyological analysis enabled us to show the chromosomal polymorphism represented by 3 variants $2n=38$, $2n=37$, $2n=36$.

The karyotype $2n=38$ consisted of 5 submetacentric chromosomal pairs (1-5), 2 subacrocentric pairs (6-7), 5 metacentric pairs (8-12), 6 acrocentric pairs (13-18) and 2 gonosomes (submetacentric X-chromosome and a small metacentric Y).

The karyotype $2n=37$ presented a Robertsonian translocation between a chromosome 15 and a chromosome 18, that gives a submetacentric chromosome, while the two homologous corresponding are free, according to Popescu *et al.* (1980).

Finally the karyotype $2n=36$ is homozygotic for the Robertsonian translocation 15-18.

Among the 14 samples analysed, the 6 collected in mountainous areas (4 males and 2 females) had $2n=36$. Among the 7 coming from flat areas, 3 subjects (2 females and 1 male) had $2n=38$, 2 males $2n=36$ and 2 females $2n=37$. All the 4 domestic pigs (3 females and 1 male) had $2n=38$.

4. Conclusions

The diploid chromosomal number in the subjects coming from mountainous areas is $2n=36$, in agreement with the results of Mauget *et al.* (1984) and Popescu *et al.* (1980).

The chromosomal polymorphism found in the subjects from the plain area lets us suppose that there were in plain area animals of unknown origin, *i.e.* released for restocking.

From the obtained results we may conclude that the technique we developed is efficient, thus a wider sample will allow us to obtain more precise information on the populations of this species.

Our hypothesis that mountainous areas, where natural selection is stronger, prevent the reproductive success of reared animals (some of which are illegally released) could be tested in the future.

We seek for a greater collaboration from the public administrations in the collection of other samples and in the control of all Wild boar farming in order to prevent a proliferation of animals with unclear chromosomal set.

The release of such animals in the wild could cause great negative effects on agriculture and modify the genetical structure of the truly wild population of *Sus scrofa*.

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