

DATA ON THE BIOCHEMICAL-GENETICAL POLYMORPHISM OF WILD BOAR IN HUNGARY

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1. Introduction

Relatively few data are available on the relationships between morphometrical parameters and biochemical-genetical attributes of Wild boar (*Sus scrofa*). Mostly the growing patterns of different parameters were analysed and few results were presented on the correlations and allometry of these characteristics. Better management of Wild boar populations requires more data about the morphological and especially about the genetical characteristics of this species. For this it is important to map the genetical structure of different free-living stocks and to designate the most valuable ones.

The purpose of this study was to evaluate the biochemical variability and differentiation of Wild boar populations in Hungary. The research program covered the following areas:

- Evaluation of biochemical methods for the analysis of enzyme-polymorphism in Wild boar.
- Search for polymorphic enzymes in Wild boar populations to detect the most polymorphic enzymes and investigation of frequent allele variations. The year-to-year variability of enzyme-polymorphism and morphological parameters were also surveyed.
- The relationships between morphological parameters (body weight-body length, body weight-height at shoulder, body weight-circumference of chest) and comparison of sex- and age-dependent variations were estimated by statistical methods.

2. Material and Methods

Body weight, body length, height at shoulder and circumference of chest data of shot animals (n=188) from both sexes were collected in the 1991/92 and 1992/93 hunting seasons. Heart, liver and kidney tissue samples were taken from the animals during evisceration and the samples were stored deep frozen until the laboratory processing.

The following enzymes were investigated: Malic-enzyme (ME, E.C. 1.1.1.40), Isocitrat-dehydrogenase (IDH, E.C. 1.1.1.42), Acid-phosphatase (ACP, E.C. 3.1.3.2), Catalase (CAT, E.C. 1.11.1.6), Hexokinase (HK, E.C. 2.7.1.1.), Glucose-dehydrogenase (GDH, E.C. 1.1.1.47). Electrophoretic and staining procedures were completed according to routine methods described in the literature (Hartl & Höger, 1986 *modified by* Ernhaft, 1991). Polymorphism and heterozygosity were determined by horizontal starch-gel electrophoresis and enzyme-specific procedures for five isoenzymes.

3. Results and discussion

The routine electrophoretic and staining methods used in Red deer studies proved to be appropriate for Wild boar. Similarly to Red deer the homogenization could be omitted which quickened the laboratory processes.

Polymorphic alleles were found in the ME-1, IDH-2, LDH-2, ACP-1, ACP-2 and HK loci. ME-1 and IDH-2 were the most variable isoenzyme loci studied. No polymorphic differ-

ences were found between the samples of 1991/92 and 1992/93 seasons.

The most important correlations are presented in table 1. No morphometrical differences were shown between the samples of 1991/92 and 1992/93 season.

On the basis of the isoenzymes the biochemical

and genetical characteristics of Wild boar and domestic pig were also compared. Lower biochemical-genetical variability of domestic pigs was found and the allelic variation of ME-1, IDH, GDH, ACP-1 in Wild boar was higher than in domestic pigs.

Table 1. Regression slopes and correlation coefficients for body size parameters.

| Parameters | Slope of regression (b) | | Correlation coefficient (r) | |
|--------------------------------------|-------------------------|------|-----------------------------|------|
| | 1991 | 1992 | 1991 | 1992 |
| Body weight - body length | 0.53 | 0.49 | 0.79 | 0.74 |
| Body weight - height at shoulder | 0.20 | 0.23 | 0.41 | 0.48 |
| Body weight - circumference at chest | 0.46 | 0.52 | 0.84 | 0.80 |

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