EVALUATION OF PrP GENOTYPE IN DIFFERENT SHEEP BREEDS BY CORRESPONDENCE ANALYSIS

Katia Capello, Granato A., Vascellari M., Bonfanti L., Marangon S. & Mutinelli F.

Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro - Padova, Italy

Corresponding author: Katia Capello, e-mail: kcapello@izsvenezie.it

INTRODUCTION

The identification of ovine PrP genotype is an important tool to understand the susceptibility to scrapie, in order to apply genetic selection programs as well as for the management of scrapie outbreaks by selective culling.

AIM OF THE STUDY

Evaluation of the association between breed and genotype by correspondence analysis to explore the structure of data using a lower dimensional display

MATERIAL AND METHODS

❖ Between January 2006 and August 2009, 1,236 blood samples were collected from 170 sheep herds in the framework of the scrapie voluntary control program of the Veneto Region (north-eastern Italy).

❖ Variables in the analysis: the isolated genotype, the allele, the level of susceptibility to scrapie, the sheep breed, and a classification of sheep breed (native vs non-native breeds).

❖ Two correspondence analysis were performed: isolated genotype vs specific breed, allele vs specific breed (relative frequencies lower than 3% not included).

RESULTS 1 » POPULATION DESCRIPTION

**Tab 1**: distribution of samples by breed (native breeds underlined)

BREED	n	%
METICCIA	330	26,70
BIELLESE	221	17,88
BROGNA	220	17,80
ALPAGOTA	170	13,75
LAMONESE	127	10,28
MASSESE	72	5,83
Other	96	7,77

Tab 2: distribution of samples by isolated genotypes
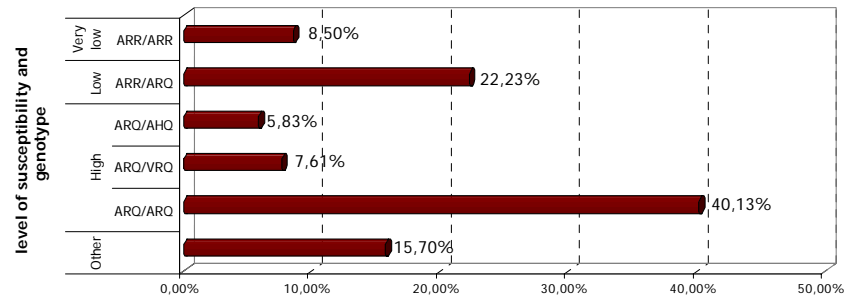
RESULTS 2 » ASSOCIATION BETWEEN ISOLATED GENOTYPES AND BREEDS

❖ 98% of total inertia explained.

❖ Horizontal dimension:

- Distinction between genotypes with a very low level of susceptibility to scrapie from genotypes with a high level of susceptibility.

- The Massese breed seemed to differ from the other breeds in terms of the distribution of genotypes.

❖ Vertical dimension:

- Native breeds with one or more isolated genotypes (top of the graph) against non-native breeds mainly characterized by a single genotype (bottom of the graph).

- ARQ/VRQ genotype appears closer to native breeds (69% of samples) than ARQ/AHQ genotype (23% of samples).
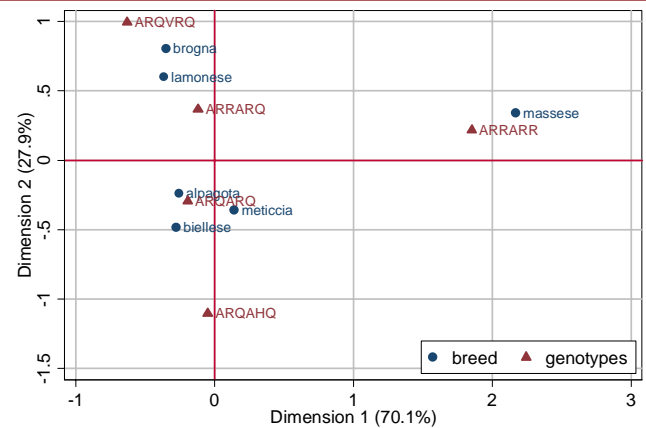

RESULTS 3 » ASSOCIATION BETWEEN ALLELES AND BREEDS

Considering the specific breed allelic distribution:

❖ The Massese breed is very dissimilar from the other breeds in terms of allelic distribution and is mainly characterised by high frequency of the ARR allele (62%).

❖ The other investigated breeds show a comparable allelic distribution and appear more associated to the ARQ allele.

Considering the allelic distribution in all investigated breeds:

❖ AHQ and VRQ are more associated to Meticcia and Brogna, respectively.

❖ No significant difference in ARQ and ARR allelic distribution between breeds was observed.

symmetric normalization
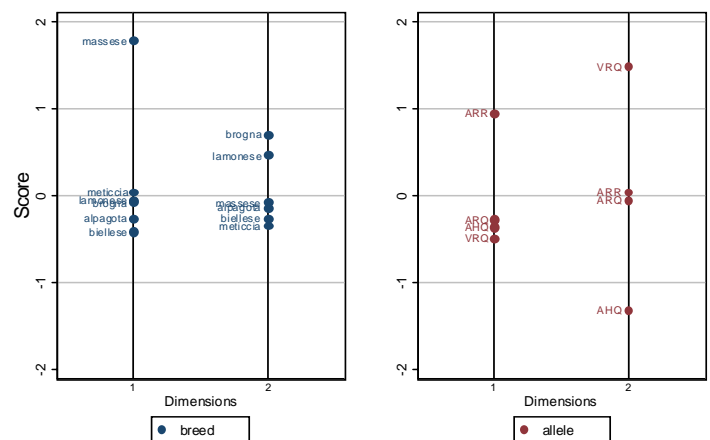
CONCLUSIONS

✓ **This statistical method provide a detailed description of the structure of the relationship among the collected data**

✓ **The identification of common pattern among breeds and genotypes is helpful to define scrapie susceptibility and to plan genetic selection programs**