

The TuBaVi project: an example of biodiversity management in Italian local chicken breeds

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INTRODUCTION

Biodiversity loss in local chicken breeds is a growing concern due to the increasing popularity of commercial chicken lines. Efforts to preserve and promote local chicken breeds can help to maintain genetic diversity. The aim of the work is to preserve the genetic variability of local poultry breeds using mating plans based on individual genetic variability indices estimated by molecular markers.

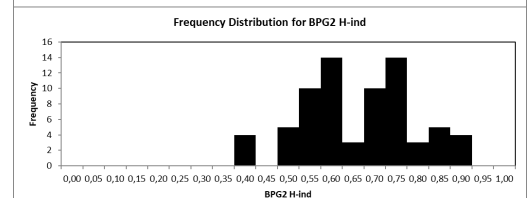
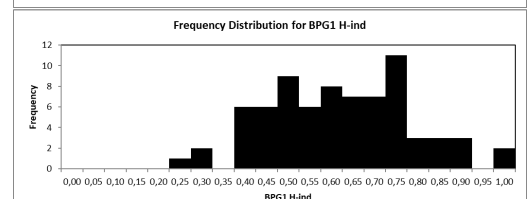
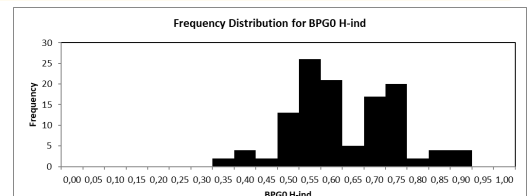
MATERIALS and METHODS

Under the TUBAVI project, the breeding animals from 17 breeds were characterized by 26 microsatellites. For each animal the heterozygosity index (H) and the parentage index (P) have been calculated. The H index is the number of heterozygous loci/number of loci analysed. This index ranges from 1 (maximum variability, all loci are polymorphic) to 0 (no locus is polymorphic). Index P is the proportion shared alleles between breeding animals. This index also ranges between 0 (no common alleles) and 1 (all common alleles). The choice of animals with high H index allows to optimize the conservation of the genetic variability, while the choice of breeding animals with low P allows to contain the inbreeding. To maximize the selection results, the two indices have been combined into a conservation index (C) calculated as difference between H and P. The index ranges from 1 (H=1 and P=0) to -1 (H=0 and P=1). Individual females are selected as breeding animals on the basis of the highest H index and the males on the basis of highest C index.

RESULTS & DISCUSSION

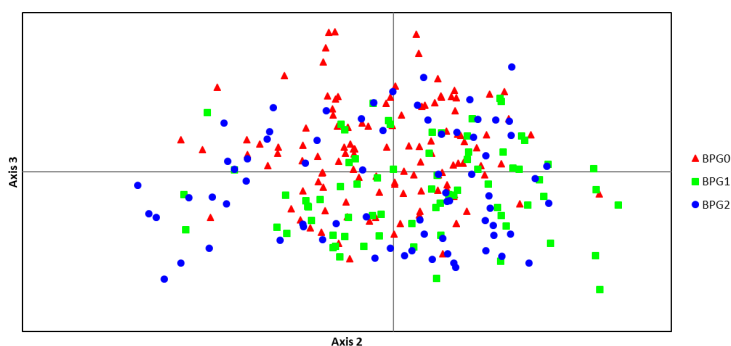
As preliminary trial, these indices have been applied to Bionda Piemontese breed over three generations. The results showed an increase in the average observed heterozygosity (from 0.65 to 0.69) and an increase by 6% in the average parentage (P). The allelic variability of the breed has been preserved. The application of the new conservation index (C) in small populations could be a valid tool to contain inbreeding. The monitoring of both heterozygosity and parentage in the offspring will allow to evaluate the results of the mating plans carried out.

	BPG0	BPG1	BPG2
N	120,00	74,00	72,00
Sum	78,09	47,37	49,55
Mean	0,65	0,64	0,69
Median	0,64	0,64	0,70
SD	0,13	0,16	0,13
SE	0,01	0,02	0,02
Min	0,36	0,30	0,43
Max	0,93	1,00	0,93



Graphical output of individual heterozygosity value (Hind) distribution

Principal Coordinates (PCA)



Principal component analysis (PCA) using a pairwise individual matrix of Nei genetic distances. The membership of BP generation is indicated using red (G0) green (G1) blue (G2)



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