GENETIC CHARACTERIZATION OF THREE TRADITIONAL ITALIAN CHICKEN BREEDS BY MICROSATELLITE MARKERS

S.P., Marelli[1], M.G., Strillacci[1], M., Gualtieri[2], P., Pignattelli[1], L., Guidobono Cavalchini[1]

[1] Istituto di Zootecnica, Faculty of Veterinary Medicine, University of Milan, via Celoria 10, 20133 Milan, Italy;

[2] Dipartimento di Scienze Zootecniche, University of Florence, via delle Cascine 5, 54144 Florence, Italy.

Introduction

The result of Red Jungle Fowl (*Gallus gallus*) domestication and selection is displayed by chicken breeds and populations showing many genetic characteristics and variants. Poultry biodiversity is considered one of the most endangered genetic resource considering the general loss of genetic variability that characterizes productive species. Information about local chicken breeds characteristics is scarce and the investigation of the occurring relationship between their genetic make-up and their performance, adaptability and resistance play an important role in their conservation. Genetic frequencies on polymorphic markers are powerful tools in assessing genetic variability at DNA level.

Materials and methods

A total of 116 subjects were analysed: Bianca di Saluzzo (n=40), Bionda Piemontese (n=36), Valdarnese Bianca (n=40). Genomic DNA was extracted from blood samples using classic procedures. All birds were genotyped at eight microsatellite loci (ADL102, ADL158, ADL176, ADL181, ADL210, ADL267, ADL136, ADL 171) isolated from domestic chicken (*Gallus gallus*). Each marker was subjected to PCR amplification in 10µl volumes with 25 ng of template DNA. The PCR products were separated by electrophoresis in 4.2% denaturing polyacrylamide gels on ABI Prism 377 DNA Sequencer equipped with Genescan and Genotyper softwares (Applied Biosystems). Allele frequencies and deviation from Hardy-Weinberg equilibrium (P-value) at the eight microsatellite loci were calculated using the GENEPOP statistic package. Particularly in case of less than five alleles, an extract P-value, by the complete enumeration method was calculated, while for more than five alleles a Markov-Chain method was computed. The heterozygosity (H) and the Polymorphism Information Content (PIC) were recorded. Factorial analysis three-dimensional distribution was carried out using the GENETIX program.

Results and Conclusions

A total of 76 alleles were detected across the 8 loci. The largest number of alleles was found in Valdarnese Bianca (63), 52 in Bianca di Saluzzo and 51 in Bionda Piemontese. In table 1 breed specific alleles per locus have been reported. The PIC and the heterozygosity values were informative for all breeds (Table 2). In the test for deviation from Hardy-Weinberg equilibrium significant deviations were recorded. Deviation from expected values may be due to inbreeding level and strong selection. Figure 1 reports the three-dimensional distribution of breeds obtained by factorial analysis. The figure shows the distribution of the three chicken breeds underlining the genetic differences between the two northern Italian breeds from the same area and the distance of the Valdarnese Bianca bred in Tuscany. The results of this preliminary study show the genetic differences occurring within the considered populations; these three breeds are important examples of typical Italian chickens particularly adapted to welfare-friendly rearing systems. Further investigations are needed to investigate

the presence of specific alleles or allelic combination coding for adaptability and commercial traits.

Keywords: biodiversity, breed conservation, Italian chicken breeds, microsatellites