Associations between microsatellite markers and milk traits in Massese sheep: preliminary results

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ABSTRACT

Current research aims to establish statistical associations between DNA microsatellites and milk chemical composition to be used for improvement procedure and genetic progress. A trial was carried out on 68 Massese ewes reared in a farm of the Tuscany. On fresh milk the following parameters were evaluated: standard chemical composition, casein and its fractions, whey proteins, pH and rheological parameters. On DNA extracted from peripheral blood, 17 microsatellites were analyzed using an ABI PRISM 310 automated sequencer. Genetic similarities among individuals have been tested using the Individual Multilocus Genotype (IMG) and classical genetic parameters using the software Arlequin. For each locus, the significance of the differences of each quality traits between the subjects carring or not carrying a given allele, was estimated using the software J.M.P. The average number of alleles per locus resulted of 7.18 and the observed heterozygosity ranged from 0.403 to 0.867 (0.677 mean value). The genetics similarity among individuals was 0.460 (0.018 SD). Five markers pointed out a significant deviation from the Hardy-Weinberg proportions (BM8124, CSN3, BM1258, BMS468 and TGLA387); we found quite a high rate of linkage disequilibrium partly because many loci mapped on the same chromosome. The study revealed several microsatellites with alleles significantly linked to milk composition traits (P<0.01). In particular the highest significance (P<0.001) has been found for the OIFNG marker, for which subjects carrying the allele 2 showed higher values of immunoglobulin and lower values for α-lactoalbumin. On the other hand, subjects carrying the allele 10 of the BL4 marker showed significantly lower value of immunoglobulin (P<0.001). We can also assume that allele 2 of BMC1009 influenced fat, while allele 9 of ILSTS42 influenced a_{30} (P<0.001). Further analyses are needed to validate these preliminary results, in particular increasing the number of subjects and of typed loci above all on the chromosomes 3 and 20 where the more interesting markers map.