Determination of Genetic Markers, Microsatellites Type, Liked to Milk Production Traits in Goats

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Abstract : Modern molecular techniques, like single marker analysis for linked traits to these markers, can provide us with rapid and accurate genetic results. In the last two decades of the last century, the applications of molecular techniques were reached a faraway point in cattle, sheep, and pig. In goats, especially in our region, the application of molecular techniques is still far from other species. As reported by many researchers, microsatellites marker is one of the suitable markers for lie studies. The single marker linked to traits of interest is one technique allowed us to early select animals without the necessity for mapping the entire genome. Simplicity, applicability, and low cost of this technique gave this technique a wide range of applications in many areas of genetics and molecular biology. Also, this technique provides a useful approach for evaluating genetic differentiation, particularly in populations that are poorly known genetically. The expected breeding value (EBV) and yield deviation (YD) are considered as the most parameters used for studying the linkage between quantitative characteristics and molecular markers, since these values are raw data corrected for the non-genetic factors. A total of 17 microsatellites markers (from chromosomes 6, 14, 18, 20 and 23) were used in this study to search for areas that could be responsible for genetic variability for some milk traits and search of chromosomal regions that explain part of the phenotypic variance. Results of single-marker analyses were used to identify the linkage between microsatellite markers and variation in EBVs of these traits, Milk yield, Protein percentage, Fat percentage, Litter size and weight at birth, and litter size and weight at weaning. The estimates of the parameters from forward and backward solutions using stepwise regression procedure on milk yield trait, only two markers, OARCP9 and AGLA29, showed a highly significant effect (p≤0.01) in backward and forward solutions. The forward solution for different equations conducted that R2 of these equations were highly depending on only two partials regressions coefficient (βi,) for these markers. For the milk protein trait, four marker showed significant effect BMS2361, CSSM66 (p≤0.01), BMS2626, and OARCP9 (p≤0.05). By the other way, four markers (MCM147, BM1225, INRA006, andINRA133) showed highly significant effect (p≤0.01) in both backward and forward solutions in association with milk fat trait. For both litter size at birth and at weaning traits, only one marker (BM143(p≤0.01) and RJH1 (p≤0.05), respectively) showed a significant effect in backward and forward solutions. The estimates of the parameters from forward and backward solution using stepwise regression procedure on litter weight at birth (LWB) trait only one marker (MCM147) showed highly significant effect (p≤0.01) and two marker (ILSTS011, CSSM66) showed a significant effect (p≤0.05) in backward and forward solutions.

Keywords : microsatellites marker, estimated breeding value, stepwise regression, milk traits

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