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AN INVESTIGATION ON RELATIONSHIP BETWEEN LACTATION MILK YIELD, SOMATIC CELL COUNT AND UDDER TRAITS IN FIRST LACTATION TURKISH SAANEN GOAT USING DIFFERENT STATISTICAL TECHNIQUES

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ABSTRACT

This study aimed to determine the relationship between lactation milk yield, (LMY), somatic cell count (SCC), and udder traits using some statistical techniques, viz. multiple linear regression, stepwise regression, use of factor analysis in multiple regression, and regression tree. Forty six Turkish Saanen Goat were used in the present investigations . These goats were milked with milking machine twice a day. The traits recorded were: daily milk yield (DMY), udder upper height (UUH), udder width (UW), udder length (UL), udder diameter (UD), teat angle (TA), udder volume (UV), somatic cell count (SCC), lactation length (LL), and lactation milk yield (LMY), Respectively. In the multiple linear regression analysis, significant effects of and LT ($P<0.01$) and TA ($P<0.01$) on LMY trait were observed. According to result of Stepwise Regression Analysis model (SRAM); TA, LL and UD had positively significant effect on the LMY trait without multicollinearity problem. Kaiser-Meyer-Olkin (KMO=0.6) and, Bartlett's test of spherity ($P<0.01$) also confirmed that factor analysis was applicable for the data. Present results from using factor analysis scores with multiple regression analysis (FASMLRA) reflected that five factors, explained 87.7 % of variation and only UV, TA, UL, UD and LL could significantly increase LMY ($P<0.01$) for factors 2-4. FASMLRA with the lowest VIF values gave more advantageous results. Regression Tree (RT) Method illustrated that, the goats with TA > 50^0 among all the goats (Node 2) had the highest LMY (297.357 lt) or Node 4 as a group of the goats with LL > 191 days among the goats with TA $\leq 50^0$ provided higher LMY average except for Node 2. If there is a verification at genetic level, the relationship between lactation milk yield (LMY), somatic cell count (SCC), and udder traits might contribute to further goat breeding to increase milk yield in the future.

Key words: Factor Analysis Scores, Milk yield, Udder trait, Stepwise Regression, Regression Tree, Saanen Goat.

INTRODUCTION

In dairy industry, milk production provides a great contribution to countries' economy and people nourishment throughout the world. In concern with milk production, milk yield as in other well-recognized quantitative traits in animal science is influenced by genetic and non-genetic factors.. Mastitis is a significant disease leading to the most economic losses in dairy industry. (Yalcin, 2000; Yalcin *et al.,* 2000; Uzmay *et al.,* 2003). To prevent mastitis, dairy breeders should take some precautions, viz. routine heath care, hygiene, and achievement of desirable genetic improvement through selection (Jouzaitiene *et al.,* 2006).

Methods which are available for mastitis diagnosis are the strip-cup, the California Mastitis Test (CMT), Wisconsin Mastitis Test (WMT), and Somatic Cell Count (SCC). Among these mentioned tests, SCC as an indicator of udder health status (Juozaitiene *et al.,* 2006) is the most well accepted method in diagnosis of Mastitis in a herd and SCC is influenced by many environmental factors (age, parity, season, temperature and stress), barn conditions and milking machine and systems (Uzmay *et al.,* 2003; Koc, 2007). These factors play a crucial role on milk yield, composition, hygiene-quality of milk, and animal's udder health (Koc, 2007).

In dairy goat, investigation of the relationship between milk yield, SCC and udder traits enables breeders to obtain beneficial clues not only for accomplishing on the subject of selection of superior goats and but also for developing better selection strategies on milk yield per goat. In a study on Damascus Goat, Mavrogenis *e al.,*(1989) stated highly heritable traits of teat length (TL), diameter (TD), 90-d and total milk production, and positive-moderately high correlations among udder traits. Accordingly, Peris *et al.* (1999) reported significant correlations between udder traits, udder volume, body weight, milk yield, and milking traits in Murciano-Gradina dairy goat. Amao *et.al.*(2003) also reported in Red Skoto Goat, significant correlations between udder traits UL, UW, UC, TL, TW, TC, and UV etc. Keskin *et al.* (2005) reported positive effects of UC and UBH on DMY in the study on the relationships between several udder traits (UBH, UD, UC, LTC, RTC, AND TA) and DMY of Akkeci Goat, by using Path Analysis and expecially significant positive correlations of DMY with UD, UC, LTC, RTC, and TA ($P<0.01$). Keskin *et al.* (2007a) investigated the relationship between daily milk yield (DMY) and 10 udder traits (upper height (UH), udder bottom height (UBH), udder depth (UD), udder width (UW), udder circumference (UC), left teat length (LTL), right teat length (RTL), left teat circumference (LTC) and right teat circumference (RTC), and teat angle (TA)) by using factor analysis scores in multiple linear regression model on Akkeci (Kilis x Saanen) crossbred goat. In a more detailed study, Cedden *et al.*, (2008) emphasized the relationship between somatic cell count, milk yield, fat percent, and some udder traits in primiparous Saanen x Kilis Crossbred goat. In the literature, reports on the relationship among milk yield with somatic cell count and udder traits together in the goat were relatively limited. To date, there has been no published knowledge on relationship of lactation milk yield with somatic cell count and udder traits in first lactation Turkish Saanen goat by using different statistical analysis techniques. Hence, the aim of the present paper was to determine the relationship of lactation milk yield (LMY) with somatic cell count (SCC), and udder traits using various statistical analysis techniques, such as multiple linear regression, stepwise regression, jointly use of factor analysis in multiple regression, and regression tree, comprehensively.

MATERIALS AND METHODS

Data Collection: Data on Forty six Turkish Saanen Goats were collected from a private company in Kılılı town of central district registered to Kahramanmaras Breeding Sheep and Goat Association. These goats were milked with milking machine twice a day. The traits recorded were: udder upper height (UUH), udder width (UW), udder length (UL), udder diameter (UD), teat angle (TA), udder volume (UV), somatic cell count (SCC), lactation length (LL), daily milk yield (DMY), and lactation milk yield (LMY), all of which are quantitative (measurable) variables, respectively. Data from Aktas *et al*. (2012) were also used with the aim of evaluating different statistical techniques in the present study, which contained various new results.

All udder measurements were recorded after morning milking at each measuring period. In addition, the udder traits at mid-lactation period were used for the present paper. As recommended before by Kaya (2005), measuring baston was used for udder traits, viz. udder lower height (ULH): udder upper height, udder width (UW) respectively. Teat angle (TA) was measured with goniometer and udder volume (UV) was measured with water immersion method on the basis of dripping water volume.

Determination of somatic cell count in milk sample: DCC (DeLaval Somatic Cell Measuring Device) was used to determine somatic cell count of the collected milk samples in Microbiology Laboratory of Agricultural Faculty of Kahramanmaras Sutcu Imam University. After dropping a few drops from milk samples into De Laval count kit, loaded cassette was put into Delaval cell counter. DCC counts somatic cells colored with DNA specific flourescent probe Propidium lodide. Amount of somatic cell count becomes numerically visible on its screen inside of one min. See Gonzalo *et al.* (2006) for more detailed information on the use of DCC device.

Statistical Analysis

Variable Structure: In the present study, lactation milk yield (LMY) was considered as a dependent (target=response) variable. In addition, all the quantitative-independent (measurable) variables are given below: udder upper height (UUH), udder width (UW), udder length (UL), udder diameter (UD), teat angle (TA), udder volume (UV), somatic cell count (SCC), lactation length (LL), and LOGSCC, which is a logarithmic transformation of SCC trait.

Multiple Linear Regression Analysis Model: In order to predict LMY from UUH, UW, UL, UD, TA, UV, LOGSCC, and LL, prediction equation for LMY can be written as follows:

$LMY = a + b_1\, UUH + b_2\, UW + b_3\, UL + b_4\, UD + b_5\, TA + b_6\, UV + b_7\, LOGSCC + b_8\, LL + e$

Where, a:intercept, b_1 , b_2 , b_3 b_4 , b_5 , b_6 , b_7 , b_8 are regression coefficients, and e: error term.

Stepwise Regression Analysis Model: By Stepwise Regression Analysis Model, significant (independent) variables (UD, TA, and LL) among UUH, UW, UL, UD, TA, UV, LOGSCC, and LL, were included in multiple regression analysis model. Prediction equation for Stepwise Regression Analysis Model can be written as follows:

$LMY = a + b_1\, UD + b_2\, TA + b_3\, LL + e$

Where, a: intercept, b_1 , b_2 and b_3 are regression coefficients, and e: error term.:

Use of Factor Analysis Scores in MLRA: The appropriateness of factor analysis was tested with ***Kaiser-Meyer-Olkin*** (KMO) measure of sampling adequacy and ***Bartlett's test of sphericity*** (Sharma, 1996).

The basic factor analysis equation in matrix form can be written as:

$\mathbf{Z} = {}^{a}\,\mathbf{F} + £$

Where **Z** is a px1 vector of variables, ^{a} is a **p**x**m** matrix of factor loadings, **F** is an **m**x**1** vector of factors and £ is a **p**x**1** vector of error or residual factors (Sharma, 1996). Due to the differences in the units of variables for factor analysis, the variables were standardized and eigen values were estimated by a correlation matrix of variables. VARIMAX rotation was utilized to facilitate interpretation of factor loadings (L_{ik}). Factor coefficients (C_{ik}) were used with the aim to obtain factor scores for the selected factors in the factor analysis. Factors whose eigenvalues are greater than 1 were included in multiple regression analysis.

Score values obtained from the chosen factors were used as explanatory variables to predict LMY of the first lactation Turkish Saanen Goat. The multiple linear regression equation for fitting standardized body weight and the following factor score equation can be formulated as below:

$LMY = a + b_1FS_1 + b_2FS_2 + b_3FS_3 + b_4FS_4 + b_5FS_5 + e$

Where a, regression constant (the value of intercept is zero); b_1 , b_2, b_3 b_4 , and b_5 are regression coefficients of Factor Scores (FS). FS is factor score and e is the error term. The significance of regression coefficients was tested by using a t-statistic.

The efficiency of multiple regression analysis explaining total variation in LMY of the first lactation Turkish Saanen Goat was determined using determination coefficient (R^2) and Root of Mean Square Error (RMSE), and Variance Inflation Factor (VIF), as an indicator of multicollinearity (Eyduran *et al.* 2009). For a trustworthy multiple linear regression or Stepwise Regression analysis, VIF for all the independent variables should be less than 10 (Karakus *et al.* 2010).

All the statistical computations except for RT analysis were performed with MINITAB (Trial Version: 15) statistical package program. (www.minitab.com).

Regression tree method: As a tree based model, Regression Tree (RT) Method, a non-parametric method, assigns the most suitable cut-off values for independent variables that can significantly influence dependent variable. The purpose of RT method is to generalize prediction rules with regard to a dependent variable, with respect to the values of independent variables (Hébert *et al.*, 2006). Regression tree method changes continuous variables into discrete variables on the basis of proper cut-off values (Camdeviren *et al.*, 2005; Tariq *et al.*, 2012b). For Regression Tree Method, F test was employed for testing significance of a continuous dependent variable in the present paper (Hébert *et al.*, 2006; Tariq *et al.*, 2012b). RT analysis was performed using SPSS (Exhaustive CHAID) statistical package program (Analyze >Classify >Tree…in the SPSS).

RESULTS AND DISCUSSION

In the literature, this is the first study to investigate relationships of lactation milk yield (LMY) with somatic cell count (SCC), and udder traits using various statistical analysis techniques, such as multiple linear regression, stepwise regression, jointly use of factor analysis in multiple regression, and regression tree in goats, comprehensively.

Result of MLRA, predicting lactation milk yield from the traits mentioned above are summarized in Table 1. . According to these results obtained from MLRA, proportion of the explained variation for LMY trait was exactly 65(%), meaning that 65(R^2%) of total variation in the LMY trait was explained by other quantitative traits (independent variables) included in the MLRA model. Result of ANOVA table belonging to MLRA showed obviously that MLRA model ($P<0.01$) building for the present study were found significant and LL ($P<0.01$) and TA ($P<0.01$) in the MLRA model significantly and positively influenced LMY trait in the present study. VIF values obtained for independent variables varied from 1.140 (LOGSCC) to 2.718 (UUH), suggesting that MLRA model could be reliable without multicollinearity problem.

Table 1. Results of Multiple linear regression analysis for original variables

Predictor	Coef	SE Coef	t	P	VIF
Intercept	-379.6	174.8	-2.17	0.036	
LL	1.1155	0.3220	3.46	0.001	1.375
UUH	-0.537	1.329	-0.40	0.689	2.718
UW	-0.370	1.423	-0.26	0.796	2.535
UL	6.672	6.465	1.03	0.309	1.712
UD	3.619	1.953	1.85	0.072	1.668
TA	2.3761	0.6794	3.50	0.001	1.673
UV	-0.00673	0.05652	-0.12	0.906	1.663
LOGSCC	24.21	19.03	1.27	0.211	1.140
S = 42,8578 R-Sq = 65,0% R-Sq(adj) = 57,4%					

LMY: lactation milk yield, UUH: udder upper height, UW: udder width, UL: udder length, UD: udder diameter, TA: teat angle, UV: udder volume, SCC: somatic cell count, LL: lactation length

Stepwise Regression Analysis Model: The Summary of Stepwise Regression Analysis for original variables is given in Table 2. In stepwise regression analysis model (SRAM), positively significant effects of TA, LL and UD traits on the LMY trait were determined, which illustrating that LMY would increase with increasing these traits. For instance, when an increase of 1^0 occurred in TA trait; LMY would increase approximately 2.29 lt. SRA model had a R^2 (%) of 62.5, which was the proportion of the variation explained by these three traits, (P<0.01). Very low VIF values for TA, LL and UD traits were 1.154, 1.072, and 1.091, respectively, with a narrow range of 1.072 to 1.154, illustrating that, no multicollinearity problem was found.

Table 2. The Summary of Stepwise Regression Analysis for original variables

Predictor	Coef	SE Coef	t	P	VIF
Intercept	-250.54	68.36	-3.67	0.001	
LL	1.1229	0.2763	4.06	0.000	1.072
UD	4.838	1.534	3.15	0.003	1.091
TA	2.2884	0.5481	4.17	0.000	1.154
S = 41,6387 R-Sq = 62,5% R-Sq(adj) = 59,8%					

LMY: lactation milk yield, UD: udder diameter, TA: teat angle, LL: lactation length

Use of Factor Analysis Scores in MLRAL In order to remove multicollinearity problem, one of the most effective approaches is to use factor analysis scores together with MLRA (FASMLRA). In the view of VIF values, present FASMLRA results with the lowest VIF values confirmed this statement compared to MLRA and SRAM, respectively. As seen from Tables 2-4, FASMLRA (S=0.638843) produced the lowest RMSE values compared with MLRA (S=42.8578) and SRAM (S=41.6387), respectively.

A Kaiser-Meyer-Olkin (KMO) of 0.60 and Bartlett's test of spherity (chi-square: 96.56; P<0.01) confirmed the suitability of the studied data for factor analysis (Table 3).

Results of factor analysis are given in Table 3. Five factors with eigenvaluesgreater than one explained 87.7 % (7.0196/8*100) of total variation in the present data. Of the explained variation, 23.8%, 19.7%, 18.3%, 13.0% and 12.9% were explained by factors 1-5, respectively. With respect to sorted-rotated factor loading and communalities in the factor analysis, communalities had a range of 0.798 to 0.977, illustrating that very high communalities which were a desirable case were found in the study, because these high communalities mean that the extracted five factors accounted for a big proportion of variance regarding the original variables.

Factor loadings permit researchers to determine the quantitative traits which will make more contribution to the formation of the extracted factors. Factor loading is the correlation between original variables and factor scores. Thus, positively high correlation (r=0.933) between UUH and FS1 was found (P<0.01), but UW was highly negatively correlated with FS1 (r=-0.872) (P<0.01) statistically. UV and TA were strongly associated with FS2 (r=-0.922 and -0.800), respectively (P<0.01). In the similar way, positive correlation coefficients were also highly estimated for UL-FS3 (r=0.857), UD-FS3 (r=0.830), LL-FS4 (r=0.923), respectively. In addition, there was a significant correlation between LOGSCC-FS5, with r = - 0.970 (P<0.01).

The results of MLRA model with latent uncorrected independent variables and LMY trait are presented in Table 4. Determination coefficient (63.7%) and Root of Mean Square Error (RMSE=0.638843) were estimated without exactly multicollinearity problem for jointly using factor score in MLRA model. In the MLRA model, no significant effects of FS1 and FS5 new-uncorrelated-latent variables on LMY trait were found as shown in Table . However, other new latent variables viz. FS2, FS3 and FS4 had very noteworthy impacts on LMY (P<0.01), respectively.

Mathematically, same signs of factor loading (Table 3) and regression coefficient (Coef) calculated for factor scores (Table 4) mean that LMY will increase in the Goat. LMY would be expected to insignificantly increase with decreasing UUH and increasing UW in respect of factor 1 as shown in the Tables 3-4, respectively.

LMY would be expected to increase when UV and TA, significantly contributing to factor 2 (P<0.01) , increased (Tables 3-4). Similarly LMY would be estimated to increase as a result of increasing UL and UD, which made a statistically significant contribution to factor 3 (P<0.01). Likewise, LMY would be expected to increase with longer LL, which was the most influential variable on factor 4 (P<0.01) (Tables 4 and 5). It was concluded that only UV, TA, UL, UD and LL could significantly increase LMY (P<0.01) in concern with factors 2, 3 and 4, which were statistically significant (P<0.05). LOGSCC positively-insignificantly affected LMY when evaluated together with fifth factor.

Keskin *et al.* (2005) reported positive influences of UC and UBH on DMY from Path Analysis, which can be seriously affected by multicollinearity problem, compared to the other traits, UD, LTC, RTC, AND TA and DMY of Akkeci Goat. In an earlier study by Keskin *et al.* (2007a), with using jointly factor scores in MLRA, four factors were extracted from 10 udder traits, and four new-latent-uncorrelated-variables were obtained with the aim of definitely removing multicollinearity problem. Among these udder traits, the positively significant effects of LTL, RTL, LTC, UD, UW, UC, and TA on DMY were reported in spite of negatively effects of UUH and UBH on the DMY. However, UV, TA, UL, UD, LL significantly influenced LMY, very positively. The only results on significant effects of TA and UD in the present study were consistent with Keskin *et al*. (2007a). Considering studies on goat, very few reports including different udder traits were available on using jointly factor analysis scores in MLRA (Keskin et.al. 2007a, b;), although there were many FASMLRA studies with various purposes on different species (Keskin *et al.*, 2007a, b; Yakubu, 2009; Cankaya *et al*., 2009; Eyduran *et al*., 2009; Eyduran *et al*., 2010; Ogah *et al*., 2009; Yilmaz *et al.,* 2011; Eyduran *et al*., 2012; Ifeanyichukwu, 2012; Tariq *et al*., 2012a).

Table 3. Results of Factor analysis for original variables

Sorted Rotated Factor Loadings and Communalities						
Variable	**Factor1**	**Factor2**	**Factor3**	**Factor4**	**Factor5**	**Communality**
UUH	0.933^{**}	-0.033	0.052	0.057	0.133	0.895
UW	-0.872^{**}	0.003	-0.010	-0.264	-0.111	0.843
UV	0.165	-0.922^{**}	0.038	-0.093	-0.056	0.890
TA	-0.154	-0.800^{**}	0.159	0.310	0.116	0.798
UL	0.278	0.054	0.857^{**}	0.103	0.153	0.848
UD	-0.202	-0.263	0.830^{**}	0.036	-0.138	0.819
LL	0.270	-0.107	0.104	0.923^{**}	0.037	0.948
LOGSCC	-0.183	0.031	-0.011	-0.039	-0.970^{**}	0.977
Variance	1.9066	1.5756	1.4631	1.0427	1.0316	7.0196
% Var	0.238	0.197	0.183	0.130	0.129	0.877
Factor Score Coefficients						
Variable	Factor1	Factor2	Factor3	Factor4	Factor5	KMO Measure of Sampling Adequacy: 0.60 Bartlett's Test of Sphericity: 96.56 (P<0.01)
LL	-0.091	0.079	-0.077	0.979	-0.071	
LOGSCC	0.126	0.012	0.011	0.057	-1.005	
UUH	0.565	-0.047	0.013	-0.218	-0.087	
UW	-0.471	-0.005	0.044	-0.057	0.105	
UL	0.103	0.163	0.626	-0.082	0.088	
TA	-0.108	-0.053	0.580	-0.059	-0.111	
UA	-0.184	-0.474	-0.037	0.251	0.140	
UV	0.189	-0.656	-0.088	-0.310	-0.106	

**P<0.01 shows statistically significant correlation between an original variable and factor scores from the related factor

LMY: lactation milk yield, UUH: udder upper height, UW: udder width, UL: udder length, UD: udder diameter, TA: teat angle, UV: udder volume, SCC: somatic cell count, LL: lactation length

Table 4. Results of Multiple Linear Regression Analysis for new-uncorrelated latent variables

Predictor	Coef	SE Coef	t	P	VIF
FS1	-0.02315	0.09523	-0.24	0.809	1.000
FS2	-0.42879	0.09523	-4.50	0.000	1.000
FS3	0.41208	0.09523	4.33	0.000	1.000
FS4	0.52626	0.09523	5.53	0.000	1.000
FS5	-0.07790	0.09523	-0.82	0.418	1.000
S = 0,638843 R-Sq = 63,7% R-Sq(adj) = 59,2%					

Regression tree (RT) Method: Regression tree (RT) diagram, drawn for finding out statistically significant traits influencing LMY is depicted in Fig 1. RT diagram reflected that merely TA, LL, and UV traits were statistically significant. . Considering significance ranking of these three traits, it was concluded that the statistically predominant trait on LMY was TA (P <0.01), followed by LL and then UV, (P<0.05) respectively.

Average LMY for Node 0, root node, a group of all the goats at the top of RT, was found as 237.652 lt (SD=65.590). Node 0 was divided into two new child nodes, Nodes 1 and 2, with respect to TA respectively. Average LMY for Node 1, which was a group of the goats with TA $\leq 50^0$ among all the goats provided for the present study, was determined to be 211.531 lt (SD=42.137). As a group of the goats with TA > 50^0 within all the goats, Node 2 yielded the highest LMY average of 297.357 lt (SD=71.688), which was compared with other Nodes in regression tree diagram. This means that the goats with TA > 50^0 could have higher LMY.

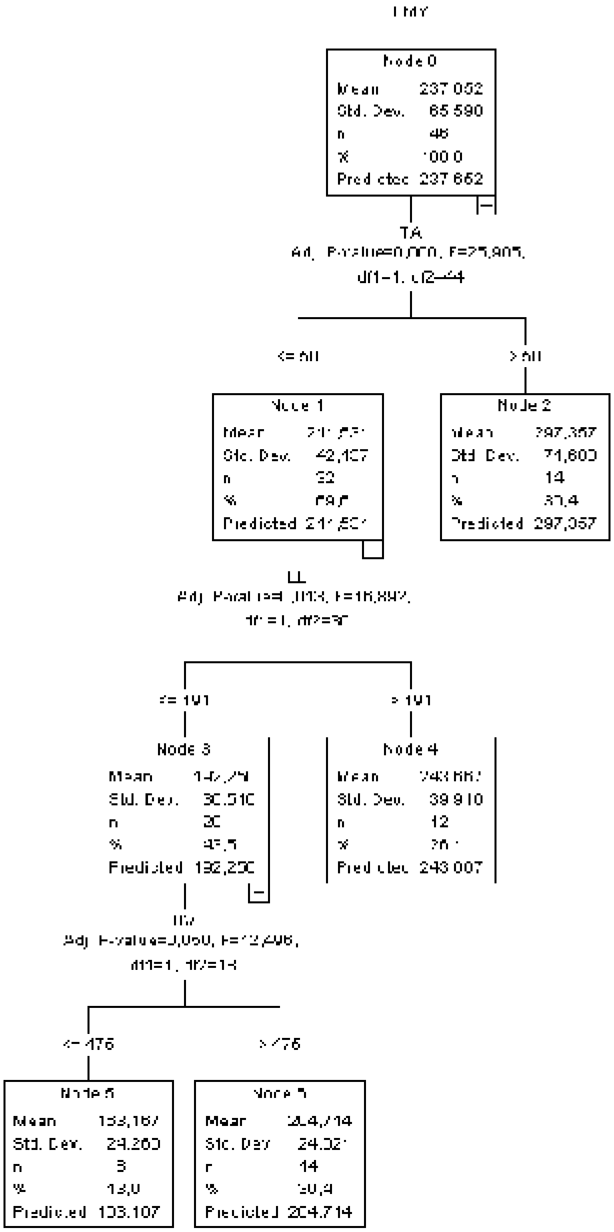

Fig 1. Regression Tree Diagram

LMY: lactation milk yield, UUH: udder upper height, UW: udder width, UL: udder length, UD: udder diameter, TA: teat angle, UV: udder volume, SCC: somatic cell count, LL: lactation length LMY of the goats with TA ≤ 50^0 (Node 1) was affected by LL and Node 1 was rebranched into the new nodes of Nodes 3 and 4 on the basis of LL, respectively. Node 3, a group of the goats with LL ≤ 191 days among the goats of TA ≤ 50^0, had an average LMY of 192.250 lt (SD=30.516). Node 4, defined as a group of the goats with LL > 191 days among the goats with TA ≤ 50^0, produced 243.667 lt LMY (SD=39.910). Compared these two Nodes, among the goats with TA ≤ 50^0, the LMY average from the goats with LL > 191 days was higher than the average from the goats ≤ 191 days.

UV significantly influenced LMY of Node 3, a group of the goats with LL ≤ 191 days and TA ≤ 50^0 (P<0.05). Node 3 was seperated once more with respect to UV trait into the new child nodes, Nodes 5 and 6, respectively. Node 5 was defined as a group of the goats with UV ≤ 475 ml among the goats with LL ≤ 191 days and TA ≤ 50^0 and its LMY average was estimated as 163.167 lt (SD=24.260). Node 6, which was a group of the goats with UV > 475 ml among the goats with LL ≤ 191 days and TA ≤ 50^0, had 204.714 lt LMY (SD=24.021).

In conclusion, Regression Tree Method illustrated that, the goats with TA > 50^0 among all the goats (Node 2) with 297.357 lt had the highest LMY in comparison with other Nodes or Node 4 as a group of the goats with LL > 191 days among the goats with TA ≤ 50^0 gave higher LMY average.

In animal science, new RT results from the study were different from those obtained by some authors, working statistical modeling on different species (Eyduran *et al.*, 2008; Mendes and Akkartal, 2009; Topal *et al.*, 2010). These results were nonissuable with each other.

In conclusion, results of the present study and earlier studies could not be discussed due to use of different breeds, traits, sample size, and especially various statistical analysis techniques.

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