

RELATIONSHIP BETWEEN GENETIC MARKERS (BM2113, ETH10, ETH225) WITH SOME BLOOD TRAITS, PROLACTIN AND CORTISOL HORMONES

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Abstract

The study was carry out in Taj Al-Nahrain research station and Wahaj Al-DNA Molecular Genetics Laboratory on Holstein-Friesian cows, from 10/12/2018 to 1/5/2019, to determine the relationship between genetic markers, BM2113, ETH10 and ETH225, with 135/125, 138/122 and 142/126 genotypes. 218/206, 220/206 and 217/207 genotypes for BM2113 genetic marker. 218/206, 220/206 and 217/207 genotypes for BM2113 genetic marker. For genetic markers ETH225, respectively with some blood traits, prolactin and cortisol hormones. The results of the study showed that there were no significant differences in the genotypes 135/125, 138/122 and 142/126 of the BM2113 genetic marker in all studied traits. In ETH10 genetic marker, 220/ 206 genotype was a highly significant increase (P \leq 0.01) compare with 217/207 and 218/206 genotypes for prolactin hormone, there were significant differences (P \leq 0.05) of 217/207 genotypes on 218/206 and 220/206 genotypes for cortisol hormone and cholesterol, there were no significant differences in total protein, albumin and globulin. The results of genetic markers ETH22 showed significant differences (P \leq 0.05) in 146/137 genotype by 4.07, as well as 140/134 genotype by 1.74, which exceeded 142/134 genotype and their relationship with the hormone prolactin, while there were no significant differences in the cortisol hormone, cholesterol, albumin, globulin and total protein.

Key words: genetic markers (BM2113, ETH10, ETH225), blood traits, prolactin, cortisol.

Introduction

Livestock is one of the most important sources around the world, Cattle occupy the highest levels of milk and meat production among farm animals (FAO, 2003). Bovine is the most common type of large domesticated animal and has an important role in the modern history of mankind when, it was domesticated 8000 to 10,000 years ago (Bollongino et al., 2012). Improving the productive and reproductive performance of farm animals, including cows, especially under traditional breeding conditions, leads to multiple difficulties, which led to a decrease in their reproductive performance, It is necessary to rely on some measures for the purpose of obtaining more adaptive and productive animals, this has led researchers to find alternatives to the traditional election, which has been followed over the past decades and requires considerable time and effort (Saleem et al., 2015). Despite genetic progress, some ancient methods, such as quantitative genetics, which were influenced by environmental factors, which reduces the accuracy of evaluation or selection, the development in molecular genetics has led to the identification of some programs that improve animal performance (Yadav *et al.*, 2017). Molecular genetic techniques allow the direct identification of genotypes by molecular markers of non-adherence to the age and sex of the animal through advanced technologies of molecular heredity (Ebegbulem and Ozung, 2013).

The aim of this study is to determine the genetic diversity of the Holstein cattle herd according to some genetic markers using microsatellite technique and its relationship with certain blood parameters, prolactin and cortisol hormones for early selection.

Materials and Methods

The study was conducted at Taj Al-Nahrain, Qadisiyah Governorate. 20 Holstein Frisian cows were used, from 10/12/2018 to 1/5/2019, the cow data were collected by the animals' ages and species through the station records. Blood analysis was carried out at the

Genotype	Prolactin	Cortisol	Cholesterol	Total protein	Globulin	Albumin			
Base pairs	nmol/l	nmol/l	(Mg/dm)	(Mg/dm)	(Mg/dm)	(Mg/dm)			
135/125	19.50 ± 2.25	63.25 ± 4.95	161.50 ± 20.45	5.83 ± 0.98	2.37 ±0.84	3.47 ± 0.28			
138/122	21.50 ± 6.06	99.25 ± 21.86	119.25 ± 23.76	5.17 ± 0.53	1.62±0.40	3.56 ± 0.27			
142/126	15.20 ± 2.53	79.80 ± 11.21	153.20 ± 10.43	5.88 ± 0.60	2.28±0.43	3.59 ± 0.22			
Sig.	N.S	N.S	N.S	N.S	N.S	N.S			
N.S: Non-significant									

Table 1: Relationship of the genetic marker BM2113 with prolactin and cortisol and some blood parameters.

Baghdad Laboratory of Pathological Analysis (Qadisiyah Governorate). The genetic part was performed in the Wahaj Al-DNA laboratory (Baghdad governorate). Samples were taken from cows prepared for study 20 blood samples of milk vein, each sample (5 mL) was placed in the anticoagulation test tube, the tubes were kept in a refrigerated container and transported directly to the analysis laboratories, for sample homogeneity, use the shaker device, use the centrifuge to separate the plasma, the analysis of cortisol and prolactin hormone, the samples were placed for two hours within the hormone device (Snibe), the chemical analysis device (mindray) used analysis of cholesterol, total protein, globulin and albumin.

Cortisol was evaluated by the preparation solutions (kit) produced by the French company Biolabo based on Tietz, (1999). Use Kit, (Bioche) to measure the concentration of prolactin, 50 microns of solution and sample were added in each hole (tube) of the Microtite plate, 100 microns of conjugater reagent enzyme were added, put in incubator at 25°C for 45 minutes, add 100 microns TMB reagent, color intensity is measured using ELTSA and a wavelength of 450 nm. Cholesterol was estimated by a solution prepared by the French company Biolabo according to Allain et al., (1974). The total protein was estimated by the prepared solutions (Kit) produced by the French company Biolabo and according to Henry, (1957). The concentration of serum bumin was determined by a solution prepared by the French company Biolabo based on the method Bush, (1998). The concentration of globulin was estimated on the basis of the difference between total protein concentration and total albumin concentration in plasma according to Otto et al., (2000).

The data were analyzed statistically using the Statistical Analysis System-SAS, (2012), significant differences were compared between averages using the Duncan, (1955), multidimensional test by applying the General Linear Model-GLM method. The Chi-square test was used to compare the percentage of allele distribution or recurrence and each genetic marker in studied cattle samples.

Results and Discussion

Table 1, shows no significant differences between the genotypes with the genotypes 135/125, 138/122 and 142/126 of the genetic markers BM2113, the percentage of prolactin hormone was 2.25, 6.06 and 2.53, cortisol hormone percentage in the genotypes was 4.95, 21.86 and 11.21, cholesterol was 20.45, 23.76 and 10.43, the total protein was 0.98, 0.53 and 0.60, globulin was 0.84, 0.40 and 2.28, albums was 0.28, 0.27 and 0.22 respectively, Daetwyler *et al.*, (2014) noted that kappa-casin reacts faster with Variant B, compared to variable A from LGB.

Table 2, showed that there were high significant differences (P<0.01) for 218/206, 220/206 and 217/207 genotypes in the ETH10 genetic marker, 220/206 genotype was superior to 217/207 and 218/206 genotype with 1.70 for prolactin hormone, there were also significant differences (P<0.01) for 217/207 and 218/206 genotypes on 220/206 genotype, the cortisol rate was 7.37 and 4.17 respectively. There were significant differences (P<0.01) between 217/207 and 218/206 genotypes on 220/206 genotype for cholesterol, as for total protein, albumin and globulin, there were no significant differences among 218/206, 220/206 and 217/207 genotypes. Farrell *et al.*, (2004) and Caroli *et al.*, (2009) found a correlation between LGB gene and the globulin in milk.

Genotype **Prolactin** Cortisol Cholesterol Total protein Globulin Albumin nmol/l nmol/l (Mg/dm)(Mg/dm)(Mg/dm)(Mg/dm)**Base pairs** 23.50±3.62 a 66.83±4.17 b 148.00±17.92 ab 2.36 ± 0.53 3.50 ± 0.17 135/125 5.84 ± 0.58 138/122 $13.00 \pm 1.70 \, b$ 104.60±16.96 a $162.80 \pm 11.28 a$ 6.14 ± 0.59 2.39 ± 0.48 3.75 ± 0.16 22.11 ± 2.42 a 142/126 $72.44 \pm 7.37 \, \mathrm{b}$ $121.88 \pm 6.98 \, b$ 5.03 ± 0.28 1.74 ± 0.26 3.28 ± 0.14 Sig. ** ** NS NS NS The averages with different letters within the same column differ significantly below the probability level of 0.05 N.S: Non-significant

Table 2: Relationship of the genetic marker ETH10 with prolactin and cortisol and some blood parameters.

Genotype	Prolactin	Cortisol	Cholesterol	Total protein	Globulin	Albumin		
Base pairs	nmol/l	nmol/ <i>l</i>	(Mg/dm)	(Mg/dm)	(Mg/dm)	(Mg/dm)		
135/125	19.67 ±4.07 ab	93.50±16.94	137.67±13.28	5.61 ± 0.44	2.01 ± 0.40	3.58 ± 0.14		
138/122	25.67±3.05 a	64.50 ± 3.41	138.83±16.17	5.37 ± 0.48	2.05 ± 0.47	3.32 ± 0.14		
142/126	$16.62 \pm 1.74 \mathrm{b}$	78.50 ± 7.62	142.50±12.24	5.64 ± 0.50	2.17 ± 0.38	3.48 ± 0.20		
Sig.	*	NS	NS	NS	NS	NS		
The averages with different letters within the same column differ significantly below the probability level of 0.05								

N.S: Non-significant

Table 3: Relationship of the genetic marker ETH225 with prolactin and cortisol and some blood parameters.

The results of table 3, showed significant differences (P<0.05) with a low percentage of individuals with 146/137 genotype by 4.07, as well as the 140/134 genotype by 1.74 in ETH225 genetic marker, which exceeded the with 142/134 genotypes and their relationship with the hormone prolactin, while cortisol, cholesterol, albumin, globulin and total protein hormone has no significant differences in 146/137, 142/134 and 140/134 genotypes, the results of some studies showed positive correlation between insulin hormone and genotype ADIPOR2 (0.235-) (Behnam *et al.*, 2014).

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