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RELATIONSHIP BETWEEN GENOTYPES OF THE HEAT SHOCK GENE HSP90, CONCENTRATIONS OF SOME BIOCHEMICAL AND ELEMENTS BLOOD PARAMETERS OF HOLSTEIN FRIESIAN COWS

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Abstract:

The experiment was conducted at Taj Al-Nahrain Research Station, north of Diwaniyah Governorate, by using 35 Holstein cows for the period between 1/3/2022 to 15/8/2022, to demonstrate the effect of the relationship between genetic polymorphisms of the heat shock gene HSP90, and some biochemical characteristics of Holstein Friesian cows. These cows were divided into three seasons as follows: the first season (11 cows), the second season (15 cows), and the third season (9 cows), based on station records. The cows were placed in semi-shaded pens with a length of 140 m and a width of 60 m for each pen, these pens were provided with freely filled water basins, after that, the genetic part was analyzed in the Molecular Genetics Laboratory of the College of Agriculture, University of Basrah. The remainder of the genetics results (Skonsk) were completed at BIONEER Laboratories Company in Seoul/Korea. As for the physiological traits, they were analyzed in the Physiology Laboratory of the College of Agriculture, University of Basrah. The results show that a significant increase of the CT and TT genotypes compared to the CC genotype on the potassium concentration in the blood of Holstein cows, with a significant increase of the CT genotype compared to the TT genotype in the concentration of urea in blood serum, there were no significant differences between all genotypes on the concentration of glucose, cholesterol, triglycerides, albumin, total protein, phosphorus, and calcium.

Keywords: heat shock gene HSP90, biochemical, elements, blood parameters, Holstein Friesian cows.

Introduction:

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Most living organisms respond to rising temperatures, starting with microorganisms, plants, and animals (Kregel, 2002), this response to heat stress occurs by stimulating biological mechanisms for the purpose of producing certain proteins known as stress proteins, which are molecular chaperones, it protects proteins from denaturation and also facilitates the refolding of proteins that can be refolded, while proteins that cannot be refolded are removed through the process of proteolysis (Tutar and Tutar, 2010). The heat stress to which the cell is exposed also causes the protein produced in it to lose its original form, which may lead to cell death, the role of the production of proteins that cause deficiency or may result in heat shock proteins that are generated to address this problem is highlighted (Jana and Maria, 2012).

The proteins that are produced in response to exposure to stress are called heat shock proteins (HSP), the first study was carried out by the Italian scientist Ritossa Ferruccio in 1962 on the Drosophila insect, it was believed that these proteins were only related to high temperatures, it has been observed that swelling occurs in chromosomes when exposed to heat, these swellings are responsible for the formation of proteins encoding the heat shock protein gene (Dai *et al*., 2007). The structure of these proteins was not described until 1974, and they were not known at that time by this name, these studies ultimately led to the identification of heat shock proteins (HSP) or so-called heat stress proteins (Ritossa 1996). Gosslau *et al*. (2001) indicated that the secretion rates of heat shock proteins increase with increasing intensity of exposure to the stressful factor and exposure time. Guerreiro *et al*. (2004) and Zulkifli *et al.* (2014) explained that many hormonal factors are involved in regulating the secretion of heat shock proteins, such as steroid hormones and corticosterone, which are secreted from the cortex of the adrenergic gland of stressed animals.

Heat shock proteins can affect the process of lipolysis, which controls the level of lipids in fat cells and thus the production of triglycerides. Some research also shows that high temperature and heat stress can lead to increased concentrations of triglycerides in cows (Xu *et al*., 2020).

This study aims to demonstrate the relationship between the genotypes of the heat shock gene HSP90 and the concentrations of some biochemical blood parameters and some blood elements of Holstein Friesian cows.

Materials and Methods:

The experiment was conducted at Taj Al-Nahrain Research Station, north of Diwaniyah Governorate, by using 35 Holstein cows for the period between 1/3/2022 to 15/8/2022, these cows were divided into three seasons as follows: the first season (11 cows), the second season (15 cows), and the third season (9 cows) based on the station's records. The animals were placed in semi-shaded pens with dimensions (140 x 60 m), it was divided into four barns, each barn containing 25 cows, was connected to the mechanical parlor, these pens were provided with freely filled water basins with salt molds suspended inside the pens. Genetic analyzes were performed in the Molecular Genetics Laboratory in Diwaniyah. The remainder of the genetics results (Skonsk) were completed at BIONEER Laboratories Company in Seoul/Korea. The biochemical parameters were analyzed in the Physiology Laboratory of the College of Agriculture, University of Basrah.

Results and discussion

Table (1) indicates the relationship between the genotypes of the heat shock gene HSP90 and some biochemical parameters, represented by the concentration of glucose, cholesterol and triglycerides, there were no significant differences between all genotypes in glucose concentration. It was a mathematical increase was observed for the CT genotype, which reached 56.59 mg/100 ml compared to the TT genotype, which had a glucose concentration of 56.06 mg/100 ml. The lowest glucose concentration was in the CC genotype, (55.53 mg/100 ml), blood glucose concentration was not affected among all genotypes, which may be due to heat shock proteins controlling blood sugar levels (Palazzo *et al*., 2018).

Table (1) The relationship between the genotypes of the heat shock gene HSP90 and the concentrations of some blood parameters (glucose, cholesterol, and triglycerides) (mean ± standard error).

Genotypes	Cow no.	Glucose (mg/ 100 ml)	Cholesterol (mg/ 100 ml)	Triglycerides (mg/ 100 ml)
CC	11	0.71±55.53	2.54±74.03	0.66±24.59
TT	10	0.77±56.06	2.94±79.59	0.59±24.09
CT	14	0.79±56.59	2.60±76.08	0.59±25.31
Sig.		NS	NS	NS

N.S: no significant differences between the means.

There was no significant effect of the genetic makeup of the heat shock gene on the concentration of cholesterol and triglycerides. The cholesterol concentration reached 74.03, 79.59 and 76.08 mg/100 ml, while the concentration of triglycerides reached 24.59, 24.09 and 25.31 mg/100 ml for the genotypes CC, TT and CT, respectively. The levels of cholesterol and triglycerides are not affected, this may be because heat shock proteins help regulate cholesterol levels in the body (Hinsu *et al*., 2016). It also controls triglyceride levels (Xu *et al*., 2020; Kassim 2017).

Table (2) shows the relationship between the genotypes of the heat shock gene HSP90 and some biochemical blood parameters for Holstein-Friesian cows, represented by the concentration of albumin, total protein, and urea, there was no significant effect of genotypes on both albumin and total protein. The albumin concentration in the TT genotype averaged 3.95 gm/100 ml, compared to the hybrid CT genotype, which reached 3.05 gm/100 ml, while it was 3.80 g/100 ml in the CC genotype.There were no significant differences in albumin concentration, it may be because the heat shock gene increases the concentration of albumin in blood serum, because the heat shock gene plays a major role in regulating the distribution of albumin in the blood (Song *et al*., 2013). As for total protein concentration, it was also noted that there was no significant effect of genotypes, the results indicate that the TT genotype had an average total protein concentration of 5.54 gm/100 ml blood serum, while the average total protein concentration for the two genotypes CC and CT was 5.27 and 5.32 gm/100 ml, respectively. Heat shock proteins interact with total protein, in addition to its role in increasing the accumulation of total protein in the kidneys, to regulate total protein production and its effectiveness (Rhoads *et al*., 2009; Kassim *et al*., 2019a).

The same table indicates that genetic makeup has a significant effect (P≤0.05) on the concentration of urea in blood serum, the hybrid CT genotype showed a significant increase (P≤0.05) at a rate of 17.45 mg/100 ml, compared to the TT genotype, which averaged 15.95 mg/100 ml, the CC genotype did not differ significantly from the TT and CT genotypes, at a rate of 16.46 mg/100 ml. The high concentration of urea in blood serum is a result of protein metabolism reactions, which increases nitrogen production and urea accumulation in the blood, as a result of the control of the heat shock protein gene, because it controls the process of regulating thermosynthesis (Desrosiers *et al*., 2012; Kassim *et al*., 2019b).

Table (2) The relationship between the genotypes of the heat shock gene HSP90 and some blood parameters (albumin, total protein and urea) (mean ± standard error).

Genotypes	**Cow no.**	**Albumin (gm/ ml)**	**Total protein (gm/ ml)**	**Urea (mg/ ml)**
CC	11	0.06±3.80	0.13±5.27	0.47±16.46 ab
TT	10	0.07± 3.95	0.14±5.54	0.30±15.95 b
CT	14	0.03±3.05	0.11±5.32	0.54±17.45 a
Sig.		NS	NS	*

Different letters within one column indicate the presence of significant differences below the 0.05 probability level. N.S: no significant differences between the means.

Table (3) shows the relationship between the genotypes of the heat shock gene HSP90 and the concentration of some minerals (phosphorus, potassium and calcium) in the blood serum of Holstein Friesian cows, noting that there was no significant effect of the heat shock gene on the concentration of both phosphorus and calcium. The phosphorus rate was 0.94, 0.96 and 0.80 mg/100 ml, and the calcium rate was 0.023, 0.022 and 0.021 mmol/L for the genotypes CC, TT and CT, respectively. The lack of significant effect may be because the heat shock gene works to balance phosphorus within living cells, by the secretion of thyroid hormones, which regulate the level of phosphorus in the blood (Hao, 2015; Kassim *et al*., 2020). Ojo and Rezaei (2018) explained that heat shock proteins regulate calcium balance in the body's cells, protecting against damage resulting from increased calcium accumulation in them.

As for potassium, the results indicated a significant increase ($P \leq 0.05$) in both the TT and CT genotypes, they recorded potassium concentrations of 8.14 and 8.53 mg/100 ml, respectively, compared to the CC genotype, the potassium concentration was 7.21 mg/100 ml.

Table (3) The relationship between the genotypes of the heat shock gene HSP90 and some blood elements (phosphorus, potassium, and calcium) (mean± standard error).

Genotypes	Cow no.	Phosphorus (mg/ 100 ml)	Potassium (mg/ 100 ml)	Calcium (mmol/L)
CC	11	0.04±0.94	0.22±7.21 b	0.003±0.023
TT	10	0.09±0.96	0.26±8.14 a	0.0009± 0.022
CT	14	0.05±0.80	0.25±8.53 a	0.0009± 0.021
Sig.		NS	*	NS

Different letters within one column indicate the presence of significant differences below the 0.05 probability level.

N.S: no significant differences between the means.

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