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Molecular characterization of Hepcidin (*HAMP* gene exon2) Gene in Selected Iron Deficiency Anemia Patients from Basrah Governorate, Iraq

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Abstract:

Anemia constitutes one of the most common blood diseases, which can be dangerous and more complex than it appears. This danger comes from the apparent lack of iron which is a vital element in various metabolic and anabolic processes. The *HAMP* gene produces a protein called Hepcidin, which has a very important role in iron metabolism. This study aimed at the molecular detection of *HAMP* gene in selected iron deficiency anemia patients, as well as healthy control, from Basra community in the south of Iraq. Forty five samples were collected from private clinics, which were divided into 33 samples for affected patients and 12 samples represented the control group. A1768 bp fragment containing HAMP exon 2was amplified using Forward: GTGGGACTTGGGGATAAGGC and Reverse: GGGCCTTGCTTTCTTGCTTC . four different polymorphisms were obtained depending on the number of mutations that occurred for the gene compared to what was recorded in the GenBank for the same gene, 3 polymorphisms, studies represented the affected and 1 represented the control, they were all registered in the GenBank under accession numbers LC713271, LC713271, LC713273, (patients' samples), and LC713274, (control samples). The polymorphisms obtained in the current study had a number of different mutations, whether silent or missense, some mutations occurred in more than one polymorphism, while some occurred in one polymorphism. It was noted that some mutations occurred in all polymorphisms of the study. When conducting a BLAST analysis, it was found that the results obtained were closer to each of the genes recorded in America and China, and this can be clearly observed in the analysis of the phylogenetic tree. The results of the analysis of the three-dimensional structure of the expected protein indicated a great match between the polymorphisms of the study . As a result of the occurrence of these mutations, the *HAMP* gene in Iraq has more than one polymorphism, these polymorphisms may be associated with the function of the gene. Therefore, further studies are needed to link this polymorphism to various traits associated with anemia.

Introduction:

Anemia is the most common hematologic disorder, iron deficiency being the leading cause worldwide (Elstrott et al., 2020). Often, anemia is the presenting sign of a more serious underlying condition that, if left untreated, can generate consequent morbidity (Portugal-Nunes et al., 2020).

The *HAMP* gene is encoding protein called Hepcidin which plays a main role to the metabolism of iron via banning the shot of iron from intestinal cells and macrophages (Melis et al., 2008). Several studies indicated that the obstruction of *HAMP* gene role will lead to an increase in iron load (Xu et al., 2021), while in common cases Hepcidin prevent surplus iron absorption in intestinal mucosa and maintains its normal level in the body (Ganz 2011). On the other hand have indicated that the activity of the Hamp gene is related to its different polymorphisms (Ganz 2006). The deficiency of hepcidin causes increase in hemochromatosis, and hepcidin excess may cause iron deficiency, iron-restricted erythropoiesis and anemia due to some mutations in the *HAMP* gene (Kanwar andKowdley 2013). Pandey et al., (2018) also indicated that the occurrence of mutations in the *HAMP* gene could lead to