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physiological and Molecular study of Lymphoma patients during and after treatment

A Thesis Submitted to the Council of college of Science /Al Muthanna University as Partial Fulfillment of the Requirements for the Degree of Master of Science in Biology

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Abstract

Lymphoma is a type of cancer that starts in lymphocytes, which are immune system cells that combat infections. These cells can be found in the bone marrow, thymus, lymph nodes, spleen, and other organs. The lymphocytes in a patient with lymphoma alter and proliferate un control ably. The aim of this study was to detection of causes lymphoma by assess the hematological and biochemical parameters in lymphoma patients. Also, detection the BCL-6 and C-myc genes that influencing patients with lymphoma and determine the sequences of both genes in terms of polymorphism and mutation and investigate for the first time in Iraq, the association between genetic mutations and illness characteristics. During the period for July - 2023 up to October –2023.

This study examined fifty samples in patients with lymphoma, as well as fifty healthy people as the control . The participants ranged in age from (5-77) years old. Hematological and biochemical assays were used to evaluate the samples according to the kind and length of therapy received by patient groups and revealed a significant rise at ($P<0.05$) when compared with control groups.

The study showed significant increase at ($P<0.05$) in white blood cells (WBC), neutrophils, platelets, but noted significant decrease at ($P<0.05$) in red blood cells (RBC), hemoglobin (HB), lymphocytes, and basophils in patients compared with control group. Additionally, the study indicated a significant rise at ($P<0.05$) in urea, creatinine, ALT, and AST in patients compared with control groups.

The study revealed For every case in this investigation, the Myc and Bcl6 sequences were examined in two the samples. The targeted sequences' genetic variations inside the amplified loci were examined in the chosen patients. After that, a direct Sanger sequencing approach was used to analyze the amplified fragments in order to determine any potential patterns of variation within the population under investigation. The sites of the examined variants within the reference genomic DNA sequences were noted. The results of the sequencing studies

revealed that one amplified fragment of the Myc and Bcl6 sequences had a single nucleic acid polymorphism (SNP). rs529015137 was the Myc-based SNP that was found in burkitt lymphoma (BL) .and rs1711523994 was the Bcl6-based SNP that was found in diffuse large B-cell (DLBCL) . It was discovered that the locations of both detected SNPs were found in the intronic regions of both examined.