THE E2F1 GENE AS IN PAN-CANCER ANALYSIS AND A POTENTIAL PROGNOSTIC BIOMARKER IN LIVER HEPATOCELLULAR CARCINOMA

Ahmed A. A. SALEM[a],

[a]Department of Biological and Biochemical Sciences, Faculty of Chemical Technology, University of Pardubice, Studentska 573, 532 10 Pardubice II, Czechia, ahmedahmedahmed.salem@student.upce.cz

This research investigates the multifaceted role of the E2F1 gene in various types of cancers, with a primary focus on liver hepatocellular carcinoma (LICH). The E2F1 gene is the first crucial member of the transcription factors family (E2Fs) which plays a pivotal key role in cell cycle regulation and proliferation, DNA repair, and also it is significant for normal cell homeostasis, uniquely induces apoptosis. To gain a deeper understanding of the gene's relevance into LICH, a comprehensive pan-cancer analysis was conducted using the TIMER2.0, GEPIA, UALCAN, Kaplan–Meier, cBioPortal, KEGG pathways analysis and concluded with validating the findings by using a public-access cohort on GEO and then further analyzed with GEO2R tool. It was found that the E2F1 gene was significantly differentially expressed in 18 tumors but highly expressed in LICH **(p<.001).** Also, it showed a significant overall survival rate **(p=.0003)** which reflected in a variation of gene expression with specific decreasing during the four pathological stage of metastasis and the correlated overall survival was significant as well. Additionally, the gene expression is correlated with other genes positively and negatively as it has shown upstream immune cell infiltration **(p<.0001).** Genetically, the gene was altered and mutated in different forms as the gene is highly active functionally in cell cycle, DNA replication and oocyte meiosis with **(p<.0001**). lastly, the E2F1 gene was validated as extreme significant downregulated gene in LICH. In summary, this study presents, for the first time, the pan-cancer relevance of E2F1 gene and underscores its potential characteristics as a prognostic biomarker in LICH. These findings suggest novel promising approaches for personalized therapeutic strategies targeting this gene as a prognostic biomarker.