EXPRESSION OF KINESIN SUPERFAMILY MEMBERS KIF2C, KIF14 AND KIF20 AS DIAGNOSTIC BIOMARKERS FOR OVARIAN CANCER

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Ovarian cancer is one of the most common malignancies of the female reproductive system [1] and has the highest mortality rate, with an overall five-year survival below 50% [2]. This is primarily due to late diagnosis caused by non-specific symptoms and the lack of effective screening methods [3]. KIF2C, KIF14 and KIF20A are mitotic kinesins involved in the regulation of mitosis and cytokinesis [4]. Given their involvement in cell cycle progression and reported associations with tumor development, altered expression of these kinesin superfamily genes represents potential as diagnostic biomarkers for ovarian cancer. This pilot study aimed to evaluate the diagnostic potential of *KIF2C*, *KIF14* and *KIF20A* by analyzing their gene expression levels and association with clinical features of ovarian cancer patients.

Gene expression levels were analyzed in 65 ovarian cancer samples, classified into three groups according to tumor histological type, using reverse transcription quantitative PCR (RT-qPCR). Association between gene expression and clinicopathological parameters were assessed, and diagnostic performance was evaluated using receiver operating characteristics (ROC) curve analysis.

Analysis of selected gene expression revealed statistically significant differences between the study groups. *KIF2C*, *KIF14* and *KIF20A* showed significantly higher expression in high-grade serous ovarian carcinoma compared with benign gynecological tumors (*KIF2C*, p = 0,03; *KIF14*, p = 0,001; *KIF20A*, p = 0,02). ROC analysis demonstrated that the gene expression biomarkers effectively distinguished between these two groups, with areas under the curve of 0,77, 0,91, and 0,82, respectively. These findings suggest that these genes could be potentially useful as diagnostic biomarkers for ovarian cancer.

Overall, *KIF2C*, *KIF14* and *KIF20A* from the kinesin superfamily emerge as promising candidates for ovarian cancer diagnosis. Variations in their expression levels could be associated with tumor histological subtype, as ROC curves demonstrate the ability to distinguish malignant from benign samples. Nonetheless, confirmation of these results through expanded and independent studies is needed to clarify their potential clinical relevance.

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