

MS04-2-2 The genetic biomarker of cervical cancer: an application of statistical and bioinformatics techniques
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Abstract

Malignant tissues in the cervix lead to cervical cancer. It is increasing women's mortality in the world. Statistical and Bioinformatics approaches are generally used to explore the genome data. To find the significant differentially expressed genes and associated pathways related to cervical cancer. From the gene expression omnibus database GSE44001, A total of 300 cervical cancer patients has been extracted for analysis. Non-parametric, semi-parametric, and parametric models have been used to find the significant genes based on clinical parameters. The survival of cancer patients highly depend on tumor diameter size and stage. The risk of death 2.92 and 2.35 times higher among patients who had tumor diameter size (4.1 mm & above) and (3.1-4.0 mm) as compared to tumor diameter size (0-3.0 mm) respectively. Total 4 genes (ABCB7, THOC2, PKN3, and HIST1H3C) were upregulated and 8 (TP63, IGF1, AIM2, ARHGAP6, RAP2B, TRIM66, CNBP, and ATG3) were downregulated. This study explores the notable genes that may responsible for cervical cancer.

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