

In silico Analysis of Differentially Expressed Genes in High-Grade Squamous Intraepithelial Lesion and Squamous Cell Carcinomas Stages of Cervical Cancer

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Abstract : Cervical cancer is one of the women related cancers which starts from the pre-cancerous cells and a fraction of women with pre-cancers of the cervix will develop cervical cancer. Cervical pre-cancers if treated in pre-invasive stage can prevent almost all true cervical squamous cell carcinoma. The present study investigates the genes and pathways that are involved in the progression of cervical cancer and are responsible in transition from pre-invasive stage to other advanced invasive stages. The study used GDS3292 microarray data to identify the stage specific genes in cervical cancer and further to generate the network of the significant genes. The microarray data GDS3292 consists of the expression profiling of 10 normal cervixes, 7 HSILs and 21 SCCs samples. The study identifies 70 upregulated and 37 downregulated genes in HSIL stage while 95 upregulated and 60 downregulated genes in SCC stages. Biological process including cell communication, signal transduction are highly enriched in both HSIL and SCC stages of cervical cancer. Further, the ppi interaction of genes involved in HSIL and SCC stages helps in identifying the interacting partners. This work may lead to the identification of potential diagnostic biomarker which can be utilized for early stage detection.

Keywords : cervical cancer, HSIL, microarray, SCC

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