MOLECULAR MARKERS IDENTIFICATION ON HNSCC USING DATA FROM DIFFERENT EXPERIMENTAL TECHNIQUES

Rodrigues, R.V.[1,3]; Silveira, N.J.F[2]; Pinheiro, D.G.[4]; Head and Neck Genome Project/GENCAPO[5]; Tajara, E.H[3]

[1]Departamento de Genética e Biologia Evolutiva, IB/USP, São Paulo; [2]Instituto de Pesquisa e Desenvolvimento, UNIVAP, SJ Campos/SP; [3]Departamento de Biologia Molecular, FAMERP, SJ Rio Preto/SP, [4]Departamento de Genética, FMRP/USP, Ribeirão Preto; [5]complete author list and addresses on: http://ctc.fmrp.usp.br/clinicalgenomics/cp/; São Paulo/SP, Brazil.

Head and neck squamous cell carcinoma (HNSCC) is one of the most common malignancies in humans. In order to investigate HNSCC biomarkers that may be relevant for prognosis and therapy, we compared SAGE (Serial Analysis of Gene Expression), microarray and proteomic data from HNSCC. A database integrating in-house SAGE and microarray data was developed. Our analysis identified 60 and 30 genes up and down-regulated in tumors, respectively. The expression level of four genes (*GNA15, KRTHA1, BST2, MFAP2*) was evaluated by quantitative PCR in matched normal/tumor samples from patients with tongue SCC. The results confirmed that at least three of these genes are dysregulated in tumors. Two genes (*BST2, MFAP2*) were upregulated in all tumors and one gene (*KRTHA1*) was downregulated in five tumors. To the best of our knowledge, this is the first study reporting SAGE data in head and neck tumors. The results, in combination with microarray and proteomic data, showed that different experimental platforms and designs offer opportunities to detect a common expression profile in HNSCC. In addition, the results demonstrated that our gene selection strategy is effective in identifying potentially relevant markers.