THE AQUAPORIN GENE FAMILY: EXPRESSION IN NORMAL AND NEOPLASTIC TISSUES

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Abstract: There are 13 known members of the human aquaporin gene family (AQP0-AQP12). The maintenance of water balance in cells is critical to the survival of all living organisms. Aquaporin water channels have been demonstrated to facilitate tumor cell migration and metastasis. Thus inhibition of aquaporins may be useful in reducing the metastatic potential of tumors. Our objective was to determine the expression of aquaporin gene family in normal and neoplastic tissues by analyzing large amounts of Serial Analysis of Gene Expression (SAGE) Tag counts. SAGE data represent absolute expression of genes. We have developed a computational pipeline to construct a dataset of expression levels (tags per 200,000) of the human aquaporin gene family from Digital Northern results of 266 SAGE libraries (188 neoplastic and 78 normal tissues) that express two housekeeping genes glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and Actin B (ACTB). The dataset was visualized using MultiExperiment Viewer (MeV) and converted into binary-encoded patterns representing evidence of gene expression. Our analysis revealed that AQP0, AQP1 and AQP3 were expressed in over 100 tissues. AQP1 and AQP4 were highly expressed in brain neoplastic tissues. AQP8 was expressed in only 5 tissues. In order to provide a translational research context to our analysis, we compared the expression levels of AQP1 and AQP4 in 20 SAGE Libraries developed from graded astrocytic tumor samples and found that at least 5-fold over-expression of AQP4 in 7 samples. In conclusion, by integrating high-dimensional SAGE data, we have provided patterns of gene expression for the human aquaporin family in normal and neoplastic tissues; and provided prioritized datasets for further analysis.

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