
The aim of our work was to establish a database for breast cancer gene expression data in order to compare human and mouse breast cancer. We identified human and mouse homologues genes and compared the expression profile of 24 human breast tumors with 6 WAP-SVT/t breast tumors (WAP-SVT/t animals, line 8). Our studies confirmed the heterogeneity in gene expression of human as well as mouse breast cancer cells. However, 63 genes were found to be differentially expressed (upregulated: 40; downregulated: 23 genes) in at least 75% of the breast tumors of both species. To differentiate between early and late events in tumor formation, we compared the 63 differentially expressed genes with a mouse data set obtained from hyperplastic mammary glands. This revealed that the majority of the early deregulated genes are cell proliferation specific. These early changes seem to be necessary although not sufficient for breast cancer formation. Late alterations concern mainly genes belonging to the category of cell communication and metabolism. Interestingly, most of the 63 conserved genes are commonly associated with tumorigenesis.