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COMPARATIVE GENE EXPRESSION PATTERNS DURING HUMAN BREAST CARCINOGENESIS USING IN VITRO MODEL

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Two types of normal human breast epithelial cells (HBECs) have already been established and characterized. Type I HBECs are deficient in gap junctional intercellular communication and are capable of anchorage-independent growth and of expressing luminal epithelial cell markers, a variant estrogen receptor (ER), and stem cell characteristics. In contrast, Type II HBECs express basal epithelial cell phenotypes and are ER-negative. Recently, we have successfully established tumorigenic cell lines (normal-extended life span-immortal-weakly tumorigenic-highly tumorigenic phase) from these normal HBECs. In the present study, we compared the gene expression patterns of more than 6400 genes in these two types of normal HBECs with those in several human breast cancer cell lines (immortal non-tumorigenic M13SV1, weakly tumorigenic M13SV1R2, highly tumorigenic M13SV1R2-N1, and poorly invasive MCF-7) using cDNA microarray technology. The result showed that the expression of keratin 5 and vimentin were elevated in the more tumorigenic human breast cancer (HBC) cells and that keratin 18 and RBP1-like protein were overexpressed in the less tumorigenic HBC cells. The others genes as well as these four genes preestimated the tumorigenesis of the HBC cells. Taken together, the expression patterns of multiple genes during human breast carcinogenesis may be useful for better understanding cancer development and prevention.

keyword : Breast Cancer, cDNA Microarray