Strategy for development of novel molecular-targeting drugs for breast cancer through gene-expression profile analysis

Toyomasa Katagiri

Division of Genome Medicine, Institute for Genome Research, The University of Tokushima

Breast cancer is the most common malignancy diagnosed among women worldwide and is the leading cause of cancer mortality. On the basis of the detailed genome-wide expression profile analysis of breast cancers, we identified dozen of therapeutic target molecules in accordance with the following criteria; 1) genes whose expressions were upregulated in large proportion of breast cancer tissues and 2) genes whose expression was not observed or undetectably in any of important vital organs 3) genes that shows growth inhibition caused by knocking-down of their expression in breast cancer cells by using RNA interference technique. Our data indicated that systematic expression profile analysis should be effective to identify therapeutic molecules for breast cancer. We here report strategies for development of anti-cancer drugs though characterization of novel therapeutic target-molecules for breast cancer.