

Application of Circulating Tumor DNA in Early Detection of Breast Cancer

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Abstract

Introduction Circulating tumor DNA (ctDNA) as a non-invasive marker that can provide more information on genetic and epigenetic alterations in tumor cells. The epigenetic modifications occur in the early stages of cancer, thus, it is considered as a target for early detection and prevention. The current study is to develop a ctDNA-probe based technology using capture, enrichment and analysis of epigenetic markers for early detection of breast cancer (BC).

Materials and Methods: ctDNA from 45 women with early stage breast cancer and 90 healthy women as control samples were isolated. Methylation analysis performed for 6 differential regions by MeDIP-Probe method and all of them were sequenced. The KLF9 gene used as an internal control for amplifying the regions despite Methylation status.

Results: The methylation analysis presented significant differences in methylation of two regions RASSF1A and HOXA10 between BC patients and healthy samples. Methylation in the regions was higher in BC than control case ($P < 0.001$).

Conclusions: Combinations of multiple methylation regions or CpG Island improved the positive predictive value for breast cancer detection. Analysis of methylation pattern of ctDNA using probe-base technology with screening methods such as mammography in high-risk women leads to noninvasive early detection of breast cancer.