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Clinical utility of cell-free DNA methylation in managing breast cancer recurrence

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A number of clinico-pathological criteria and molecular profiles have been used to stratify breast cancer (BC) patients into high and low risk groups. Currently, there are still no effective methods to determine which patients harbor micrometastatic disease after standard BC therapy and who will eventually develop local or distant recurrence. Cell-free (cf) DNA has attracted attention for clinical use in the context of risk prediction, prognostication and prediction of response to chemotherapy in human cancer. Several groups including ours have reported the detection of tumor-associated methylation changes in cfDNA extracted from plasma or serum. We are specifically interested in the use of cfDNA methylation biomarkers for the prediction of cancer metastasis in the early stage setting. Accordingly, we are validating a DNA methylation signature, referred to as CpG4C, which discriminates metastatic BC from healthy individuals or disease free survivors using a targeted bisulfite amplicon sequencing approach. In addition, we have been investigating whether a surge of cfDNA levels after cytotoxic chemotherapy affects the sensitivity and specificity of the CpG4C assay. Lastly, we are also working on determining the technical and biological limits of detection of CpG4C in plasma. CpG4C is a potential blood-based biomarker that could be advantageous at the time of surgery and/or after the completion of chemotherapy to indicate patients with micrometastatic disease who are at high-risk of recurrence, and who could benefit from additional therapy.

Biography

Bodour Salhia is an Assistant Professor at the University of Southern California and is a Translational Genomics Scientist with extensive knowledge and expertise in mechanisms that underlie tumorigenesis and tumor biology. She received her Honors Bachelor of Science Degree (1998), Master of Health Science (2001) and PhD (2006) degrees in Human Molecular and Cellular Biology from the University of Toronto. She completed a Post-doctoral fellowship (2006-2011) at the Translational Genomics Research Institute (Phoenix, Arizona) in cancer genetics and epigenetics. She has published more than 30 papers in peer-reviewed and reputed journals.

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