EuroSciCon

October 08-09, 2018
Moscow, Russia

4th Edition of World Congress on
Cancer Research, Survivorship and Management Conference

Irina Gromova, Arch Cancer Res 2018, Volume 6
DOI: 10.21767/2254-6081-C3-011

In depth –omic analysis of tumor interstitial fluid of human breast: Association with intrinsic tumor subtypes and clinical outcome

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Breast cancer (BC) is one of the most common cancers in woman with more than 1,300,000 cases each year worldwide. Recent studies have revealed extensive genetic diversity even within the same class of breast tumor. Such heterogeneity severely affects key cancer pathways and drives phenotypic variations posing a significant challenge to cancer medicine. Despite tremendous efforts, no robust blood markers for BC patients have been identified so far, mainly due to difficulties in monitoring tumor heterogeneity and a high dilution factor in blood. The multidirectional signaling events within tumor-stroma setting are implemented through the tumor interstitial fluid (TIF) which forms the interface between circulating bodily fluid (lymph and blood) and intracellular fluid. TIF provides and facilitates the exchange of ions, proteins, cytokines, miRNAs and glycans between various cellular components within local interstitial space. As the concentration of potential cancer-specific biomolecules within the local tumor milieu is estimated to be several orders higher as compared to serum/plasma, TIF is currently considered as a promising source for biomarker discovery which provides an access to the entire complement of molecules externalized (i.e. secreted, excreted or shredded) from tumor cells and local microenvironment into tumor interstitium. Comprehensive multi-omics profiling of molecular complement of breast TIF aimed the identification of integrated biomolecular signature(s) that could enable to stratify tumor types, reflect the degree of tumor aggressiveness and potentially provide a basis for blood-based testing for breast cancer screening in a future. The synergistic integration of results from multidimensional platforms with advanced bioinformatics and system biology tools will improve our understanding of intercellular communication and signaling pathways in BC and will lead to identification of diagnostically relevant biomarker signatures that can be appropriate for accurate profiling of BC diversity.

Biography

Irina Gromova graduated from Moscow State University, Russia. She completed her PhD in Molecular Biology at the Institute of Gene Biology, Russian Academy of Science, Moscow. Soon after that, she was invited as a Guest Scientist to University of Aarhus, Department of Molecular Biology where she was working as Associate Professor until 2000. She is working in Institute of Cancer Biology, Danish Cancer Society and her study is dedicated to understanding of breast cancer complexity aiming to develop and validate diagnostic, prognostic, and predictive biomarkers for clinical decision-making. She has published more than 90 papers in highly citied journals and is serving now as a Leader of Breast Cancer Biology group.

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