Stefania Brandini et al., Madridge J Cancer Stud Res. 2018
http://dx.doi.org/10.18689/2640-5180.a3.002

NGS Approach for New Ovarian Cancer Biomarker Discovery

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Ovarian cancer is the sixth most common cancer in women and is called 'the silent killer' as most women are not diagnosed until the cancer has already spread, thus resulting in low chances of survival. Given the complex and heterogeneous nature of this neoplasm, it is crucial the identification of molecular biomarkers that might be used for focused and efficient diagnosis, prognosis and therapy.

In order to contribute to the identification of new biomarkers for ovarian cancer, we used the Next Generation Sequencing (NGS) technology allowing simultaneous testing of the coding and non-coding RNAs from 21 samples belonging to the most representative histological types of ovarian, serous and endometrioid carcinomas.

Among the molecular factors involved in the process of tumor transformation, many small noncoding miRNAs and their target genes have been found. Some of these genes have already been reported to be involved in cell proliferation and death pathways, and might be considered as possible targets for specific treatment purposes.

The differentially expression analysis revealed more than one thousand mismatches in the tumor expression profiles of both long and miRNAs in comparison to the control tissues. These data shed light on new possible molecular biomarkers for ovarian cancer.

Biography:

Stefania Brandini is a biologist with a Ph.D. in 'Genetics, Molecular and Cellular Biology' obtained in January 2017 at the University of Pavia. Since 2010 she worked and collaborated with different research teams acting in various environments (i.e. University, hospital and CNR) and experienced the methods used in genetics and molecular biology. Recently, she focused on cancer epigenetics and in particular on the characterization of new biomarkers useful for the diagnosis/prognosis/therapy of proliferative diseases by NGS methods. She was co-author of 6 original articles, 2 of which selected for the covers of the journal Molecular Biology and Evolution.