BANQUET KEYNOTE TALK

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(Tallac)

Application of Functional Genomics to Oncology Practice: Opportunities, Successes, Failures and Barriers

Panos Anastasiadis & George Vasmatzis
Mayo Clinic
USA

Abstract: Radical improvement in cancer care can be accomplished by individualizing patient management via the application of genomics and functional model systems into clinical practice. Recent breakthroughs in immunotherapy (i.e. checkpoint inhibitors) and targeted therapies (i.e. NTRK inhibitors) have shown that therapy of advanced cancers might become agnostic to the organ of origin, arguing for a more individualized approach to patient care. Emerging genomics technologies, data integration and visualization platforms are powerful tools to determine the state of the individual's tumor and point to tailored treatments. Furthermore, an efficient combination of comprehensive genomics with 3D microcancer functional model systems can further refine treatment decisions. However, applying such disruptive technologies in clinical practice is not trivial. Regulatory, financial and clinical barriers will be discussed.

Speaker Bio-Sketch: Dr. Anastasiadis is the Chair of the enterprise-wide Department of Cancer Biology, co-director of the Cell Biology Program at the Mayo Clinic Cancer Center, and executive member of the Center for Biomedical Discovery. He is also a professor and consultant in the Department of Cancer Biology. Dr. Anastasiadis is widely recognized for his work in the cell-cell adhesion field, has served in several NIH study sections as member and Chair, and more recently serves on the R35 MIRA study section at NIGMS. His research program focuses on cell-cell adhesion signaling events, regulation of Rho GTPases during cell adhesion, transformed cell growth and/or migration, as well as the establishment of cell polarity in adherent and migrating cells. Published papers in Nature Medicine, Nature Cell Biology, Journal of Cell Biology and Cancer Research demonstrate the laboratory's high impact research. Related to cell adhesion, his lab recently reported the crosstalk between apical cell-cell junctions and the RNAi machinery to regulate the expression and localization of select miRNAs and mRNAs in order to inhibit epithelial cell growth. As a result of his pre-clinical work, Dr. Anastasiadis is involved in multiple translational and clinical studies. Finally, in collaboration with the Center for Individualized Medicine he has also launched the Ex Vivo project in multiple cancer types and across Mayo Clinic sites.

Speaker Bio-Sketch: Dr. Vasmatzis is the co-director of the Biomarker Discovery Program, within the Center for Individualized Medicine. He is also an Associate professor and consultant in the Department of Molecular Medicine and a member of the Mayo Clinic Cancer Center. His research program consists of bioinformatics specialists, molecular biologists, epidemiologists, and pathologists. By training and experience, Dr. Vasmatzis has a unique set of skills in engineering, computational biology, bioinformatics and genomics. He recognizes the critical importance that each team member plays to the success of a given project or that of a program as a whole. He works tirelessly to maintain a team spirit. This team has demonstrated success in discovery and translation of several biomarkers as well as developing evidence-based models that should help clinicians stratify (cancer) patients in order to provide each individual with the appropriate care. Published papers in Journal of Clinical Oncology, Cancer Research and BLOOD further demonstrate the laboratory's discovery, validation, and translation capabilities. With the recent advances in Next Generation Sequencing (NGS) technologies his laboratory have been engaging in massive sequencing to scan the genome of cancer cells for abnormalities that can be used for clinical purposes such as diagnosis and stratification of patients for optimal treatment. He has developed MPseq, an accurate and inexpensive whole genome sequencing platform that has been used to detect structural variants. MPseq is a combination of a protocol and algorisms that can deliver a detailed description of all DNA rearrangements at a resolution that can show how individual genes are disturbed thus providing necessary novel insight for correct clinical interpretation.