PGDx HEARD THROUGH THE PIPELINE

February 2016

TECHNOLOGY SPOTLIGHT

Selecting a Neoantigen Prediction Approach for Immunotherapy Research and Developement

Neoantigens are short, potentially immunogenic, peptide sequences created through the development of somatic mutations in cancer cells. These neoantigens are presented on the surface of the tumor cell by major histocompatibility complex (MHC) molecules where they are recognized by T-cells and can trigger an immune response. Neoantigen identification has become important for several aspects of immunotherapy research:

- To aid in the identification of relevant T-cell populations that are involved in mounting an immunological response against a patient's own tumor as recently reported in Science by Dr. Steven Rosenberg's group at NCI as well as other investigators
- To be used as targets for the development of personalized immunotherapy vaccines
- Identification of shared neoantigens, which may be targets for the development of chimeric antigen receptor (CAR) T-Cell therapies

Next generation sequencing can be leveraged for the accurate identification of neoantigens through coupling of highly sensitive and specific whole exome sequencing (WES) approaches with advanced bioinformatics tools.

Dr. Drew Pardoll and team at Johns Hopkins Kimmel Cancer Center have used ImmunoSELECT™ to identify candidate neoantigens in lung and colorectal cancer patients who have received anti-PD-1 immunotherapy **(Register for upcoming PGDx webinar to learn more)**.

The CancerXOME™ portion of ImmunoSELECT™ captures the coding regions of >20,000 genes from tumor and normal samples, and has been optimized for a variety of samples including low abundance, poor quality DNA samples, and those derived from FFPE tissue. The tumor and matched normal are sequenced in parallel to accurately identify somatic sequence mutations and copy number changes. The somatic mutations identified using this approach are then evaluated using highly specific prediction tools to prioritize the most relevant mutation-derived neoantigens for targeted immunotherapies.

Key features of PGDx's ImmunoSELECT™ research service for accurate identification of candidate neoantigens:

- Unparalleled accuracy of cancer exome sequencing - 95% assay sensitivity and 99.99999% assay specificity for tumors with at least 70% tumor purity, with a limit of detection as low as 10% mutant allele frequency (MAF) at 150x average total sequencing coverage
- Inclusion of a matched normal to ensure all mutations reported are somatic in nature
- Accurate HLA genotyping using WES eliminates the need for additional tests
- Prediction and prioritization of the most relevant neoantigens from exome sequencing based somatic mutations

"ImmunoSelect™ provides a novel platform for the comprehensive analysis of a patient's tumor to better understand response to checkpoint inhibitors, immune cell therapies, cancer treatment vaccine development, and other immunotherapy approaches." -Mark Sausen, Ph.D., VP R&D

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WEBINAR

Genomic Approaches for the Advancement of Neo-Antigen Understanding in Immunotherapy

Dr. Victor Velculescu, M.D., Ph.D.
Professor of Oncology and Co-Director of Cancer Biology
Johns Hopkins Kimmel Cancer Center

Founder
Personal Genome Diagnostics

Dr. Drew Pardoll, M.D., Ph.D.
Abeloff Professor of Oncology and Director of Cancer Immunology

Johns Hopkins Kimmel Cancer Center

Theresa Zhang, Ph.D.
Vice President of Research Services

Personal Genome Diagnostics

ABOUT

Cancer immune therapies have recently demonstrated exciting clinical benefits for a number of cancer types. Somatic mutations in an individual's cancer cells encode neoantigens. Clinical responses to cancer immune therapies including T cell transfer and checkpoint blockade are primarily mediated by neoantigen specific reactivity. Advances in next-generation sequencing and bioinformatics prediction allow for the rapid and affordable identification of neoantigens in individuals, which have profoundly impacted immuno-oncology drug development.

LEARNING OBJECTIVES

- Overview of Cancer Genomics
- Understand how neoantigen prediction can adapt response to immunotherapy in certain populations
- Learn more about PGDx technologies for advancing the value of prediction for response to immunotherapies

UPCOMING EVENTS

Arrange a Meeting

18-19 FEB — **The Biomarker Conference**
San Diego, CA
Applications of circulating cell-free tumor DNA (ctDNA)

15-17 MAR — **World CDx Europe**
London, UK
Aligning drug-CDx co-development

25-26 FEB — **Biomarkers Congress**
Manchester, UK
Applications of circulating cell-free tumor DNA (ctDNA)

21-22 MAR — **Circulating Biomarkers**
Boston, MA

6-11 MAR — **Molecular Med TRI-CON**
San Francisco, CA
Novel clinical applications of cancer genomics

4-7 APR — **Molecular Diagnostics Europe**
Lisbon, Portugal
Application of circulating cell-free tumor DNA (ctDNA)

WE'RE GROWING

John K. Simmons, Ph.D.

Manager of Research Services
Personal Genome Diagnostics

John Simmons joins PGDx from NCI where his research focused on identifying therapeutic strategies for multiple myeloma through chemical genomic approaches. He will be working closely with our customers in application of PGDx technologies as well as future directions for PGDx R&D. John received his B.S. from American University and Ph.D. in Tumor Biology from Georgetown University. John received the MMRF Research Fellow award to support his work in developing systems-level approaches for drug combination.

Julie Meyer

Business Development Manager
Personal Genome Diagnostics

Julie Meyer joins PGDx to focus on our Pharma and Biotech customers in the eastern half of the US. She is highly experienced in the genomics field having managed the Gene Expression Core Facility at Roswell Park Cancer Institute until 2004 followed by 11 years' experience at Qiagen. Julie is a graduate of the University of Rochester. At PGDx Julie is looking forward to working with existing and new customers to advance biomarker discovery and cancer therapeutics development.