PRODUCTS, INFORMATION, AND SCIENTAINMENT ISSUE 17 | 2017

Uncovering checkpoint biomarkers page 16

How are your antibodies validated?*

page 22

Going further with flow

page 28

Antibody gifts for anybody

page 30

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Illuminating the immune system

* See page 22 for full details regarding validation.

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INSIDE IMMUNO-ONCOLOGY RESEARCH

Immuno-oncology (I-O) is considered by some to be one of the most promising anti-cancer therapeutics.^[1] In general, I-O manipulates the body's own immune response to mount an attack against tumor cells.

Recent breakthroughs in I-O research translate into a paradigm shift with regards to attacking cancer.^[2] Advances in I-O results in long-lasting tumor regression where surgery, radiotherapy, chemotherapy, and targeted therapy had proved less effective previously.^[3, 4, 5] Two of the hottest areas for I-O research today are checkpoint inhibitors and chimeric antigen receptor (CAR) T cell therapy. The two models are wildly different and both offer unique advantages.

Regulating immune checkpoints to empower the immune system

Immune checkpoints are cell pathways crucial in maintaining a normal immune response and protecting tissues from damage when the immune system is activated. Tumor cells dysregulate immune checkpoints and use it as a mechanism of immune resistance. Understanding immune checkpoints in natural killer (NK) cells and T cells is a main focus of research as these cells regulate both the adaptive and innate immunity surrounding the tumor (Figure 1). Immunity is maintained through a combination of cells interacting with their environment. T cell–mediated responses are among the best studied because they:

- are involved in a multitude of immune functions within the tumor environment,
- are highly regulated by both stimulatory and inhibitory signals,
- mediate immunity through membrane receptors and secretory factors that are considered to be easily druggable. Other immune cells such as NK cells and B cells are also being studied for anti-cancer receptor targets.

There has been dramatic progress in recent years in the advancement of checkpoint inhibitors that are able to direct and regulate T lymphocyte proliferation and function. These inhibitors interfere with the signaling pathways that can activate or inhibit cell events to directly or indirectly modulate the activity of immune cells. Only a small fraction of immune checkpoints are being characterized and developed for therapeutic purposes. CTLA-4 was one of the first immune checkpoint pathways to be targeted by therapeutic antibodies and achieved US Food and Drug Administration (FDA) approval. Other checkpoint pathway targets are being developed and include: PD-1, LAG-3, KIR, and OX40. Integration of multiple pathways ondifferent cell types can provide a more successful chance to shrink the tumor size and provide long-term immunity against cancer.

Chimeric antigen receptor (CAR) T cell therapy

Many I-O therapeutics are mass-produced antibody or fusion proteins. Chimeric antigen receptor (CAR) T cell therapy breaks that mold by being a modified patient cell that acts as an anti-cancer therapeutic (Figure 2). CAR T cell therapy utilizes genetically modified T cells to attack and kill the cancer cells. T cells do not normally identify cancer cells as foreign bodies, which would mark them for destruction. For immunotherapy to work, T cells are genetically manipulated to enable them to identify the cancer cells as an enemy and kill them as they would other foreign bodies. These T cells are genetically modified with CARs containing antibody-based recognition domains directed against cell-surface antigens linked to intracellular signaling sequences to overcome the tumor's tolerance.^[5] Once created, these modified cells are reintroduced into the patient with either a chemotherapy or other anti-cancer drugs. CTL019 is an example of a successful CAR T cell therapy as it is a patient-



Figure 2. CAR T cell therapy combines personalized medicine with targeted therapeutics. derived T cell engineered to express anti-CD19 single-chain variable fragment to shrink indicated B cell malignancies. These findings are encouraging as the field of personalized medicine develops toward mainstream therapy. The question still remains if CAR T cell therapy can be used to effectively treat a wide array of solid tumor types.

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KEY GENE EXPRESSION I-O TOOLS

How qPCR, dPCR, NGS, and microarrays are used to study cancer

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Additionally, they offer an excellent solution for orthogonal verification for data obtained from broad-panel studies using next-generation sequencing (NGS) or microarrays. As the value of such studies progress towards future gene therapies, lentivirus vectors are used to deliver genetic payload into T cells for random integration into genome of target cell. There is a strong need to quantitate the lentiviral load and determine the knock-in regions in the genome where the virus gets integrated. The Applied Biosystems[™] QuantStudio[™] 3D Digital PCR platform and assays can be used to precisely and accurately quantify the lentiviral load, that may in the future be used to correlate the response to treatment.

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UNCOVERING CHECKPOINT BIOMARKERS



An interview with Lisa Butterfield, PhD

Professor of Medicine, Surgery and Immunology

Director, UPCI Immunologic Monitoring and Cellular Products Laboratory, University of Pittsburgh Cancer cells cloak their identity to avoid detection from host defense cells by exploiting genes important to differentiate between self and non-self. Though cells in a tumor mass may go undetected by the immune system, their presence leaves behind molecular clues. Researchers like Lisa Butterfield are sleuthing using archived blood and tumor samples to find biomarkers and capture the presence of these tumor cells.

What is the role of the research laboratory in clinical trials? What is the role of your biomarker core facility in clinical trials?

I direct a research laboratory and a cancer center core facility for the immunologic monitoring and development of cellular products. Initially, we support bench-tothe-bedside development by performing translational research and development. Once the clinical trial is rolling, we process and bank both blood and tissue samples in a standardized fashion. Immunological assays are used to elucidate the drug mechanism of action in these clinical research samples and find potential prognostic and predictive biomarkers.

Our core is useful for clinical trials as we have standard operating procedures in place. Competency training is paramount for everyone who touches clinical research samples. This means all samples are processed the same way to minimize variables, reduce error and noise, and to maximize meaningful signal. We also have a large bank of healthy donor serum. While each subject can serve as their own control when we are looking for a change over baseline during time course studies, we also have a big collection of healthy, noncancer donors that are used as a comparison to cancer subjects, giving us an accurate baseline to know what is normal and what is not.

How does a group start the process for biomarker validation?

After discovering a potential biomarker, there is a roadmap to standardization and validation. The Society for Immunotherapy Cancer (SITC) released open-access white papers outlining the analytical and clinical validation of immunotherapy biomarkers. There are 5 white papers and a meeting summary report, all found here on the society's website: **sitcancer.org/research/ biomarkers**

How did your core facility become involved with the SARC028 clinical trial?

SARC028 is the first clinical study of PD-1 blockade in sarcomas. The SARC cooperative group and their clinical leads, Drs. Hussein Tawbi and Melissa Burgess, were responsible for starting and coordinating this clinical trial. Our collaboration formed to standardize handling and banking of blood samples in order to look for mechanisms of action and biomarkers of the immune-tumor response.

Let's set the stage for the SARC028 clinical trial. Can you give us the background for the study?

In a sense, PD-1 upregulation on lymphocytes is an activation marker. T cells upregulate their expression of PD-1 when exposed to antigen, and that includes tumor antigen. Tumors across a spectrum can upregulate PD-ligand 1 (PD-L1) and express it on the surface of both the tumor cell and myeloid cells in the tumor. PD-1 upregulation and binding to PD-L1 induces T cells to reduce their activity or shut them off. Antibodies that block the PD-1 pathway are designed to interfere with downregulation of T cell activity and allow them to do a better job of eradicating the tumor.

What role did PD-L1 play in the SARC028 trial?

The role of PD-L1 had not yet been investigated in sarcomas. However, it has been hypothesized that patients with higher levels of PD-L1 in tumors are more likely to respond to therapy. The investigators recruited a diverse set of sarcoma patients to test which subset would most likely respond to PD-1 therapy. They collected and analyzed tumor samples for the correlation between PD-L1 expression and positive response to therapy. My group was responsible for testing serum samples to look for generation of tumor antigen–specific immunity and novel "Our goal is to identify a robust biomarker, then create a panel to test for which patients would benefit from PD-1 blockade."

prognostic markers to better understand which patients would respond to therapy.

SARC028 found some subgroups of sarcoma patients did not benefit particularly well from the PD-1 pathway blockade. However, there were subsets of patients who did benefit. We found from our biomarker testing that there were novel correlations between soluble PD-1 and PD-L2, and clinical outcomes. Some of our other investigations found possible soluble factors markers, such as IL-15, which correlated with a positive anti-tumor kind of immune milieu in the serum. Our goal is to identify a robust biomarker, then create a panel to test for which patients would benefit from PD-1 blockade.

Can you talk about liquid biopsy and what are the challenges with liquid biopsy?

Finding checkpoint biomarkers from tumors is difficult because the biopsy is an invasive procedure. Ideally, the best tumor samples are taken at points where standard of care biopsies and surgical resections occur. Repeatedly taking a solid tumor sample at different times in the trial is a challenge. Blood samples are more attractive as collection is minimally invasive, can be drawn at any time point and in a reasonable amount. Serum can be aliquoted and easily stored at –80°C for future testing.

How are the ProcataPlex panels* for the Luminex platform applied in the SARC028 trial?

Multiplex measurement of soluble forms of the immune checkpoint receptors and ligands is novel. There have been only a few preliminary suggestions that the soluble forms play a role and this is the first evidence that measuring these soluble factors correlates with treatment in these sarcoma patients, and may have clinical utility to potentially predict who might benefit from

a given therapy.

Detection of 65 cytokines, chemokines, and growth factors in a single Luminex[®] assay was also a favorable trait as it combines many analytes into a single assay and with small sample volumes. This diversifies the use of Luminex-based immunoassays for broad biomarker discovery and validation rather than only for testing a specific hypothesis.

What do you think is the future of biomarkers in immunooncology research?

An important evolution is taking place. Traditionally, we only had easy access to blood and not the solid tumor, and we were also investigating very small numbers of good clinical responders. After years of looking in the blood, there were not many robust biomarker signals from those methods and samples, from the few clinical responders. Advancements in biotechnology and pharmaceutical fields provided new technologies and research is to now examine both tumor and blood samples for markers from the much higher number of clinical responders who are receiving these more effective drugs. We can now better understand what is happening in the tumor and this can then be applied to finding those signals and biomarkers in the blood.

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Anass Jawhari Chief Scientific Officer CALIXAR

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EVERYDAY HERO Ameet Chimote, PhD

Department of Internal Medicine, Division of Nephrology, University of Cincinnati

The challenge: I have been working as a postdoctoral research associate in Dr. Laura Conforti's laboratory (Department of Internal

Medicine, University of Cincinnati) for the past 7 years. The main research focus of our laboratory is to study the role played by the K⁺ ion channels in the function of T lymphocytes and their implications in cancer. Previously, I had shown *in vitro* that exposure to hypoxia and adenosine (pathological conditions in solid tumors) inhibited these ion channels. The next logical step for me was to evaluate the expression and function of these ion channels in solid tumors. I was fortunate to avail the resources of University of Cincinnati Cancer Institute's Tumor Bank in procuring surgically resected solid tumor samples from head and neck cancer patients. However, I had no experience in isolating T cells from solid tumors; furthermore, another challenge was that I could not isolate the tumor-infiltrating lymphocytes (TIL) by enzymatic dissociation because I needed to preserve the T cell function. **The solution:** Try, try, and try, till you succeed! Under the guidance of my mentor, I "troubleshooted" protocols for isolating TILs based on published procedures in literature and consulted with technical support from companies until I could successfully isolate fully functional T cells from surgically resected head and neck tumors without using any enzymatic dissociation. The cell number I would isolate would vary from patient to patient; but for all of the samples the cell number of the infiltrated lymphocytes was much lower than what I expected. I learned to work with that small cell number and I was able to measure Ca²⁺ fluxes in these cells by flow cytometry and also phenotype them. To complete the "story", I did immunofluorescence staining for ion channel expression and functional markers in sections from these tumors.

Next steps: This was my first foray in the realm of "Translational Research" and I enjoyed the experience very much. Currently there is a lot of interest in studying ion channels in cancer T cells as potential targets for cancer immunotherapy. I want to build up on my experience and technical expertise gained from this project and continue to investigate ion channels in cancer T cells and decipher whether any "defects" in these ion channels can lead to the lack of immune response in cancers.

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HOW ARE YOUR ANTIBODIES VALIDATED?

Every year, researchers waste valuable time and money using antibodies that do not perform as intended

In September 2015, Thermo Fisher Scientific helped organize and supported a group of leading researchers from institutions throughout the world to draft a set of proposed standards for the best ways to validate* antibody specificity.

The International Working Group for Antibody Validation (IWGAV) published their proposed strategies in *Nature Methods* in September 2016. In the fall of 2016, many of the IWGAV members, as well as representatives from antibody producers, pharmaceutical companies, and leading academic research labs, met at an event coordinated by the Global Biological Standards Institute (GBSI) to further study this topic. This meeting reviewed and validated the IWGAV's proposed standards and discussed ways to implement the standards across the industry.

As a result of our active discussions and key participation in these forums, we have seen a clear consensus develop around several impactful practices to help further advance antibody validation. These new guidelines will add to the extensive application validation* already performed for Invitrogen[™] antibodies and will focus on confirming antibody specificity. Testing antibodies for application validation* is critical and must be carried out with the utmost rigor, but it can be a further challenge to confirm antibody specificity. By combining both application validation* and specificity testing, we aim to ensure that antibodies meet the highest possible standards of overall antibody validation.*

^{*} The use or any variation of the word "validation" refers only to research use antibodies that were subject to functional testing to confirm that the antibody can be used with the research techniques indicated. It does not ensure that the product(s) was validated for clinical or diagnostic uses.

Advanced verification testing methods



Immunoprecipitation-mass spectrometry (IP-MS)

IP-MS: testing using immunoprecipitation followed by mass spectrometry to identify atibody targets



Genetic modification

Knockout: expression testing using CRISPR-Cas9 cell models

Knockdown: expression testing using RNAi to knock down gene of interest



Independent antibody verification (IAV)

IAV: measurement of target expression is performed using two differentially raised antibodies recognizing the same protein target



Biological verification

Cell treatment: detecting downstream events following cell treatment

Relative expression: using naturally occurring variable expression to confirm specificity

Neutralization: functional blocking of protein activity by antibody binding

Peptide array: using arrays to test reactivity against known protein modifications

Orthogonal method: correlation using both antibody dependent and independent method

These specificity verification methods are being used to systematically validate the Invitrogen[™] antibody portfolio. In addition, Invitrogen[™] antibodies than 60,000 reference citations.

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- Over 50 diverse target species

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DOB: 1972

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Figure 1. Antibody internalization process.

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Invitrogen[™] pHrodo[™] iFL dyes dramatically increase fluorescence as pH changes from basic to acidic (Figure 2). Attachment of an iFL pHrodo dye to your antibody makes for a fast, effective, and unambigious signal to determine antibody internalization.

Clear internalization of Herceptin™ antibody in breast cancer cells



Figure 2. Herceptin antibody conjugates of aminereactive pHrodo iFL Red dye traffic into SKBR3 cells overexpressing Her2 protein (Image from Invitrogen[™] EVOS[™] FL Auto Imaging System).

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EFFICIENT INTERNALIZATION OF HERCEPTIN[™] ANTIBODY

Figures 3 and 4 show binding and internalization using flow cytometry and high-content image anlaysis.

Specific binding and internalization of Gazyva[™] obinutuzmab in CD20+ cells

Cell Binding of Alexa Fluor™ 647 SiteClick™ conjugates



Figure 3. Cells from triplicate samples were analyzed on the Invitrogen™ Attune™ NxT Flow Cytometer with AutoSampler to show binding specificity and internalization of Gazyva™ obinutuzmab to CD20+ cells. Nonspecific binding and internalization was not in observed in CD20- cells.

Efficient tracking of internalization events



Figure 4. Conjugated Herceptin[™] antibody internalizes into Her2+ cells over time. Her2cells provide minimal signal. Cells from triplicate samples were analyzed on the Thermo Scientific[™] CellInsight[™] CX5 platform.

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PROTEONICS: INSIGHTS INTO CANCER SIGNALING

Quantitative analysis of AKT/mTOR pathway using western blotting and IP-MS techniques

Because the AKT/mTOR pathway plays a central role in tumor progression and anticancer drug resistance, the quantitative measurement of this pathway's protein expression and posttranslational modifications (PTMs) is vital to cancer research.^[1] A major limitation when measuring the protein levels in the AKT/mTOR pathway is the lack of rigorously verified methods and reagents. Because many biologically relevant proteins are present in very limited quantities, immunoprecipitation (IP) is commonly used as a tool for enriching protein targets before detection and quantification by western blotting and mass spectrometry (MS).^[2,3] Western blotting is a foundational proteomics research application, yet the potential of the application to determine subtle differences in protein expression and protein modification states is limited by shortcomings in detection

reagent selection and instrumentation. The IP-MS method enables the enrichment of signaling pathway proteins, revealing proteinprotein interactions and PTMs.^[4] Multiplex IP coupled with MS (mIP-MS) further enhances this workflow by simultaneously quantifying multiple proteins and their phosphorylation states in a specific signaling pathway.* Here we demonstrate improved western blot detection using the new Invitrogen™ iBright[™] FL1000 Imaging System and compare the results to mIP-MS methodology by analyzing a specific set of protein targets in the AKT/mTOR pathway. The iBright FL1000 Imaging System is a CCD-based western blot imaging instrument, featuring advanced automated features, a powerful 9.1 megapixel camera, and Smart Exposure[™] optimized exposure technology.

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Invitrogen[™] iBright[™] FL1000 Imaging System (Cat. No. A32752)



Figure 1. Western blotting of phospho AKT/mTOR pathway proteins; (A) pPRAS40, (B) pAKT, (C) pp70S6K, (D) pmTOR.



Figure 2. mIP-MS assays allows quantitation of low abundant phosphorylated AKT/mTOR pathway proteins. All 7 phospho targets were quantified across all three lysates conditions.

Smart Exposure technology rapidly determines optimal exposure time, which helps minimize the potential for overor underexposed images and the need to repeat exposures to get the desired signal. Together, the system's high sensitivity camera and Smart Exposure technology enables the acquisition of subtle differences in protein expression.

For the western blot and mIP-MS analysis, HCT116 cells were grown and serum-starved for 24 hours prior to the following treatments: untreated, stimulated (15 min in 12.8 nM hIGF-1), inhibited, then stimulated (1 hour in 50 µM LY294002 plus 15 min in hIGF-1). Subsequent to treatments, cells were lysed with Thermo Scientific[™] Pierce[™] IP-Lysis buffer (Cat. No. 87788) supplemented with 1X HALT[™] Protease and Phosphatase inhibitor cocktail (Cat. No. 78440). Protein concentration of lysates was determined with the Thermo Scientific[™] Pierce[™] BCA Assay (Cat. No. 23225).

For the western blot detection and quantification, 20 µg of each cell lysate was then diluted in electrophoresis reducing sample buffer and run on Invitrogen[™] Novex[™] Tris-Glycine 4-20% gel (Cat. No. XP04200BOX). After electrophoresis, proteins were transferred to nitrocellulose membrane (Cat. No. 88018) using the Thermo Scientific[™] Pierce[™] Power Blotter (Cat. No. 22824) and Thermo Scientific[™] Pierce[™] 1-Step Transfer Buffer (Cat. No. 84731). Membranes were blocked in Thermo Scientific[™] StartingBlock[™] (TBS) Blocking Buffer (Cat. No. 37542) for 1 hour at room temperature and then incubated with primary antibodies overnight at 40°C, rocking gently. Antibody was washed in TBST and protein was detected using Invitrogen[™] Goat anti-rabbit Horseradish Peroxidase Conjugate (Cat. No. 32460) and Thermo Scientific[™] SuperSignal[™] West Dura Extended Duration Substrate (Cat. No. 34076). Images were acquired using the iBright FL1000 Imaging System (Cat. No. A32752). For the mIP-MS sample preparation and analysis, please refer to the article in BioProbes Vol 75; pp. 19-22. Figures 1 and 2 show the correlation between western blotting and mIP-MS.

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* Original article published in *BioProbes 75 Journal of Cell Biology Applications*.

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Figure 1. Mouse plasmacytoid dendritic cell (pDC) gating and analysis. (A) a gate was made on live cells using Invitrogen[™] SYTOX[™] AADvanced[™] Dead Cell Stain (Cat. No. S10274; channel BL3, 640 nm longpass fi Iter), (B) live cells were then gated on CD19 cells (channel VL1, 450/40 nm bandpass (BP) filter). (C) a 2-parameter plot of CD45R/B220 vs. CD317 was used to detect pDCs (channel BL1, 530/30 nm BP filter; and channel BL2, 574/26 nm BP filter); pDCs were identified as dual B220+/ CD317⁺ (upper right quadrant) and comprise 0.851% of live CD19 cells, which is 0.194% of total splenocytes. A collection rate of 500 μ L/ min was used to acquire 1.3 million total cells; total acquisition time was 23 minutes-3x faster than the same sample run on a traditional hydrodynamic focusing cytometer.

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