Adaptive Biotechnologies and Collaborators to Present Six Studies Leveraging Immunosequencing in Lymphoid, Non-Small Cell Lung, and Colorectal Cancers at the 2017 American Society of Clinical Oncology Annual Meeting

May 30, 2017

Seattle, WA – May 31, 2017 – Adaptive Biotechnologies, the leader in combining next-generation sequencing (NGS) and expert bioinformatics to profile T- and B-cell receptors of the adaptive immune system, and its collaborators will present six studies during the 2017 American Society of Clinical Oncology® (ASCO®) meeting in Chicago, June 2-6. Presentations and posters will demonstrate how Adaptive Biotechnologies' immunoSEQ® platform and clonoSEQ® Assay are enabling researchers to characterize T-cell and B-cell repertoires in tumor tissue and in peripheral blood to identify prognostic biomarkers, potential biomarkers of response, toxicity, and to assess measurable residual disease (MRD) in multiple tumor types.

"Profiling the adaptive immune system is a vital element in cancer drug development, diagnosis and treatment," says Dr. Harlan Robins, head of innovation and co-founder of Adaptive Biotechnologies. "We are gratified to collaborate with such a distinguished, diverse group of scientists and researchers in their efforts to discover and advance novel therapies in the war against cancer."

Representatives from Adaptive Biotechnologies will be exhibiting at ASCO booth #18113 to answer questions about its immunosequencing technologies.

Oral Abstract and Poster Presentation Highlights

Abstract #11500: TCR repertoire sequencing of 254 resected non-small cell lung cancers to reveal TCR clonality in normal tissues compared to tumor tissues

Presenter: Alexandre Reuben, PhD, University of Texas MD Anderson Cancer Center, Houston, TX

Oral Abstract Session: Sunday June 4, 8:00 AM – 11:00 AM

Location: S406

Abstract #3090, Poster #185: Association of CMB305 or LV305-induced and baseline anti-NY-ESO-1 immunity with survival in recurrent cancer patients

Presenter: Seth Pollack, MD, Fred Hutchinson Cancer Research Center, Seattle, WA

Poster Session: Monday June 5, 8:00 AM – 11:30 AM

Location: Hall A

Abstract # 9585, Poster #9585: Clonality of T cell repertoire in the tumor (TME) and peripheral blood of regionally advanced melanoma patients (pts) treated with neoadjuvant ipilimumab (ipi) and high dose interferon-α (HDI)

Poster Session: Saturday June 3, 1:15 PM – 4:45 PM

Location: Hall A

Abstract #8036, Poster #362: Daratumumab, bortezomib and dexamethasone (DVd) vs bortezomib and dexamethasone (Vd) in relapsed or refractory multiple myeloma (RRMM): Efficacy and safety update (CASTOR)

Poster Session: Monday June 5, 8:00 AM – 11:30 AM

Location: Hall A

Abstract #8025, Poster #351: Daratumumab, lenalidomide, and dexamethasone (DRd) vs lenalidomide and dexamethasone (Rd) in relapsed or refractory multiple myeloma (RRMM): Efficacy and safety update (POLLUX)

Poster Session: Monday June 5, 8:00 AM – 11:30 AM

Location: Hall A

Abstract #7552, Poster #314: Circulating tumor DNA assessment in patients with diffuse large B-cell lymphoma following CAR-T therapy

Poster Session: Monday June 5, 8:00 AM – 11:30 AM

Location: Hall A

Abstract #7509, Poster #271: CD19 CAR-T cells combined with ibrutinib to induce complete remission in CLL.

Poster Session: Monday June 5, 8:00 AM – 11:30 AM

Location: Hall A

Poster Discussion Session: Monday June 5, 1:15 PM – 2:30 PM

Location: E354b

Abstracts for Publication

Abstract # e14639: T-cell population expansion in response to allogeneic cancer vaccine alone (DPV-001) or with granulocyte-macrophage colony-stimulating factor (GM-CSF) or imiquimod (I) for definitively-treated stage III NSCLC patients (pts)

Citation: J Clin Oncol 35, 2017 (suppl; abstr e14639)

Author(s): Bernard A. Fox, Brian C. Boulmay, Rui Li, Kyle T Happel, Christopher Paustian, Tarsem Lal Moudgil, Sachin Puri, Christopher Dubay, Yoshinobu Koguchi, Adi Mehta, Fridtjof Lund-Johansen, Brenda K Fisher, William L Redmond, Carlo Bruno Bifulco, Augusto Ochoa, Hong-Ming Hu, Traci Hilton, Walter John Urba, Rachel E. Sanborn; Robert W. Franz Cancer Research Center, Earle A. Chiles Research Institute, Providence Cancer Center, Portland, OR; Louisiana State University, New Orleans, LA; Providence Cancer Center, Portland, OR; LSU Health Sciences Center, New Orleans, LA; UbiVac, Portland, OR; Department of Immunology, Oslo University Hospital, Rikshospitalet, Oslo, Norway; Earl A. Chiles Research Institute, Portland, OR

Abstract:
Background: The DPV-001 DRibble is a dendritic cell-targeted microvesicle (proteasome blocked autophagosome) vaccine derived from an adenocarcinoma and a mixed histology cell line. It contains multiple TLR agonists and > 130 potential NSCLC antigens, many as prospective altered-peptide ligands. In preclinical studies, DRibble immunotherapy provided significant anti-cancer effects in a dozen models. We hypothesize that DRibble' vaccination efficacy can be attributed to their capacity to present tumor-derived short-lived proteins (SLiPs) and defective ribosomal products (DRiPs) that are typically not processed and presented by professional antigen presenting cells and against which the host may be less tolerant.

Methods: Pts received induction cyclophosphamide, 7 vaccines every 3-weeks, then every 6 weeks x 4 more doses. Pts were randomized to receive DRibble alone (A), or with I (B) or GM-CSF (C). PBMCs /serum were collected at baseline and at each vaccination to assess changes in antibodies (Ab) (ProtoArray and microsphere affinity proteomics), peripheral lymphocyte populations (flow cytometry) and T cell receptor (TCR) repertoires (Adaptive immunoSEQ).

Results: 13 pts were enrolled (Arm A: 5; B: 4; C: 4). We previously reported that vaccination induced or increased IgG Ab responses against targets over-expressed by NSCLC. Patients receiving DPV-001 had a significant ($p < 0.04$) increase in total (CD4 + CD8) TCRs that increased 10 fold over baseline compared to normal controls (independent from trial, n = 3) and the increase in CD4 clones was similar to that seen following ipilimumab (melanoma pts, independent from trial, n = 9). Analysis of a resected metastasis (progressing on treatment), identified brisk infiltration of T cells and tumor that was strongly PD-L1+.

Conclusions: Vaccination with DPV-001 expanded populations of T cells over that observed in controls and the increase in CD4 T cells was similar to that observed in patients receiving ipilimumab and may represent vaccine-reactive T cells. Clinical Trial Identifier: NCT01909752, Support: R44 CA121612 Clinical trial information: NCT01909752

Abstract #e15133: Similar T-cell repertoires of tumor infiltrating lymphocytes and Crohn's-like lymphoid reaction in colorectal cancer

Citation: J Clin Oncol 35, 2017 (suppl; abstr e15133)

Author(s): Asaf Maoz, Joel K Greenson, Marilena Melas, Ryan O Emerson, Marissa Vignali, Harlan Robins, Chenxu Qu, Stephanie Schmit, Mila Pinchev, Kevin J McDonnell, Gad Rennert, Stephen B. Gruber; University of Southern California Norris Comprehensive Cancer Center, Los Angeles, CA; University of Michigan Hospital, Ann Arbor, MI; Adaptive Biotechnologies, Seattle, WA; Moffitt Cancer Center, Tampa, FL; CHS National Israeli Cancer Control Center, Haifa, Israel

Abstract:
Background: Tumor infiltrating lymphocytes (TILs) and Crohn's-like Lymphoid Reaction (CLR) are independently associated with improved survival in colorectal cancer (CRC). Whereas TILs are localized within tumors, CLR are extra-tumoral lymphocytic aggregates. The origins and relationships of the T-cell repertoire of TILs and the T cells within CLR of the colorectal cancer tumor microenvironment are unknown.

Methods: Expert pathology review identified and circled areas of invasive adenocarcinoma and areas containing CLR from 13 CRC patients for

macrodissection from formalin fixed paraffin embedded (FFPE) slides. DNA was extracted from matched tumor and CLR areas for multiplex PCR sequencing of the CDR3 region of the T-cell receptor beta chain (TCRβ), using the immunoSEQ platform. This approach permits 1) estimating the T-cell content of each sample, 2) measuring the clonality of the T-cell repertoire as a measure of diversity, and 3) quantifying the overlap and similarity of T-cell repertoires across samples.

Results: The T-cell content (Spearman's $r_s = 0.56$, $p = 0.046$) and clonality (Spearman's $r_s = 0.66$, $p = 0.014$) were highly correlated among matched tumor and CLR samples. The ten most frequently identified TIL clones were found at similar frequencies in matched CLR enriched tissues. Comparisons of all the clones detected in tumor and matched CLR tissue demonstrated substantial similarity of these immune repertoires, with an average of 186 shared clones between samples. This degree of similarity was significantly greater than published reports of the similarity of the T-cell repertoire of colorectal tumors and adjacent normal tissue ($p = 1.1e-5$).

Conclusions: The T-cell repertoire of CLR is highly similar to the tumor infiltrating T-cell repertoire, providing supporting evidence for the hypothesis that tumor-specific antigen presentation and lymphocyte maturation occur within CLR.

About Adaptive Biotechnologies®

Adaptive Biotechnologies is the pioneer and leader in combining high-throughput sequencing and expert bioinformatics to profile T-cell and B-cell receptors. The accuracy and sensitivity of its immunosequencing platform, technologies and products are enabling laboratories around the world to drive groundbreaking research in cancer and other immune-mediated diseases. Adaptive also translates immunosequencing discoveries into clinical diagnostics and therapeutic development to improve patient care. For more information please visit adaptivebiotech.com.

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