Inhibition of A2AR induces anti-tumor immunity alone and in combination with anti-PD-L1 in preclinical and clinical studies.

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PHASE 1/1B CLINICAL TRIAL DESIGN



Successive cohort expansion based on pre-defined rules (Clinical Activity: CR/PR or SD > 3 months) ^{*} Others: Prostate, head & neck, MSI+ CRC, or baldder

IMMUNE MODULATION BY CPI-444 IN PERIPHERAL BLOOD

PD-1⁺ T cells are reportedly enriched for neo-antigen specific anti-tumor clones, indicating CPI-444 may induce tumor-specific T cell expansion PD-1 expression is induced in most patients following CPI-444 treatment.





Fresh blood was collected at day 0 and day 28 and the following day cells were stained for PD-1 and T cell lineage markers for flow cytometry

CPI-444 MODULATES TCR REPERTOIRE IN PERIPHERY





CPI-444 INCREASES IMMUNE INFILTRATION INTO TUMORS





CPI-444 Alone



CPI-444 INCREASES T EFFECTOR GENE SIGNATURE



CPI-444 Alone CPI-444 + Atezolizumab

CPI-444 treatment induces expression of IFN response genes in tumors

TCR CLONALITY ASSOCIATES WITH TUMOR REGRESSION

Subjects with TCR diversity are enriched for tumor regression and changes in peripheral TCR repertoire following CPI-444 treatment.





Baseline TCR Clonality in Peripheral Blood

Baseline TCR Clonality in Peripheral Blood

PBMCs were collected at day 0 and between day 28 and day 56. Deep sequencing of TCRb and Moristia and clonality calculations were performed by Adaptive Biotechnology. Subjects with T cell receptor clonality within normal range (< 0.2) are enriched for tumor regression and changes in peripheral T cell receptor repertoire following CPI-444 treatment.

ANTI-TUMOR IMMUNITY INDUCED IN RESPONDING RCC PT.



ELIMINATION OF CIRCULATING TUMOR DNA

SOMATIC

ALTERATION

2.5%

1 SNV

CLINICAL ACTIVITY OF CPI-444 ± ATEZOLIZUMAB



GENE SIGNATURE CORRELATES WITH CLINICAL RESPONSE



Gene expression levels were determined from pre treatment tumor biopsies using the Nanostring Pan Cancer Immune Profiling panel with the addition of custom genes. Differential expression analysis was performed to determine gene expression differences between subjects with a best change in tumor size showed no growth (less than or equal to zero) vs. those with tumor growth (greater than zero). A composite T-effector was calculated as the geometric mean of its composite genes; both the t-effector signature and a number of its component genes were expressed more highly in screen biopsy samples from subjects with no tumor compared to subjects with tumor growth. For each gene shown, the z-score for each individual was calculated and used to display by color on the heatmap.

CONCLUSIONS

• Immune activation in both peripheral blood and tumor tissues observed in patients treated with single agent CPI-444 or in combination with atezolizumab

1. Increased frequencies of PD-1+ activated T cells in peripheral blood

GENE 3

GENE 4

GENE 5

0%

0 SNV

4 SNV

- 2. Significant expansion of TCR repertoires in peripheral blood in patients with high TCR diversity at baseline
- 3. Increased tumor CD8 infiltration as well as induction of interferon induced genes in tumor tissues

• Early clinical data suggests pre-existing T cell infiltration or activation is not required for tumor regression with either single agent or combination regimens

• This is consistent with the hypothesis that inhibition of A2AR signaling stimulates T cell infiltration and activation in the tumor microenvironment in both inflamed and non-inflamed tumors