OncoPept is a end-to-end genomic solution to discover novel therapeutics and biomarkers in the cancer immunotherapy space

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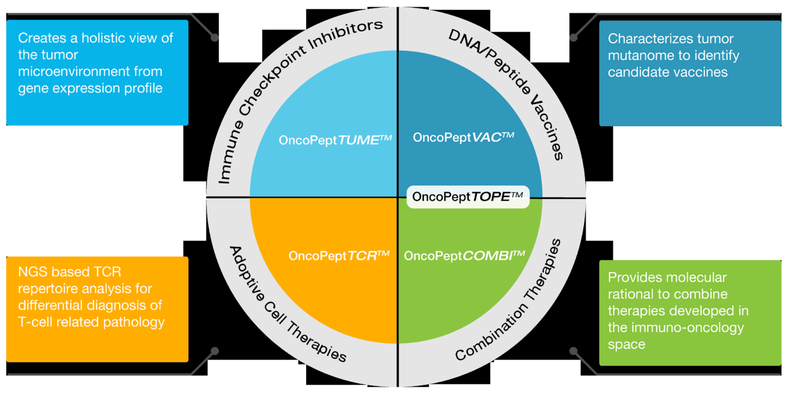
Introduction

Cancer immunotherapeutics engage the body's immune system to fight cancer. Two recently approved checkpoint control antibodies Ipilimumab and Nivolumab target the PD-1 receptor on T-cells blocking the negative signaling that attenuates T-cell activation. The release of brakes maintains the T-cells in their activated state. Activated $CD8^+$ cytolytic T-cells (CTLs) recognize and eliminate tumor cells by recognizing peptides derived from mutated cellular proteins. Identifying T-cell-activating cancer mutations will lead to the development of novel therapeutics including peptide vaccines and engineered T-cell receptors.

What is OncoPept

OncoPept is an integrated platform that combines powerful analytics to analyze exome and RNA-seq data to quantitate the epithelial, stromal and immune cell infiltration, thereby producing a holistic view of the tumor and the tumor microenvironment. By assessing the T-cell neo-epitope burden and the immune phenotype of the tumor, OncoPept helps to identify novel drug targets and biomarkers of response to cancer immunotherapy drugs.

Figure 1. OncoPept accelerates discovery research in immuno-oncology space

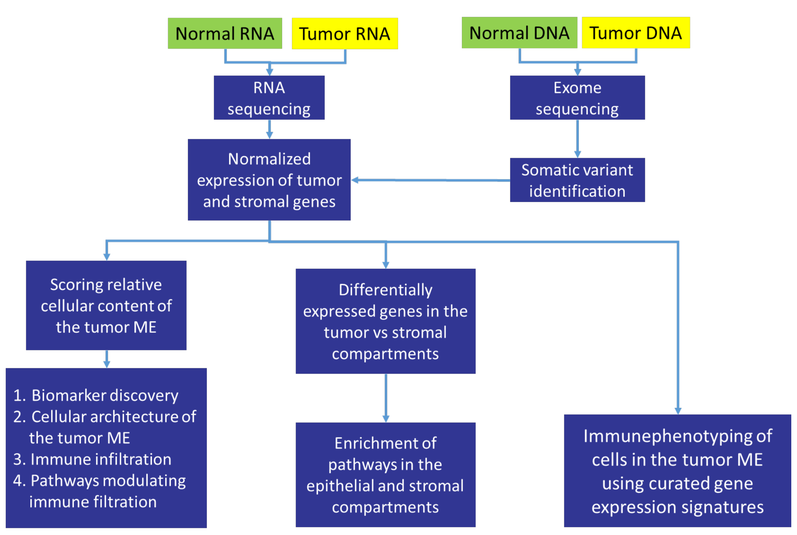


OncoPept*TUME*

Provides immune phenotyping of the tumor microenvironment to discover potential biomarkers that can predict patient response to enable the success of checkpoint inhibitor treatment in preclinical and clinical settings.

Gene expression data analysis captures the state of the tumor microenvironment at any given point of time and provide valuable information on the response of tumors to checkpoint inhibitors and combination therapies

Figure 2. OncoPept*TUME* workflow



OncoPept*TUME* applications in different stages of drug development

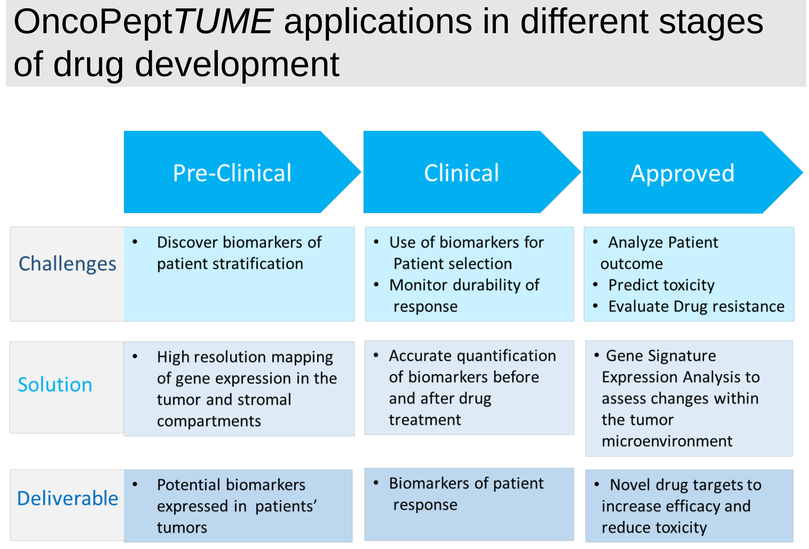


Figure 3. Analysis of tumor microenvironment in Head and Neck Cancer samples from India

Tumors

OncoPept*VAC*

Delivers prioritized neo-epitopes for the development of cancer vaccines. The analysis pipeline delivers prioritized neo-epitopes from exome and RNA-seq data by taking them through multiple selection steps that include identifying all genetic alterations in the sample, creating peptides from SNVs, frameshifted proteins and fusion proteins, assessing the mutant allele expression, HLA binding, processing of peptides by proteasomal and immunoproteasomal cleavage and TAP binding. The output is a short list of somatic mutations that has the potential to activate $CD8^+/CD4^+$ T-cells.

Figure 4. OncoPept*VAC* workflow

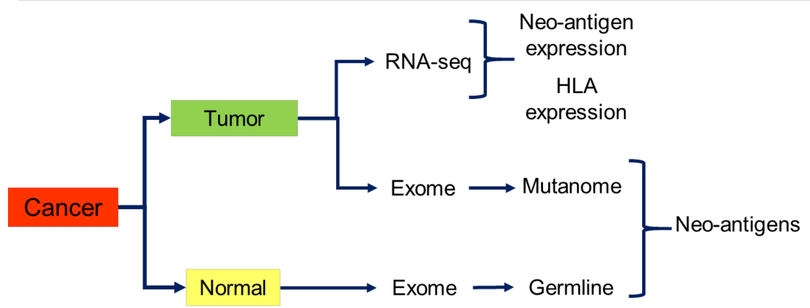


Figure 5. OncoPept*VAC* application in different stages of drug development

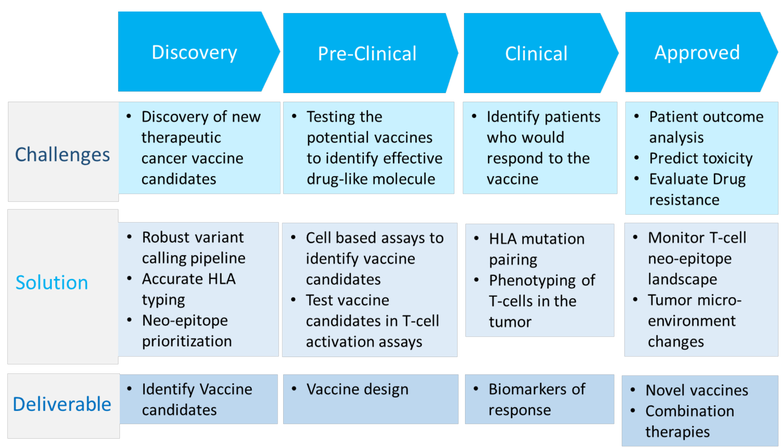


Figure 6. OncoPept*VAC* case study in H&N cancer: Mutation profile and gene expression

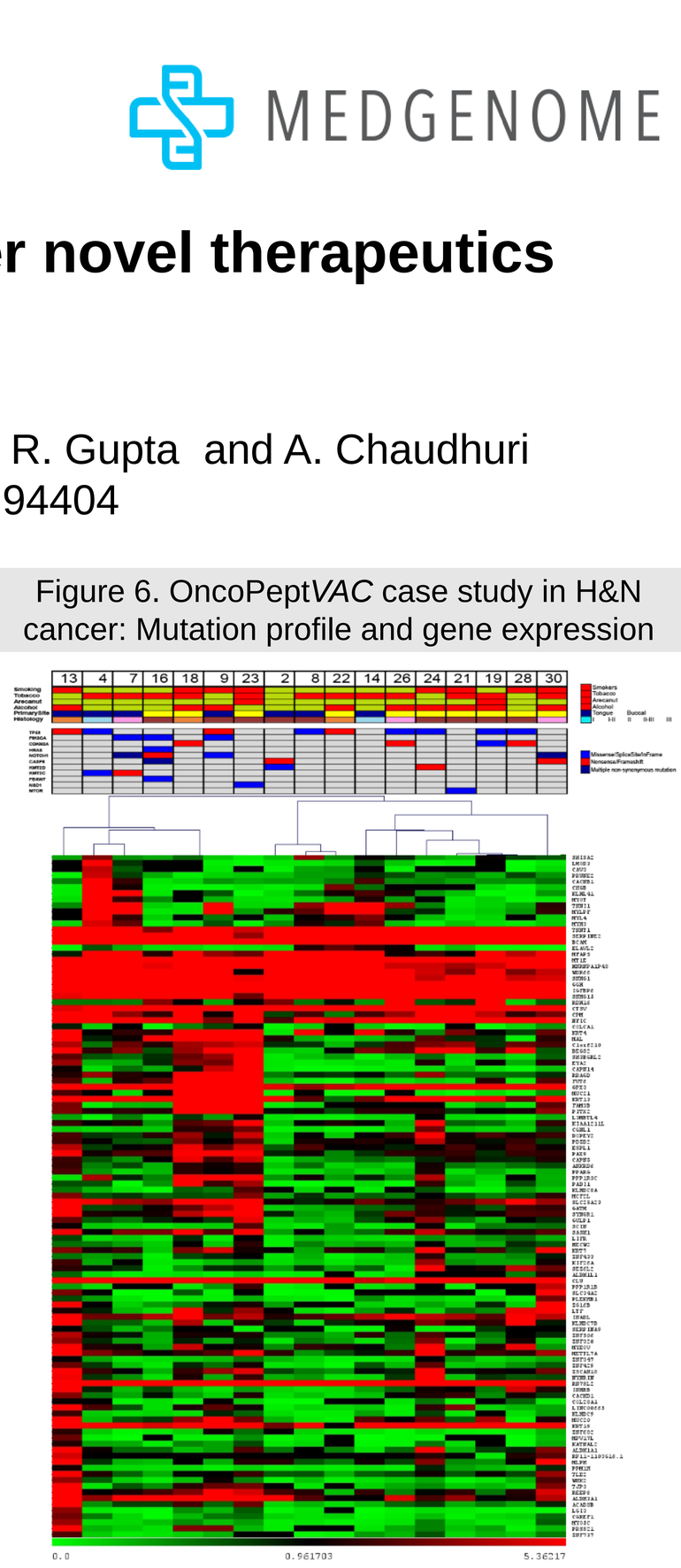


Figure 7. Expression of wild-type and mutant alleles in the tongue and buccal samples

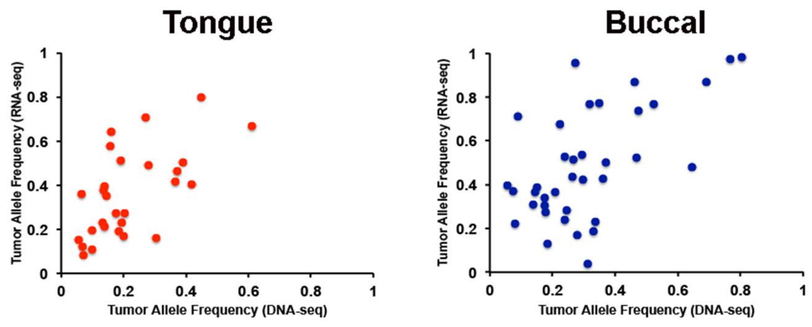
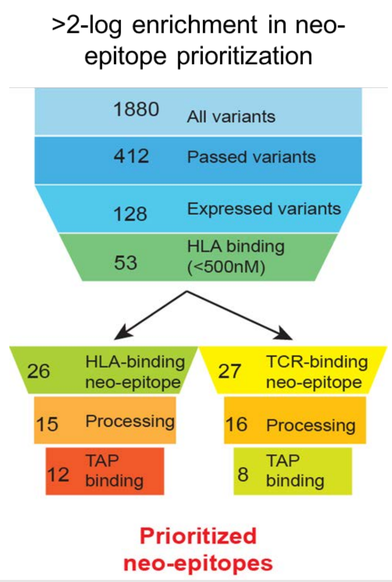


Figure 8. Example of neo-epitope prioritization in a sample of tongue cancer



Conclusion

- OncoPept provides an end-to-end genomic solution to address challenges in the cancer immunotherapy space
- OncoPept*TUME* captures the tumor microenvironment to predict how tumors will respond to IO therapies
- OncoPept*VAC* provides greater ammunition to treat tumors by identifying cancer vaccines