



Overview

- •Hypothesis: Tumor clones surviving checkpoint inhibition therapy harbor mutations more prone to immune avoidance.
- •Approach: Tumors from melanoma patients collected before and after nivolumab immunotherapy (n=41) were analyzed with Ancer, an advanced neoepitope screening platform that combines proprietary machine learning-based CD8 and CD4 epitope mapping tools with removal of inhibitory Treg epitopes [1,2].
- •<u>Results</u>: Mutations gained after nivolumab therapy are less immunogenic and more tolerogenic compared to mutations found prior to therapy.
- •Response to therapy is associated with Ancer results.
- •**Summary**: Our Ancer analysis suggests that nivolumab therapy affects the immunogenicity and tolerance profiles of newly generated mutations in a manner that is consistent with the concepts of immunoediting and immune camouflaging.

Approach – Ancer analysis of melanoma samples

- •Forty-one pairs of mutanomes collected before (*Pre*) and while on (*Post*) nivolumab therapy were retrieved from [7].
- •Pre and Post mutanomes were compared to identify deleted, maintained, and newly acquired mutations.
- •Immunogenic and tolerance potentials were calculated for all mutations with Ancer.



Clones **sensitive** to checkpoint therapy



Clones **acquired** under checkpoint therapy



•This study demonstrates the utility of immunogenicity screening tools in the Ancer platform for streamlined designs of personalized cancer vaccines. •Our Ancer analysis suggests tumors reduce their immunogenicity (less neoepitopes) and increase their tolerance potentials (mutations more likely to be tolerated) in response to nivolumab therapy. Mutations acquired **after immunotherapy are more "stealth"** than mutations found prior to therapy. •Ancer can be employed to **identify novel biomarkers** associated with clinical responses. Tumor neoepitopes become more similar to self in patients that respond to nivolumab therapy. •These results highlight that identifying relevant mutations for precision immunotherapy (e.g. personalized vaccines) will become more difficult once patients are treated with a checkpoint inhibitor. Specializec tools, such as JanusMatrix are needed to correctly and quickly identify immunogenic mutations.

Tumor homology with self as a biomarker for response to checkpoint inhibitor therapy

Guilhem Richard¹, Gary D. Steinberg^{1,2}, Nicole Ruggiero¹, William D. Martin³, Anne S. De Groot^{3,4} ¹EpiVax Therapeutics, Inc., Providence, RI, USA, ²NYU Langone Health, New York, NY, USA, ³EpiVax, Inc., Providence, RI, USA, ⁴University of Georgia, Athens, GA, USA

Background - Mutanome-Directed Cancer Immunotherapy Based on 25 Years of Experience in Epitope Mapping



Tolerance potential (JanusMatrix)



Results - Checkpoint therapy affects tumor immune profile

- Mutations are less immunogenic (less neoepitopes) in tumors collected after nivolumab therapy Mutations acquired after nivolumab therapy have low immunogenicity
- Mutations acquired after nivolumab therapy are likely to be tolerated due to high homology with self antigens
- immune system.



Summary and Conclusions

nivolumab therapy.

JanusMatrix) suppress IFNg production to EVT-CT26 vaccine [6]

Results - Ancer analysis is associated with response to therapy

• Tumors increase their tolerance potential (JanusMatrix homology scores) after

 \rightarrow Change in tolerance is associated with response to therapy.

	Keterences
	1. De Groot. et al., Front Immunol. 2020; 11: 442
k	2. Richard G. et al., Expert Rev Vaccines. 2022 Feb;21(2):173-184
	3. Liu R. et al., Hum Vaccin Immunother. 2015 11:9, 2241-2252
	4. Wada Y. et al., Sci Rep. 2017 Apr 28;7(1):1283
	5. Jang H. et al., Hum Vaccin Immunother 2020 Sep 1;16(9):2042-2050
b	6. Richard G. et al., Proceedings: AACR Annual Meeting 2019; March 29-April 3, 2019; Atlanta, GA
	7. Riaz N. et al., Cell 2017; 171, 934-949