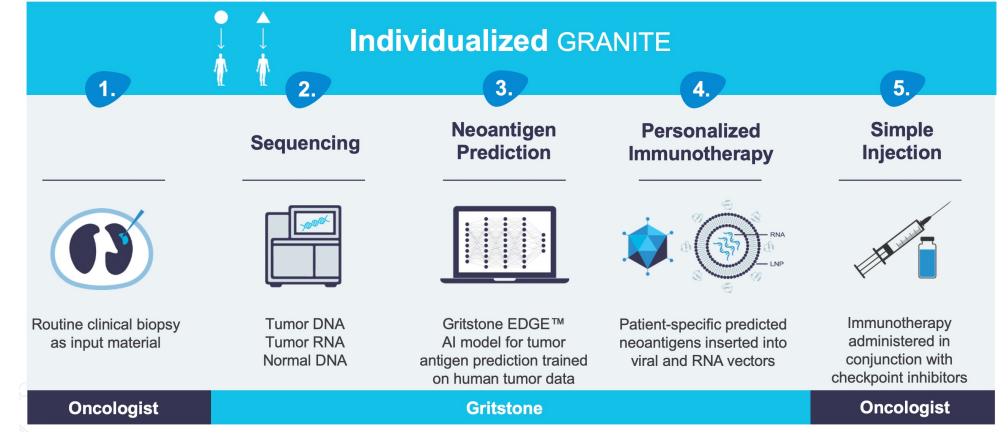
Comprehensive ctDNA monitoring provides early signal of clinical benefit with a novel personalized neoantigen directed immunotherapy for late-stage cancer patients

Desiree Schenk, Rita Zhou, Alexis Mantilla, Oliver Spiro, Taylor Patch, Adrienne Johnson, Daniel Navarro Gomez, Brian S. Henick, Chih-Yi Liao, Sameek Roychowdhury, Steve Maron, Benjamin Solomon, Alexander I. Spira, Daniel V. T. Catenacci, Andrew R. Fergusson, Raphael F. Rousseau, Karin Jooss, <u>Matthew J. Davis</u>.



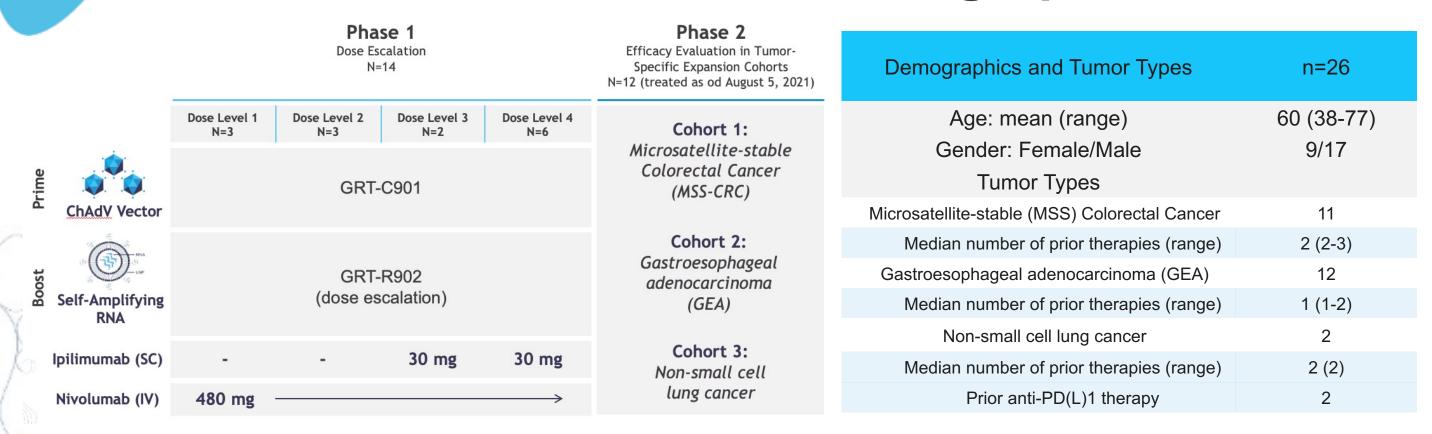
Abstract: Neoantigen directed immunotherapy holds promise for patients with solid tumors devoid of immune infiltration to benefit from immune checkpoint immunotherapy (CPI). A heterologous prime-boost vaccination approach consisting of a Chimpanzee Adenovirus (ChAd) prime and multiple self-amplifying mRNA (samRNA) boosts, delivering 20 neoantigens, has been evaluated in a Phase 1/2 clinical trial in late-stage solid tumor patients in combination with nivolumab and ipilimumab (NCT03639714). Neoantigen dynamics, tumor burden and genomic correlates of response were studied over time in 25 patients (12 GEA, 2 NSCLC, 11 MSS-CRC).

GRANITE process workflow



Methods: Exome sequences from archival (sample used for neoantigen selection), baseline (start of immunization) and on-treatment biopsies were analyzed for 25, 16 and 10 patients, respectively. Paired preand post-vaccine tumor transcriptomes were analyzed for 6 patients. Personalized capture baits were designed for all non-synonymous mutations detected in archival biopsies (mean 144; range: 67-402) for ctDNA monitoring. Longitudinal ctDNA samples were collected monthly on treatment (mean 7; range: 1-18). ctDNA duplex UMI libraries were captured and sequenced to a target mean raw depth >80,000x and reduced to 3x per strand consensus duplex reads.

Phase 1/2 clinical trial and demographics



SC = subcutaneous GRT-C901 = chimpanzee adenovirus encoding 20 neoantigens GRT-R902 = self-amplifying mRNA in lipid nanoparticles encoding same neoantigens as GRT-C901

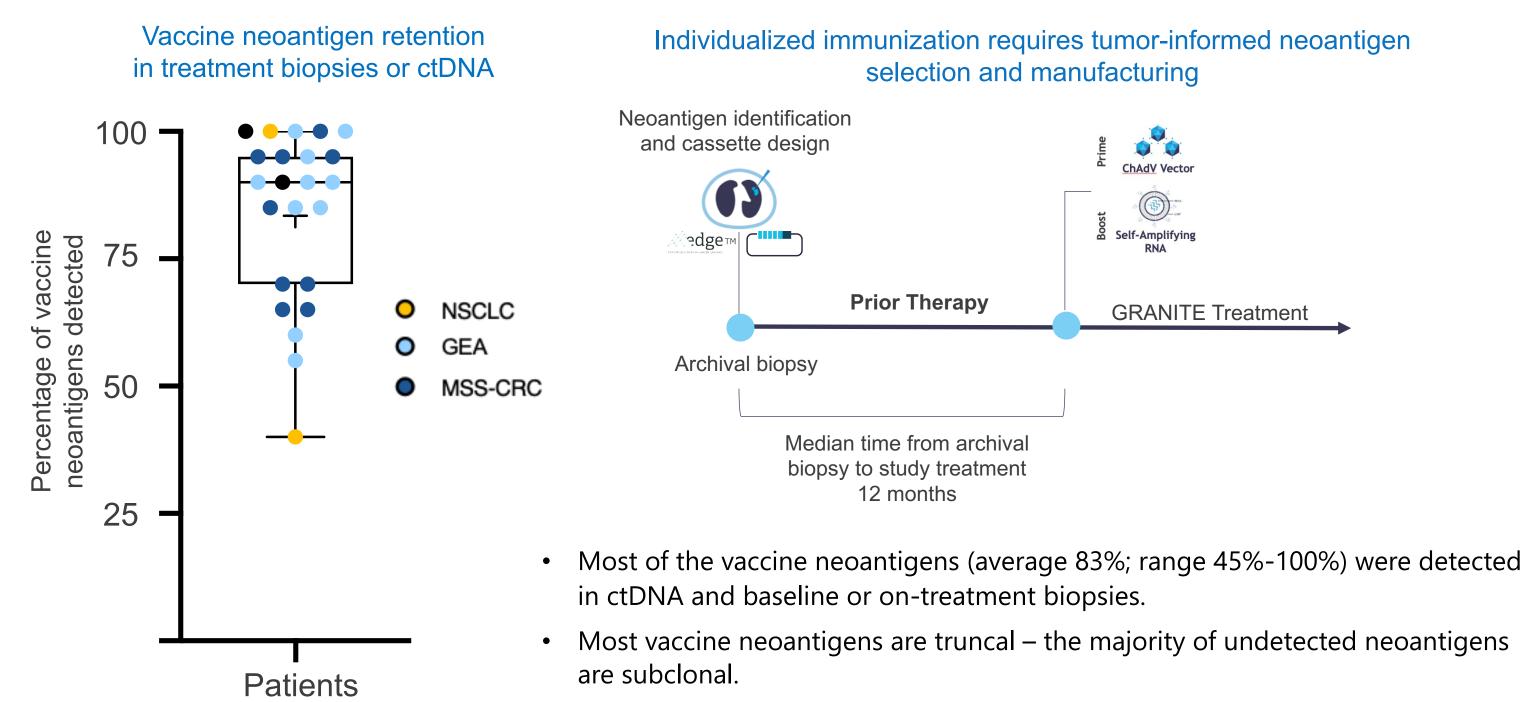
N=26 is the number of patients enrolled – G26 has not been analyzed yet.

AACR ANNUAL MEETING APRIL 8-13, 2022 • #AACR22 O22 New Orleans

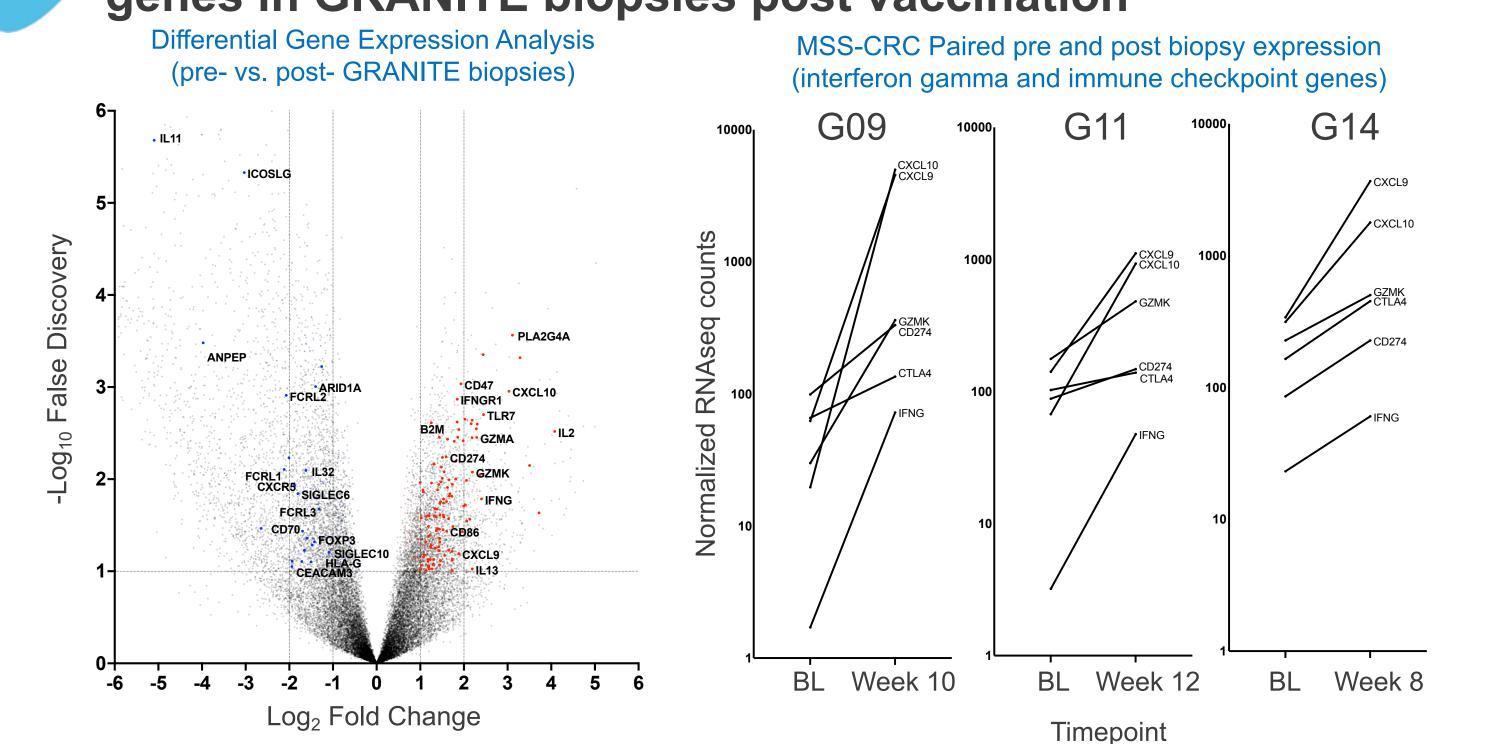
Patient tumors – prior to GRANITE – are immune deserts PD-L1 mRNA expression vs. Tumor Mutational Burden Interferon Gamma (IFN-γ) mRNA expression signature O GEA Lung Adenocarcinoma Lung Adenocarcinoma MSS-CRC MSI-CRC Gastric Melanoma Lung Adenocarcinoma Lung Adenocarcinoma

TMB calculated based on all somatic mutations called divided by WES bait set size Average IFN-γ score utilizing established gene set across GRANITE and relevant PANCAN TCGA tissue types (LUAD, LUSC, COAD, SKCM): J Clin Invest. 2017;127(8):2930-2940

Most vaccine neoantigens are retained through prior treatments including chemotherapy



Increase in interferon gamma and immune infiltration related genes in GRANITE biopsies post vaccination

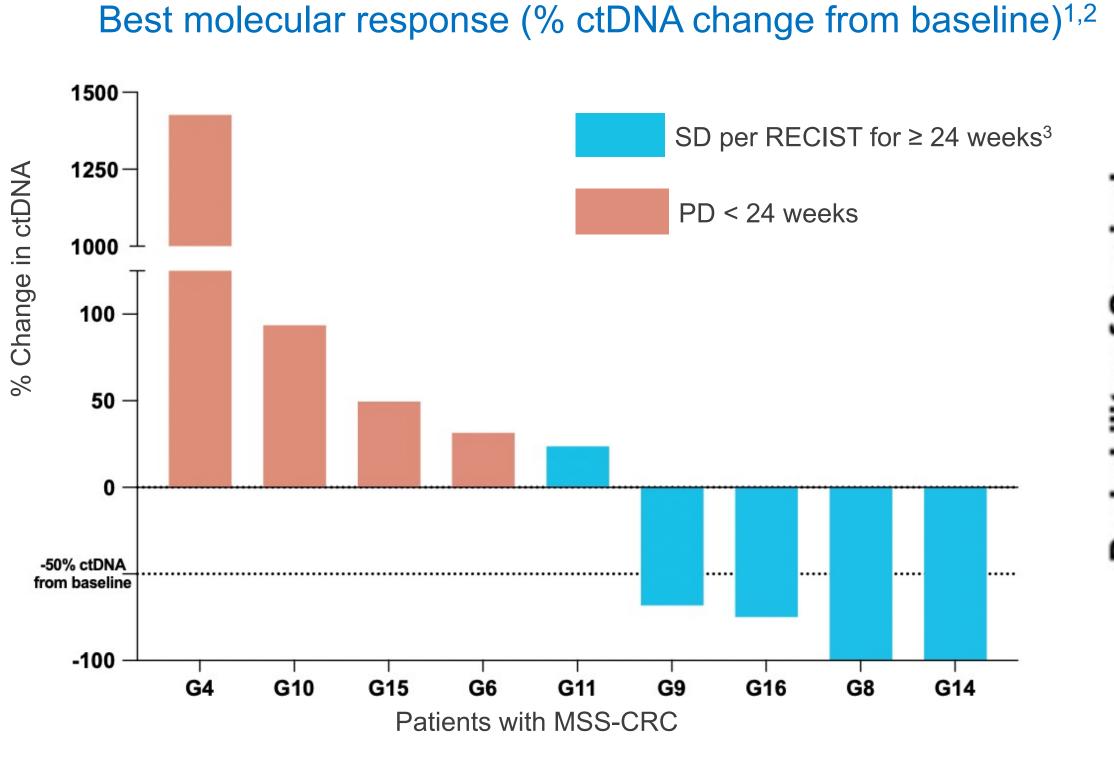


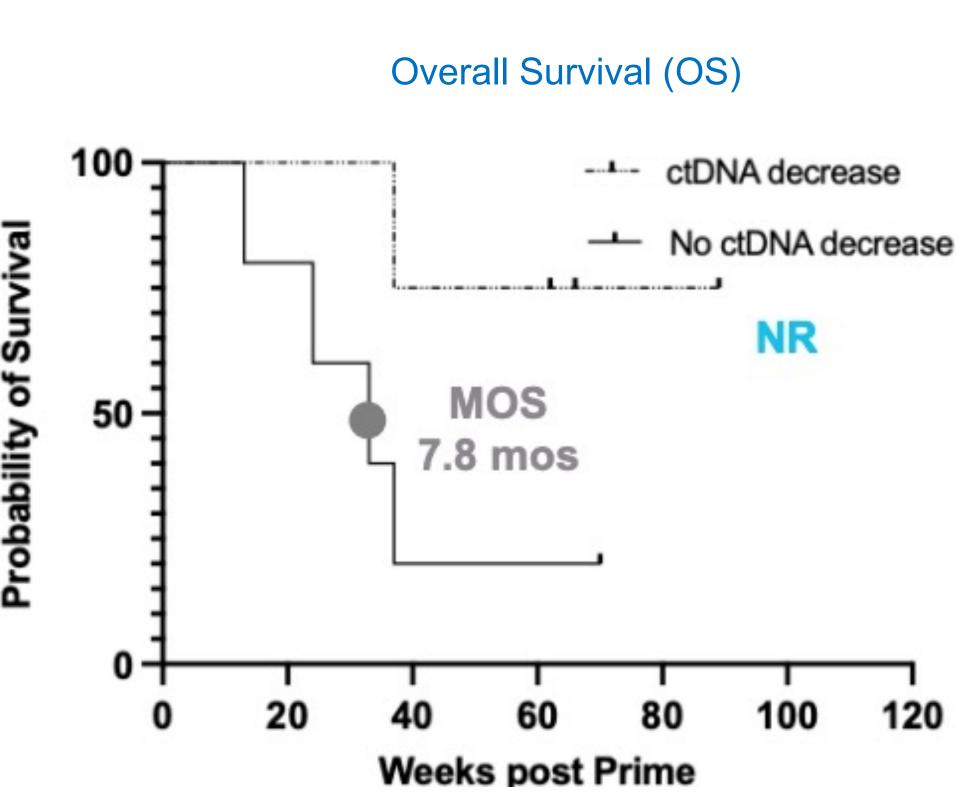
Differential gene expression analysis from 6 paired pre- and post-vaccine biopsies (3 GEA and 3 MSS-CRC – G09 with molecular response (MR*)) demonstrated significant upregulation in gene signatures associated with immune-inflamed tumor microenvironments including interferon gamma responses and immune checkpoint genes

Pre-treatment biopsies include manufacturing (MFG) and baseline (BL) when available.
On-Treatment (OT) - G01 post-vaccine collected at week 80 (EOT) all others collected at weeks 8-14 post ChAd prime

*MR = > -50% decrease in ctDNA from baseline

ctDNA molecular response is associated with OS in patients with advanced stage MSS-CRC





- . ctDNA assessment based on Gritstone-developed, tumor-informed assay
- ctDNA assessment not available for the 3 most recently treated patients
 Patients G14 and G16 with PD at week 16 and 9 respectively not confirmed on subsequent scans through week 24

SD=stable disease; PD=progressive disease

Acquired resistance in antigen presentation pathway at 12 months of therapy suggesting vaccine induced immune pressure on tumor

Molecular response achieved for >7 months before subclonal TAP1 biallelic loss-of-function mutations are identified in ctDNA

G08: 50-year-old Female with Metastatic MSS-CRC
Received two prior lines of therapy

Prior Therapy

Variable

Biochemical
Biomarker

CEA elevated
Biomarker

Liver Enzymes
Elevated

Decrease in target lesions of 17% over first 48 weeks on study treatment

TMB (mut/MB)

PD-L1

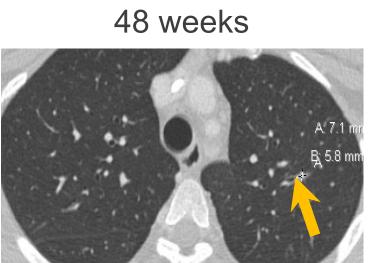
C10

Progression at 65 weeks based on appearance of a new non-target liver lesion

Baseline

A 10.7 mm

B 8.0 mm



Data cut-off 05 Jan 2022

Longitudinal ctDNA dynamics (Vaccine neoantigens)

Longitudinal ctDNA dynamics (subclonal escape mutations)

— Average mutated hGE/mL

— NLRC5 Q1035fs
— NLRC5 N1805T
— TAP1 W139*
— TAP1 L299fs

— TAP1 L299fs

G08 ctDNA dynamics in panel 2 and 3 as an example of the correlation of vaccine targeted neoantigens and all monitored mutations. Across the GRANITE patient cohort mean neoantigen variant allele frequency (VAF) strongly correlated with all monitored mutations VAF ($R^2 = 0.90$, p < 0.0001) through treatment.

*hGE/ml=Mutated haploid genome equivalents, calculated from cfDNA concentration (ng/ml) and VAF.

Conclusion

- Majority of neoantigens are retained in tumor while vaccine is being manufactured
- Comprehensive ctDNA longitudinal monitoring enables real-time assessment of response/resistance and potentially provides more useful predictive information than traditional RECIST radiologic assessment in the context of this novel immunotherapy
- Neoantigen-directed Immunotherapy appears to drive clinical benefit in patients with advanced MSS-CRC, with molecular response elicited in 4/9 treated subjects and correlated with prolonged progression-free survival and overall survival