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Conclusions: We confirmed a priori identified risk factors for poor prognosis in the larger and COVID-19 cohort and performed initial analysis of lab parameters, informing risk assessment.

Clinical trial identification: NCT03453470.

Legal entity responsible for the study: COVID-19 and Cancer Consortium (CC19).

Funding: Has not received any funding.

Disclosure: P. Grivas: Honoraria (self), Research grant/funding (institution): Astrazeneca; Honoraria (self), Research grant/funding (institution): Bayer; Honoraria (self), Speaker Bureau/Expert testimony: Bristol-Myers Squibb; Honoraria (self), Research grant/funding (institution): Clovis Oncology; Honoraria (self), Research grant/funding (institution): Denovo; Honoraria (self), Research grant/funding (institution): Merck; Honoraria (self), Research grant/funding (institution): Pfizer; Honoraria (self): Roche; Honoraria (self): Seattle Genetics; Honoraria (self), Research grant/funding (institution): QED Therapeutics; Research grant/funding (institution): Kurelet; Research grant/funding (institution): Bavarian Nordic; Research grant/funding (institution): Debiopharm; Research grant/funding (institution): Immunomedics; Research grant/funding (institution): Oncogenex; J. Warner: Advisory/Consultancy: IBM Watson Health; Advisory/Consultancy: Westat; Leadership role, Shareholder/Stockholder/Stock options: HimOnC.org LLC; Travel/Accommodation/Expenses: American Society of Clinical Oncology; Research grant/funding (institution): National Cancer Institute. Y. Shyr: Advisory/Consultancy: Roche; Advisory/Consultancy: Novartis; Advisory/Consultancy: Pfizer; Advisory/Consultancy: Johnson & Johnson; Advisory/Consultancy: GlaxoSmithKline; Advisory/Consultancy: Speaker Bureau/Expert testimony: Astrazeneca; Advisory/Consultancy: Janssen; Advisory/Consultancy: Travel/Accommodation/Expenses: Biogen; Advisory/Consultancy: Travel/Accommodation/Expenses: Janssen; Advisory/Consultancy: Advisory/Consultancy, Speaker Bureau/Expert testimony: Eisai; Advisory/Consultancy, Travel/Accommodation/Expenses: Janssen; Advisory/Consultancy: Travel/Accommodation/Expenses: Bristol-Myers Squibb; Advisory/Consultancy: Travel/Accommodation/Expenses: F. Hoffmann-La Roche; Advisory/Consultancy: Research grant/funding (institution): Merck Sharp & Dohme; Honoraria (self), Advisory/Consultancy: Eli Lilly; Advisory/Consultancy: Genentech; Advisory/Consultancy: BMS; Advisory/Consultancy: Amgen; B. Haam: Advisory/Consultancy, Research grant/funding (institution): AstraZeneca; Advisory/Consultancy, Research grant/funding (institution): Merck; Advisory/Consultancy, Research grant/funding (institution): Boehringer-Ingelheim; Advisory/Consultancy, Research grant/funding (institution): AbbVie; Advisory/Consultancy, Research grant/funding (institution): Cyt性格; Advisory/Consultancy: Spectrum; Advisory/Consultancy: Takeda; Advisory/Consultancy, Research grant/funding (institution): Guardant Health; Advisory/Consultancy: Foundation One; Advisory/Consultancy, Research grant/funding (institution): Genentech; Research grant/funding (institution): AbbVie; Research grant/funding (institution): AstraZeneca; Research grant/funding (institution): Eli Lilly; Advisory/Consultancy: G1 Therapeutics; Advisory/Consultancy, Spectrum; Advisory/Consultancy: Invatea; Advisory/Consultancy: Sandoz; Advisory/Consultancy: Samsung; Advisory/Consultancy: Beyond Spring; Advisory/Consultancy, Travel/Accommodation/Expenses: Bayer; Advisory/Consultancy: Mylan; Research grant/funding (institution): Amgen. B.J. Rini: Advisory/Consultancy, Research grant/funding (institution), Travel/Accommodation/Expenses: Merck; Advisory/Consultancy, Research grant/funding (institution): Roche; Advisory/Consultancy, Research grant/funding (institution): Bristol-Myers Squibb; Travel/Accommodation/Expenses: P: Advisory/Consultancy, Research grant/funding (institution): AVED; Advisory/Consultancy: Arrawee; Advisory/Consultancy, Research grant/funding (institution), Travel/ Accommodation/Expenses: BMS; Advisory/Consultancy: Janus: 3M; Advisory/Consultancy, Research grant/funding (institution): Synthorx; Advisory/Consultancy, Surface Oncology; Shareholder/Stockholder/Stock options: PTC Therapeutics; Research grant/funding (institution): Blueprint Therapeutics; Research grant/funding (institution): Boehringer-Ingelheim; Advisory/Consultancy, Research grant/funding (institution): Takeda; Advisory/Consultancy, Research grant/funding (institution): Merck; Advisory/Consultancy, Research grant/funding (institution): Guardant Health; Advisory/Consultancy, Foundation One; Advisory/Consultancy, Research grant/funding (institution): Genentech; Research grant/funding (institution): Gilead; Travel/Accommodation/Expenses: E.R. Squibb Sons LLC. All other authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.08.2131

LBA73

The ORF1b of SARS-CoV-2 encodes an immunodominant epitope restricted by HLA-A*01:01

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Background: A large global effort is ongoing to develop vaccines against SARS-CoV-2, the causative agent of COVID-19. While there is accumulating information on the antibody response against SARS-CoV-2, less is known about the presentation of viral antigens that are targeted by CD8 T cells. Such knowledge will be of high value to gain fundamental insights into the antigenic landscape of SARS-CoV-2 recognized by CD8 T cells, to develop tool allowing focused analysis of the SARS-CoV-2 specific T cell responses, and to look for therapeutic options. However, whether, and how, current vaccine designs are covering the CD8 T cell recognized antigens.

Methods: To address this issue, we have analyzed samples from 18 COVID-19 patients for CD8 T cell recognition of 500 predicted SARS-CoV-2-derived epitopes restricted to 10 common HLA-A and HLA-B alleles. For each HLA allele, the top 50 epitopes were selected based on predicted binding affinity and presented in a peptide pool for high throughput cellular and functional analysis. To probe for CD8 T cell recognition of the selected epitope-HLA complexes, we made use of our in-house technology based on multiplexing of peptide-HLA multimers conjugated to fluorescent dyes.

Results: In addition to previous studies showing D8 T cell reactive epitopes derived from the spike protein of SARS-CoV-2, we have identified several CD8 T cell reactive epitopes derived from other SARS-CoV-2 genes. These data suggest that a variety of immunodominant properties across patients positive for HLA-A*01:01. Investigation of the functional status of part of the identified responses (including 4 responses specific for the immunodominant epitope) revealed that the T cell responses were
Disparities in cancer during the COVID-19 pandemic: COVID-19 and cancer outcomes study (CCOS)

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Methods: CCOS is a multicenter prospective cohort study designed to define the impact of the pandemic on cancer care delivery and outcomes. The CCOS cohort comprised consecutive outpatients with cancer seen at two US cancer centers from March 2 to March 6, 2020 (index visit). Data was collected at baseline, retrospectively from the preceding 3 months, and prospectively at 3-month follow up per patient. Changes in numbers of visits were compared using Wilcoxon signed rank tests. Correlates of increases in telehealth visits and decreases in in-person visits were evaluated using multivariable logistic regression models. Adjusted Odds ratios (aOR) and 95% confidence intervals (CI) were reported.

Results: Of 2365 included patients, 1219 (51.6%) had a decrease in in-person visit frequency during the pandemic period relative to the preceding 3 months. Conversely, 760 (32.2%) had an increased frequency of telehealth visits (decrease in in-person and increase in telehealth visits; both p<0.001). 128 (5.4%) patients developed COVID-19. Compared to White patients, Black and Hispanic patients were less likely to have telehealth visits, had no significant change in frequency of in-person visits, and were more likely to develop COVID-19 (Table).

Conclusions: Significant disruptions to routine cancer care were observed during the pandemic period relative to the prior 3 months. Racial and ethnic barriers to the adoption of telehealth, and related socioeconomic factors, place these vulnerable populations simultaneously at disproportionate risk for decreased cancer-related visits and COVID infection, thereby exacerbating existing racial and ethnic health disparities.

Legal entity responsible for the study: The authors.

Funding: Has not received any funding.

Disclosure: All authors have declared no conflicts of interest.