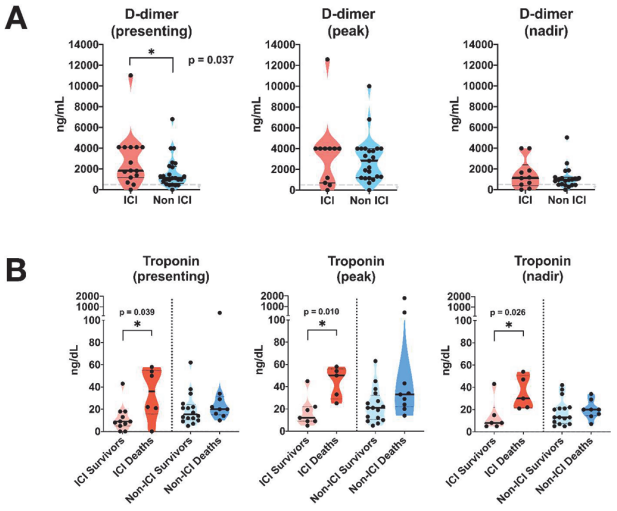

Abstract 481 Figure 3 Significant lab values in cancer patients with COVID-19
(A) Comparison of D-dimer levels between patients taking ICI in last year and non-ICI controls. Patients with ICI use had elevated presenting D-dimer level (median 1850 vs. 1123 ng/mL) compared to non-ICI patients. (B) Comparison of troponin levels between survivors and COVID-19 deaths within ICI and non-ICI case control cohorts. Elevated presenting, peak, and nadir troponin levels were related to COVID-19 mortality in ICI patients (p = 0.04, 0.01, 0.03) but not in non-ICI patients. Laboratory results were taken at date closest to presentation for COVID-19 (presenting), as well as peak and nadir values throughout COVID-19 course or within 21 days of presentation. Dots represent individual patient values, the solid black line represents median, and thin black lines represent 25% and 75% percentiles. The vertical dotted line separates the two cohorts (ICI vs. non-ICI). Gray lines indicate normal reference ranges for each laboratory test. Violins show range and kernel density estimate distributions of each group. The Wilcoxon rank-sum test was used to calculate p-values. (*) $p < 0.05$, (**) $p < 0.01$, (***) $p < 0.001$).

the clinical and operational research data used in this project. The content is solely the responsibility of the authors.

Ethics Approval This project was approved by the Partners Healthcare Institutional Review Board (#2020P000851).

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482 COVID-19 IN PATIENTS WITH LUNG CANCER RECEIVING IMMUNOTHERAPY. A REPORT FROM AN SPANISH ACADEMIC CENTER

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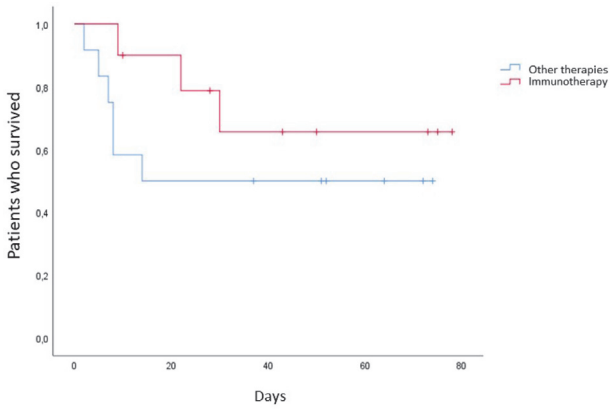
Background COVID-19, caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was declared pandemic in March 2020. We know that patients with cancer represent a high risk population. Lung cancer have an already damage lung that may affect the evolution and outcomes of these patients.[1–3] The aim of this study is to report the characteristics and outcomes of patients with lung cancer receiving immunotherapy and SARS-CoV-2 infection.

Methods We retrospectively collected sociodemographic and clinical data from patients with lung cancer and COVID-19 diagnosis who were admitted to La Paz University Hospital (Madrid, Spain) from March 1 to May 7, 2020. Survival analysis was performed using the Kaplan-Meier method and log-rank test. Hazard ratios and corresponding 95% confidence intervals were estimated with the use of Cox proportional-hazards regression models.

Results A total of 29 patients were included. Baseline characteristics are depicted in table 1. Non-small-cell lung cancer (NSCLC) was reported in 93% of the patients and 69% were at advanced stage at the time of COVID-19 diagnosis. Eighty-two percent of the patients were admitted to the hospital and 75% received experimental therapy for COVID-19, including hydroxychloroquine (HCQ) (N=9), HCQ plus azithromycin (N=11) or lopinavir/ritonavir (N=2). A total of 12 patients developed acute distress respiratory syndrome (ADRS) at a median time of 7 days from COVID-19 diagnosis. ADRS was managed with steroids in 75% of the patients. Thirteen (44.8%) deaths were reported, 11 of them were considered to be COVID-19 related. Death occurred at a median time of 8 days. In the univariate analysis, diabetes mellitus, respiratory failure at the time of admission, presence of multilobar infiltrates and SDRA were associated with death.Twenty-two patients were on systemic treatment, of whom 10 patients were receiving immunotherapy alone (N=7) or in combination with chemotherapy (N=3) at the time of COVID-19 diagnosis. No significant association with the development of ADRS (P=0.38) or death (P=0.41) was found between patients on immunotherapy versus other systemic therapies. Overall survival was not reached in the immunotherapy group vs 14 days in patients on other systemic therapies (P=0.25), see figure 1.

Abstract 482 Table 1 Clinical characteristics
ECOG PS, Eastern Cooperative Oncology Group Performance Status; NSCLC, Non-Small-Cell Lung Cancer; SCLC, Small-Cell Lung Cancer; CT, chemotherapy; ICI, immune checkpoint inhibitors; TKI, tyrosine-kinase inhibitors

Table 1. Baseline characteristics	
Male sex, nº (%)	20 (69)
Age, Median (range)	69 (48-85)
Race, nº (%)	
• Caucasian	28 (96.6)
• Hispanic-American	1 (3.4)
ECOG PS, nº (%)	
• 0	9 (31.0)
• 1	11 (37.9)
• 2	5 (17.2)
• 3-4	4 (13.8)
Smoking history, nº (%):	
• Current smoker	8 (27.6)
• Former smoker	18 (62.1)
• Non-smoker	3 (10.3)
Comorbidities, nº (%):	
• HTA	18 (62.1)
• DM	8 (27.6)
• COPD/Asthma	17 (58.6)
• Obesity (BMI≥30)	4 (13.8)
Lung cancer features, nº (%):	
• NSCLC	27 (93.1)
• SCLC	2 (6.9)
Stage at COVID diagnosis, nº (%)	
• I	2 (6.9)
• II	1 (3.4)
• III	6 (20.7)
• IV	20 (69.0)
Antineoplastic treatment at COVID diagnosis, nº (%):	
• None	7 (24.1)
• CT	8 (27.6)
• ICI	7 (24.1)
• CT + ICI	3 (10.3)
• TKI	4 (13.8)
Previous thoracic radiotherapy, nº (%)	6 (20.7)
Previous lung surgery, nº (%)	8 (27.3)
Uncontrolled disease at the time of COVID-19 diagnosis, nº (%)	9 (31.0)



Abstract 482 Figure 1 Overall survival. Overall survival in patients with lung cancer treated with immunotherapy vs other therapies

Conclusions We found that patients with lung cancer represent an extremely vulnerable population, with a poor prognosis after COVID-19 diagnosis. Treatment with immunotherapy may also be considered a risk factor. Emphasis on prevention and treatment based on evidence-based medicine is crucial in our daily practice.

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Ethics Approval The study was approved by Hospital Universitario La Paz Institution's Ethics Board, approval number PI-4147

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483 ASSOCIATION OF COVID-19 INFLAMMATION WITH ACTIVATION OF THE C5A-C5AR1 AXIS

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Background Coronavirus disease 2019 (COVID-19) is a new pandemic disease caused by infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The C5a anaphylatoxin and its receptor C5aR1 (CD88) play a key role in the initiation and maintenance of several inflammatory responses, by recruiting and activating neutrophils and monocytes in the lungs.

Methods We provide a longitudinal analysis of immune responses, including immune cell phenotyping and assessments of the soluble factors present in the blood and broncho-alveolar lavage fluid (BALF) of patients at various stages of COVID-19 severity: paucisymptomatic, pneumonia and acute respiratory distress syndrome (ARDS)

Results We report an increase in soluble C5a levels proportional to COVID-19 severity and high levels of C5aR1 expression in blood and pulmonary myeloid cells, supporting a role for the C5a-C5aR1 axis in the pathophysiology of ARDS. Avdoralimab, an anti-C5aR1 therapeutic monoclonal antibodies (mAbs) prevented C5a-mediated human myeloid cell recruitment and activation, and inhibited acute lung injury (ALI) in human C5aR1 knockin mice.

Conclusions These results support the evaluation of avdoralimab to block C5a-C5aR1 axis as a mean of limiting myeloid cell infiltration in damaged organs and preventing the excessive lung inflammation and endothelialitis associated with ARDS in COVID-19 patients

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Ethics Approval Human study protocol was approved by the Committee for the Protection of Persons Ile-de-France III – France (#2020-A00757-32). Animal experiments were approved by the ministere de l'enseignement superieur, de la recherche et de l'innovation – France (APAFIS#25418-2020051512242806 v2).

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Data sharing, handling, and access

484 BIOTURING BROWSER: INTERACTIVELY EXPLORE PUBLIC SINGLE CELL SEQUENCING DATA

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Background Single-cell sequencing technology has opened an unprecedented ability to interrogate cancer. It reveals significant insights into the intratumoral heterogeneity, metastasis, therapeutic resistance, which facilitates target discovery and validation in cancer treatment. With rapid advancements in throughput and strategies, a particular immuno-oncology study can produce multi-omics profiles for several thousands of individual cells. This overflow of single-cell data poses formidable challenges, including standardizing data formats across studies, performing reanalysis for individual datasets and meta-analysis.

Methods N/A

Results We present BioTuring Browser, an interactive platform for accessing and reanalyzing published single-cell omics data. The platform is currently hosting a curated database of more than 10 million cells from 247 projects, covering more than 120 immune cell types and subtypes, and 15 different cancer types. All data are processed and annotated with standardized labels of cell types, diseases, therapeutic responses, etc. to be instantly accessed and explored in a uniform visualization and analytics interface. Based on this massive curated database, BioTuring Browser supports searching similar expression profiles, querying a target across datasets and automatic cell type annotation. The platform supports single-cell RNA-seq, CITE-seq and TCR-seq data. BioTuring Browser is now available for download at www.bioturing.com.

Conclusions N/A

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