Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

1674MO ACE2 and TMPRSS2 expression by clinical, HLA, immune, and microbial correlates across 34 human cancers and matched normal tissues: Implications for SARS-CoV-2

R. Bao[1], K. Hernandez[2], L. Huang[3], J.J. Luke[1]

[1]University of Pittsburgh Medicine, UPMC Hillman Cancer Center, Pittsburgh, PA, USA; [2]Medicine, University of Chicago, Chicago, IL, USA; [3]Center for Research Informatics, University of Chicago, Chicago, IL, USA

Background: Pandemic COVID-19 by SARS-CoV-2 infection is facilitated by the ACE2 receptor and protease TMPRSS2. Patients with cancer may be at particularly high risk for SARS-CoV-2 infection and deleterious outcomes to the disease. A better understanding of potential host risk factors, notably *ACE2* and *TMPRSS2*, in malignant tissues may inform considerations surrounding SARS-CoV-2 and COVID-19 in patients with cancer and more broadly in the general population.

Methods: We performed a large-scale integrated study of *ACE2* and *TMPRSS2* gene expression in 10,038 patients with cancer across and within organ systems, by normal *versus* tumor. We investigated its correlative pattern with clinical factors (age, gender, race, BMI and smoking history, etc.), HLA, immune signatures, and commensal microbiome.

Results: Matched normal tissues generally display higher *ACE2* and *TMPRSS2* expression compared with tumor, with digestive organs expressing the highest levels. No consistent association was observed between clinical groups or HLA genotypes and *ACE2*/*TMPRSS2* levels, after adjusting for tissue-specific expression. *ACE2* expression showed a significant correlation with clinically relevant immune signatures including interferon-stimulated genes and the T cell-inflamed phenotype, and with macrophage cell subsets. Single-cell RNAseq analysis demonstrated little to no *ACE2* or *TMPRSS2* expression in lymphocytes or macrophages. *ACE2* and *TMPRSS2* showed a distinctive correlative pattern with 75 bacterial taxa in normal tissues particularly from colorectal cancers (gram-negative to positive ratio = 2.6:1). LASSO regression models integrating multi-dimensional correlates revealed immune and microbiota are among the top-ranked features predicting *ACE2* expression, while epithelial cell abundance is the dominant predictor for *TMPRSS2*.

Conclusions: We investigated *ACE2* and *TMPRSS2* expression across clinical, genetic, immune, and microbiome domains. We identify novel associations with the microbiota and confirm host immunity associations with gene expression. We hope these data may better inform clinical considerations surrounding risk stratification and prevention approaches.

Legal entity responsible for the study: The authors.

Funding: Search Results Web results U.S. Department of Defense.

Disclosure: All authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.08.1739

1675MO Screening of COVID-19 disease based on chest CT and PCR for cancer patients undergoing radiotherapy in a French coronavirus hotspot

R. Sun, S. Achkar, S. Ammari, S. Bockel, N. Douir, G. Mevel, K. Diop, S. Corbin, F. Hubert, G. Brusadin, M. Merad, A. Laville, K. Ka, A. Bossi, S. Rivera, C. Chargari, E. Deutsch

Radiotherapy, Gustave Roussy Cancer Campus, Villejuif, France

Background: The coronavirus disease (COVID-19) pandemic has caused 180,000 confirmed cases in France with more than 28, 000 deaths as of May 19. A large part of COVID-19 patients seem asymptomatic and cancer patients may be more vulnerable. We evaluated a screening strategy combining chest computed tomography (CT) and PCR for patients treated with radiotherapy (RT).

Methods: A screening strategy was organized from March 18, in our RT department. An inspiratory breath hold chest acquisition was proposed during the CT simulation for RT. Images was reviewed by a radiologist according to the CO-RADS classification. A nasal swab with a polymerase chain reaction (PCR) assay was proposed by the radiation oncologist in case of evocative imaging or clinical context. For patients who were already undergoing RT at this time, a PCR was proposed in case of evocative symptoms and before concomitant chemotherapy.

Results: From March 18 to May 1, 2020, 507 CT simulation were performed for 449 patients, including 445 chest acquisition. 237 of the chest CT (53%) showed lung abnormalities, of which 34 (8%) were COVID-19 compatible (CO-RADS $\geq$ 3). 102 patients were tested by PCR after the chest CT. 24 of the 449 (5.3%) patients were considered as COVID-19 patients: 19 had positive PCR, and five were considered positive on the basis of imaging despite PCR-negative PCR. Four of the patients (17%) were diagnosed during RT: 3 on routine screening before chemoradiotherapy, and one on symptoms. Four patients needed several PCR for the diagnosis of COVID-19 with six confirmed false negative PCR (Sensitivity (Se)= 76 % (19/25)). Three PCR positive patients had no evocative lung images (Se = 84%). During this period, an additional 169 patients whose CT simulation was prior to March 18, were also undergoing RT. Among them, six patients (3.6%) were diagnosed with COVID-19 by PCR during RT, performed for symptoms in 4 cases and on screening for the other 2. Of the 30 COVID-19 patients, only 8 (27%) had symptoms at the time of diagnosis. Twelve patients (40%) reported no symptoms and benefited from screening.

Conclusions: This study confirms the high proportion of asymptomatic patients with COVID-19 and suggests the value of screening by CT and PCR during COVID-19 pandemics.

Legal entity responsible for the study: The authors.

Funding: Has not received any funding.

Disclosure: R. Sun: Travel/Accommodation/Expenses: AstraZeneca. E. Deutsch: Advisory/Consultancy: Roche, BMS, Boehringer, Astrazeneca, Lilly Amgen and Merck-Serono. All other authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.08.1740

1676MO Prevalence and clinical impact of asymptomatic or mildly symptomatic SARSCoV-2 infection among actively treated cancer patients during COVID-19 pandemic in Italy

A. Zambelli[1], V. Fotia[2], T. Bosetti[2], G. Negrini[3], A. di Croce[2], C. Moro[2], P.L. Poletti[2], A.C. Bettini[4], E. Arnoldi[4], C. Messina[2], B. Merelli[4], A.P. Callegaro[5], L. Chiudinelli[6], S. Mosconi[7], C. Tondini[2]

[1]Oncologia, Azienda Ospedaliera Papa Giovanni XXIII, Bergamo, Italy; [2]Oncology, ASST Papa Giovanni XXIII, Bergamo, Italy; [3]Medical Oncology, Azienda Ospedaliera Papa Giovanni XXIII, Bergamo, Italy; [4]Oncology, Azienda Ospedaliera Papa Giovanni XXIII, Bergamo, Italy; [5]Microbiology, ASST Papa Giovanni XXIII, Bergamo, Italy; [6]Interdepartmental Centre for Health Technology, University of Pavia, Pavia, Italy; [7]Oncology and Ematology department, Azienda Ospedaliera Papa Giovanni XXIII, Bergamo, Italy

Background: The European SARS-CoV-2 pandemic had its first epicentre in Italy, particularly in the area of Bergamo. In spite of a significant mortality rate, in the majority of cases the spectrum of COVID-19 ranges from asymptomatic to mildly symptomatic infection. No information is available on the prevalence and clinical impact of asymptomatic or mildly symptomatic SARS-CoV-2 infection among actively treated cancer patients during pandemic.

Methods: From April 1st, 2020 to the end of the month, 560 consecutive and unselected patients, scheduled for anticancer treatment at our facility and without clinical suspicious of COVID-19, were evaluated and tested for SARS-CoV-2. We implemented a two-step diagnostics, including a rapid serological immunoassay for anti-SARS-CoV-2 IgG/IgM and a pharyngeal swab RT-PCR assay in case of IgM seropositivity.

Results: In 560 patients, 172 (31%) resulted positive for SARS-CoV-2 IgM/IgG antibodies, regardless of type of cancer, stage and treatment. All IgM-seropositives were then tested with RT-PCR pharyngeal swabs and 55/146 (38%) proved to be SARS-CoV-2 carriers, with slightly difference b/w mildly symptomatic *vs.* asymptomatic patients (38 *vs.* 17). Therefore, the two-step procedure allowed the identification of 55 (10%) silent carriers in the whole study population and magnified the number needed to test (NNT) with the pharyngeal swab RT-PCR assay to detect a silent virus carrier (NNT: 2.6 *vs.* 10, with or without serological selection). At a very early follow up (8 wks), in 114 SARS-CoV-2-seropostive/RT-PCR-negative patients, who continued their anticancer therapies, none but one developed a symptomatic COVID-19 illness.

Conclusions: Among cancer patients, the two-step diagnostics strategy with serology followed by pharyngeal swab for asymptomatic or mildly symptomatic SARS-CoV-2 infection is feasible and effective and can help selecting cancer patients on treatment who might be silent carriers of the virus. The early safety outcome of patients previously exposed to SARS-CoV-2 supports the recommendation to continue active treatment, at least in the case of negative RT-PCR test.

Legal entity responsible for the study: The authors.

Funding: Has not received any funding.

Disclosure: All authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.08.1741

1677MO COVID-19 mortality in hospitalized cancer patients is not significantly affected by chemotherapy or other anti-cancer treatments

L. Lee[1], T. Starkey[1], J-B. Cazier[1], R. Kerr[2], G. Middleton[3]

[1]Institute of Cancer and Genomic Sciences, University of Birmingham, Birmingham, UK; [2]Department of Oncology, Churchill Hospital University of Oxford, Oxford, UK; [3]Institute of Cancer and Genomic Sciences, University of Birmingham, Birmingham, UK

Background: Individuals with cancer, particularly those who are receiving systemic anti-cancer treatments, have been postulated to be at increased risk of mortality from SARS-CoV-2 related coronavirus disease (COVID-19). This conjecture has considerable impact on the treatment of cancer patients and large, multi-centre data to support this assumption is lacking due to the contingencies of the pandemic.