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.

The rate of seroconversion 15 days after documented SARS-COV2 on RT-PCR was therefore significantly lower in cancer patients versus HCWs (30% versus 71%, $P = 0.04$). Importantly, six of the seven serodiagnostic-negative cancer patients had received cytotoxic therapy or major surgical intervention in the previous 4 weeks, compared with none of the five remaining patients ($P = 0.003$). None of these patients died.

In this series, 5 of 85 (5.9%) and 13 of 244 (5.4%) cancer patients and HCWs, respectively, had detectable Ab against COVID-19. However, cancer patients had a significantly lower detection rate of SARS-COV2 Ab 15 days or later after symptoms and RT-PCR+ testing. Anti-SARS-COV2 Ab were more often undetectable in patients receiving cancer treatments in the month before testing. Additional studies will be needed to confirm whether immune response to the virus is influenced by recent cancer treatments.

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Available online 1 May 2020

https://doi.org/10.1016/j.annonc.2020.04.475

FUNDING

This work was supported by NetSARC (INCA and DGOS) and RREPS (INCA and DGOS), RESOS (INCA and DGOS) and LYRICAN [grant number INCA-DGOS-INSERM 12563], Association DAM's, Eurosarc [grant number FP7-278742], la Fondation ARC, Infosarcome, InterSARC (INCA), LabEx DEvweCAN [grant number ANR-10-LABX 0061], PIA Institut Convergence Francois Rabelais PLAsCAN [grant number PLASCAN, 17-CONV-0002], Ligue de L'Ain contre le Cancer, La Ligue contre le Cancer, EURACAN [grant number EC 739521].

DISCLOSURE

The authors have declared no conflicts of interest.

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Do patients with cancer have a poorer prognosis of COVID-19? An experience in New York City

The outbreak of coronavirus disease 2019 (COVID-19) emerged in late 2019 in Wuhan, China, and has been spreading rapidly. As the infection has become widespread, concern for the influence of COVID-19 on patients with cancer has grown. Zhang et al.[1] reported a retrospective case study of 28 COVID-19-infected cancer patients with an astonishingly high mortality rate (28.6%). However, as Oh[2] pointed out, the result cannot be applied to other countries with different cancer epidemiology and practice. We herein sought to determine whether patients with cancer in the USA have a poorer prognosis of COVID-19 by analyzing the electronic medical records of Mount Sinai Health System (MSHS) in New York City.

We analyzed the electronic medical records (EMR) of MSHS from 1 March 2020 to 6 April 2020, using Epic SlicerDicer software, Verona, WI. We extracted data (sex, age, comorbidities, intubation, and mortality status as of 8 April) from patients who were positive for the COVID-19 RT-PCR test during this period. MSHS waived Institutional Review Board approval since this research used only deidentified, aggregate-level data.

A total of 5688 patients had COVID-19, and there were 334 patients (6%) with cancer among them (57, 56, 23, 18, and 16 patients with breast, prostate, lung, urothelial, and colon cancer, respectively). Without adjusting for age groups, patients with cancer were intubated significantly more frequently [relative risk, RR (95% confidence interval, CI); 1.89 (1.37—2.61)], but the rate of death was not significantly different. By stratifying patients by age groups, we detected a significantly increased risk of intubation in patients with cancer aged 66—80 years [RR (95% CI); 1.76 (1.15—2.70)]. No significant difference in intubation risk was found in other age groups. Additionally, patients younger than 50 years with cancer had a significantly higher mortality rate [RR (95% CI); 5.01 (1.55—16.2)]. However, the mortality rates of COVID-19 in cancer patients were lower than those in patients without cancer in age groups older than 50 years, though they were not statistically significant (Table 1).

Cytokine-associated lung injury is a potential etiology in severe cases of COVID-19.[3] Patients with cancer have impaired immune systems, which may decrease the frequency of overwhelming lung inflammation, contributing to these patients' non-inferior mortality rates.[4,5] Nevertheless, in young populations, whose mortality rate from COVID-19 is very low in general, baseline fragility in cancer patients may lead to a relatively higher rate of deaths.

Table 1. Relative risk of intubation or death in patients with or without cancer stratified by age groups

Age (years)	Intubation (event/total)		Relative risk (95% CI)	Death (event/total)		Relative risk (95% CI)
	With cancer	Without cancer		With cancer	Without cancer	
All	37/334	314/5354	***1.89 (1.37–2.61)***	37/334	518/5354	1.15 (0.84–1.57)
≤50	2/53	52/2035	1.48 (0.37–5.90)	3/53	23/2035	***5.01 (1.55–16.2)***
51–65	8/84	113/1557	1.31 (0.66–2.60)	4/84	117/1557	0.63 (0.24–1.68)
66–80	22/143	104/1191	***1.76 (1.15–2.70)***	15/143	173/1191	0.72 (0.44–1.19)
≥81	5/54	45/571	1.17 (0.49–2.83)	15/54	168/571	0.94 (0.60–1.48)

The numbers of italics and bold are with statistical significance (P value <0.05).

The unclear causation between COVID-19 and intubation or death is a limitation in this aggregate-level data analysis. Additionally, the heterogeneity of cancer types and varying stages of the disease may obscure the rationale of our findings. However, this is the first report on the prognosis of COVID-19 patients with cancer in the USA. The relatively large number of patients in the study allowed for the adjustment of age, which is one of the strongest prognostic factors. Further study based on the individual patients' data is warranted for a better understanding of the risk of COVID-19 in cancer patients.

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Available online 21 April 2020

https://doi.org/10.1016/j.annonc.2020.04.006

ACKNOWLEDGEMENTS

We wish to thank the timely help given by Satoshi Miyashita, MD at Mount Sinai Beth Israel in organizing the study group.

FUNDING

None.

DISCLOSURE

All authors report no conflicts of interest.

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Germline-somatic fluidity in guiding patient care

In this novel and important work, the authors attempt to most closely approximate the true germline sequence using different combinations of control tissue, paired with tumour tissue.[1] This was done to accurately determine germline variants, thus guiding clinical care. The model applied in this study accounts for the reality of blood being far more imperfect a surrogate for the germline than currently thought. This is due to its representing only one germ cell layer, frequent clonal expansions, and decreased leukocyte survival in the face of different genetic aberrations, thereby underrepresenting certain germline or mosaic variants.[2] The study's approach of using multiple different tissue types and looking for similarities is logical; however, the choice of tissues, driven by availability, introduces bias, with thyroid tumour tested twice and lymphoid tissue four times. Additionally, performing whole exome sequencing on tumours is less sensitive than targeted panels due to artifactual noise. In order to most closely approximate what is germline, endodermal, ectodermal, and mesodermal tissue should be compared, without the need to look at parental sequence, thereby accounting for the multitude of mutations in parental germ cells and only neglecting post-zygotic mutations prior to trilaminar disk formation.[3] Additionally, this study disregards revertant mosaicism, which is known to occur, and is at times a necessary feature of disease.[4]

The authors state that the true germline sequence can be most closely approximated through sequencing multiple non-tumorous tissues, and this determination can alter patient care, mitigating unnecessary action and resource utilization. It is our assertion that *even if* the true germline sequence can be determined, the binary mindset of germline-versus-somatic with ascribed clinical significance is an oversimplification that can result in improper patient treatment. Each result should be contextualized to patient care. In the cancer predisposition setting, this manifests on