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May to December 2021. We described the molecular profile of the tumor samples and also the characteristics of these patients. Results: We analyzed data from 53 patients, and about 55% of them were male. Their median age was 71 years old. Smokers or former smokers accounted for 43%. Programmed cell death ligand 1 (PD-L1) expression was analyzed by TPS (tumor proportion score); it was negative (<1%) in 51% of the cases and only 11% had a high expression (≥50%). At the moment of diagnosis, 54% of the patients were metastatic. The most common mutation was TP53, detected in 54% of tumor samples. The most frequent druggable drive mutations were in EGFR, ERBB2, ALK and ROS1, found respectively in 38%, 9%, 9% and 5% of the patients. TP53 was also the most common comutated gene, found in 45% patients with other mutations. TP53 alterations were observed most commonly in association with EGFR mutations. Tumor mutational burden (TMB) analysis was available in 86% of the cases; 41% of all patients had a low TMB (1-5 mutations/Mb) and only 5% had a high TMB (≥ 20 mutations/Mb). Conclusions: this analysis showed that patients of our service had similar molecular tumor profile as previously reported in other studies: EGFR alteration as one of the main drive mutations, TP53 alterations as being the most common comutated gene, and most of the patients with low TMB. Also, our data about PD-L1 expression are in agreement with the results of a brazilian study previously published. Knowing the molecular tumor profile of the patients with NSCLC is essential, and more studies are necessary in this poor region of Brazil, to better understand this population genomic profile, allowing physicians to individualize the treatment and offer the best option for each case. Contributing to a faster diagnosis, in our service the NGS is performed as a reflex molecular testing requested by our pathologists, after a diagnosis of squamous cell carcinoma in non-smokers or adenocarcinoma. Keywords: genomic profile, non-small cell lung cancer, NGS

Introduction: New York City was the first place in the US to record a COVID-19 case on March 1, 2020, and soon became the epicenter of the pandemic. Because of the large number of hospitalized patients, Governor Cuomo imposed a halt on all elective care from March 22 to June 8, 2020. Such action resulted in delayed cancer screening rates, care and treatment. However, no study has quantified the effect of the “pause” on cancer stage at diagnosis, one of the best indicators of cancer prognosis. We analyze here data from the Mount Sinai Health System cancer registry; we chose lung cancer as an example of a condition where early diagnosis can dramatically modify survival. Methods: Lung cancer cases diagnosed between January 1, 2018 and February 28, 2021 (n=1884) at the Mount Sinai Health System were identified from Mount Sinai’s cancer registry, based on ICD-10 codes of C34.x. Only analytic cases (00-22) were included, based on Commission on Cancer guidelines. For multi-tumor or multi-hospital cases, unique patients were identified by selecting the earliest date of diagnosis. The ratio of the number of monthly cases in 2020-2021 over the average number of monthly cases in 2018 and 2019 was calculated. The percent of monthly diagnoses with early (0/I/II), late (III/IV) and unknown stage over the total number of monthly diagnoses was examined and was compared to the average percent in 2018 and 2019 from the same month. Results: The number of diagnoses sharply dropped in March 2020, reaching a minimum in April (78% lower than pre-pandemic averages), and returned to near pre-pandemic levels by July 2020, began to decline again in January and February 2021 (35% lower than pre-pandemic averages) (Figure 1a). Stages 0/I/II dropped to 21.9% of total in May 2020, while stage III/IV hit 75% in April 2020. Early stage diagnoses dropped again to 23.5% of total, while late stages increased to 64.7% of total in February 2021 (Figure 1b). The percent of stage III/IV diagnoses in April of 2020 was 1.79 times greater than the pre-pandemic average, the percent of stage 0/I/II diagnoses was 50% lower. The percent of stage 0/I/II cases increased between August 2020 and January 2021, but in February 2021 it was 50% lower than pre-pandemic levels, and the percent of stage III/IV diagnoses was 1.3 times greater than pre-pandemic levels (Figure 1c). Conclusions: This descriptive analysis suggests an immediate negative impact on lung cancer diagnoses of COVID-19 restrictions, which affected screening, early detection, and drastically reduced any patient’s contact with the health system that would have prompted an early lung cancer diagnosis. The increase in late stage diagnoses during pandemic surges may reflect the fact that only sick patients with symptoms, and acute events that require immediate care were seeking hospital attention. The data suggests that we will likely observe an increase in lung cancer mortality in the next few months and years, as consequence of stage shift at diagnosis associated with the COVID-19 pandemic. Keywords: Lung cancer, Covid-19, Stage shift

Introduction: Lung cancer is associated with rising disease burden, most in advanced stages with brain as the predominant metastatic site. Patients with EGFR mutations are more susceptible to develop brain metastasis (BM) than EGFRwt. BM predicts poor prognosis often in advanced stages with brain as the predominant metastatic site. Lung cancer is associated with rising disease burden, most in advanced stages with brain as the predominant metastatic site. Patients with EGFR mutations are more susceptible to develop brain metastasis (BM) than EGFRwt. BM predicts poor prognosis often leading to changes in treatment. We aimed to understand this clinical context that requires deeper scientific investigation. Methods: BRAINMETS was a multicentric, cross-sectional, interventional study to estimate the presence of BM in NSCLC patients (stage III unresectable or stage IV) in EGFRm NSCLC Patients at the time of diagnosis. Patients with previous primary brain tumors or other malignancies and prior systemic anti-cancer treatment were excluded. MRI assessment was performed within 7 days after inclusion, except those with previous MRI or diagnosis of BM with CT-scan. Descriptive analysis were conducted with results reported as frequencies and medians. Results: A total of 73 patients were enrolled. Demographics and clinical characteristics of overall population and subgroups according to BM are presented in Figure 1 and Table 1, respectively. Brain imaging data at first visit was available for 58.9% (n=43) patients (MRL 67.4%; CT