GENE PROFILING OF LUNG CANCER AMONG NON- SMALL CELL LUNG CANCER PATIENTS IN ALEXANDRIA, EGYPT.

Waleed Arafat, Abbas Omar, Suzan Mohamed Helal,* Sherif Farouk EL Zawawy,** Evalyne Nyakerario Obeya

Department of Clinical Oncology and Nuclear Medicine, Pathology,* Oncology and Nuclear Medicine, ** Faculty of Medicine, University of Alexandria

INTRODUCTION

Lung cancer is among the most common cancers worldwide. Data from the International Agency for Research on Cancer indicate that it is the second most common cancer worldwide with an incidence of 2,206,771 cases in 2020 after breast cancer. It is the most common cause of cancer related mortality with estimated 1.8 million lung cancer related deaths in 2020 according to the WHO. Over time, various oncogenic driver mutations have been discovered in non-small cell lung cancer. This has made it possible to categorize this disease into therapeutically useful molecular subgroups, leading to the creation of target therapies that have resulted in better clinical outcomes. These genetic mutations include EGFR, ALK, ROS 1, KRAS, BRAF, HER 2, NTRK, MET and RET alterations. Studies have shown that the prevalence of some genetic markers may vary with race and ethnicity with majority of previous studies having been done on the Caucasian population.

AIM OF THE WORK

The primary objective of this study was to find out the genetic profiles of NSCLC patients seen in Alexandria University Clinical Oncology Department, Egypt. The secondary objectives were to evaluate the prevalence of various genetic profiles, to determine the clinicopathological characteristics as well as to estimate survival in these patients.

PATIENTS AND METHODS

The study was carried out in the Alexandria University Hospital, Clinical oncology department. It included 60 patients with NSCLC who presented to the oncology department between January 2020 and July 2022.The study population consisted of NSCLC patient cases of all stages whose medical records were complete and Formalin fixed, paraffin embedded (FFPE) tumor samples were available. Ethical approval was obtained from the Hospital's ethics department and informed consent was gotten from the patients. This was a retrospective study looking at genetic profiles of lung cancer patients who had presented to the hospital's oncology department between January 2020 to January 2021.

Data was also collected prospectively from patients seen between February 2021 and July 2022. Information on biodata, clinical and pathologic characteristics was retrieved from the patients' medical records and compiled using a checklist. This was followed by molecular analysison FFPE tumor samples using gene sequencing, real time PCR and immunohistochemistry.

RESULTS

There were 45 (75%) males and 15 (25%) females. The median age at presentation was 58.5 years, range (38-84) years. Majority 42 (70%) of the patients were smokers. The most common histology was adenocarcinoma present in 86.7% of the cases. Other histological subtypes included squamous cell carcinoma, 11.7%and large cell carcinoma, 1.7%. 90% of the patients had stage IV disease. Genetic mutations were detected in 17 (28.3%) samples. EGFR was the most frequently detected mutation in 10 (16.7 %) patients. Other mutations include ALK (3.33%) and ROS 1 (3.33%). BRAF, KRAS, NRAS and NTRK were each detected in 1.7% of the cases. PDL-1 was positive in 16.7 % of the patients.

Table: Distribution of the studied cases according to different genetic markers in detail (n = 60)

Gene	Samples tested		Wild		Mutant	
	No.	%	No.	%	No.	%
ALK	60	100.0	58	96.7	2	3.3
EGFR	55	91.6	45	75	10	16.7
BRAF	23	38.3	22	36.7	1	1.7
HER 2	23	38.3	23	38.3	0	0.0
KRAS	23	38.3	22	36.7	1	1.7
PIK3CA	23	38.3	23	38.3	0	0.0
NRAS	23	38.3	22	36.7	1	1.7
ROS 1	21	35.0	19	31.7	2	3.3
NTRK	19	31.7	17	28.3	1	1.7

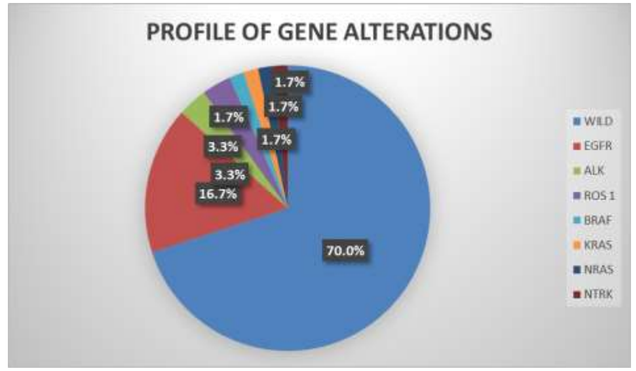

Figure: Distribution of the studied cases according to mutational status

CONCLUSION

The median age at diagnosis is 58.8 years and NSCLC is more common in males (75%) than females. Adenocarcinoma is the most common histologic subtype of present in 87.5% of the cases and majority of the patients presented with IV disease. The genetic profile was fairly similar to that of the Caucasian population, although with a lower incidence for KRAS mutations (EGFR 16.7%, ALK 3.3%, ROS-1 3.3%, BRAF 1.7%, KRAS 1.7% NRAS 1.7%, NTRK 1.7%).This study revealed rare co-existing EGFR/ROS 1 mutations and complex EGFR mutations present in 1.7% of the cases.