A Real-World Molecular Epidemiological Study of Non-Small-Cell Lung Cancer (NSCLC) Patients from Western India

Ashish Joshi1  Reshma Korgavkar2  Kshitij Joshi1  Vashishth Maniar1  Pritam Kalaskar1  Pradip Kendre1  Udip Dilip Maheshwari1  Chandrashekhar Pethe1  Smith Sheth1  Sonal Dhande1

1 Department of Oncology and Hematology, Mumbai Oncocare Center, Borivali and Vile Parle, Mumbai, Maharashtra, India
2 Department of Research and Clinical Trials, Mumbai Oncocare Center, Borivali and Vile Parle, Mumbai, Maharashtra, India

South Asian J Cancer

Abstract

Background The molecular characterization of advanced non-small-cell lung cancer (NSCLC) has unveiled genomic alterations such as EGFR gene mutations, KRAS gene mutations, ROS1 gene rearrangements, EML4-ALK rearrangements, and altered MET signaling. The objective of this molecular epidemiological study was to report the clinical, pathological, and molecular profile of NSCLC patients from western India.

Patients and Methods This real-world study of NSCLC patients was performed at a chemotherapy day-care center in western India. The clinical, pathological, and molecular data were collected from the patient’s medical records after obtaining the Ethics Committee permission for the study. The study was conducted according to the ethical principles stated in the latest version of Helsinki Declaration, and the applicable guidelines for good clinical practice.

Results A total of 182 (58.7%) men and 128 (41.3%) women with a median age of 63 years (range: 22–93 years) were included in the study. Of the total 310 patients, 195 (62.9%) were nonsmokers whereas 81 (26.1%) had a past history of smoking. EGFR, EML4-ALK Fusion Gene, KRAS, ROS1 gene rearrangement, and PD-L1 were positive in 42 (22.3%), 12 (9%), 2 (28.6%), 3 (12.5%), and 3 (25%) patients, respectively. One patient had concurrent EGFR mutation along with ROS1 gene rearrangement.

Conclusions Oncogenic driver mutations are present in Indian NSCLC patients. Molecular testing should be performed for all patients of advanced NSCLC to identify those that can benefit from newer generation of targeted or immunotherapies.

Keywords

► NSCLC
► KRAS
► EGFR
► EML4-ALK
► ROS1
► PD-L1

How to cite this article: Joshi A, Korgavkar R, Joshi K, et al. A Real-World Molecular Epidemiological Study of Non-Small-Cell Lung Cancer (NSCLC) Patients from Western India South Asian J Cancer 2022;00(00):00–00.

© 2023. MedIntel Services Pvt Ltd. All rights reserved.
This is an open access article published by Thieme under the terms of the Creative Commons Attribution-NonDerivative-NonCommercial-License, permitting copying and reproduction so long as the original work is given appropriate credit. Contents may not be used for commercial purposes, or adapted, remixed, transformed or built upon. (https://creativecommons.org/licenses/by-nc-nd/4.0/)
Introduction

The purpose of this molecular epidemiological study is to report the clinicopathological and molecular profile of non-small-cell lung cancer (NSCLC) patients in community oncology setup from western India.

Materials and Methods

This real-world study of NSCLC patients was performed at the Mumbai Oncocare Center, a chemotherapy day-care center in western India. The clinical, pathological, and molecular data were collected from the patient’s medical records after obtaining the Ethics Committee permission (reference number NSCLC/MOC/2K19RS05) for the study. The study was conducted according to the ethical principles stated in the latest version of Helsinki Declaration, and the applicable guidelines for good clinical practice.

Formalin-fixed, paraffin-embedded tissue blocks were used for the mutation analysis. EGFR and KRAS mutations were tested using polymerase chain reaction (PCR)/Sanger sequencing method. Deoxyribonucleic acid (DNA) was extracted using a commercially available blood DNA extraction kit, following the manufacturer’s instructions. A nested PCR protocol was followed using gene-specific primers to amplify the desired region of the EGFR gene that is required to be sequenced. Four PCR amplicons, each representing Exons 18, 19, 20, and 21, were generated. A similar protocol was followed to amplify the target region of the KRAS gene that is represented by a 214 bp PCR amplicon. The PCR products were purified using an exonuclease and an alkaline phosphatase enzyme and sequenced using the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Thermofisher Scientific). The sequenced products were purified by ethanol precipitation, air dried, and suspended in water. Sequence analysis was performed on an Applied Biosystems genetic analyzer as per the standard protocol provided by the manufacturer; EGFR mutations (Exon 18[G719A/C/S]; Exon 19 Deletions; Exon 20 [T790M]; Exon 21 [L858R (CTG to CGG) and L861Q (CTG to CAG)]) and KRAS mutations (12 Gly12Asp [GGT > GAT]; 12 Gly12Ala [GGT > GCT]; 12 Gly12Val [GGT > GTT]; 12 Gly12Ser [GGT > AGT]; 12 Gly12Arg [GGT > CTG]; 12 Gly12Cys [GGT > TGT]; 13 Gly13Asp [GGC > GAC]) were then detected using a standard wild-type transcript ID, respectively, as reference to detect the presence or absence of the mutations. ALK gene rearrangement was detected using the Vysis ALK Break Apart Rearrangement Probe Kit (Abbott Molecular, Abbott Park, Illinois, United States). Cases were considered positive for ALK rearrangement when >15% of a minimum of 100 tumor cells showed split signals or single red signals. ROS1 fluorescence in situ hybridization assay was performed using a dual-color break-apart probe (Zytolight Spec ROS1; ZytoVision, Germany). For PD-L1 immunohistochemistry (IHC) assay, sections of 4 µm thickness were stained with anti-PD-L1 (SP263) rabbit monoclonal primary antibody and a matched rabbit immunoglobulin G-negative control with an OptiView DAB IHC Detection Kit on the Ventana BenchMark ULTRA automated staining platform. For the SP142 assay, sections were stained with anti-PD-L1 (SP142) rabbit monoclonal primary antibody and a matched rabbit immunoglobulin G-negative control with an OptiView Amplification Kit, on the Ventana BenchMark ULTRA automated staining platform.

Categorical variables were analyzed using Pearson chi-squared or Fisher’s exact test, whichever was appropriate, and presented in the form of number and percentage. Logistic regression was performed to compare the study groups. The width of the resultant confidence intervals (CIs) for parameters to be estimated was constructed with a significance level of 0.05, that is, a 95% CI. Furthermore, multiple logistic regression was performed to check the significance of independent variables. Statistical analysis was performed using SAS version 9.4 (SAS Institute Inc. Mumbai Oncocare Centre, 2nd Floor, Majithia Apartments, God’s Gift Premises, Co-op. Society Ltd, Swami Vivekananda Rd, above Irla, Vile Parle, Mumbai, Maharashtra 400056).

Results

A total of 310 NSCLC patients were included in the study. There were 182 (58.7%) men and 128 (41.3%) women with a median age of 63 years (range: 22–93 years). Of the 310 patients, 81 (26.1%) were smokers whereas 195 (62.9%) were nonsmokers. Of the study population, 249 (80.3%) patients had adenocarcinoma whereas 48 (15.5%), 5 (1.6%), and 8 (2.6%) patients, respectively, had squamous cell carcinoma, adenosquamous carcinoma, and poorly differentiated carcinoma. Stage at presentation was III and IV in 25 (8.1%) and 285 (91.9%) patients, respectively. Performance status was 0, 1, 2, and 3 in 5 (1.6%), 82 (26.5%), 61 (19.7%), and 15 (4.8%) patients, respectively.

EGFR, EML4-ALK Fusion Gene, KRAS, ROS1 gene rearrangement, and PD-L1 were positive in 42 (22.3%), 12 (9%), 2 (28.6%), 3 (12.5%), and 3 (25%) patients, respectively. One patient had concurrent EGFR mutation along with ROS1 gene rearrangement.

The distributions of EGFR mutations, EML4-ALK Fusion Gene, ROS1 gene rearrangement, KRAS, and PD-L1 were studied with regard to individual variable of gender, age, tobacco chewing, smoking history, alcohol intake, histology stage, and performance status. EGFR mutations showed significant association with adenocarcinoma histology (p < 0.05) whereas EML4-ALK Fusion Gene showed significant association with age (p = 0.0025) and alcohol intake (p = 0.0057). ROS1 gene rearrangement showed significant association with tobacco chewing (p = 0.0047).

Discussion

The incidence of KRAS gene mutation in NSCLC has been reported in the range of 24% whereas the incidence of EGFR mutations has been reported in the range of 13%, 47%, and 51.8% across Caucasian, Asian, and Indian population, respectively. With an incidence of KRAS gene mutation of 28.6%, the results of our study are consistent with the previously published reports. The 22.3% incidence of EGFR mutations in our study is way below the previously published reports from India. The ALK gene
rearrangement incidence of 9% in our study confirms the findings of previously published reports. A higher rate of EGFR mutation and ALK gene rearrangement rate have been reported in females as compared with males along with a positive correlation with never smokers as compared with smokers in the previously published studies.\textsuperscript{2–5} The prevalence of ROS1 gene in NSCLC has been reported in the range of 0.9–2.6\%.\textsuperscript{6,7} Among Indian population, three independent studies by Suryavanshi et al,\textsuperscript{8} Joshi et al,\textsuperscript{9} and Mehta et al\textsuperscript{10} have reported ROS1-rearranged NSCLC in 2.9\%, 4.1\%, and 2.82\% patients, respectively. Contrary to the previous reports, the incidence of 12.5\% for the ROS1 gene rearrangement in our study is the highest reported incidence to date. The results of Express study in locally advanced or metastatic NSCLC showed a real-world prevalence of PD-L1 expression \(\geq 50\%\) and \(\geq 1\%\) in 50\% and 52\% patients, respectively.\textsuperscript{11} The 25\% incidence of PD-L1 expression in our study is way below the findings of Express study.

Our study demonstrated a positive correlation of EGFR mutation in adenocarcinoma histology group (20.21\%, \(p = 0.0102\)). Similarly, a positive correlation of EML4-ALK fusion gene was observed for the age group of 40–60 years (7.46\%, \(p = 0.0025\)) as well as teetotaller group (7.46\%, \(p = 0.0057\)). A positive correlation of ROS1 gene rearrangement was observed in tobacco chewing group although the same was equally distributed among tobacco users and nontobacco users. One case in the present study had concurrent EGFR mutation along with ROS1 gene rearrangement. This observation is consistent with two of the previously published reports.\textsuperscript{6,10} Although a greater number of females in our study had EGFR mutation and ROS1 gene rearrangements, the results were not statistically significant. Similarly, our study did not demonstrate a significant association of never smokers vis-à-vis EGFR mutation, EML4-ALK Fusion Gene, and ROS1 gene arrangements although the same has been reported in the literature.\textsuperscript{2–5,10}

**Conclusion**

Our study reports the clinical, pathological, and molecular profile of NSCLC patients at a chemotherapy day-care center in western India. The molecular characterization of advanced NSCLC has unveiled different genomic alterations that are paving the way for improved treatment outcomes as well as personalized treatment to the individual patient. Our study reassures the importance of molecular testing in the NSCLC with an aim to identify patients that can benefit from newer generation of targeted or immunotherapies.

**Ethical Statement**

The study was conducted according to the ethical principles stated in the latest version of Helsinki Declara-

**Source(s) of Support**

Nil.

**Declaration**

No research support was sought from any commercial agency related directly or indirectly to the subject of this article.

**Conflict of Interest**

The authors declare that they have no conflict of interest.

**References**