



Category: Cancer Genomics

Mutational profiling of KRAS and its association with non-small cell lung carcinoma in Indian Kashmiri population

Naseer Ue Din Shah¹, Md Niamat Ali^{1*}, Syed Mudassar² and Mosin Saleem Khan²

¹Cytogenetic and Molecular Biology Research Laboratory, Centre of Research for Development, University of Kashmir, Srinagar 190006, J&K, INDIA

²Department of Clinical Biochemistry, University of Kashmir, Srinagar 190006, J&K, INDIA

Presenting author: naseershah2009@gmail.com

Abstract

Lung cancer represents commonest cancer worldwide, with a high mortality rate as the disease becomes clinically apparent at advanced stages. The most common molecular alterations observed in NSCLC lie in the mutations of KRAS. These mutations occur in 15–30% of NSCLC and are more frequent in adenocarcinoma. We have screened prospectively all newly diagnosed patients with NSCLC (n=70) for the ability to be analysed for KRAS mutations. Seventy, blood samples of Non-small cell lung cancer were collected from Department of Hematology, Sheri-i- Kashmir Institute of Medical Sciences (SKIMS). Blood DNA was extracted from these cases. DNA sequencing was performed on all the samples for detection KRAS codon 12, 13 activating mutations. Mutation status was compared with patient clinicopathological characteristics. The prevalence of KRAS mutation rate in NSCLC in the Kashmiri population was 30%. The significant association was seen between KRAS gene mutation and histological types of lung cancer. The higher frequency was seen in adenocarcinoma (ADC) (28.84%) than squamous cell carcinoma (SCC) (6%). The difference was statistically significant (OR=0.81, 95% CI=0.257- 2.588, p < 0.01). Among the different stages, the higher frequency of KRAS (exon 2) mutation was reported in NSCLC patients in advanced stage (38.09%) than the early stages (17.85%). The difference was statistically significant (OR=0.353, 95% CI= 0.112- 1.116, p<0.05). A statistically significant difference was reported between smokers and non-smokers with respect to the KRAS (exon 2) mutation (OR= 4.899, 95%CI =1.273- 18.77, p < 0.01). The significantly higher frequency of this mutation was reported in NSCLC patients (29.16%) with metastasis (OR= 0.941 95% CI= 0.319-2.775, p < 0.03). KRAS (exon 2) mutation is a common molecular alteration in NSCLC and occurs most predominantly on codon 12, 13, characterizing 30% of the total mutations found in Kashmiri population. These mutations are significantly associated with clinicopathological characteristics of patients.

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