J Clin Cell Immunol 2014, 5:5
http://dx.doi.org/10.4172/2155-9899.S1.019

OMICS Group Conferences
Accelerating Scientific Discovery

3rd International Conference and Exhibition on
Clinical & Cellular Immunology
September 29-October 01, 2014 DoubleTree by Hilton Baltimore-BWI Airport, USA

Association of interleukin 1 β polymorphism with mRNA expression and risk of non small cell lung cancer

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Introduction: Interleukin-1beta (IL- 1β), a key proinflammatory cytokine encoded by the interleukin 1 beta gene, has been associated with chronic inflammation and plays an important role in lung inflammatory diseases including lung cancer. Elevated levels of Interleukin 1 proteins, in particular interleukin 1 beta greatly enhance the intensity of the inflammatory response.

Aim: To study the role of interleukin 1 beta -31 C>T and -511 T>C polymorphism in the pathogenesis of non small cell lung cancer (NSCLC).

Materials and Methods: 190 non small cell lung cancer patients and 200 healthy age, sex, smoking and dwelling matched controls were used for polymorphic analysis by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) followed by sequencing. Normal tissues of 48 histopathologically confirmed non small cell lung cancer patients were taken for mRNA expression analysis. Quantitation of interleukin 1 beta was carried out by quantitative real time PCR.

Result: The T/T genotype of Interleukin 1 beta-31 gene was significantly associated with increased risk of NSCLC [(P=0.001, OR-2.8 (95%CI 1.52-5.26)]. The interleukin I beta −511 T>C does not show any difference between the non small cell lung cancer and control group (P=0.3, OR-0.72 (95%CI 0.41-1.28). Quantitative analysis of mRNA showed significant association with interleukin 1 beta T allele as compared to the interleukin 1 beta -31C allele (p=0.006).

Conclusion: We conclude that lung cancer risk genotype interleukin 1 beta -31TT results in increased expression of Interleukin 1beta mRNA in lung cancer patients. Our data suggest that this genotype (IL1β -31TT) in the interleukin 1 beta regulatory region provide a microenvironment with elevated inflammatory stimuli and thus increasing the risk for lung cancer.

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