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

KIR Genotyping in the selected population in Andhra Pradesh, India

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Background: The population is not always homogeneous in relation to the representation and functioning of genes. Therefore, the presence of allogenicity is a universal phenomenon. The profound variability is noticed among the members of the human population with reference to the resistance against infections and late-on-set of diseases. In this line, a few sets of alleles which come under the domain of immune function namely KIRs (Killer Cell immunoglobulin-like receptor genes) and HLA-I have been chosen to report in the population of Puttaparthi (India).

Objectives: The genotyping of the population is the current ongoing focus of our team wherein the distribution of the following alleles has been taken up in the mixed ethnic groups of Puttaparthi as a prelude to earmark them as genotypic markers in future studies relating to susceptible diseases.

Methods: The PCR protocols for the identified immune related genes viz., KIR-2DL1, 2DL2, 2DL3, 2DL4, 2DL5, 3DL1, 3DL2, 3DL3, 3DS1, 2DS1, 2DS2, 2DS3, 2DS4, 2DS5, 2DP1, 3DP1; HLA- C1 and HLA- C2 have been standardized.

Results & Interpretation: In the present study, except KIR 2DL2, the other non-framework inhibitory KIR genes were represented at higher percentage and ranged from 57% to 80%in the chosen population which would suggest its higher survival adaptation. Interestingly, majority of activating KIR genes were least represented and varied between 5% to 32.5% which is also in compliance with the survival adaptation of the chosen population. The carrier gene frequencies of KIRs were compared with the other populations' viz., Chinese Mongolian, Chinese Han, Greek and Brazilian data. The expected heterozygosity of KIR alleles and their rank in gene diversity among the population of Puttaparthi were also discussed.

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Expression of Epstein-Barr virus (EBV)-encoded latent membrane protein 1(LMP-1) in patients with nasopharyngeal carcinoma (NPC) is associated with a worse clinical prognosis

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The Epstein-Barr virus (EBV)-encoded latent membrane protein 1 (LMP1) is a key effector of EBV-mediated B cell transformation. LMP1 displays oncogenic properties in fibroblasts, and induces a wide range of effects in B cells and a variety of growth-promoting effects in human epithelial cells. The constitutive activation of these signaling cascades explains LMP1's ability to induce morphological and phenotypic effects in cells. Taken as a whole, these findings demonstrate that LMP1 can induce profound effects in epithelial cells, many of which may account for its oncogenic properties. There is now strong evidence supporting a role of EBV encoded LMP-1 protein in the pathogenesis of nasopharyngeal carcinoma (NPC), but also, there are other molecular pathology variables which can predict clinical outcome in these patients. Accordingly, we aimed to systematically analyze LMP1 immunoexpression in patients with non-endemic NPC and do a correlation with clinicopathological features and patients survivals. Our data suggest that LMP1 expression could be correlated with a poorer clinical outcome and prognosis in patients with NPC. To our knowledge, this series is the first one published in non-endemic/non-white population of NPC; and supports the importance to explore the molecular signaling pathways to provide a substantial opportunity for identification of novel diagnostic and prognostic biomarkers that could improve individual treatment in patients with NPC.

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