

# Euro Health Care and Fitness Summit

September 01-03, 2015 Valencia, Spain

## Association of cytotoxic T-lymphocyte antigen-4 (CTLA4) gene variants with non-dermato malv vitiligo

Yaswanth Ala<sup>1</sup>, Raja Narasimha Rao<sup>2</sup> and Parveen Jahan<sup>3</sup>

<sup>1</sup>Osmania University, India

<sup>2</sup>South Central Railway Hospital, India

<sup>3</sup>Maulana Azad National Urdu University, India

**Background:** The cyto-toxic T lymphocyte antigen4 (CTLA4) is a negative regulator of T-cell function and encodes a surface molecule with inhibitory effects on activated T cells. Variation in CTLA4 gene has been genetically associated with a number of autoimmune diseases including vitiligo, an acquired pigmentary disorder resulting from loss of melanocytes.

**Aim:** The present study is aimed at investigating the role of functional polymorphisms of CTLA-4 gene (rs11571317C>T, rs231775A>G and rs5742909C>T) in susceptibility to vitiligo.

**Methods:** Genotyping was performed by PCR-RFLP and ARMS-PCR in a total of 410 subjects (200 vitiligo patients and 210 normal healthy controls). Data was subjected to appropriate statistics.

**Results:** The two polymorphisms rs11571317 and rs5742909 showed a significant association with vitiligo. The multifactor dimensionality reduction (MDR) analysis of CTLA-4 gene revealed a strong synergy between rs11571317 and rs231775. The two locus model (rs11571317 and rs5742909) and three locus model (rs11571317, rs231775 and rs5742909) was observed to be the best models (with cross validation 10/10) showing the two fold and three fold increased risk respectively towards vitiligo (OR: 2.0, 95% CI: 1.3-3.2 and OR: 3.3, 95%CI: 2.16-5.17respectively). By Multiple logistic regression analysis gender and rs231775 showed the significant variation ( $p < 0.05$ ). Haplotype blocks C-A-T and T-G-C conferred significant protection (OR: 0.42, 95% CI: 0.23-0.78,  $p = 0.005$  and OR: 0.48, 95% CI: 0.26-0.88,  $p = 0.018$  respectively) and C-G-C a two-fold increased risk towards vitiligo (OR: 1.72, 95% CI: 1.04-2.86,  $p = 0.036$ ).

**Conclusion:** Our findings suggest the role of CTLA-4 in the vitiligo pathogenesis and for the first time we report the association of rs11571317 and rs5742909 polymorphisms in relation to vitiligo.

### Biography

Yaswanth Ala has completed his Master's in Biotechnology from Osmania University and pursuing PhD in Genetics. He is a member of Indian Immunology Society and presented more than 10 papers in national and international conferences.

[yashwanthala@gmail.com](mailto:yashwanthala@gmail.com)

### Notes: