

3rd International Conference on **Genomics & Pharmacogenomics**

September 21-23, 2015 San Antonio, USA

Evidence of association of interleukin-23 receptor gene polymorphisms with Egyptian rheumatoid arthritis patients

Gehan Hamdy

Cairo University, Egypt

Background: The identification of additional genetic risk factor is an on-going process that will aid in the understanding of Rheumatoid Arthritis (RA) aetiology. A genome-wide association scan in Crohn's Disease (CD) highlighted the Interleukin-23 Receptor (IL23R) gene as a susceptibility factor. Since the IL-23/IL-17 pathway is known to associate with other autoimmune disease, including rheumatoid arthritis and systemic sclerosis, we hypothesized that IL23R could be a shared susceptibility gene. The rare allele of IL23R single nucleotide polymorphism (SNP) rs11209026 (Arg381Gln) confers strong protection against CD. Our aim was to analyze IL23R SNP (rs11209026, rs2201841, and rs10889677) and to detect its association with RA in Egyptian patients.

Methods: A group of Egyptian patients with RA (n=120) and apparently healthy persons as controls (n=120) was genotyped for rs11209026, rs2201841 and rs10889677 by real time/polymerase chain reaction (real-time/PCR) for the first SNP and restriction fragment length polymorphism/PCR (RFLP/ PCR) in the last two SNPs.

Results: Our data emphasise that the AA genotype of rs11209026 (Arg381Gln) was significantly associated with RA patients compared to the controls (p value=0.001). We did not find any significant association between either rs2201841 or rs10889677 and the development of rheumatoid arthritis (p value=1.000 & 0.562, respectively).

Conclusion: Our results suggest that IL23 receptor AA genotype variant of rs11209026 would contribute to RA aetiology; consequently, it might be a genetic marker for RA. We need to address the sub-group of patients who will benefit from the selective suppression of the IL23 signaling which would represent new perspectives toward a personalized therapy of RA patients by further studies.

Biography

Gehan Hamdy has completed here MBCh from Kasr El Ani Hospital, Cairo University, Egypt and Postdoctoral studies from same University. She is Assistant Professor of Internal Medicine. She has published more than 10 papers and 3 case reports in reputed journals.

gegehamdy@gmail.com

Ranomics: Eliminating variants of unknown significance (VUS) in genetic testing

Cathy Tie

Ranomics Inc., USA

In this evolving age of personalized health care, genetic testing companies are sequencing disease-associated genes in a fast and cost-effective fashion. This has given rise to multi-million dollar enterprises such as 23 and me, which specializes in determining disease-risk based on consumer DNA samples. However, the majority (>90%) of genetic variations that may increase disease-risk are rare and unique in nature and have not undergone rigorous scientific analysis, these variations are referred to as Variants of Unknown Significance (VUS). Paradoxically, this prevents personalized genetic testing companies from providing personalized insights into the health and disease risk of their consumers and additionally limits the number of diseases they can predict associated risks for. At Ranomics, we strive to overcome the barrier of VUS using high-throughput genetic techniques in model organisms. By exploiting our ability to test human gene function in the model organism *Saccharomyces cerevisiae* using gold-standard complementation techniques, we are systematically generating all possible genetic variations of conserved disease-associated genes and quantifying the functional implications of every genetic variation. The resulting database will be accessible to personalized genetic testing companies such that they can confidently reported on the functional implications and associated disease risk of the rare genetic variations identified in their consumers.

cathy@ranomics.com