Pediatric Rheumatology

BioMed Central

Oral presentation

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14.5 Rheumatoid Arthritis susceptibility loci; STAT4, TRAF1/C5 and 6q23 region, are also associated with Juvenile Idiopathic Arthritis

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from 15th Paediatric Rheumatology European Society (PreS) Congress
London, UK. 14–17 September 2008

Published: 15 September 2008

Pediatric Rheumatology 2008, **6**(Suppl 1):S32 doi:10.1186/1546-0096-6-S1-S32

This abstract is available from: http://www.ped-rheum.com/content/6/S1/S32

Background

Recent genome wide association studies (GWAS) of many complex diseases have successfully identified novel susceptibility loci. An emerging observation is that a number of loci are associated with more than one condition, particularly in the cases of autoimmune diseases.

In view of the shared pathology of adult inflammatory arthritis and juvenile idiopathic arthritis (JIA) we hypothesised that loci identified in GWAS of rheumatoid arthritis (RA) may also have a role in JIA.

Aims

To test whether markers at three recently identified RA susceptibility loci, STAT4, TRAF1/C5 and 6q23 region, are also associated with JIA.

Methods

Previously associated SNPs for each of the three regions (11 SNPs in total) were selected for investigation. Genotyping was performed using Sequenom MassArray. DNA was available for 855 UK Caucasian JIA cases and 3599 controls. Genotype frequencies were compared between cases and controls using the trend test implemented in PLINK.

Results

Strong evidence for association was seen for both STAT4 (strongest effect rs7574865 OR 1.24 95%CI 1.1–1.4, ptrend = 0.0008) and TRAF1/C5 (strongest effect rs2900180 OR 1.23 95%CI 1.1–1.38, ptrend = 0.0004). The 6q23 region showed weak evidence for association with JIA (rs6920220 OR 1. 17 95% CI 1.01–1.36, ptrend = 0.03). In all cases the associated allele was the same as for RA and the effect sizes were similar.

Conclusion

We have identified three novel JIA susceptibility loci. These findings are currently being validated in a North American JIA cohort. Fine mapping and functional studies will be required to elucidate how these polymorphisms contribute to disease.