

Poster presentation

The TRAF1/C5 region is a risk factor for polyarthritis in juvenile idiopathic arthritis

HM Albers*¹, FAS Kurreeman¹, JJ Houwing-Duistermaat¹, DMC Brinkman¹, SSM Kamphuis², HJ Girschick³, C Wouters⁴, MAJ van Rossum⁵, W Verduyn¹, REM Toes¹, TWJ Huizinga¹, MW Schilham¹ and R ten Cate¹

Address: ¹Leiden University Medical Center, Leiden, Netherlands, ²Erasmus Medical Center – Sophia Children's Hospital, Rotterdam, Netherlands, ³University of Wuerzburg, Wuerzburg, Germany, ⁴University Hospital Gasthuisberg, Leuven, Belgium and ⁵Emma Children's Hospital AMC, Amsterdam, Netherlands

* Corresponding author

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Background

Juvenile idiopathic arthritis (JIA) is a chronic disorder in which both genetic and environmental factors are involved. Recently we identified the *TRAF1/C5* region (located on chromosome 9q33-34) as a risk factor for rheumatoid arthritis (RA) ($p_{\text{combined}} = 1.4 \times 10^{-8}$) [1]. In the present study the association of the *TRAF1/C5* region with the susceptibility to JIA was investigated.

Methods

A case-control association study was performed in 338 Caucasian JIA patients and 511 healthy individuals. We genotyped SNP rs10818488 as a marker for the *TRAF1/C5* region.

Results

The A-allele was associated with the susceptibility to Rheumatoid Factor (RF) negative polyarthritis with an 11% increase in allele frequency (OR 1.54, 95% CI 1.09–2.18; $p = 0.012$). This association was stronger when combining subtypes with a polyarticular phenotype (OR 1.46, 95% CI 1.12–1.90; $p = 0.004$). In addition, we observed a trend towards an increase in A-allele frequency in patients with extended oligoarthritis versus persistent oligoarthritis (49% and 38% respectively); $p = 0.055$.

Conclusion

Apart from being a well replicated risk factor for RA, *TRAF1/C5* also appears to be a risk factor for the RF negative polyarthritis subtype of JIA and, more generally, seems to be associated with subtypes of JIA characterized by a polyarticular course.

References

1. Kurreeman FA, Padyukov L, Marques RB, Schrodi SJ, Seddighzadeh M, Stoeken-Rijsbergen G, Helm-van Mil AH van der, Allaart CF, Verduyn W, Houwing-Duistermaat J, et al.: **A candidate gene approach identifies the TRAF1/C5 region as a risk factor for rheumatoid arthritis.** *PLoS Med* 2007, **4**:e278.