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Genomic and epigenomic analysis in South Asian RA [Abstract]

PLEASE CITE THE PUBLISHED VERSION

<https://doi.org/10.1093/rheumatology/key075.155>

PUBLISHER

© the Author. Published by OUP on behalf of the British Society for Rheumatology

VERSION

AM (Accepted Manuscript)

PUBLISHER STATEMENT

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REPOSITORY RECORD

Mastana, Sarabjit S.. 2019. "Genomic and Epigenomic Analysis in South Asian RA [abstract]". figshare.
<https://hdl.handle.net/2134/33676>.

Genomic and epigenomic analysis in South Asian RA

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Accepted on 23 March 2018

Rheumatoid arthritis (RA) is a chronic musculoskeletal disease of unknown aetiology. RA is an inflammatory autoimmune disease affecting around 1% of the world's population. A mixture of genetic and environmental factors like gender, smoking, ethnicity and socioeconomic status contribute to RA pathology with heritability estimated at 60%. The human leukocyte antigen (HLA) region accounts for around 30% of genetic variance in RA. However, other areas of the genome, in particular inflammatory pathways have become the focus of research. RA is a complex polygenic and multifactorial disease and has not been analysed comprehensively among South Asians. In this presentation we present our results of genomic (individual loci and polygenic risk scores) and epigenomic analysis on a cohort of South Asian severe RA patients from the East Midlands and contextualise the similarities and differences with reference to other ethnic groups. The use of genetic results for personalised medicine and treatment of RA would be discussed.

SIG session at the British Society for Rheumatology Annual Conference 2018, Tuesday 1 to Thursday 3 May at the ACC in Liverpool, UK.