Role of genetics studied in rheumatoid arthritis development

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Genetic predisposition is increased across patients with pre-rheumatoid

arthritis (RA), according to a study published online Aug. 12 in *Arthritis & Rheumatology*.

Marc P. Maurits, from the Leiden University Medical Center in the Netherlands, and colleagues examined whether established genetic predictors for RA differentiate healthy controls (HC), clinically suspect arthralgia (CSA), and RA (1,015, 479, and 1,146 participants, respectively, in the Dutch population). CSA patients were assessed for conversion to inflammatory arthritis for a period of two years and were classified as converter (CSAc) or nonconverter (CSAnc; 84 and 395, respectively).

The researchers found that compared with both CSA and CSAc, the polygenic risk score (PRS) was increased in RA (mean, 1.31 versus 1.07 and 1.12, respectively). In anticitrullinated protein antibody (ACPA)-negative participants, the distribution of PRS differed strongly when comparing CSA, especially CSAc, with RA (1.05 and 0.97, respectively, versus 1.20), while CSA differed from both healthy controls and RA in ACPA-positive (1.25 versus 1.05 and 1.41 percent, respectively). Human leukocyte antigen-shared epitope (HLA-SE) was more prevalent in RA than CSA (0.64 versus 0.45). The prevalence of HLA-SE differed more strongly within ACPA-positive participants: 0.43, 0.48, 0.59, 0.66, and 0.79 for HC, CSAnc, CSA, CSAc, and RA, respectively.

"We observe that the prevalence of two genetic markers (primarily HLA-SE and secondarily a PRS) differs between healthy controls, CSA patients, and RA patients, especially within the ACPA-positive strata of these populations," the authors write. "Our results contribute to our growing understanding of the etiology of RA."

More information: Marc P. Maurits et al, The Role of Genetics in Clinically Suspect Arthralgia and Rheumatoid Arthritis Development: a

Large Cross-Sectional Study, *Arthritis & Rheumatology* (2022). DOI: 10.1002/art.42323