Abstract

**OBJECTIVE:** Large-scale genetic association studies have identified >20 rheumatoid arthritis (RA) risk alleles among individuals of European ancestry. The influence of these risk alleles has not been comprehensively studied in African Americans. We therefore sought to examine whether these validated RA risk alleles are associated with RA risk in an African American population.

**METHODS:** Twenty-seven candidate single-nucleotide polymorphisms (SNPs) were genotyped in 556 autoantibody-positive African Americans with RA and 791 healthy African American control subjects. Odds ratios (ORs) and 95% confidence intervals (95% CIs) for each SNP were compared with previously published ORs for RA patients of European ancestry. We then calculated a composite genetic risk score (GRS) for each individual based on the sum of all risk alleles.

**RESULTS:** Overlap of the ORs and 95% CIs between the European and African American populations was observed for 24 of the 27 candidate SNPs. Conversely, 3 of the 27 SNPs...
Most common single-nucleotide polymorphisms associated with rheumatoid arthritis in persons of European ancestry confer risk of rheumatoid arthritis in African Americans.

(CCR6 rs3093023, TAGAP rs394581, and TNFAIP3 rs6920220) demonstrated ORs in the opposite direction from those reported for RA patients of European ancestry. The GRseq analysis indicated a small but highly significant probability that African American patients relative to control subjects were enriched for the risk alleles validated in European RA patients (P = 0.00005).

**CONCLUSION:** The majority of RA risk alleles previously validated for RA patients of European ancestry showed similar ORs in our population of African Americans with RA. Furthermore, the aggregate GRseq supports the hypothesis that these SNPs are risk alleles for RA in the African American population. Future large-scale genetic studies are needed to validate these risk alleles and identify novel RA risk alleles in African Americans.

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