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Original Communications

Crohn's Disease in Caucasians and African Americans, as Defined by Clinical Predictors and Single Nucleotide Polymorphisms

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Objectives:

To compare three aspects of Crohn's disease (CD) between African Americans and Caucasians: (1) demographic data and environmental factors affecting CD susceptibility, (2) disease presentation and clinical course, and (3) genetic susceptibility via the use of single nucleotide polymorphism (SNP) data for inflammatory bowel disease (IBD) susceptibility loci.

Methods:

Clinical data and peripheral blood were obtained from 1032 patients (554 CD patients and 478 controls) derived from a clinically well-defined university-based medical and surgical digestive disease practice and included those who were diagnosed with IBD. Genomic DNA was extracted and polymerase chain reaction (PCR) amplification and genotyping were performed for 11 SNPs, including the NOD2, IL-23r, OCTN1, and the IGR gene variants.

Results:

A total of 554 patients with CD were included in this study: 53 African Americans (10%), 485 Caucasians (87%), and 15 of other races (3%). The strongest demographic predictor of CD in African American patients was a family history of IBD. Ileocolic disease (L3) was the most common site involved in both African Americans and Caucasians, while the penetrating phenotype (B3) was the most common CD disease behavior in both races. Genotype association analysis showed a significant association between 2 IL23r gene SNPs and CD susceptibility in African Americans ($p = .016$ and $.028$, respectively).

Conclusions:

We believe this study is the first to report on genotype-phenotype associations in African American CD patients and compare findings to Caucasian CD patients within the same geographic area. We found no association between NOD2 gene SNPs and CD susceptibility in African Americans patients ($p > .05$).

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Keywords

gastrointestinal; African Americans; tobacco; genes

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