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**Abstract**

Endemic helminthic infection is a major public-health problem and affects a large proportion of the world's population. In Australia, helminthic infection is endemic in Aboriginal communities living in tropical northern regions of the continent. Such infection is associated with nonspecific (polyclonal) stimulation of IgE synthesis and highly elevated total serum IgE levels. There is evidence that worm-infection variance (i.e., human capacity of resistance) and total serum IgE levels may be related to the presence of a major codominant gene. The beta chain of the high-affinity IgE receptor, Fc epsilon R1-beta, has been previously identified as a candidate for the close genetic linkage of the 11q13 region to IgE responses in several populations. We show a biallelic RsaI polymorphism in Fc epsilon R1-beta to be associated with total serum IgE levels ($P = .0001$) in a tropical population of endemically parasitized Australian Aborigines ($n = 234$ subjects). The polymorphism explained 12.4% of the total residual variation in serum total IgE and showed a significant ($P = .0000$) additive relationship with total serum IgE levels, across the three genotypes. These associations were independent of familial correlations, age, gender, racial admixture, or smoking status. Alleles of a microsatellite repeat in intron 5 of the same gene showed similar associations. The results suggest that variation in Fc epsilon R1-beta may regulate IgE-mediated immune responses in this population.