Natural resistance-associated macrophage protein 1 gene polymorphisms in rheumatoid arthritis.

胡朝榮

Yen JH;Lin CH;Tsai WC;Ou TT;Wu CC;Hu CJ;Liu HW

摘要

Abstract

Objectives

To investigate the association of natural resistance-associated macrophage protein 1 gene (NRAMP1) polymorphisms with rheumatoid arthritis (RA) in Taiwan.

Methods

NRAMP1 polymorphisms were determined from 113 RA patients and 74 healthy controls using the polymerase chain reaction/restriction fragment length polymorphism method.

Results

The genotype frequencies of NRAMP1 823 C/C, 1703G/G (543D/D), and 1729 + 55 del 4 TGTG+/+ (244/244) were significantly higher in patients with RA than in controls. Similar findings were also evident in allele frequencies and allele carriage frequencies of 823C, 1703G (543D), and 1729 + 55 del 4 TGTG+ (244). The associations of these polymorphisms with RA were independent of HLA-DR4. Linkage disequilibria could be found between 823C and 1703G, and between 1703G and 1729 + 55 del 4 TGTG+. The estimated haplotype frequency of NRAMP1 823C/1703G/1729 + 55 del 4 TGTG+ was significantly increased in RA patients compared with controls. We also found that patients with 823 C/C had a significantly lower prevalence of rheumatoid nodule than those without 823 C/C.

Conclusion

NRAMP1 823C, 1703G (543D), and 1729 + 55 del 4 TGTG+ (244) are precipitating factors for the development of RA in Taiwan. The estimated NRAMP1 823C/1703G/1729 + del 4 TGTG+ haplotype is associated with susceptibility to RA. NRAMP1 823 C/C prevents the development of rheumatoid nodule in RA patients.