Preliminary study of the clonal characteristics of the TCR BV subfamilies in T cells in the peripheral blood from patients with uveitis

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ABSTRACT. The aim of this study was to investigate the characteristics and polymorphisms of the T-cell receptor BV complementarity-determining region 3 (TCR BV CDR3) gene in peripheral blood mononuclear cells (PBMCs) from patients with uveitis to provide an experimental basis for studying the pathogenesis of this disease. RT-PCR amplification of 26 subfamilies of the TCR BV CDR3 gene and immune spectratyping analysis were used to study the pedigree drift of TCR BV CDR3 in PBMCs from the uveitis patients. The following results were obtained: 1) the vast majority of the TCR BV CDR3 spectra in PBMCs in 5 healthy subjects fit the normal (or Gaussian) distribution. The distributions of the TCR BV CDR3 spectra in 4 patients with uveitis were non-normal and showed an abnormal peak including a widowed peak trend, a partial peak, and an irregular abnormal peak. 2) In the 26 TCR BV subfamilies, the abnormal peak frequency was different
in the various subfamilies. The BV2 and BV17 (both 3/4) subfamilies had higher frequencies of the non-normally distributed abnormal peak. The BV5.2, BV6, BV15, and BV18 subfamilies showed no abnormal peaks. 3) TCR BV2 and BV17 yielded an abnormal peak in 3 HLA-B27-negative patients; however, no such abnormalities were detected in HLA-B27-positive patients. The abnormal expression of some TCR BV subfamilies in PBMCs from patients with uveitis may be associated with the immune pathogenesis of the disease. Our study provides the basis for further investigations into the pathogenesis of uveitis.

**Key words:** BV subfamily; Complementarity-determining region; Uveitis; T-cell receptor; Immune scanning spectratyping analysis