Immuno-Related Gene Polymorphisms associated with Acute Myeloid Leukemia

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Abstract

Though the pathogenesis of acute myeloid leukemia (AML) is still unknown, accumulating evidence has revealed that immune response plays a vital part in the pathogenesis. Here, we investigated the involvement of 24 single-nucleotide polymorphisms (SNPs) of immuno-related genes, including cytokines (IL2, IL4, IL9, IL-12A, IL-22, IFNG, and TGFB1), transcriptional regulatory genes (TBX21, STAT1, STAT3, STAT5B, STAT6, GATA3, FOXP3, and IRF4), and others (IL2RA IL6R NFKBIA), in 269 AML inpatients and 200 healthy controls. Furthermore, we analyzed the relationship between the SNPs and clinical characteristics. Immuno-related SNP genotyping was performed on the Sequenom MassARRAY iPLEX platform. All the SNPs in healthy controls were consistent with Hardy–Weinberg equilibrium. All final p values were adjusted by Bonferroni multiple testing. Our results showed that IL-22 (rs2227491) was significantly associated with the white blood cell (WBC) counts. STAT5B (rs6503691) showed a close relationship with the recurrent genetic abnormalities in patients with AML. We verified the negatively independent effect of age and risk of cytogenetics on overall survival (OS). More importantly, the GG genotype of IL-12A (rs6887695) showed a negative impact on AML prognosis independently. Furthermore, the relative expression of IL-12 was decreased in GG genotype, no matter under codominant or recessive model. However, no correlation was observed between the SNPs mentioned above and disease susceptibility, risk stratification, and survival. Our findings suggest that immuno-related gene polymorphisms are associated with prognosis in AML, which may perform as novel inspection targets for AML patients.

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