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POSTER ABSTRACTS

632.CHRONIC MYELOID LEUKEMIA: CLINICAL AND EPIDEMIOLOGICAL

Analysis the Relationship between Clonal Hematopoiesis and Cardiovascular Events in Chronic Myeloid Leukemia Based on Next-Generation Sequencing Technology

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B ackground With the development and clinical application of high-throughput sequencing technologies and cytogenetics, the genetic complexity of hematopoiesis is better understood. Studies have found that there are gene mutations in hematopoietic stem cells that leading to subsequent clonal hematopoiesis (CH) phenomenon. Moreover, several recent studies have linked the occurrence of cardiovascular events with CH, and individuals with CH had a doubled risk of coronary heart disease and a fourfold increased risk of myocardial infarction. CH also exists in CML, and with the widespread application of second- and third-generation TKIs, the occurrence of cardiovascular adverse events had become one of the difficulties in the management of CML patients. Therefore, analyzing the relationship between additional gene mutations and cardiovascular adverse events in CML patients based on Next-Generation Sequencing (NGS) technology will provide new directions and ideas for the precise management of CML patients.
O bjective Analyzing the relationship between clonal hematopoiesis and cardiovascular events in CML patients based on NGS technology.
Method Using NGS technology to find hematological tumor-related gene mutations in CML patients, and analyzing their relationship with cardiovascular adverse events in CML patients.
R esult A total of 149 CML patients were tested by NGS in this study, and were detected 152 clinically significant mutations. The mutations mainly involved genes related to epigenetic and activated signaling pathways, most of which were detected only in patients with drug resistance/intolerance to tyrosine kinase inhibitors (TKIs). The genes with higher mutation frequency were FAT1, GSTM1, ABL1, CUX1, EP300, ASXL1, TET2, CEBPA and so on. In this study, a total of 40 patients had cardiovascular events during treatment. When analyzing the risk factors of cardiovascular events in CML patients, it was found that patients with cardiovascular events were older [the median age were 58 (23-74) years vs 39 (16-73) years, $P<0.001$], and the duration of taking second-generation TKIs was also longer [the median time were 38 (0-102) months vs 16 (0-66) months, $P=0.001$]. When analyzing the relationship between gene mutations and cardiovascular events in CML, it was found that ASXL1, DNMT3A, EZH2 and other genes were more frequently detected in CML patients with cardiovascular events. Among them,DNMT3A mutation was associated with the occurrence of cardiovascular events in CML patients (RR 23.3, $P=0.003$). In addition, we also found that CCND1, CYP2C19 and NTRK2 gene mutations were only detected in patients without cardiovascular events significantly.
C onclusion CML patients with cardiovascular events are older, take second-generation TKIs for a longer time, and have a higher incidence of DNMT3A gene mutation; CCND1, CYP2C19, NTRK2 gene mutation may be a protective factor for cardiovascular events in CML patients.

Disclosures No relevant conflicts of interest to declare.

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