



Significance of detecting IgH and TCR γ gene rearrangements in patients with hemopoietic malignancies by real-time quantitative PCR

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ABSTRACT. The aim of our study was to investigate the association of IgH and TCR γ gene rearrangements in hematological malignancies with the disease and clinical application. IgH and TCR γ gene rearrangements were determined in 69 paraffin and bone marrow specimens with SYBR Green I fluorescent dye and RQ-PCR method, including 21 paraffin-embedded tissues of the onset cases and 48 bone marrow samples, representing 15 ALL and 25 AML cases. After chemotherapy, 8 cases were NHL; the 10 cases of the negative control group were healthy people. Among the ALL cases, the IgH rearrangement occurred in 80.0%, the TCR γ rearrangement in 46.7%,

and both gene rearrangements in 46.7%. Among the AML cases, the IgH rearrangement occurred in 72.0%, the TCR γ rearrangement in 68.0%, and both gene rearrangements in 60.0%. In the lymphoma cases, the IgH rearrangement occurred in 93.1%, the TCR γ rearrangement in 51.7%, and both gene rearrangements in 44.8%. In the negative control group, the 10 cases were all negative. There was the phenomenon of “sequence-non-fidelity” in the hematologic malignancies; the detection rate of both genes was much higher than that of the single gene. The application of the RQ-PCR method in the detection of IgH and TCR γ gene rearrangements in hematologic malignancies has important clinical significance in MRD monitoring.

Key words: Real-time quantitative PCR; Fluorescent dye; Hematological malignancies; IgH gene; TCR γ gene; Gene rearrangement