Abstract

We established next generation sequencing (NGS)-based assays for the detection of rearranged immunoglobulin (Ig) and T-cell receptor (TR) genes (Ig heavy chain complete/incomplete, TR gamma and delta). We used these assays for minimal residual disease (MRD) detection and antigen repertoire analysis in children with acute lymphoblastic leukaemia (ALL).

We compared MRD levels in 210 paediatric ALL samples detected by NGS and by quantitative PCR (qPCR), which is a current gold standard for MRD detection. We showed that both methods provide highly comparable results and that NGS results are more specific for relapse prediction. The better specifity of NGS was also proven on 40 post-transplant samples, where qPCR can provide false positive MRD results. We showed that repertoire diversity at day 78 is an independent prognostic factor in paediatric ALL.

Besides the above-mentioned advantages NGS-based MRD detection is cheaper and faster than qPCR. Before NGS-based MRD monitoring can safely replace qPCR, the extensive standardization of the method must be performed, as well as the evaluation of its prognostic relevance on a larger group of patients.

Keywords: Minimal residual disease, Next Generation Sequencing, Ig/TR rearrangements