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Improved clonality detection in Hodgkin lymphoma using a semi-nested modification of the BIOMED-2 PCR assay for *IGH* and *IGK* rearrangements: A paraffin-embedded tissue study

[Background] The BIOMED-2 PCR protocols targeting IGH and IGK genes may be useful for detecting clonality in Hodgkin lymphoma (HL). The clonality detection rates, however, have not been very high with these methods using paraffin-embedded tumor sections. We previously described the usefulness of the semi-nested BIOMED-2 *IGH* assay in B-cell malignancies. In this study, we devised a novel semi-nested BIOMED-2 *IGK* assay. [Methods] Employing 58 cases of classical HL, we carried out the standard BIOMED-2, BIOMED-2 followed by BIOMED-2 re-amplification, and BIOMED-2 followed by semi-nested BIOMED-2, all targeting *IGH* and *IGK*, using paraffin-embedded tissues. [Results] In both *IGH* and *IGK* assays, semi-nested assays yielded significantly higher clonality detection rates than the standard assays and re-amplification assays. Clonality was detected in 13/58 (22.4%) classical HL cases using the standard *IGH*/*IGK* assays while it was detected in 38/58 (65.5%) cases using semi-nested *IGH*/*IGK* assays. The detection rates were not associated with the HL subtypes, CD30-positive cell density, CD20-positive cell density, or Epstein–Barr virus (EBV) positivity. [Conclusion] Tumor clonality was detected in nearly two thirds of classical HL cases using semi-nested BIOMED-2 *IGH*/*IGK* assays using paraffin tumor sections. These semi-nested assays may be useful when the standard *IGH*/*IGK* assays fail to detect clonality in histopathologically suspected HLs.