

## ORIGINAL ARTICLE

### T Cell Receptor- $\gamma$ Gene Analysis of CD30<sup>+</sup> Large Atypical Individual Cells in CD30<sup>+</sup> Large Primary Cutaneous T Cell Lymphomas

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The hallmark of primary cutaneous CD30<sup>+</sup> large T cell lymphoma are large lymphoid tumor cells, at least 75% of which, by definition, must be positive for CD30. The relatively benign clinical course of this lymphoma type has been explained with CD30-induced apoptosis, on the assumption that expression of CD30 defines the tumor clone; however, this hypothesis has not been tested on the molecular level to date. In this study we analyzed CD30<sup>+</sup> cells in four patients with primary cutaneous CD30<sup>+</sup> large T cell lymphoma by single cell polymerase chain reaction of T cell receptor- $\gamma$  genes followed by sequencing. Here, we demonstrate that most of the large CD30<sup>+</sup> atypical cells possessed identical T cell receptor- $\gamma$  gene rearrangements, indicative of clonal proliferation. Nevertheless, polyclonally rearranged T cells were present in all CD30<sup>+</sup> samples studied. In addition, one patient showed a second clone in a separate biopsy and three of four patients showed chromosomal imbalances as revealed by comparative genomic hybridization. Taken together, our data suggest that the CD30<sup>+</sup> population in primary cutaneous CD30<sup>+</sup> large T cell lymphoma indeed contains the tumor clone, thus providing molecular support for a link between clinical course and CD30-related signaling. Importantly, however, CD30 expression does not define the tumor clone as bystander T cells, as well as occasional additional clones, are also present in this population.