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ERRATUM

Erratum to: Two morphologically and immunophenotypically distinct cell populations within a composite lymphoma arise from a common precursor

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The articles was published with errors to table citation. Please find correct information here:
Clinical Summary, Histologic and Immunophenotypic Analysis. This information is summarized in Tables 1 and 2 and cytogenetic studies in Table 3.

DNA sequence analysis of the amplified JH regions from three of the four cases (cases 1, 3, and 4) revealed identical sequences in the two distinct malignant cell populations. DNA sequencing could not be performed in case 2 because one of the sequencing reactions failed and there was inadequate specimen to repeat it after the FR analysis had been completed. The results from the molecular analysis of the JH regions of all four cases are presented in Table 5.

Three cases (2, 4, and 5) were subjected to analysis of VH rearrangement by performing PCR with primers targeting the different framework regions followed by capillary electrophoresis. In this approach, DNA was extracted from paraffin-embedded tissue sections containing both malignant lymphoid components, followed by three multiplex PCR reactions, each targeting one of the three framework regions (FR1, 2, and 3) of the immunoglobulin heavy chain variable region. The PCR products were analyzed by capillary electrophoresis. In case 2, single peaks of 117, 258, and 322 bp of PCR products were present in the electropherograms. In case 4, single peaks of 321 and 256 bp of PCR products were present with FR1 and FR2 primers. A double peak of 124 and 127 bp was present with FR3 primer. The 127-bp peak was very small compared to the stronger 124-bp peak. In case *5,* single peaks of 343, 278, and 148 bp corresponding to the FRI, FR2, and FR3 regions were identified in the electropherograms (Fig. 4 and Table 6).

The online version of the original article can be found at http://dx.doi.org/10.1007/s12308-011-0101-0.

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