SKIN CANCER (OTHER THAN MELANOMA)

ARRAY-BASED CGH OF PRIMARY CUTANEOUS CD8+ AGGRESSIVE EPIDERMOTROPIC CYTOTOXIC T-CELL LYMPHOMA

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Introduction: Primary cutaneous CD8+ aggressive epidermotropic cytotoxic T-cell lymphoma (pcAECyTCL) is a rare aggressive cutaneous lymphoma still considered as a provisional entity in the last WHO classification. Its pathogenesis and molecular mechanisms are still unknown, and only two individual cases have so far been molecularly characterized.

Objectives: The aim of this study was to deeply investigate chromosomal imbalances in patients with pcAECyTCL at the time of diagnosis.

Material and Methods: Tumor samples of 20 patients were analyzed using an array-comparative genomic hybridization (a-CGH) approach. In order to validate the CGH results, the 9p21.3 locus in the CDKN2A region was investigated by means of fluorescence in situ hybridisation (FISH) using formalin-fixed, paraffin-embedded tissues.

Results: Numerous genomic aberrations were present in all the patients and, putting these together as a whole, they affected all the chromosomes. However, no specific profile of recurrent copy number alterations (CNAs) was found. Most of the gains involved regions previously described in other aggressive cutaneous lymphomas such as 7q, 8q24.3, and 17q, whereas the most significant CNA was the loss of 9p21.3 (CDKN2A–CDKN2B), which has already been found in a variety of malignant tumors and is associated with aggressive cutaneous T-cell lymphomas.

Conclusions: In brief, CGH analysis revealed a large number of CNAs with only few recurring regions that probably do not represent driving events. The genomic instability found in this aggressive variant of cutaneous lymphoma may therefore be a secondary event but, at the time of the diagnosis of pcAECyTCL, the genomic integrity of tumor cells is

already compromised.