Abstract #8 | Poster

Genetic lesions in nodular lymphocyte-predominant Hodgkin lymphoma and T cell/histiocyte-rich large B-cell lymphoma identified by whole genome sequencing

T. Rausch[3], H. Schäfer[1], J. Bein[5], F. Mölder[6], L. Beeck[6], B. Kölsch[1], S. Borchert[1], V. Benes[3], T. Halbsguth[2], U. Brunnberg[2], T. Oellerich[2], T. Tousseyn[4], M. Ponzoni[7], M.-L. Hansmann[5], J. Köster[6], R. Küppers[6], **S. Hartmann**[1]

[1] *University Hospital Essen, Institute for Pathology, Essen, North Rhine-Westphalia, Germany*
[2] *University Hospital Frankfurt, Internal Medicine 2, Frankfurt, Hesse, Germany*
[3] *EMBL, Heidelberg, Baden-Württemberg, Germany*
[4] *University Hospital KU Leuven, Pathology, Leuven, Belgium*
[5] *University Hospital Frankfurt, Frankfurt, Hesse, Germany*
[6] *University Hospital Essen, Essen, North Rhine-Westphalia, Germany*
[7] *Scientific Institute San Raffaele, Pathology, Milan, Italy*

Nodular lymphocyte-predominant Hodgkin lymphoma (NLPHL), also called nodular lymphocyte-predominant B-cell lymphoma, is a rare malignant lymphoma characterised by a few large tumour cells expressing B-cell antigens in an inflammatory background. T-cell/histiocyte-rich large B-cell lymphoma (THRLBCL) is now considered to be closely related to NLPHL. Little is known about the mutational spectrum of the lymphoma cells in primary NLPHL and THRLBCL due to the rarity of the diseases and the technical challenges of analysing these tumours. Therefore, the aim of the present study was to elucidate mechanisms contributing to the pathogenesis of NLPHL and THRLBCL by whole genome sequencing of laser microdissected tumour cells from seven cases. We observed a heterogeneity of transforming events, with cases showing abundant somatic mutations, others with a predominance of structural variations, and cases with few aberrations. The genes that were most frequently affected by aberrations encode factors influencing JAK-STAT, NF-κB, and WNT signalling, and apoptosis regulators. However, the mutated genes were often not the typical targets known from classical HL, such as *SOCS3* or *N4BP1*. Two cases showed recurrent rearrangements of *BCL6* and *CD74*. In conclusion, our data enrich our understanding of NLPHL and THRLBCL and highlight common and distinct features with classical Hodgkin lymphoma.