

international consensus and flow cytometry (FCM) became a promising method. We have shown the specificity and reliability of KIR3DL2 as a positive marker for SCs, and introduced KIR3DL2 in our routine panel. Here, we report our 4 years expertise for initial diagnosis in 130 patients. Our results are discussed in the light of the latest recommendations from the EORTC CLTF which provided a comprehensive literature review looking for an universal blood-class MF/SS definition.

Methods: FCM including CD7, CD26, and KIR3DL2 labelling was performed. Patients were diagnosed according to the ISCL/EORTC classification for CTCL. We also took into account the latest recommendations from EORTC defining B2 stage when CD4+CD26- cells is $\geq 1000/\text{mm}^3$. We gathered the samples at diagnosis for 33 SS, 35 MF, 8 EMF and 54 patients with inflammatory skin diseases (ISD). 2 groups of patients were defined, according to their CD4+T-cell absolute counts: group A ($\geq 1000/\text{mm}^3$) and group B ($< 1000/\text{mm}^3$).

Results: A strong positive correlation between KIR3DL2+ and CD4+CD26-T-cell count was found in group A (60 patients) ($r = .81$, $p < .0001$). A value of KIR3DL2+T-cells $\geq 200/\text{mm}^3$ (25/29 SS patients) allowed a specificity of 90% and a sensitivity of 86% for the diagnosis of SS. In group B, only results expressed as percentages were relevant. All patients with KIR3DL2+ T-cells $\geq 10\%$ were SS, whereas 42% of remaining MF or ISD had CD4+CD26- cells $\geq 30\%$, including 7/8 EMF.

Conclusion: Our results suggest that the detection of KIR3DL2+T-cells improves the biological diagnosis of SS, especially when CD4+T-cell count is $< 1000/\text{mm}^3$. We propose to introduce this parameter as a tumoral marker into the blood classification, in association with CD26 for the diagnosis of SS and EMF.

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1p36 deletion is associated with TNFRSF14 mutations in primary cutaneous follicle center lymphoma

Bence Batai¹, Ambrus Gángó¹, Martin Varga¹, Dóra Kapczár¹, Gergo Papp¹, Márta Marschalkó¹, Eniko Kuroli¹, Tamás Schneider², Judit Csomor¹, András Matolcsy¹, Csaba Bódör¹, Ágota Szepesi¹

¹Semmelweis University, Budapest, Hungary

²National Institute of Oncology, Budapest, Hungary

Background: Primary cutaneous follicle center lymphoma (PCFCL) is an indolent variant of follicular lymphoma (FL) with limited information available on the genetic background of the disease. The genetic hallmark of nodal FL, the t(14;18) translocation, affecting the *BCL2* gene, is rare in PCFCL. Loss of 1p36, the most common secondary chromosomal abnormality in nodal FL, has been recently reported in 16.7% of PCFCL cases. The mutation analysis of *TNFRSF14*, the candidate gene in the 1p36 region has not yet been performed.

Aims: Since the data is scarce about the genetic background of PCFCL we assessed the frequency of 1p36 deletion and t(14;18) translocation and analyzed the mutation status of *TNFRSF14* and *EZH2*. We evaluated the prognostic relevance of the identified alterations.

Methods: 21 cases were analyzed using interphase fluorescence in situ hybridization with *BCL2* break apart and 1p36/1q25 dual color probes. Sanger sequencing was used to investigate *TNFRSF14* and *EZH2* mutations and immunohistochemistry was used to assess *BCL2* and *EZH2* protein expressions.

Results: 1p36 deletion occurred in 22% (5/21), *BCL2* gene break in 10% (2/20) of the PCFCL cases. Mutations of the candidate tumor suppressor gene of the 1p36 region, *TNFRSF14* were detected in 4/17 (23, 5%) cases with 2 cases presenting with concurrent 1p36

deletion, resulting in complete loss of functional *TNFRSF14*. *EZH2* hotspot mutations at Y641, A682 and A692 were not found. High *EZH2* protein expression associated with a *BCL2* negative phenotype was observed in 43% (9/21) of the cases. *BCL2* gene break or 1p36 deletion did not impact the prognosis, however they showed association with advanced stages at diagnosis ($p = 0.016$) and a tendency of shorter event free survival ($p = 0.052$).

Conclusions: 1p36 deletion co-occurs with acquired *TNFRSF14* mutations, suggesting a role of this tumor suppressor gene in the development of a subgroup of PCFCL. High *EZH2* protein expression associated with *BCL2* negative phenotype is common and might represent an ideal therapeutic target.

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T-cell receptor clonality analysis with the Biomed-2 PCR as a diagnostic tool in cutaneous T-cell lymphomas

Hanna Kresbach¹, Emmanuella Guenova²

¹Department of Dermatology, Kepler University, Linz, Austria

²Department of Dermatology, University Hospital Zurich, Zurich, Switzerland

Early and precise diagnosis of cutaneous T-cell lymphomas (CTCL) is a challenge. The identification of T-cell receptor (TCR) clonality plays an important part in the diagnostic process. Polymerase chain reaction (PCR)-based clonality assessment following the Biomed-2 protocol is an everyday gold standard method in the assessment of the T-cell receptor clonality. We aimed to assess the sensitivity and specificity of this diagnostic method, based on a complete dataset collected over a 5-year period from 2012 to 2017 in our specialized tertiary center.

We reviewed the diagnostic TCR-PCR results and the medical records of 292 patients with a suspicion for CTCL. There was an overall prevalence of CTCL in 57.9% of the cases. Monoclonal rearrangement of the TCR showed a relatively high specificity (76.4%) but low sensitivity (68.6%), when dominant PCR peaks were classically interpreted as monoclonal T-cell populations when 3 times higher than the third highest PCR peak. By changing the cut-off and considering dominant PCR peaks to represent monoclonal T-cell populations only when 5 times higher than the third highest PCR peak, sensitivity and specificity of the test changed to 59.8% and 83.7% respectively.

Taken together, we confirmed the diagnostic value of the TCR clonality analysis with the Biomed-2 PCR in the workup of CTCL. By adjusting the cut-off value and considering dominant PCR peaks to represent monoclonal T-cell populations only when 5 times higher than the third highest PCR peak, specificity of the test improved. However, the cost of this increased specificity was lower sensitivity and lower screening utility of the test.

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'T-cell versus T-cell': Tumour infiltrating lymphocytes in mycosis fungoides show a remarkably homogeneous exhaustion profile across a heterogeneous patient population

Duncan Murray¹, Suzy Eldershaw¹, Jack McMurray¹, Hayden Pearce¹, Nathaniel Davies¹, Paul Moss¹, Julia Scarisbrick²

¹Institute of Immunology & Immunotherapy, Birmingham, United Kingdom

²University Hospitals Birmingham, Birmingham, United Kingdom