The applicability of a simple gene expression assay for the classification of peripheral T-cell lymphomas

Peripheral T-cell lymphomas (PTCLs)
- highly heterogeneous and rare tumors
- ~ 1/3 of PTCLs remain unclassifiable: PTCL-NOS

270 lymphoma samples (multicentric T-cell lymphoma consortium (TENOMIC) of the Lymphoma Study Association (LYSA))

Reverse transcriptase-multiplex ligation-dependent probe amplification gene expression profiling (RT-MLPA) assay

20 genes
- 17 markers relevant to T-cell immunology and lymphoma biopathology
- 1 EBV-related transcript
- Variants of RHOA (G17V) and IDH2 (R172K/T)

Identification of 33/33 RHOAG17V and 9/10 IDH2 R172K/T mutations

• Unsupervised hierarchical clustering
  • 21/21 ALK/positive anaplastic large cell lymphoma
  • 16/16 extranodal NK/T-cell lymphomas
  • 6/6 hepatosplenic T-cell lymphomas
  • 13/13 adult T-cell leukemia/lymphomas

• Support vector machine (SVM) predictor model based on RT-MLPA data
  Attributed a molecular class to 27/77 not specified T-cell lymphomas:
  • 17 T\textsubscript{FH}
  • 5 cytotoxic ALK-negative anaplastic
  • 5 NK/ T-cell leukemia/lymphomas

Drieux et al., Haematologica, 2020