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#### **EHA-TSH Hematology Tutorial on T-Cell Lymphomas**

June 29-30, 2024 | Ankara, Türkiye



#### Session 1

New classification and epidemiology of T cell diseases

June 29, 2024









# Updated classification and molecular evaluation of nodal T-cell lymphomas

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#### DISCLOSURE

• Sandoz (Consultancy, non-financial)



#### **Learning objectives**

After attending this presentation, you will be able to:

- 1. Understand the updates in the classification of nodal T-cell lymphomas based on the latest WHO and ICC guidelines
- 2. Recognize the molecular characteristics of these lymphomas
- 3. Explore potential prognostic and therapeutic implications based on specific genetic alterations



#### **Peripheral T-cell lymphomas**

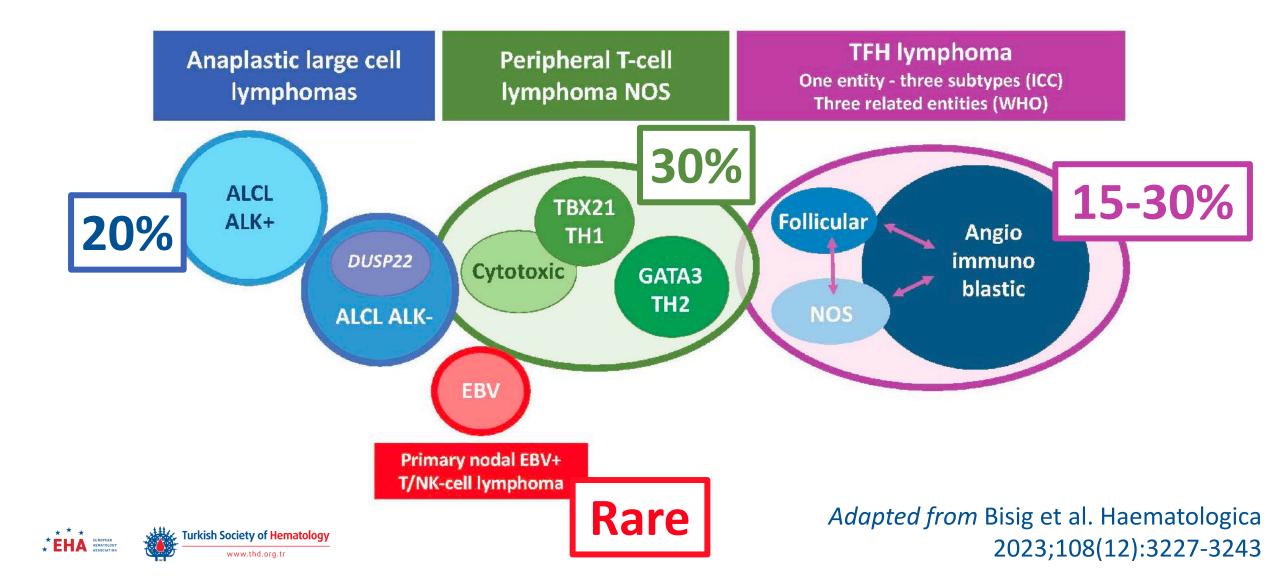
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- Diverse group of neoplasms (> 30 entities) that arise from mature NK or T cells
- 10% of all lymphomas in Western countries up to 20% in Asia

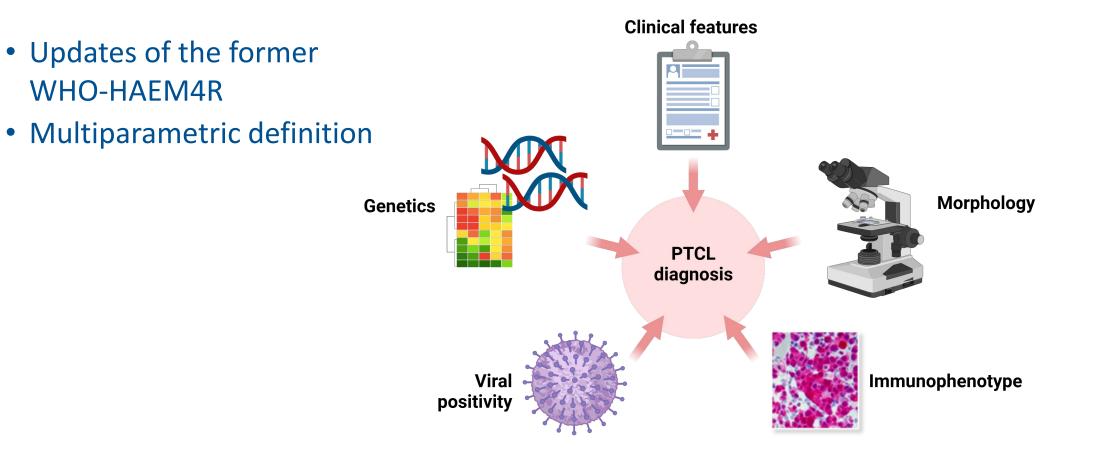




#### **Nodal T-cell lymphomas**



#### **New classifications: ICC and WHO-HAEM5**



International Consensus Classification (ICC)  $\rightarrow$  Campo et al. Blood. 2022;140(11):1229-1253 5<sup>th</sup> World Health Organization classification of hematological malignancy  $\rightarrow$  Alaggio et al. Leukemia 2022;36:1720–1748

#### **New classifications: ICC and WHO-HAEM5**

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WHO-HAEM4R	ICC 2022	WHO-HAEM5		
Anaplastic large cell lymphoma, ALK-positive	Anaplastic large cell lymphoma, ALK-positive	Anaplastic large cell lymphoma, ALK-positive		
Anaplastic large cell lymphoma, ALK-negative	Anaplastic large cell lymphoma, ALK-negative	Anaplastic large cell lymphoma, ALK-negative		
<ul> <li>Nodal lymphomas of T follicular helper origin</li> <li>Angioimmunoblastic T-cell lymphoma</li> <li>Follicular T-cell lymphoma</li> <li>Nodal peripheral T-cell lymphoma with TFH phenotype</li> </ul>	<ul> <li>Follicular helper T-cell lymphoma</li> <li>TFH lymphoma, angioimmunoblastic type</li> <li>TFH lymphoma, follicular type</li> <li>TFH cell lymphoma, NOS</li> </ul>	<ul> <li>Nodal T-follicular helper (TFH) cell lymphoma</li> <li>Nodal TFH lymphoma, angioimmunoblastic type</li> <li>Nodal TFH cell lymphoma, follicular type</li> <li>Nodal TFH cell lymphoma, NOS</li> </ul>		
Not listed as an entity (PTCL, NOS)	Primary nodal EBV+ T-cell/NK-cell lymphoma	EBV+ nodal T- and NK-cell lymphoma		
Peripheral T-cell lymphoma, NOS	Peripheral T-cell lymphoma, NOS	Peripheral T-cell lymphoma, NOS		



# ANAPLASTIC LARGE CELL LYMPHOMA

Heterogeneous group
 Distinct morphology
 Uniform CD30 expression



#### ANAPLASTIC LARGE CELL LYMPHOMA

WHO-HAEM5 and 2022 ICC define 4 forms of ALCL:

□ Anaplastic lymphoma kinase (ALK)-positive

□ ALK-negative

Primary cutaneous

□ Breast implant–associated



#### **ANAPLASTIC LARGE CELL LYMPHOMA**

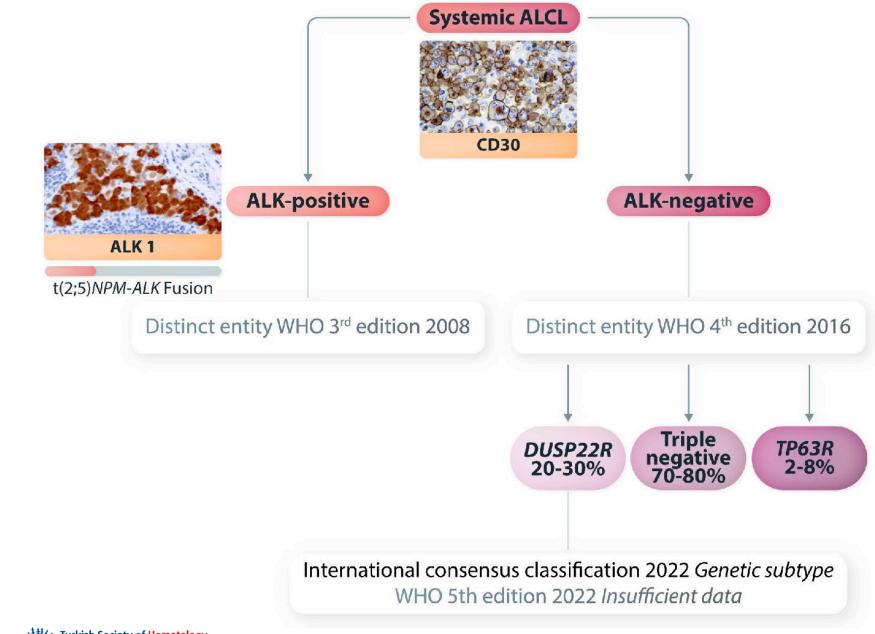
Anaplastic lymphoma kinase (ALK)-positive
 ALK-negative



Localized

Primary cutaneousBreast implant-associated





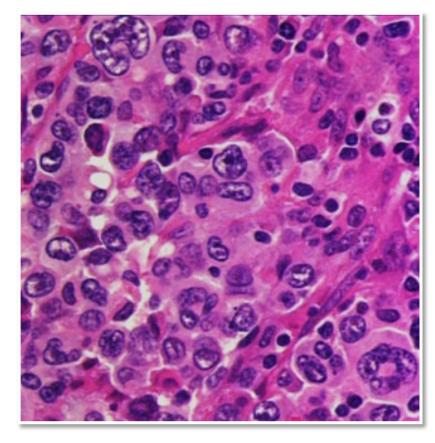


Adapted from Savage et al. Haematologica 2023;108(6):1463-1467

#### **MICROSCOPIC FEATURES**

- Lymph node architecture is usually effaced
- Sinusoidal infiltration
- Hallmark cells: large kidney- or horseshoeshaped nuclei
- Other cells may have immunoblastic features
- Histological patterns of ALK+ ALCL:

Common	60%
Lymphohistiocytic	10%
Small cell	10%
Hodgkin-like	<5%

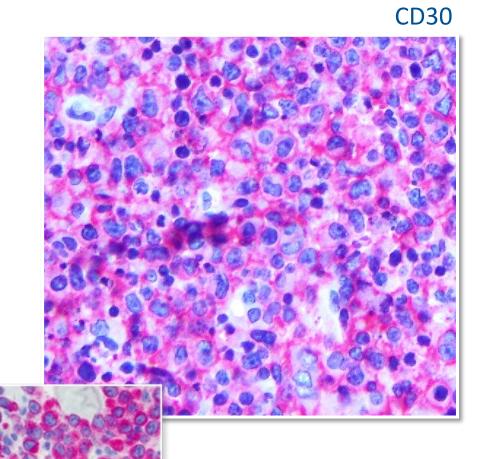


Hallmark cells



#### IMMUNOPHENOTYPE

- Diffuse and uniform CD30 expression
- Most ALCLs are CD4+ and express cytotoxic markers (perforin, TIA1 and granzyme B)
- Frequent loss of pan-T-cell markers ("null" phenotype")







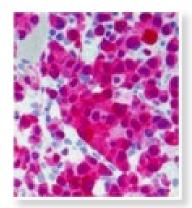
# **ALK-positive ALCL**

Young males (median age, 30-35 years)

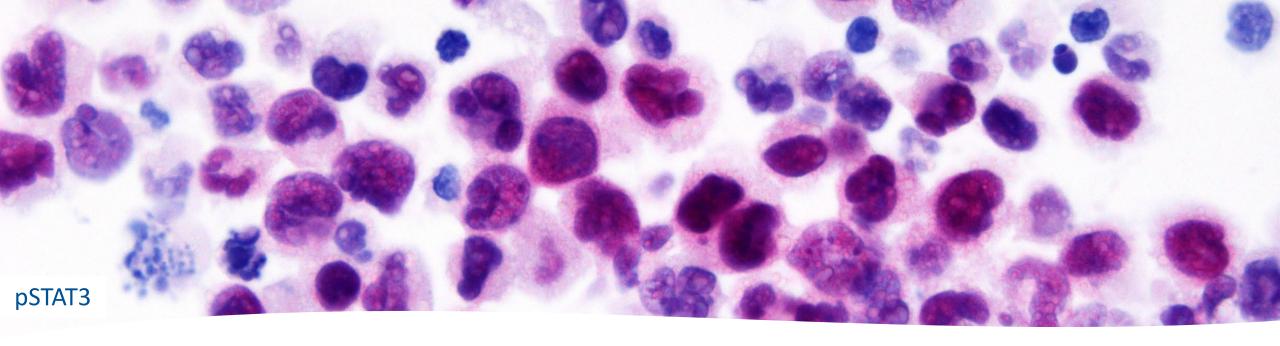
Rare leukemic presentation

ALK translocation on 2p23: NPIM1 t(2;5)(p23;q35) [80%]
TPM3 t(1;2)(q25;p23) [20%]
CLTC t(2;17)(p23;q23) [2%]
Others (ATIC, MSN, ...) Nuclear +
 cytoplasmatic

Cytoplasmatic ± membranous ALK







MOLECULAR FEATURES ALK+ ALCL

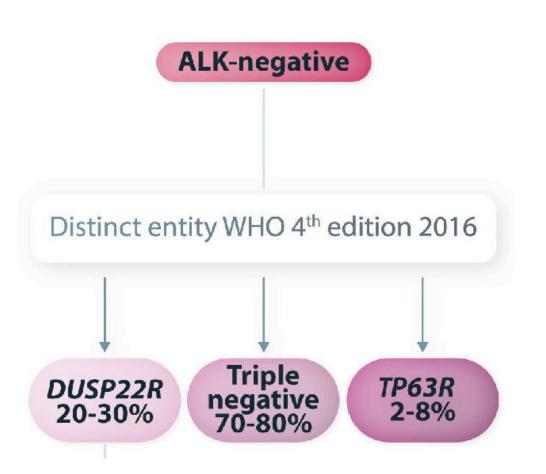


- ALK fusion proteins have constitutive tyrosine kinase activity
- Nuclear phospho-STAT3 (pSTAT3) is detected in nearly all cases
- Recurrent mutation in NOTCH1 (20%) and TP53 (11%)

# **ALK-negative ALCL**

- Older patients
- More aggressive than ALK+ ALCL

 Rare cases harboring both TP63-R and DUSP22-R





# «Triple negative» ALCL

#### JAK/STAT pathway activation

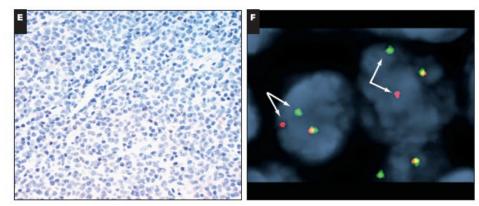
- Activating mutations in *JAK1*, *JAK3*, and *STAT3*
- Tyrosine kinase gene fusions (STAT3::JAK2, NFKB2::TYK2, and NCOR2::ROS1)
- $ROS1 \rightarrow receptor tyrosine kinase (RTK) with structural homology to ALK$
- Granzyme B and PD-L1/CD274, transcriptional targets of STAT3, are highly expressed

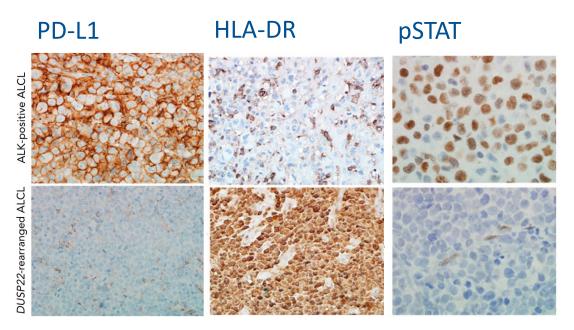


#### **DUSP22-R ALCL**

- Absence of JAK/STAT3 pathway activation
- Absent expression of PD-L1 and high expression of CD58 and HLA class II
- DNA hypomethylation
- Absent expression of cytotoxic molecules
- LEF1+
- MSC E116K mutation (30%)

#### Tia1 FISH DUSP22





Adapted from Luchtel et al. Blood 2018; 132(13):1386-1398 Adapted from Parrilla Castellar et al. Blood 2014; 124(9):1473-1480



#### **TP63-R ALCL**

- TP63-R  $\rightarrow$  fusion transcripts
- The most common is TBL1XR1::TP63, corresponding to inv(3)(q26q28)

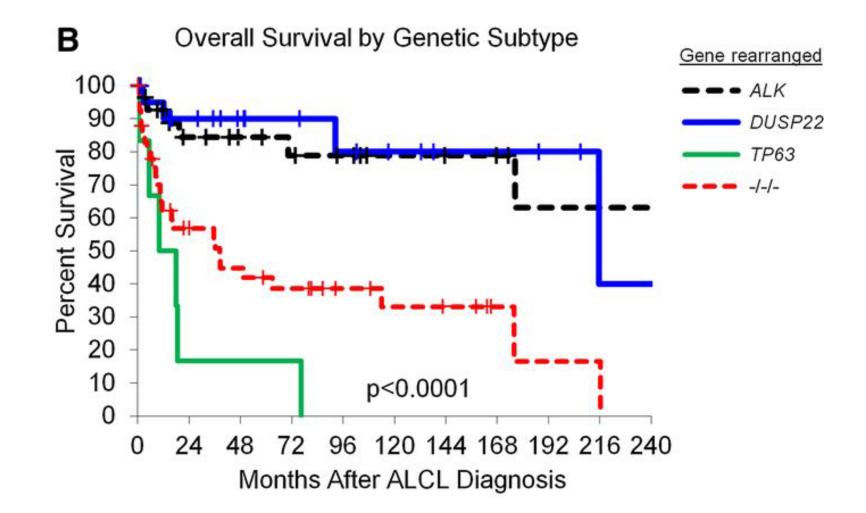
- Immunohistochemistry for p63 is highly sensitive although not specific
- Useful to select cases for TP63 FISH

TBL1XR1/TP63

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#### **PROGNOSIS**





Adapted from Parrilla Castellar et al. Blood 2014; 124(9):1473-1480

#### **PROGNOSIS – DUSP22-R**

	First author (Study location/group)					
Feature	Parilla-Castellar (Mayo) <sup>6</sup>	Pedersen (Denmark) <sup>10</sup>	Hapgood (BC Cancer) <sup>12</sup>	Onaindia (Spain) <sup>11</sup>	Sibon (LYSA) <sup>13</sup>	Qiu (MDACC) <sup>14</sup>
DUSP22-R cases, N	22	5	12	4	47	22
DUSP22-R among	30	19	19	18	45	28
ALK-negative cases, %						
Treatment, %						
CHOP(like)	90	100	92	50 <sup>b</sup>	94°	90
Consolidative auto-SCT	5	50 <sup>d</sup>	8	0	19	27
Missing treatment data	36			25		
5-year PFS, %	nr	nr	40	nr	57	40 <sup>d</sup>
5-year OS, %	90	80	40	100	65	40







# T-FOLLICULAR HELPER CELL LYMPHOMA

TFH phenotype
 GEP similar to normal Tfh cells
 Similar molecular landscape



#### T-FOLLICULAR HELPER CELL LYMPHOMA

WHO-HAEM4R (2017) → «umbrella category» that included AITL, follicular T-cell lymphoma, and nodal PTCL with TFH phenotype

**ICC and WHO-HAEM5**  $\rightarrow$  TFHL is a single entity with 3 subtypes:

Angioimmunoblastic-type

□ Follicular-type

□ TFHL, NOS

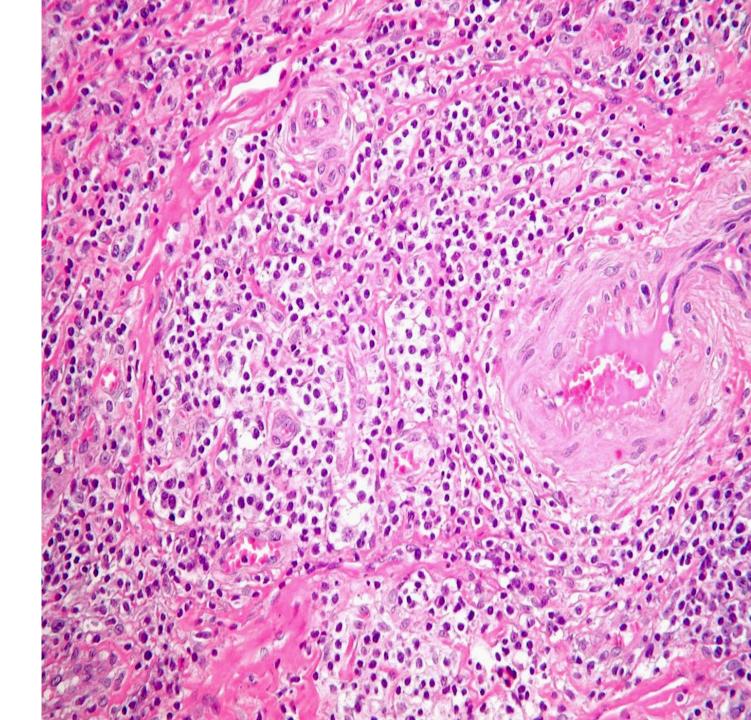




# AITL-type MICROSCOPIC FEATURES

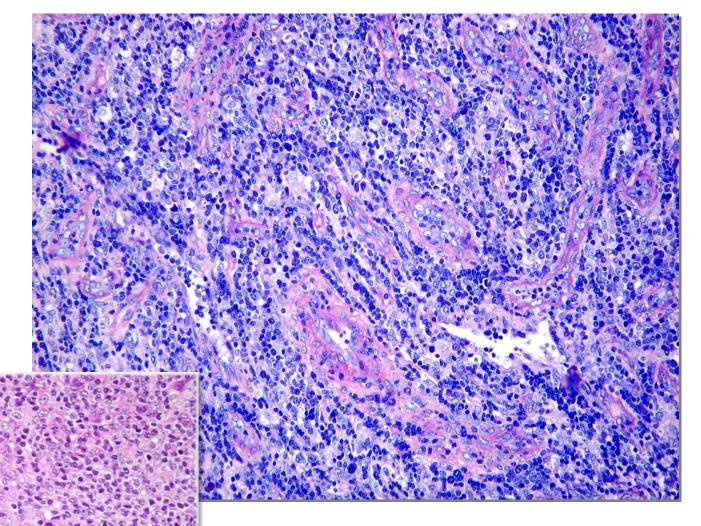
- Perifollicular (Patterns 1-2) or Diffuse (Pattern 3)
- Small- to medium-sized lymphocytes, often with pale, clear cytoplasm
- Inflammatory background:
  - Small lymphocytes
  - Immunoblasts (HRS-like)
  - Histiocytes
  - Eosinophils





# AITL-type MICROSCOPIC FEATURES

- Prominent, branching high endothelial venules
- Proliferation follicular dendritic cells (FDCs)

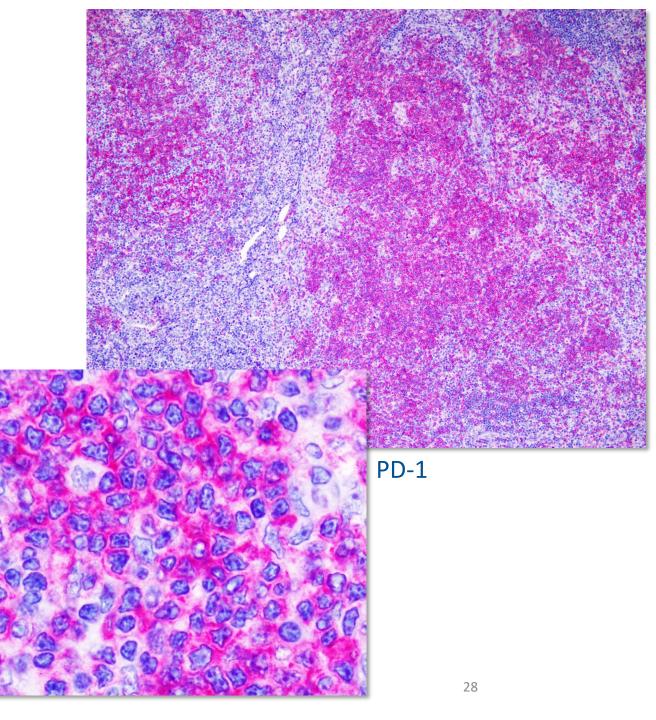




# **FOLLICULAR-type** MICROSCOPIC FEATURES

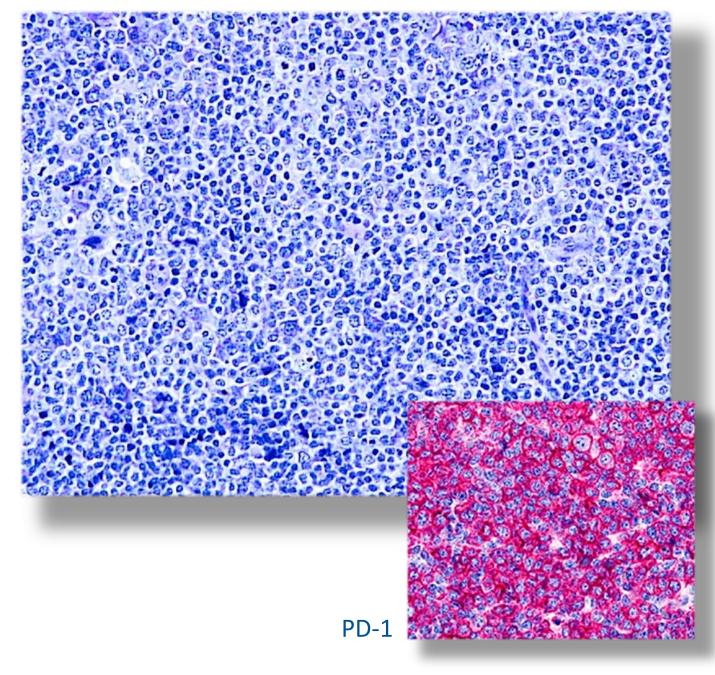
- Lacks characteristic features of AITL
- Two distinct patterns:
  - FL-like pattern: resembling follicular lymphoma
  - PTGC-like pattern: large nodules
     reminiscent of progressive
     transformation of germinal centers
- Absent/minimal HEVs and FDCs proliferation of





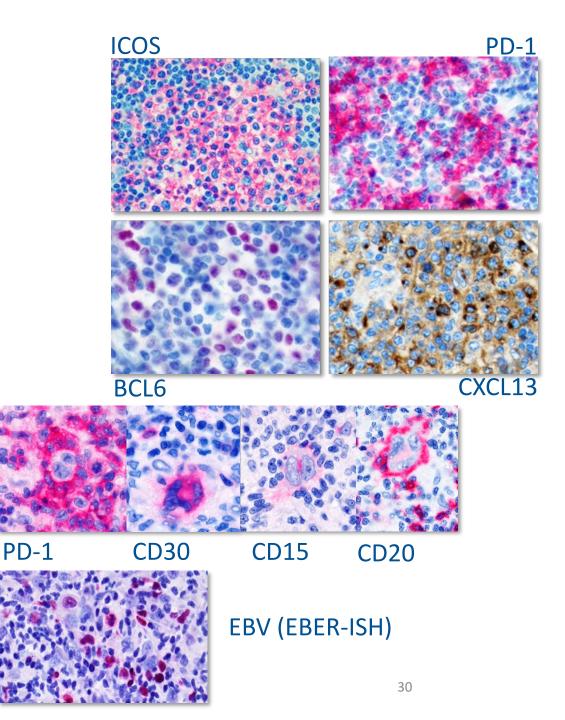
# **TFHL, NOS** MICROSCOPIC FEATURES

- TFHL-NOS lack features of AITL and TFHL-F
- The lymph node architecture is usually effaced
- Medium- to large-sized CD4+ cells expressing at least 2 TFH markers



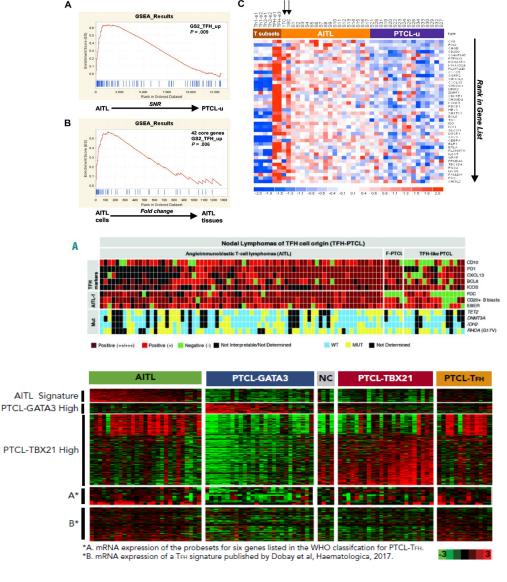
### IMMUNOPHENOTYPE

- Neoplastic cells
  - CD4+
  - Preserved expression of CD2, CD3, and CD5 with loss/diminished expression of CD7
  - At least 2 TFH markers (CD10, BCL6, CXCL13, ICOS, and PD1) are positive
- Intermingled B-immunoblasts (CD20+/CD30+), often associated with Epstein-Barr virus (EBV) infection



#### **MOLECULAR FEATURES**

- The 3 subtypes share gene expression signatures and mutational profiles
- In 2007, GEP analyses identified the TFH cell as the cell of origin of AITL
- Further analysis identified additional nodal PTCLs with GEP features of TFH derivation



de Leval et al. Blood 2007;109(11):4952-4963 Dobay et al. Haematologica 2017;102(4):e148-e151 Heavican et al. Blood 2019;133(15):1664-1676



#### **MOLECULAR FEATURES**

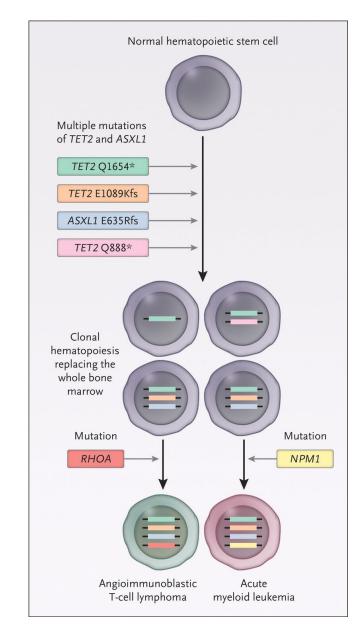
- Frequently mutated genes include RHOA, TET2, DNMT3A, and IDH2
- *RHOA* G17V [50%-70%] binds to VAV1 → accelerating T-cell receptor (TCR) signaling
- *RHOA* G17V expression in CD4 T cells led to TFH differentiation

Lemonnier F et al. Blood 2012;120(7):1462-1469 Palomero et al. Nat Genet 2014;46(2):166-170 Sakata-Yanagimoto et al. Nat Genet 2014;46(2):171-175 Vallois et al. Blood 2016;128(11):1490-1502 Lemonnier F et al. PNAS 2016;113(52):15084-15089



#### **MOLECULAR FEATURES**

- Recurrent mutations in epigenetic modifier genes (*TET2*, *IDH2*<sup>R17</sup>, and *DNMT3A*)
- Also found in healthy individuals with clonal hematopoiesis
- Possible multistep pathogenesis of TFHL:
  - Girst hit»: TET2 +/- DNMT3A
  - Gircle second hit": RHOA G17V, other genes



Tiacci et al. NEJM 2018;379(10):981–4 Lewis et al. Blood Adv 2020;4:2261–2271





- The overall prognosis of patients with TFHL is poor (3-year OS ~ 50%)
- Lenalidomide + CHOP: *DNMT3A* mutations are associated with shorter response rate to chemotherapy and adverse PFS
- Co-occurrence of TET2/IDH/DNMT3A mutation was associated with shorter PFS and OS



Lemonnier et al. Blood Adv 2021;5(2):539-548



PRIMARY NODAL EBV–POSITIVE T/NK-CELL LYMPHOMA



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#### PRIMARY NODAL EBV–POSITIVE T/NK-CELL LYMPHOMA

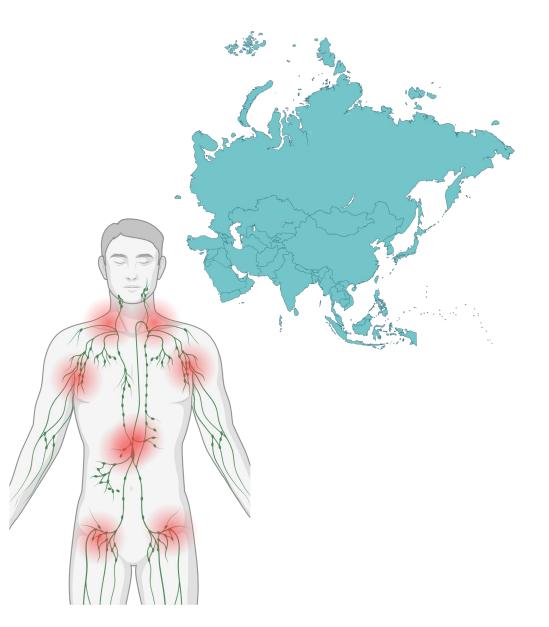
- Most EBV+ T/NK-cell lymphomas arise in extranodal sites (e.g ENKTL)
- Primary nodal EBV+ nTNKLs are much rarer
- Classified as a variant of PTCL-NOS in WHO-HAEM4R
- New distinct entity in ICC and WHO-HAEM5

WHO-HAEM4R	ICC 2022	WHO-HAEM5	
Not listed as an entity (PTCL, NOS)	Primary nodal EBV+ T-cell/NK-cell lymphoma	EBV+ nodal T- and NK-cell lymphoma	



## **CLINICAL FEATURES**

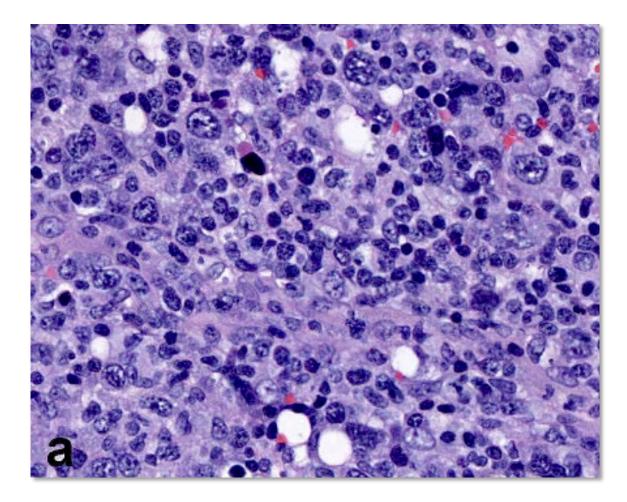
- East Asia (≈ ENKTL)
- Usually affecting the elderly, advanced stage disease
- Often associated with immunodeficiency
- Lymphadenopathy with or without extranodal involvement
- No nasal involvement
- Advanced-stage disease and B symptoms



#### Ng et al. Haematologica 2018;103:278–287

### **MICROSCOPIC FEATURES**

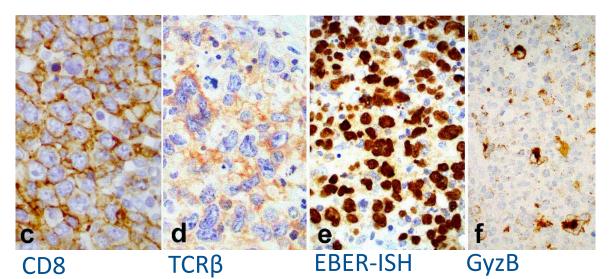
- Medium- to large-sized lymphocytes (mimicking DLBCL)
- Angiocentric infiltration and necrosis are uncommon (≠ ENKTL)

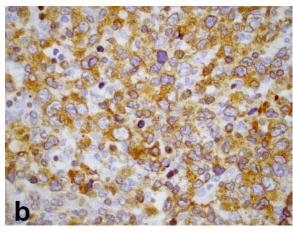




## IMMUNOPHENOTYPE

- Positive for pan-T-cell markers and cytotoxic molecules
- Usually CD8+/CD56-
- Frequent loss of CD5
- In situ hybridization for EBV-encoded small RNAs (EBER ISH) is positive by definition
- Type 2 EBV latency pattern



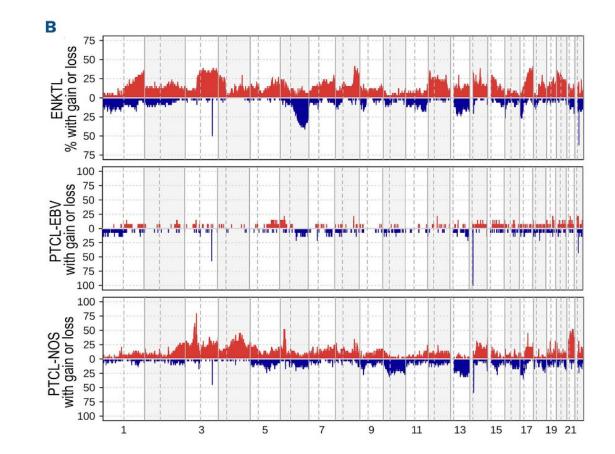


CD3

#### Adapted from Wai et al. Haematologica 2022;107(8):1864-1879

### **MOLECULAR FEATURES**

- Predominantly of T-cell origin (80% clonal rearrangement of TCR genes)
- Mutations in *TET2* (64%), *PIK3CD* (33%), *DDX3X* (20%), and *STAT3* (19%)
- Lower genomic instability than ENKTL or PTCL-NOS

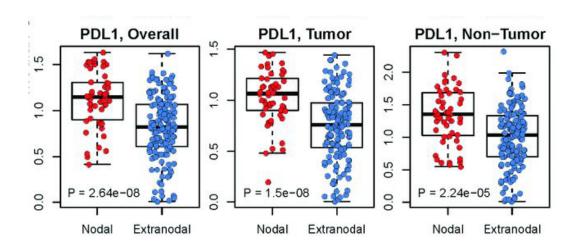


Adapted from Wai et al. Haematologica 2022;107(8):1864-1879



### **MOLECULAR FEATURES**

- Upregulation of genes related to
  - Cytotoxic activation
  - □ JAK/STAT signaling
  - □ Immune-related pathways (CD274/PD-L1)

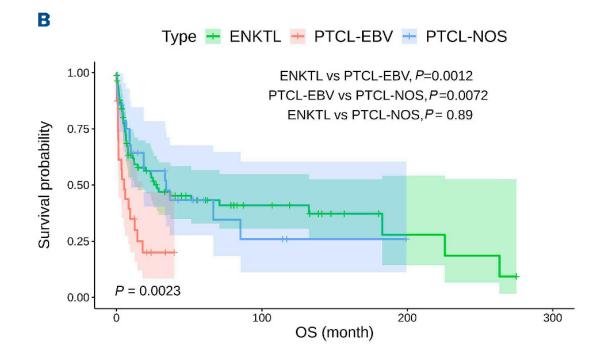


#### Adapted from Ng et al. Haematologica 2018;103:278–287



#### **PROGNOSIS**

- Poor outcomes compared with ENKTL or PTCL-NOS
- Median OS is 2.5 to 8.9 months



#### Adapted from Wai et al. Haematologica 2022;107(8):1864-1879





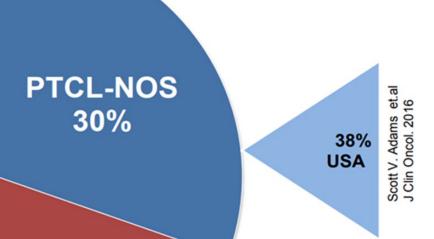
## PERIPHERAL T-CELL LYMPHOMA, NOT OTHERWISE SPECIFIED



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#### PERIPHERAL T-CELL LYMPHOMA, NOT OTHERWISE SPECIFIED

- Heterogeneous category
- Diagnosis of exclusion: nodal mature T-cell lymphomas that cannot be assigned to a specific entity





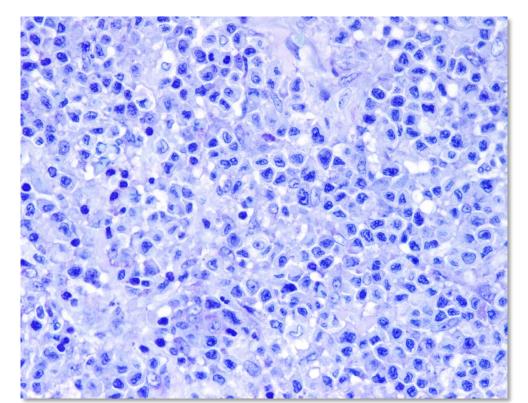
### **MICROSCOPIC FEATURES**

- Paracortical or diffuse pattern
- Wide spectrum of cytologic features

medium-sized cells with irregular nucleai (most often)

□ small or large-sized T cells

Inflammatory background

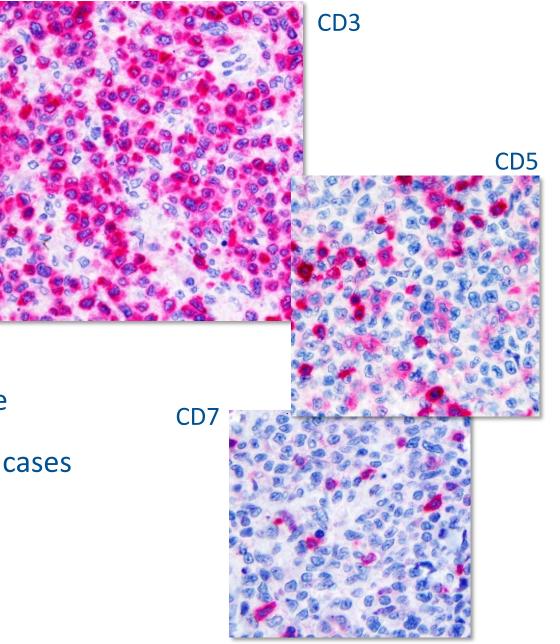


- Epithelioid histiocytes can be numerous in so-called Lennert lymphoma
- Scattered HRS-like and/or EBV-positive B-immunoblasts



### IMMUNOPHENOTYPE

- Mature T-cell phenotype
- Aberrant loss or diminished expression of one or more pan-T-cell markers (CD2, CD3, CD5, CD7, and TCR)
- Mostly CD4+/CD8-  $\rightarrow$  exclude TFH phenotype
- Cytotoxic molecules are positive in a subset of cases  $\rightarrow$  exclude EBV+



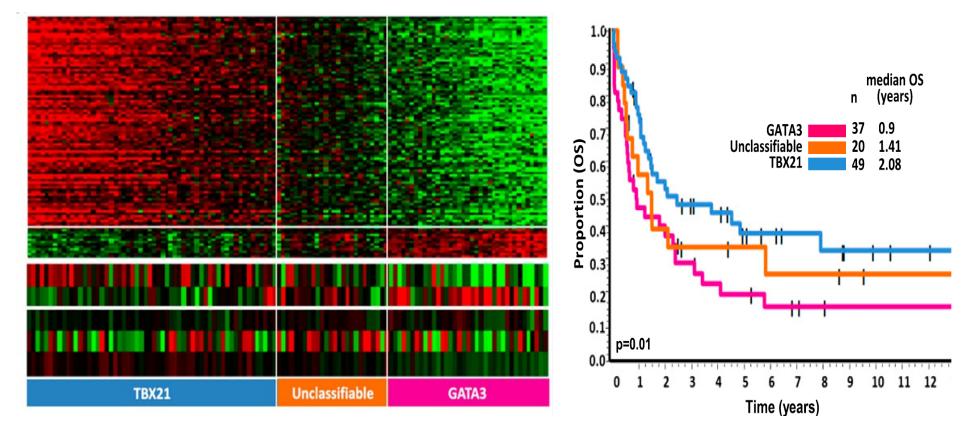
### **MOLECULAR FEATURES**

- Highly heterogeneous and complex genomic landscape
- Recurrent mutations in genes associated with:
  - □ TCR pathway (*PLCG1* and *CARD11*)
  - □ JAK/STAT pathway (JAK3, STAT3, and SOCS1)
  - Cell cycle (TP53, CDKN2A, and ATM)
  - □ DNA methylation (*TET2* and *DNMT3A*)
- TP53 and CDKN2A mutations and/or deletions
- Fusion genes involving FER and VAV1



#### **MOLECULAR FEATURES – TBX21 and GATA3**

Two distinct molecular subtypes have been recognized by GEP





#### *Adapted from* lqbal et al. Blood 2014;123:2915–2923

### **MOLECULAR FEATURES – TBX21 and GATA3**

#### PTCL-TBX21

- □ Th1-like signature
- □ High expression of TBX21 and EOMES and their target genes (CXCR3, IL2RB, CCL3, and IFNG)
- □ Fewer of copy number alterations (CNAs)
- Frequent mutations in genes associated with DNA methylation
- □ More favorable prognosis

#### **PTCL-GATA**3

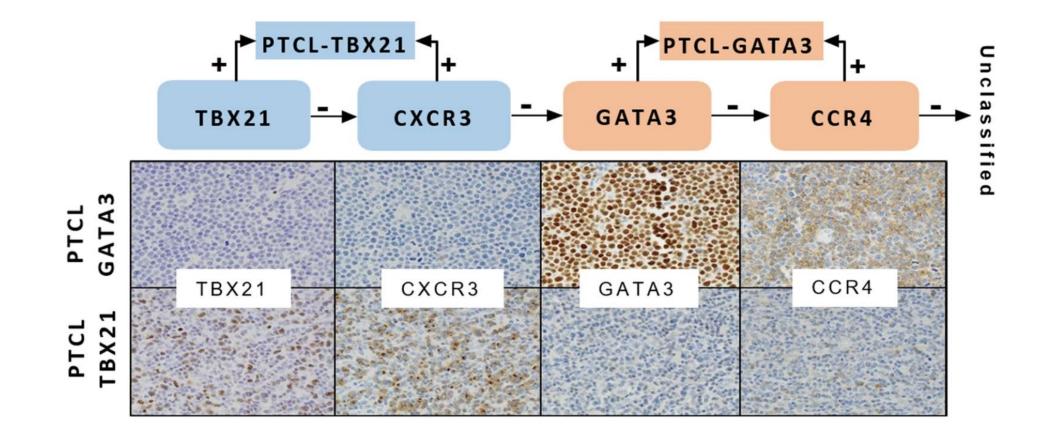
#### □ Th2-like signature

- □ High expression of GATA3 and its target genes (CCR4, IL17RA, CXCR7)
- □ Higher level of CNAs
- Loss/ mutation of tumor suppressor genes (CDKN2A/B-TP53 & PTEN-PI3K)
- Poorer prognosis



Heavican et al. Blood 2019;133:1664–1676

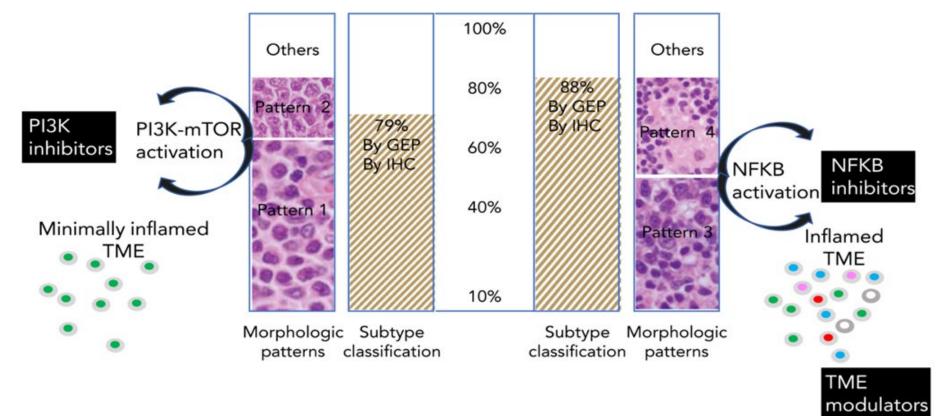
### How to diagnose in daily practice?



\* EHA REALFACTOR TUrkish Society of Hematology www.thd.org.tr

Amador et al. Blood 2019;134:2159–2170

#### PTCL-GATA3 PTCL-TBX21



	Cell of origin	
T <sub>H</sub> 2 (?)	T <sub>H</sub> 1 (?)	
	Clinical outcome	
Worse	Poor	



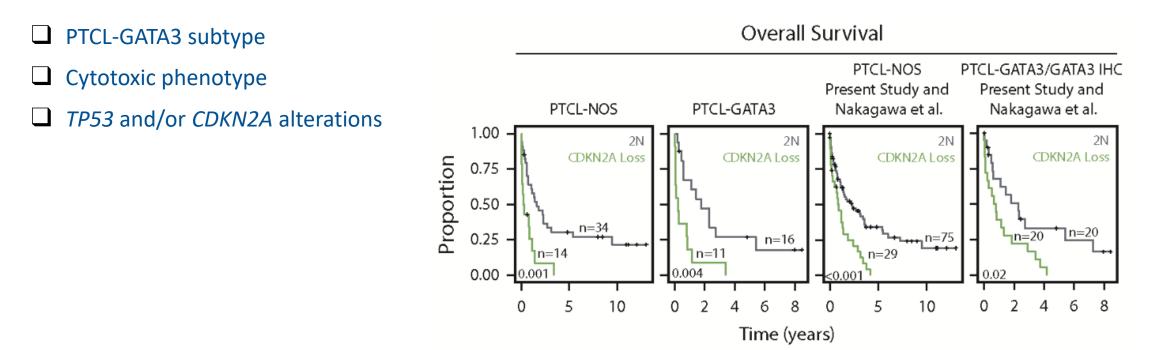
#### Adapted from Carbone A, Gloghini A. Blood 2019;134(24):2120-2121

#### **PROGNOSIS**

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- Poor response to therapy, frequent relapses, and short OS
- Molecular features associated with inferior OS:



Heavican et al. Blood 2019;133:1664–1676





# Thank you

