



## The 65th ASH Annual Meeting Abstracts

## ORAL ABSTRACTS

## 621.LYMPHOMAS: TRANSLATIONAL-MOLECULAR AND GENETIC

**Polytypic B-Cells, B-Cell Lymphoproliferative Disorders/Lymphomas, and Neoplastic T-Cells Divergently Differentiate from *TET2*-/*DNMT3A*-Mutated Clonal Hematopoiesis in Patients with Follicular Helper T-Cell Lymphomas/Lymphoproliferative Disorders**

Natasha Lewis, MD<sup>1</sup>, Kseniya Petrova-Drus, MD PhD<sup>1,2</sup>, Rohan Sardana, MD<sup>1</sup>, Qi Gao, DCLS<sup>3</sup>, Shenon Sethi, MBBS<sup>1</sup>, Wenbin Xiao, MD PhD<sup>1</sup>, Mikhail Roshal, MD PhD<sup>3</sup>, Jeeyeon Baik, BA, MPH<sup>1</sup>, Himanshu Bhurtel, BS<sup>1</sup>, Alison Moskowitz, MD<sup>4</sup>, Steven M. Horwitz, MD<sup>4</sup>, Ahmet Dogan, MD PhD<sup>1</sup>

<sup>1</sup> Department of Pathology and Laboratory Medicine, Hematopathology Service, Memorial Sloan Kettering Cancer Center, New York, NY

<sup>2</sup> Department of Pathology and Laboratory Medicine, Molecular Diagnostics Service, Memorial Sloan Kettering Cancer Center, New York, NY

<sup>3</sup> Memorial Sloan Kettering Cancer Center, New York

<sup>4</sup> Memorial Sloan Kettering Cancer Center, New York, NY

## Introduction:

Patients with follicular helper T-cell lymphomas/lymphoproliferative disorders (TFH-LPDs) commonly develop B-cell lymphoproliferative disorders and lymphomas (B-LPDs), but the pathophysiology is incompletely understood. TFH-LPDs often arise from *TET2*-/*DNMT3A*-mutated clonal hematopoiesis (CH). Here we show *TET2*/*DNMT3A* mutations are commonly shared by polytypic B-cells (PBCs), B-LPDs, and TFH-LPDs, with the latter two often carrying additional unique mutations.

## Methods:

Pathology database search at Memorial Sloan Kettering identified patients with TFH-LPDs and PBCs or B-LPDs available for genotyping. If available, myeloid cells were also genotyped. PBCs lacked aberrancies by morphology and flow cytometry (FC) immunophenotyping (including polytypic light chain expression). TFH-LPDs and B-LPDs were defined using International Consensus Classification criteria. Genotyping assays included targeted next-generation sequencing (NGS) with (n=13) or without (n=8; cases 1, 4, 9, 10, 15, 16, 17, 22) a matched germline control and droplet digital PCR (n=4; cases 2, 3, 5, 6). Genotyping was performed on bulk samples or FC-sorted cells, including T-, B-, and myeloid as available. In bulk samples, mutations with allele frequencies (VAFs) >2x the percentage of neoplastic T- and myeloid cells combined in B-LPD samples and of neoplastic T- and total B-cells in bulk blood (PB)/bone marrow (BM) samples were considered present in B-LPD or myeloid compartments, respectively. A >2% VAF cutoff was utilized. EBV status was assessed using EBER in situ hybridization on tissues, serum EBV DNA by quantitative PCR, and/or evaluation of off target EBV reads by NGS. Statistical analyses utilized Mann-Whitney U tests.

## Results:

In total, 25 patients (10 female, 15 male; median age 70 [range 38-82] years) with TFH-LPDs (19 TFH lymphoma, angioimmunoblastic type, 4 TFH lymphoma, NOS, 2 T-LPD with TFH phenotype [defined by morphologically and/or immunophenotypically atypical T-cells with both TFH-like phenotypes and genomic alterations that did not fulfill morphologic criteria for diagnosis of lymphoma]) were identified. The TFH-LPDs harbored *TET2* (25/25, 100%), *DNMT3A* (12/25, 48%), *RHOA* p.G17 (15/25, 60%), and *IDH2* p.R172 (9/25, 36%) mutations (Figure 1A).

PBCs from 11 patients were evaluated (7 EBV+, 3 EBV-, 1 EBV unknown; 5 from lymph node, 4 PB, 2 BM). PBCs from 7/11 (64%) shared identical *TET2* (n=6; median VAF 0.11 [range 0.02 - 0.27]) and/or *DNMT3A* (n=3; median VAF 0.05 [range 0.03-0.49]) mutations with corresponding TFH-LPDs. PBCs in 1 patient harbored a unique mutation (*TET2*). Four of 8 (50%) patients in which myeloid cells were assessed harbored identical *TET2* and/or *DNMT3A* mutations in the myeloid, PBC, and TFH-LPD compartments.

B-LPDs were evaluated from 14 patients (5 diffuse large B-cell lymphoma, 5 polymorphic B-LPD, 2 follicular lymphoma, 1 B-LPD, NOS, 1 plasma cell myeloma; 11 EBV+, 3 EBV-; 9 from tissue, 4 PB, 1 BM). Polymorphic B-LPDs showed atypical polymorphic morphology and an abnormal B-cell immunophenotype by FC and/or a clonal IgH gene rearrangement. The B-LPD, NOS showed an abnormal CD5-/CD10- immunophenotype with light chain restriction by FC without available tissue

for morphologic evaluation. Nine of 14 (64%) B-LPDs shared identical mutations with corresponding TFH-LPDs ( *TET2* [n=9; median VAF 0.42 (range 0.10- 0.56)], *DNMT3A* [n=5; median VAF 0.27 (range 0.05-0.50)], *TET3* [n=1; VAF 0.32]). Myeloid compartments in 9/12 (75%) patients shared identical *TET2* and/or *DNMT3A* mutations with B- and/or T-LPDs. B-LPDs more commonly harbored additional mutations absent in corresponding TFH-LPDs than PBCs (12/14 [86%] vs 1/8 [13%] evaluated by NGS; p=0.001). Unique mutations in B-LPDs involved epigenetic/transcriptional regulation (n=14, e.g. *TET2*, *KMT2D*, *SETD5*), signaling pathways (n=22, e.g. *DTX1*, *KRAS*, *EPHA5*), and DNA damage response (n=3, e.g. *ATM*, *CHEK2*, *BRCA2*). Incidences of shared and unique mutations did not significantly differ among EBV+ and EBV- cases.

Conclusions:

Both PBCs and B-LPDs in TFH-LPD patients are commonly EBV+ and share *TET2/ DNMT3A* mutations with TFH-LPDs, consistent with common origin from CH. B-LPDs more often harbor additional unique mutations than PBCs. Thus, CH mutations and EBV activation in B-cells may predispose TFH-LPD patients to B-LPDs, which may develop with additional private genomic aberrations aiding transformation (Figure 1B).

**Disclosures Lewis:** United States Drug Testing Laboratories: Consultancy, Membership on an entity's Board of Directors or advisory committees. **Roshal:** Physicians' Education Resource: Other: Provision of services; **Celgene:** Other: Provision of services; **Auron Therapeutics:** Other: Ownership/Equity interests; Provision of services; **NGM:** Other: Funding; **Roche:** Other: Funding; **Beat AML:** Other: Funding. **Baik:** Pauling.AI: Current Employment. **Moskowitz:** Merck: Honoraria, Research Funding; **ADC Therapeutics:** Research Funding; **Bristol-Myers Squibb:** Research Funding; **Beigene:** Research Funding; **Incyte:** Research Funding; **Seattle Genetics:** Honoraria, Research Funding. **Horwitz:** Takeda: Consultancy, Research Funding; **Tubulis:** Consultancy; **Crispr Therapeutics:** Research Funding; **Millenium:** Research Funding; **Seattle Genetics:** Research Funding; **Verastem/SecuraBio:** Research Funding; **Trillium Therapeutics:** Consultancy, Research Funding; **Affimed:** Research Funding; **Celgene:** Research Funding; **Daiichi Sankyo:** Consultancy, Research Funding; **Kyowa Hakko Kirin:** Consultancy, Research Funding; **ONO Pharmaceuticals:** Consultancy; **SecuraBio:** Consultancy; **Shoreline Biosciences, Inc.:** Consultancy; **ADC Therapeutics:** Research Funding; **Yingli Pharma Limited:** Consultancy; **Cimieo Therapeutics:** Consultancy; **Abcuro Inc.:** Consultancy; **Auxilium Pharma:** Consultancy. **Dogan:** Incyte: Consultancy; **Peer View:** Honoraria; **Loxo:** Consultancy; **EUSA Pharma:** Consultancy; **Physicians' Education Resource:** Consultancy, Honoraria; **Seattle Genetics:** Consultancy; **Takeda:** Other: Research Funding; **Roche:** Other: Research Funding.

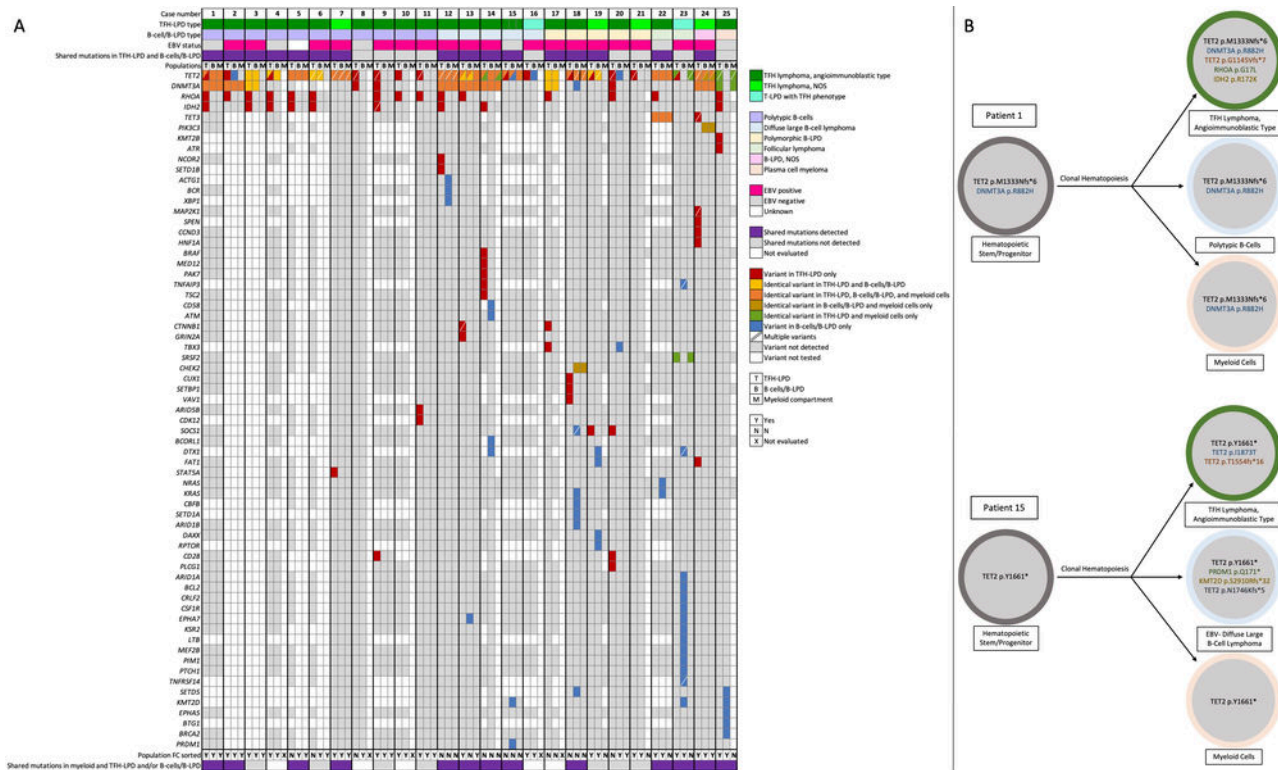


Figure 1

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