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ORAL ABSTRACTS

618.ACUTE LYMPHOBLASTIC LEUKEMIAS: BIOMARKERS, MOLECULAR MARKERS AND MINIMAL RESIDUAL **DISEASE IN DIAGNOSIS AND PROGNOSIS**

STAG2/LMO2 Gamma-Delta ($\gamma \delta$) T-ALL: Identification and Characterization of an Extremely High Risk Group of T-ALL in the Very Young

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Background

Methods

The prognosis of pediatric T-cell acute lymphoblastic leukemia (T-ALL) has improved with minimal residual disease (MRD)stratified therapy, however, gamma delta T cell receptor positive ($\gamma \delta$) T-ALL remains a high-risk (HR) group. Limited studies have explored the clinical and genomic characteristics of $\gamma\delta$ T-ALL, prompting us to conduct a comprehensive analysis of this entity and to identify determinants of outcome.

Through a consortium of 13 groups, we assembled a cohort of 200 patients up to 25 years of age with $\gamma\delta$ T-ALL enrolled in clinical trials between 2000 and 2018. Clinical data of patients with non- $\gamma\delta$ T-ALL enrolled on the same clinical trials were collected (n = 1,067). Complete remission (CR) was defined when bone marrow (BM) showed M1 cytomorphology and/or MRD <1% without evidence of extramedullary disease at end of induction/consolidation (EOI/EOC) and failure to achieve CR was considered treatment failure. A total of 76 $\gamma\delta$ T-ALL samples were analyzed by whole genome (WGS) and/or transcriptome (RNAsea) sequencina.

The frequency of $\gamma \delta$ T-ALL was 8.0% of T-ALL cases. Patients with $\gamma \delta$ T-ALL exhibited a higher rate of poor prednisone response (P<0.01), MRD > 1% at day 15 (P<0.01), at EOI (P<0.01) and EOC (P<0.01), compared to non- $\gamma\delta$ T-ALL cases. Furthermore, patients with $\gamma\delta$ T-ALL showed significantly worse 5-year event free survival (EFS, 65% v. 78%, P<0.01) and overall survival (OS, **ORAL ABSTRACTS** Session 618

77% vs 83%, P=0.048). Almost all relapses of $\gamma\delta$ T-ALL were isolated BM, while the central nervous system was the main site of relapse in non- $\gamma\delta$ T-ALL, suggesting slow treatment response and chemo-resistance to the current treatment in $\gamma\delta$ T-ALL. However, $\gamma\delta$ T-ALL showed a higher rate of toxic death during treatment (7.6% vs 4.0%, P<0.01), suggesting the need for different therapeutic strategies and risk-classification, rather than treatment intensification.

Strikingly, patients less than 3 years of age with $\gamma\delta$ T-ALL exhibited significantly poor EFS (33% v. 70% [3-10 years] and 73% [>10], P<0.01) and OS (49% v. 78% [3-10] and 82% [>10], P<0.01) (**Fig. A**), a difference not observed in non- $\gamma\delta$ T-ALL. MRD >1% at EOI showed poor EFS (51% v. 96% [MRD<0.01%] and 91% [1%>MRD>0.01%], P<0.01) and OS (66%).

Integrated analysis of WGS and RNAseq identified enrichment of several genomic subtypes in $\gamma\delta$ T-ALL, including STAG2/LMO2, hyperdiploidy with recurrent gains of chromosomes 8, 10, 11, 13q and 19, a recently identified "LMO2 γδlike" subtype with distinct gene expression and LMO2/MYC/MYCN alterations, TLX3-rearranged (-R), and PICALM::MLLT10. No TAL1 nor TLX1-R were detected. STAG2/LMO2 was associated with age at diagnosis before 3 years, and extremely poor outcome, with 4 out of 5 cases dying within three years of diagnosis (Fig. B).

Of 24 STAG2/LMO2 T-ALL (additional 5 non- $\gamma\delta$, 13 TCR unknown cases), 22 of which were diagnosed by age three. All STAG2/LMO2 cases had alterations resulting in LMO2 activation and STAG2 inactivation, most commonly a single rearrangement between these two genes, and upregulation of HBE1, the LIN28-let7 pathway and stem cell proliferation pathways, suggesting a fetal hematopoietic origin.

STAG2 has a critical role in the maintenance of enhancer-promoter looping mediated by the cohesin complex. To examine the consequences of STAG2 alterations, we performed integrated genomic/epigenomic analysis of the STAG2/LMO2 (MOLT-14 and PER-117) and STAG2 knockout (KO)/addback T-ALL lines. Chromatin loop sizes defined by H3K27ac HiChIP was highest in STAG2/LMO2 lines compared to other T-ALL. Following restoration of STAG2 expression in MOLT-14, CD34 and ID1/2 were down-regulated and H3K27ac was enriched in pathways related to T-cell differentiation. STAG2 KO in the non-STAG2/LMO2, LMO2-activated line PF382 identified genes also upregulated in STAG2/LMO2 primary samples, including CDK4 and STAG1. STAG2 KO lines exhibited partial compensation of STAG2 binding sites by STAG1 and upregulation of $\gamma\delta$ -related genes, RORC and ID1/3. High throughput screening of 2,050 small molecules identified efficacy of HDAC, CDK and PARP inhibitors in STAG2/LMO2 lines.

Conclusion

Very young onset $\gamma\delta$ T-ALL, but not non- $\gamma\delta$ T-ALL, is enriched for the STAG2/LMO2 subtype and is a very high risk form of T-ALL. STAG2 loss perturbs chromatin organization and hematopoietic differentiation. Moreover, we demonstrate efficacy of novel therapeutic approaches that are needed to cure this form of leukemia.

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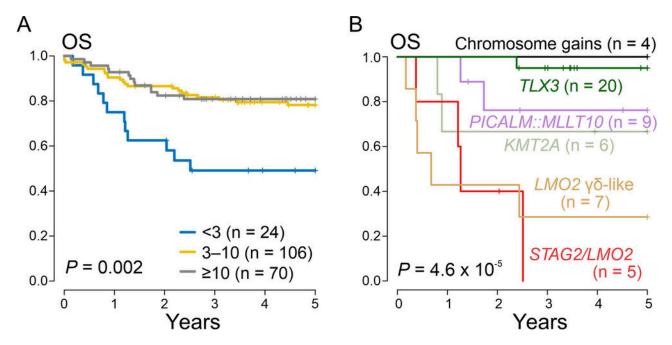


Figure 1

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