had no impact - splenectomy vs no splenectomy (median OS 11.22 vs 7.05 months, P = 0.113), hematopoietic stem cell transplantation (HSCT) vs no HSCT (median OS 14.40 vs 11.30 months, P = 0.662) and chemotherapy vs no chemotherapy (median OS 11.39 vs 10.02 months, P = 0.323).

Also, there was no difference in OS observed between different treatment modalities [chemo only (143 patients), splenectomy only (21 patients), chemo with splenectomy (51 patients), chemo with HSCT (12 patients), splenectomy with chemo and HSCT (10 patients)]. Compared to no treatment, only splenectomy with chemotherapy was prognostic for OS (18.6 vs 2.9 months, P = 0.030).

On multivariate analysis, female gender (HR 0.664 95% CI 0.462-0.954; P = 0.027) and splenectomy (HR 0.611 95% CI 0.418-0.892; P = 0.011) were associated with better OS, whereas chemotherapy and HSCT had no impact (HR 1.010 95% CI 0.634-1.608; P = 0. 967 and HR 0.951 95% CI 0.563-1.607; P = 0. 852, respectively).

Conclusion: In this large real-world cohort based analysis of HSTCL, female gender and treatment with splenectomy were associated with better OS, while chemotherapy and HSCT failed to improve survival.

Keywords: Aggressive T-cell non-Hodgkin lymphoma

No conflicts of interest pertinent to the abstract.

223 | SUBTYPES OF MATURE T AND NK CELL LYMPHOMAS ACCORDING TO 2016 WHO CLASSIFICATION. PRELIMINARY REPORT OF THE INTERNATIONAL PROSPECTIVE T-CELL PROJECT 2.0

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Introduction: Mature T and NK-cell lymphomas represent a heterogeneous group of lymphoid disorders (29 subtypes according to the 2016 WHO classification) arising from mature T cells of post-thymic origin with different morphological characteristics, phenotypes, and clinical presentation. Following the success of the T Cell Project (TCP), which allowed the analysis of more than 1,500 cases of peripheral T-Cell lymphomas (PTCLs) collected prospectively in 18 Countries, in 2018 the TCP 2.0 was launched. Here we report the global distribution of PTCLs, from the cases registered so far based on the locally established histological diagnosis.

Methods: The TCP2.0 (ClinicalTrials.gov Identifier: NCT03964480) is a prospective, international, observational study which adapts to changes made in the new WHO classification.

Results: Since the beginning of the study (October 2018), 648 patients with newly diagnosed PTCL were registered by 75 active centers across 14 countries. Of these data, 594 patients have been validated by the centralized trial office. Overall, PTCL-NOS, Anaplastic large cell lymphoma (ALCL) ALK-negative, and Angioimmunoblastic T-cell lymphoma (AITL), represent the most frequent subtypes, representing 31.3%, 18,9% and 13,5% of cases, respectively.

As reported in Table 1, PTCL-NOS represents the most frequent subtype worldwide, whereas Adult T-cell leukemia/lymphoma was more frequent in Brazil, AITL and ALCL ALK-negative in Australia/India, and ALCL ALK-positive in North America and Europe. Extranodal NK/T-cell lymphoma, nasal type was relatively frequent in Brazil and quite rare in the other Latin America Countries. Finally, many sub-types represent less than 5% of cases in all geographic areas.

Conclusions: The TCP2.0 continues to recruit very well, despite the difficulties linked to the COVID-19 pandemic, and may represent a useful resource for the prospective study of this group of rare lymphomas.

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Keywords: Aggressive T-cell non-Hodgkin lymphoma, Pathology and Classification of Lymphomas

Conflicts of interests pertinent to the abstract

E. A. Hawkes

Other remuneration: Takeda, Roche

Subtypes (ICD-O code)	Total N (%)	Australia/India N (%)	Brazil N (%)	Hispanic America N (%)	North America/Europe N (%)
PTCL, NOS (97023)	**186 (31,3)**	**54 (32,3)**	**93 (31,4)**	**23 (33,8)**	**16 (25,4)**
Lymphoepitelioid lymphoma	3 (0,5)	0 (0,0)	1 (0,3)	2 (2,9)	0 (0,0)
ALCL, ALK – (97153)	**112 (18,9)**	**40 (24)**	**53 (17,9)**	**12 (17,6)**	**7 (11,1)**
AITL (97053)	**80 (13,5)**	**27 (16,2)**	**32 (10,8)**	**8 (11,8)**	**13 (20,6)**
PTCL-TFH (97023)	1 (0,2)	0 (0,0)	0 (0,0)	0 (0,0)	1 (1,6)
ENKTCL (97193)	69 (11,6)	19 (11,4)	39 (13,2)	3 (4,4)	8 (12,7)
ATLL (98273)	59 (9,9)	5 (3,0)	46 (15,5)	6 (8,8)	2 (3,2)
ALCL, ALK + (97143)	52 (8,8)	11 (6,6)	24 (8,1)	7 (10,3)	10 (15,9)
HSTCL (97163)	10 (1,7)	5 (3,0)	4 (1,4)	1 (1,5)	0 (0,0)
SPTCL (97083)	10 (1,7)	6 (3,6)	2 (0,7)	0 (0,0)	2 (3,2)
EATL (97173)	7 (1,2)	0 (0,0)	2 (0,7)	4 (5,9)	1 (1,6)
MEITL (97173)	2 (0,3)	0 (0,0)	0 (0,0)	1 (1,5)	1 (1,6)
LGL leukaemia (98313)	2 (0,3)	0 (0,0)	0 (0,0)	1 (1,5)	1 (1,6)
CLPD-NK (98313)	1 (0,2)	0 (0,0)	0 (0,0)	0 (0,0)	1 (1,6)
Total	**594**	**167**	**296**	**68**	**63**

224 | CIRCULATING TUMOR DNA BY HIGH-THROUGHPUT SEQUENCING OF T CELL RECEPTOR MONITORED TREATMENT RESPONSE AND PREDICTED TREATMENT FAILURE IN T CELL LYMPHOMAS

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Introduction: Next-generation sequencing (NGS)-based circulating tumor DNA (ctDNA) detection is a promising monitoring tool for lymphoid malignancies. Studies for T cell lymphoma are limited.

Objective: To explored whether next-generation sequencing (NGS)-based circulating tumor DNA (ctDNA) detection is applicable to T cell lymphoma and assessed its performance in clinical settings.

Methods: We first identified tumor clones, identified as any CDR3 sequences that accounted more than 5%, by TCR sequencing in pathological specimens. Then use these sequences to capture circulating tumor DNA in plamsa. Any non-zero result in the plasma was considered positive molecular disease. Results of ctDNA were compared with PET/CT or the clinical outcome.

Results: 30 tumor and 74 blood samples were analyzed in our study. Malignant clone was identified in 23 of the 30 (76.7%) tumor samples through high-throughput sequencing (HTS) combined with PCR. We detected the same tumor clone in plasma in 18 out of the 23 (78.3%) patients. Circulating tumor DNA fraction correlated with lactate dehydrogenase (LDH) ($r = 0.52$, $p = 0.017$), high level of ctDNA predicted treatment failure ($p = 0.0003$) and there was a trend patients with high ctDNA burden would have poorer PFS. Furthermore, ctDNA changed in concordance with clinical outcome and was more sensitive than PET/CT. Also, recurrence of ctDNA was an important clue for relapse.

Conclusion: In conclusion, our study indicated that ctDNA monitoring was suitable for T cell lymphoma. High level of pretreatment ctDNA was a poor prognosis factor and changes of ctDNA correlated well with clinical courses and was sensitive to find early relapse.

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Keywords: Liquid biopsy

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