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TO THE EDITOR:

Molecular profiling identifies at least 3 distinct types of posttransplant lymphoproliferative disorder involving the CNS

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Posttransplant lymphoproliferative disorder (PTLD) is an immunodeficiency-associated lymphoproliferative disorder defined as occurring in the posttransplant setting. The risk factors for development of PTLD include Epstein-Barr virus (EBV) serostatus, type of organ transplant, intensity and type of immunosuppressive regimens, patient age, and presence of genetic polymorphisms (eg, HLA).¹⁻⁸ PTLD with involvement of the central nervous system (PTLD-CNS) is a rare posttransplant complication, often with poor prognosis. PTLD-CNS has most commonly been observed after renal transplantation and typically occurs later after transplant (mean, >9 years) when compared with its EBV⁺ systemic counterpart.⁸

Prior studies of systemic PTLD demonstrated various molecular alterations in critical oncogenic pathways, such as clonal immunoglobulin gene rearrangement, somatic mutations of *RAS* and *TP53*, translocations of *MYC* and *BCL6*, and aberrant somatic hypermutation of proto-oncogenes including *BCL6*, *PIM1*, *PAX5*, and *MYC*.⁹⁻¹⁸ Notably, PTLD cases showed a substantially lower frequency of oncogenic molecular aberrations compared with sporadic lymphomas in immunocompetent patients. In this setting of PTLD with minimal oncogenic alterations, EBV is thought to be the predominant driver of lymphoproliferation. However, the genetic landscape of PTLD involving the CNS is not well established, with the most comprehensive study including cases of PTLD-CNS demonstrating that EBV⁺ and HIV⁻ cases had a low burden of somatic mutations with a lack of alterations in *MYD88*, *CD79B*, *PIM1*, and *CDKN2A/B* known to be frequent in adult-type *MYD88*-mutant primary CNS large B-cell lymphoma (PCNS-LBCL), as well as mutations in *TP53*, *NKFBIE*, and *GNA13* that we recently described as frequent in pediatric-type *MYD88*-wild-type PCNS-LBCL.¹⁹⁻²³

Here, we sought to investigate the clinical, pathologic, and molecular characteristics of PTLD-CNS to better identify factors that may be useful in risk stratification of this patient population. Through a multi-institutional collaboration, we assembled a cohort of 24 patients with PTLD-CNS (Figure 1; supplemental Tables 1 and 2). Twenty-one patients had undergone solid organ transplantation, and 3 had undergone bone marrow transplantation. Patient #22 had severe combined immunodeficiency and Nijmegen breakage syndrome, and patient #8 had Down syndrome. The remaining patients did not have any

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The full clinical, pathologic, and molecular data are available in the supplemental Data available with the online version of this article. Further original data are available on request from the corresponding author, Kwun Wah Wen (kwun.wen@ucsf.edu).

Sequence data from the 14 PTLD-CNS lesions have been deposited at the Sequence Read Archive (SRA) under BioProject ID PRJNA950018 (<https://dataview.ncbi.nlm.nih.gov/object/PRJNA950018>).

The full-text version of this article contains a data supplement.

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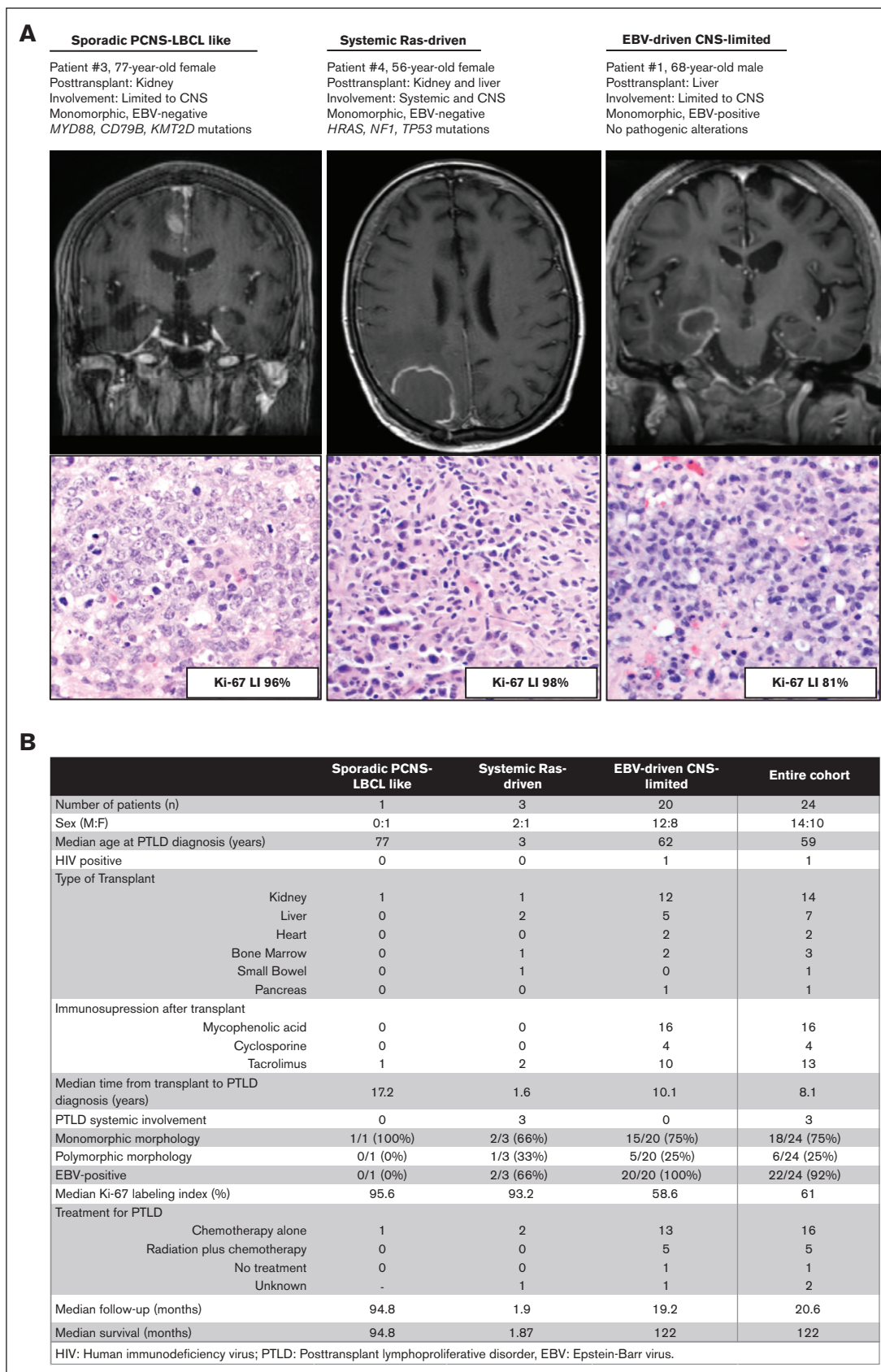


Figure 1.

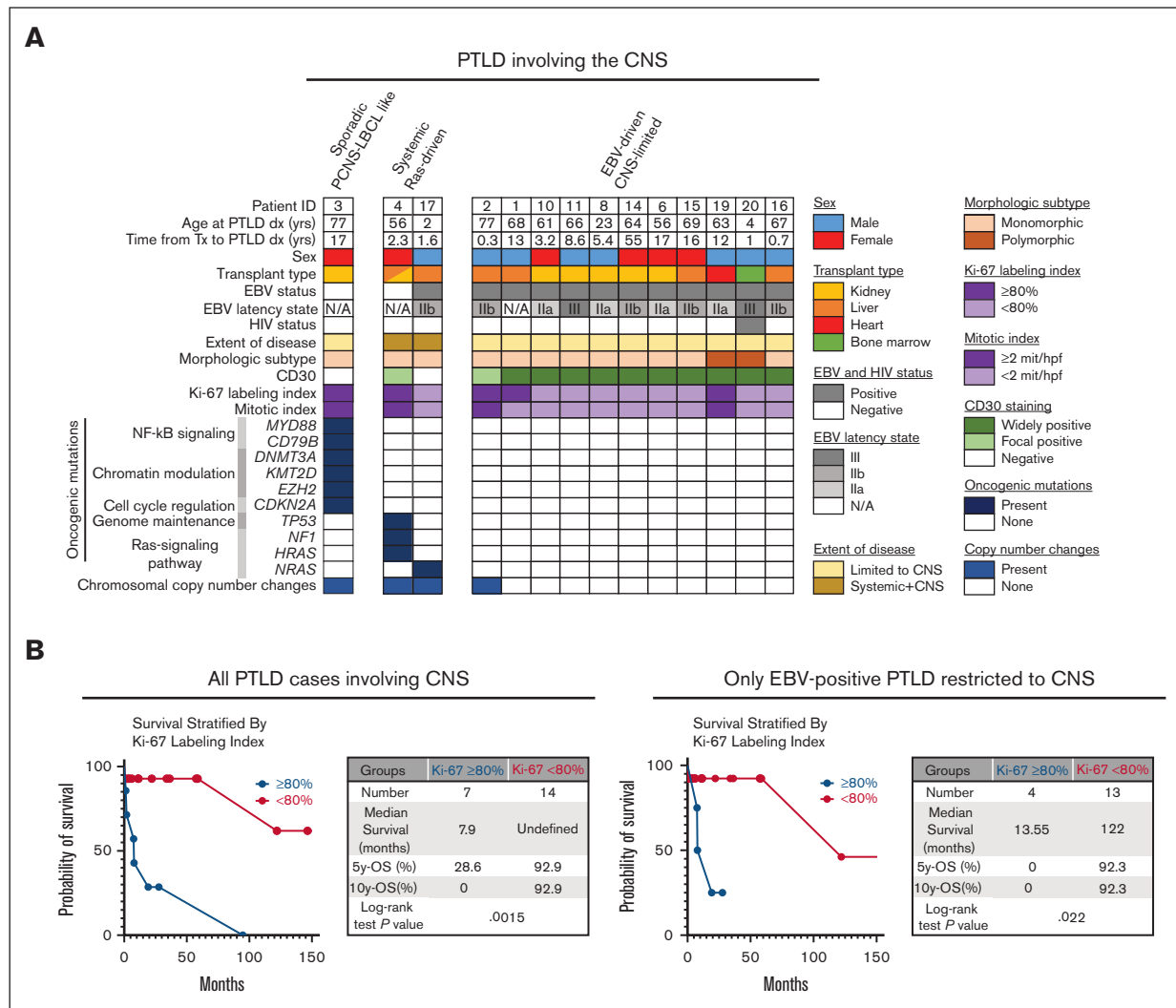


Figure 2. Integration of genomic profiling and clinicopathologic features identifies 3 distinct types of PTLD-CNS. (A) Oncoprint of genomic profiling results and clinical data from the PTLD-CNS cohort. Stratification was performed according to EBV status by in situ hybridization, presence or absence of systemic extra-CNS involvement, and pathogenic molecular alterations involving RAS family oncogenes (*HRAS* and *NRAS*) and known lymphoma oncogenes and tumor suppressor genes (*MYD88*, *CD79B*, *KMT2D*, and *CDKN2A*). (B) Kaplan-Meier survival analysis of patients with PTLD-CNS stratified by Ki-67 LI using a cutoff of 80%.

known innate immunodeficiency or tumor predisposition syndromes. The median time from organ transplant to development of PTLD-CNS was 8.1 years. Of 24 patients, 21 patients had PTLD with exclusive CNS involvement, whereas the other 3 patients also had PTLD at systemic sites (2 gastrointestinal and 1 nodal involvement) outside the CNS. The median age at time of PTLD-CNS diagnosis was 59 years (range, 2-77 years). Eighteen PTLD cases demonstrated monomorphic morphologic features resembling LBCL, whereas 6 PTLD cases demonstrated polymorphic morphology with variable composition of small-to-large sized B cells admixed with T cells and plasma cells (Figure 1A; supplemental Tables 3 and 4). Patients were treated with various combinations of dexamethasone, high-dose

methotrexate, and rituximab, along with other accompanying agents in a subset. Five patients were additionally treated with radiotherapy. The median survival of all patients with PTLD-CNS was 122 months, and the 5-year and 10-year overall survival rates were 67.5% and 50.6%, respectively. The University of California San Francisco Institutional Review Board approved this study, which was conducted in accordance with the Declaration of Helsinki.

Targeted next-generation DNA sequencing and genome-wide copy number analysis were performed (Figure 2; supplemental Tables 5 and 6; supplemental Methods). Based on integration of the molecular features, EBV status, and presence or absence of

Figure 1. Clinical and pathologic features of the 3 identified types of PTLD involving the CNS. (A) Preoperative T1-weighted postcontrast magnetic resonance imaging and hematoxylin and eosin-stained sections from representative patients with sporadic PCNS-LBCL-like, systemic Ras-driven, and EBV-driven CNS-limited PTLD-CNS showing intraparenchymal mass lesions with contrast enhancement and significant edema in the surrounding white matter. Ki-67 LI is shown. (B) Summary of clinical and pathologic features of the multiinstitutional cohort of patients with PTLD-CNS.

systemic extra-CNS involvement, we identified 3 distinct types of PTLD-CNS, which we term “sporadic PCNS-LBCL like,” “systemic Ras-driven,” and “EBV-driven CNS-limited.”

Sporadic PCNS-LBCL like: The PTLD in patient #3 was EBV⁻ and showed an activating *MYD88* hotspot missense mutation, a *CD79B* mutation, a *CDKN2A* homozygous deletion, and deleterious mutations in chromatin modulators including *DNMT3A*, *EZH2*, and *KMT2D*. The molecular signature was overall similar to sporadic EBV⁻ PCNS-LBCL in immunocompetent older adults. This patient died at 94.8 months after diagnosis.

Systemic Ras-driven: In 2 patients (#4 and #17) with both systemic and CNS involvement, there were activating mutations in RAS oncogenes. In patient #4, the PTLD was EBV⁻ and demonstrated an *HRAS* p.Q61K hotspot mutation, along with *NF1* and *TP53* inactivating mutations. This patient died at 1.9 months after PTLD-CNS diagnosis. In patient #17, the PTLD was EBV⁺ and demonstrated an *NRAS* p.Q61K hotspot mutation. This patient was alive at last follow-up at 146.6 months.

EBV-driven CNS-limited: In 11 patients, the PTLD was EBV⁺ and restricted to the CNS. There was no clinical or radiographic evidence of systemic involvement. Evaluation by next-generation sequencing did not demonstrate oncogenic alterations in any of the evaluated genes, and only 1 of the 11 cases demonstrated clonal chromosomal gains/losses, whereas the other 10 cases showed normal diploid genomes.

Next, we sought to determine associations of any relevant clinical, pathologic, and molecular features with clinical outcomes for our PTLD-CNS cohort using Cox proportional hazards univariate models (supplemental Table 7). Kaplan-Meier stratification of the entire PTLD-CNS cohort based on a Ki-67 labeling index (LI) of $\geq 80\%$ or mitotic index of ≥ 2 per high-power field, determined as optimal cutoff values by the Liu method (supplemental Table 8), demonstrated an association with worse survival (log-rank test, $P = .0015$ and $P = .0092$, respectively) (Figure 2B; supplemental Figure 1). This association of worse survival with Ki-67 LI of $\geq 80\%$ was also found in the subgroup of patients with EBV⁺ PTLD with exclusive CNS involvement (log-rank test, $P = .0092$), as well as the subgroup of patients with PTLD-CNS with monomorphic morphology (log-rank test, $P = .02$) (supplemental Figure 2A).

Overall, through integration of molecular and clinicopathologic features, we have demonstrated that PTLD involving the CNS is a heterogeneous disease category comprising at least 3 distinct biologic types. The sporadic PCNS-LBCL-like type demonstrated a molecular profile with *MYD88* and *CD79B* mutations similar to sporadic EBV⁻ adult-type *MYD88*-mutant primary CNS-LBCL,²² which suggests that the pathogenesis is similar to that of conventional EBV⁻ PCNS-LBCL in immunocompetent adults. The systemic Ras-driven type was defined by systemic extra-CNS involvement and activating RAS family oncogene mutations, similar to those reported in systemic PTLD.^{9,10} We speculate that PTLD-CNS with concurrent systemic involvement and activating RAS mutations is biologically similar to systemic PTLD with RAS mutations and may represent CNS spread of systemic Ras-driven PTLD. The lack of oncogenic alterations in EBV-driven CNS-limited cases distinguished them from the sporadic PCNS-LBCL-like and systemic Ras-driven types. Our findings support that PTLD-CNS is a molecularly heterogeneous category of lesions,

and perhaps true CNS-restricted PTLDs are devoid of oncogenic molecular alterations and driven primarily by EBV reactivation. Future studies of additional cases are needed to confirm these findings of at least 3 distinct types of PTLD-CNS.

Various clinical risk factors such as multiorgan involvement, older patient age, earlier onset after transplantation, lack of response to reduced immunosuppression, and CNS involvement are known to be associated with worse prognosis for PTLD.^{24,25} Here, we found that high proliferative activity defined by a Ki-67 LI of $\geq 80\%$ conferred worse survival in patients with PTLD-CNS. Confirmation of the prognostic utility of proliferative activity in future independent studies is important for prospective clinical risk stratification of PTLD-CNS.

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Contribution: All authors had access to clinical, pathologic, and molecular data and contributed to this study as follows: E.G., C.-H.G.L., D.A.S., and K.W.W. designed the study and contributed to specimen collection, clinical and pathologic data collection, pathologic review, data analysis, statistical analysis, and wrote the manuscript; D.A.S. and K.W.W. supervised the study; M.P. contributed to statistical analysis; R.S.O. contributed to pathologic review; K.S. performed the digital Ki-67 quantification; S.F.-P., K.M., A.T., H.V., S.P., C.J.D., J.N., D.R.B., E.H., S.P.F., R.S.O., J.L.R., A.W.B., T.T., and A.P. contributed to specimen collection, data collection, and pathologic review; and all authors critically reviewed the manuscript and approved its submission.

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