Background: Pretreatment nutritional status has been noted to be an important prognostic factor in various types of malignancies, but its prognostic significance is not still investigated in diffuse large B-cell lymphoma (DLBCL) patients in the rituximab era.

Method: A retrospective cohort of 297 patients with newly diagnosed DLBCL treated with rituximab, cyclophosphamide, doxorubicin, vincristine, and prednisone (R-CHOP) were analyzed to reveal the prognostic significance of the controlling nutritional status (CONUS) score. The CONUS was calculated by the serum albumin concentration, the total peripheral lymphocyte count, and the total cholesterol concentration, which has been developed to screen nutritional status in the early stage of the diseases.

Result: The mean follow-up duration was 39.9 months (95% confidence interval [CI], 36.7-43.3 months). At a CONUS cutoff of <2 vs ≥2, a trend towards longer 5-year progression-free survival (PFS, CONUS 0 vs 1/2, 76.5% vs 63.6%, respectively; \( P = .088 \)) was observed in all of the treated patients. In germinal center (GC) type subgroup, the lower CONUS group showed a significantly longer 5-year PFS (CONUS 0 vs 1/2, 80.1% vs 69%, respectively; \( P = .048 \)). Five-year PFS and overall survival (OS) were significantly better in patients with the lower Glasgow prognostic score (GPS), the lower Ann Arbor stage, the better Eastern Cooperative Group (ECOG) performance status, and the lower international prognostic indices (IPI). In multivariate analysis, the lower international prognostic indices was the only significant poor prognostic factor for PFS (hazard ratio [HR], 2.56; 95% CI, 1.33-4.91; \( P = .005 \)), but for OS, the GPS (HR, 2.1; 95% CI, 1.07-4.51; \( P = .019 \)) and the ECOG performance status (HR, 2.2; 95% CI, 1.07-4.51; \( P = .33 \)) were significant prognostic factors.

Conclusion: Pretreatment nutritional status calculated by the CONUS has the possibility of predictive value of progression-free survival in DLBCL patients treated with rituximab-based regimen, especially in GB type patients.

Keywords: diffuse large B-cell lymphoma (DLBCL); prognostic indices; rituximab

PROGNOSTIC ROLE OF THE NEUTROPHIL-TO-LYMPHOCYTE RATIO IN PATIENTS WITH PRIMARY CENTRAL NERVOUS SYSTEM LYMPHOMA

Introduction: Neutrophil-to-lymphocyte ratio (NLR) is one of parameters complete blood cell count (CBC) tests provide and has been reported to be an easily-accessible prognostic marker in aggressive cancer including non-Hodgkin lymphoma (NHL). Primary CNS lymphoma (PCNSL) is an extranodal NHL with highly aggressive features. However, the importance of NLR has never been assessed in PCNSL.

Methods: This retrospective study enrolled 62 biopsy-proven patients whose baseline NLR was available and reviewed their medical records.
to compare high (≥2.0) and low NLR group in terms of clinical characteristics and outcomes.

Results: The low NLR group showed significantly better response rates to induction chemotherapy vs the other one (P = .041). With a median follow-up of 41.5 months, the high NLR group revealed significantly worse 3-year overall survival (OS) (42.5 vs 71.2%; P = .031), and 3-year progression-free survival (PFS) (37.3 vs 60.1%; P = .028).

In univariable Cox analysis, high NLR at diagnosis was a poor prognostic factor for both 3-year OS (HR, 2.64; 95% CI, 1.06-6.58; P = .038) and 3-year PFS (HR, 2.41; 95% CI, 1.07-5.42; P = .034). However, multivariable analyses adjusting for IELSG score and induction chemotherapy regimen showed no statistical significance albeit high NLR’s tendency towards worse 3-year OS (HR, 2.36; 95% CI, 0.99-5.64; P = .053) and worse 3-year PFS (HR, 2.01; 0.92-4.36; P = .079).

Conclusions: In conclusion, given the fact that it is simple and easy to obtain, NLR might play a potential role in prognostication of PCNSL from the very beginning of patient journey.

Keywords: non-Hodgkin lymphoma (NHL); primary CNS lymphoma (PCNSL); prognostic indices

### TABLE 1 Univariable analyses for overall survival and progression-free survival

|          | OS          | PFS          |
|----------|-------------|--------------|
|          | HR (95% CI) | p            | HR (95% CI) | p            |
| NLR <2   | 1           |              | 1           |              |
| ≥2.0     | 2.64 (1.06, 6.58) | 0.038       | 2.41 (1.07, 5.42) | 0.034       |
| Age ≤60  | 1           |              | 1           |              |
| >60 years old | 2.36 (0.99, 5.64) | 0.053       | 2.01 (0.92, 4.36) | 0.079       |
| ECOG ≤1  | 1           |              | 1           |              |
| >1       | 2.43 (1.11, 5.32) | 0.026       | 1.62 (0.78, 3.34) | 0.196       |
| IELSG ≤2 | 1           |              | 1           |              |
| >2       | 3.25 (1.24, 8.52) | 0.016       | 2.22 (0.97, 5.01) | 0.060       |
| Location | Non-deep    |              | Deep lesion | 0.69 (0.31, 1.51) | 0.349       |
|          | Normal      |              | Elevated   | 1.62 (0.20, 12.8) | 0.649       |
| LDH      | Normal      |              | Elevated   | 2.59 (1.15, 5.84) | 0.022       |
| Induction regimen | R-mop 1 | 5.90 (0.80, 43.8) | 0.083      | 4.04 (0.96, 17.0) | 0.056      |
| CRP      | Normal      |              | Elevated   | 0.71 (0.23, 2.17) | 0.547       |
| PLR      | <97         |              | ≥97        | 2.82 (0.97, 8.18) | 0.057       |
| RDW      | <14.2       |              | ≥14.2      | 3.41 (1.27, 9.17) | 0.015       |

Abbreviations: HR, hazard ratio; CI, confidence interval; ECOG, Eastern Cooperative Oncology Group; IELSG, International Extranodal Lymphoma Study Group; WBRT, Whole Brain Radiation Therapy; PLR, Platelet-to-lymphocyte ratio.

### Introduction

Aggressive non-Hodgkin B cell lymphomas are a heterogeneous group that is usually divided into established categories, such as Burkitt lymphoma and subtypes of diffuse large B cell lymphoma. Advances in genomic profiling have confirmed that these categories have characteristic oncogenic mechanisms, but also reveal significant number of cases that are intermediate between established categories; leading to difficulties in diagnosis, prognosis, and prediction of treatment outcome. Another recent development is the availability of large databases containing genomic molecular data with linked clinical variables and outcome information. Here, we investigate whether using these databases to search for sets of patients with molecularly similar profiling represents a viable alternative to category-based methods, and preliminary findings are presented.

### Methods

Using several publicly available and study-specific datasets, we determined genes consistently associated with prognosis. Molecular similarity between patients was defined using the correlation coefficient of prognostic gene expression, and this was further.