00537 A Clinico-genotypic Index to Predict Survival Outcomes in de novo Composite Diffuse Large B-cell Lymphoma Arising From Follicular Lymphoma

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Aims: Composite follicular lymphoma with diffuse large B-cell lymphoma (FL/DLBCL) is rarely studied and prognostic indicators remain scarce. This aim of this study was to examine clinico-pathological features of patients with FL/DLBCL and investigate relevant predictors of survival outcome.

Methodology: Patients who were consecutively established with concomitant FL/DLBCL at diagnosis (n=117) from 2001-2017 at the National Cancer Centre Singapore and Singapore General Hospital were retrospectively analyzed. Survival analyses were performed using the Kaplan-Meier method and multivariate Cox proportional models.

Result: The cohort consisted of 78 men and 39 women with a median age of 60 years (range, 24-90). Most patients (87%) received Rituximab-based regimens as their initial treatment. The cell of origin by Han's algorithm was GCB in 57%, ABC in 37% and unknown in 6%. Eight patients (6.8%) were double-hit for c-MYC, BCL2 and/or BCL6 rearrangements. In a multivariate model inclusive of known clinico-pathological parameters, presence of B symptoms ($p = 0.0074$), ECOG score ≥1 ($p = 0.0001$), double-hit genotype ($p = 0.0018$), use of chemotherapy regimens other than R-CHOP ($p = 0.001$) and lack of complete response to first-line therapy ($p = 0.0001$) were independently prognostic for worse OS. These factors, excluding B symptoms, were similarly prognostic for progression-free survival (PFS). Classification by cell of origin was not prognostic. A Clinico-Genotypic Index derived from pointwise addition of the five independent adverse parameters revealed four prognostic risk groups accounting for 25%, 32%, 21%, and 22% of the cohort, with a predicted 10-year OS of 94%, 72%, 52%, and 0%, respectively ($p < 0.0001$). Median OS for the highest risk group (score 3-4) was only 13.7 months.

Conclusion: A Clinico-Genotypic Index derived from clinical and molecular factors can classify patients with composite FL/DLBCL into distinct prognostic groups. Han's algorithm has no prognostic value in this disease entity.