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POSTER ABSTRACTS

623.MANTLE CELL, FOLLICULAR, AND OTHER INDOLENT B CELL LYMPHOMAS: CLINICAL AND EPIDEMIOLOGICAL

Spectrum and Clinical Features of Gene Mutations in Chinese Follicular Lymphoma

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Background: Follicular lymphoma (FL) is the most common indolent lymphoma with variable biologic presentation and heterogeneous clinical outcomes, and some of patients experiences early progression and have inferior survival outcomes. Next-generation sequencing (NGS) identified recurrently mutated genes in FL. While few studies on gene mutations in Chinese FL patients have been identified in the real world, this present study aimed to characterize the genomic landscape and provide insights into the biomarkers of high-risk FL populations.
Methods: 590 FL patients were reviewed, and 100 patients with sufficient samples were enrolled in our cohort. We performed targeted sequencing of 521 lymphoma-related genes based on NGS in this study.
Results: A total of 207 genetic alterations were detected in 99/100 patients. T NFRSF14, CARD11, and NOTCH3 mutations were common in FL1-2 patients compared to FL3a patients ($p = 0.025$, 0.0036, and 0.0047, respectively). SOCS1 mutations were more common in patients with Ki-67 index > 30% ($p = 0.324$), and PRDM1 mutations were more common in patients who experienced progression of disease within 24 months (POD24) (33.3% vs. 0%, $p = 0.008$). We observed a trend that patients with a high mutation load (with ≥ 6 mutated genes) showed decreased PFS compared with patients with < 6 mutated genes ($p = 0.068$). For patients who received R-CHOP-like regimens, the multivariate COX proportional hazard modeling identified TP53, TNFAIP3, and SOCS1 mutations as independent risk factors of PFS (HR 6.76, 95% CI 1.81 to 25.18, $p = 0.004$; HR 3.68, 95% CI 1.06 to 12.82, $p = 0.041$; HR 5.07, 95% CI 1.81 to 21.73, $p = 0.029$). TP53 and TNFAIP3 were significant independent predictors of PFS when testing with either FLIPI ($p = 0.029$) or FLIPI2 ($p = 0.023$) in multivariable analysis.
Conclusion: Our study depicted genomic characterization of real-world Chinses FL patients and demonstrated TP53, TNFAIP3 and SOCS1 mutations can help identify high-risk patients.

Disclosures Yuan: *AcornMed Biotechnology Co., Ltd.:* Current Employment.

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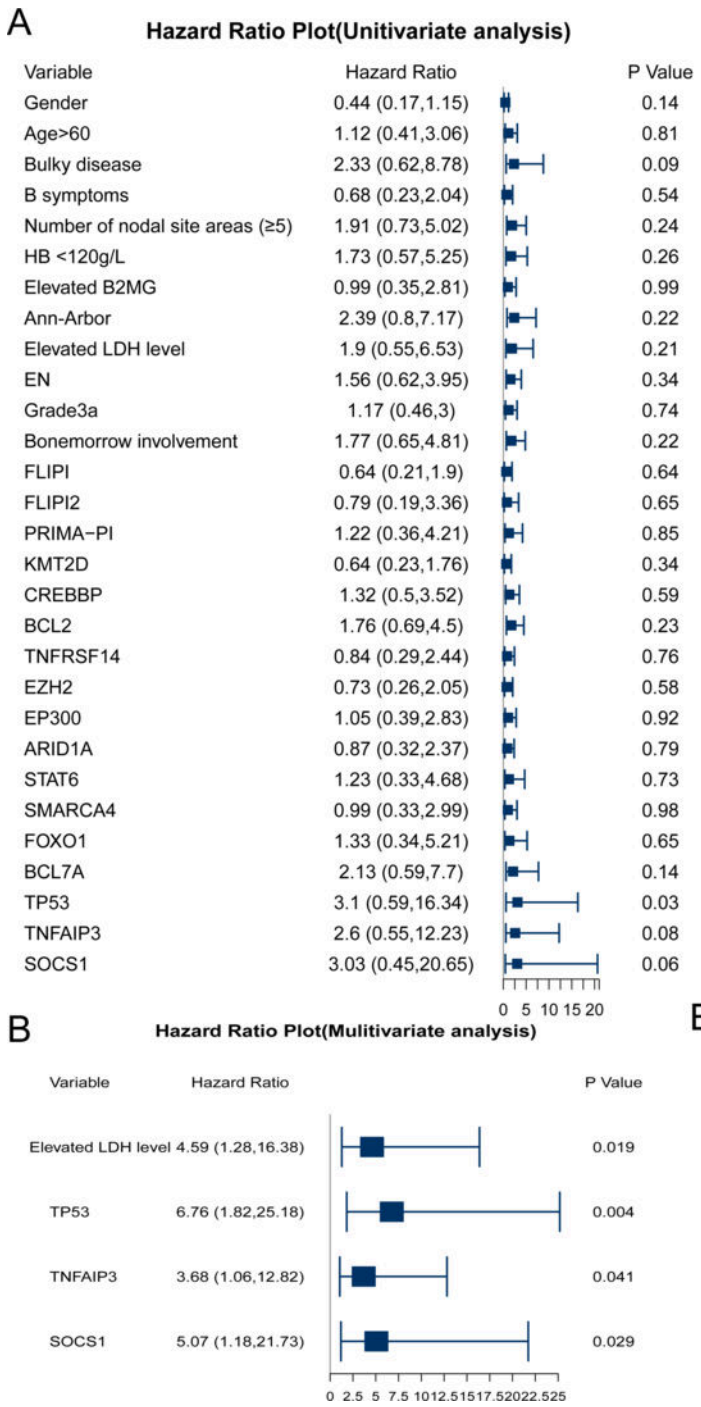

Figure 1

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