The role of artificial intelligence in differential diagnosis and prognostic significance of Small B-cell lymphoma

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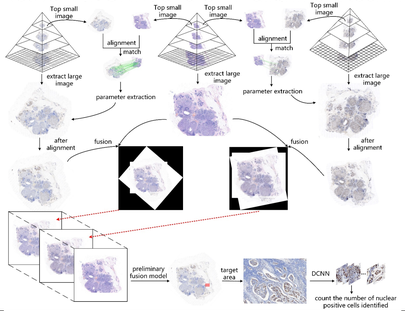
Introduction

- MCL and CLL/SLL have atypical immunophenotypic features that predispose to misclassification.
- Pathological immunohistochemistry (IHC) is clinically used to differentiate MCL from CLL/SLL. Due to subjective judgment of pathologists, and difficulty reading quantitative data, pathological diagnosis results are time-consuming and laborious to obtain, with the accuracy to be verified.
- Artificial intelligence (AI) technology will be a reliable pathologist aid.
- In this study, we expect to use AI technology to explore the differential diagnosis and prognostic significance of immunohistochemical indicators in MCL and CLL/SLL.

Methods

- **Patient Samples** Pathological sections of 52 cases with a pathological diagnosis of MCL and 14 instances of SLL at our hospital from April 2017 to April 2022, together with the data of patients.
- **Principles of AI technology** Pathology slides were scanned using an intelligent pathology analyzer by extracting images and initial fusion. The rate of IHC lesion site positivity, i.e., quantitative data, was calculated using Deep Convolutional Neural Network (DCNN) and SITF alignment techniques.

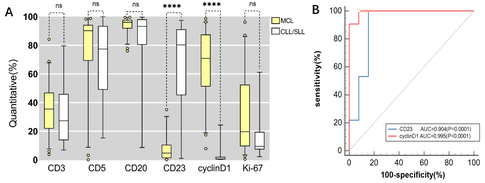


Methods(cont.)

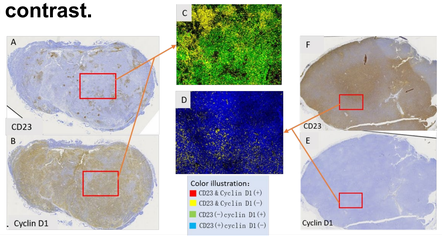
- **Grouping of immunohistochemical quantification** CD5 and CD20 expression ≥ 30% was considered positive, otherwise negative. The median served as a threshold for quantifying high and low expression of each immunophenotype.
- **Statistical analysis** ROC curve analysis to obtain cut-off values. The primary endpoints overall survival time (OS) and progression-free survival (PFS). Survival analysis was performed using the Kaplan-Meier method.

Results

CD23 and Cyclin D1 are significant markers for identifying MCL and CLL/SLL. A cut-off value of ≤35.02% for CD23 (AUC=0.904; P<0.0001) and >24.26% for Cyclin D1 (AUC=0.995; P<0.0001) was favored for the diagnosis of MCL.



The virtual multiplex immunofluorescence technique was used to label CD23 and Cyclin D1 in MCL and CLL/SLL pathology specimens to obtain pseudo-color maps with sharp contrast.

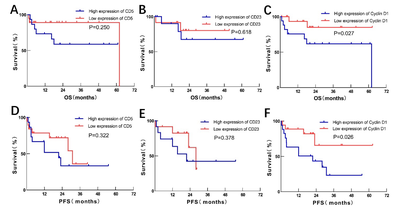


Results(cont.)

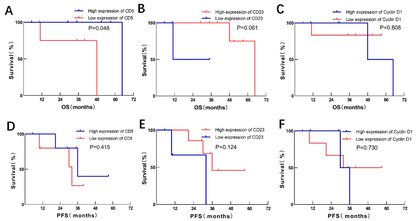
The model consisting of CD20, CD5, CD23, and Cyclin D1 was used to diagnose MCL or CLL/SLL with 100% accuracy.

Model	Total	MCL	CLL/SLL
CD20+CD5+CD23-Cyclin D1+	26	26 (100%)	0 (0)
CD20+CD5+CD23+Cyclin D1-	8	0 (0)	8 (100%)
CD20+CD5-CD23-Cyclin D1+	2	2 (100%)	0 (0)
CD20+CD5-CD23+Cyclin D1-	1	0 (0)	1 (100%)

Among MCL patients, the 3-year OS rates were (90.0±9.5) % and (60.2±11.8) % (P=0.027), and the 3-year PFS rates were (64.5±19.9) % and (23.6±12.7) % (P=0.026) in the Cyclin D1 low and high expression groups, respectively.



The OS was prolonged in the CD5 high expression group compared to the low expression group in CLL/SLL patients (64.7 months vs. 48.0 months, P=0.048).



Conclusions

- When the expression of CD23 was 35.02%, and Cyclin D1 was 24.26%, it may be helpful to identify MCL and CLL/SLL.
- AI could help pathologists classify and diagnose lymphomas more accurately and quickly.
- The models consisting of CD20, CD5, CD23, and Cyclin D1 show high accuracy in the differential diagnosis of both diseases.
- High expression of Cyclin D1 is associated with poor prognosis and increased risk of recurrence in MCL. CLL/SLL patients with low CD5 expression suggest a poor prognosis.

References

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