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Single-cell sequencing analysis of paired PBMC and BMMC samples from AL patients

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Objectives : Systemic light chain amyloidosis (AL) is the most common type of systemic amyloidosis, kidney and heart are the most commonly affected organs. The diagnosis of AL depends on the presence of amyloid deposition of immunoglobulin light chain or heavy light chain as a precursor protein confirmed by biopsy, the existence of monoclonal immunoglobulin or free light chain in blood or urine, or the monoclonal plasma cells /B cells found in bone marrow examination, but lack of diagnostic biomarkers. Here, we performed single-cell methods in AL patients with renal damage.
Methods : In this study, paired peripheral blood mononuclear cell (PBMC) and bone marrow mononuclear cell (BMMC) of 5 newly diagnosed AL patients were collected, including 3 healthy controls. Single-cell sequencing and antibody repertoire sequencing were used to explore related characteristics.
Results : κ light chain (n=1) and λ light chain (n=4) were included in the 5 AL patients. The results showed that AL patients had some different expression patterns compared with the healthy control, and AL patients contained more plasma B cells. Most of the marker genes were enriched in protein binding and N-glycan biosynthesis related pathways. Some patients contained specific amplified clones, such as the variable region of antibody V1-33 in subject AL2 had significantly amplified clone while the V4-30-4 in subject AL5. The top five up-regulated genes were RHOB, CTSW, HSPA5, KRTCAP2 and MZB1, while the top five down-regulated genes were BTG1, CD79A, CD37, HLA-DRB1 and JUND.
Conclusions : Single-cell results revealed that AL patients with kidney damage contained specific transcriptional features and differentially expressed genes were discovered. These findings can provide theoretical basis for the discovery of diagnostic biomarkers in AL patients with kidney injury in the future.