Vgll3 causes discoid lupus-like fibrosis in a mouse model of lupus
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Lupus erythematosus (LE) is a systemic autoimmune disease that can occur in isolation or in the context of systemic lupus erythematosus (SLE). SLE is often disfiguring, and no FDA-approved therapies for CLE exist. Further, evidence suggests skin inflammation in CLE can provoke systemic autoimmune disease, including precipitating dangerous kidney inflammation. Thus, understanding CLE pathogenesis has great potential to alleviate patient suffering.

In this study, we used a standardized murine model of CLE that develops both skin and systemic inflammation, similar to human disease. We employed single-cell RNA-sequencing (scRNA-seq) and spatial sequencing to investigate the transcriptional and spatial arrangement of the cellular players in CLE. We found unique populations of skin keratinocytes, fibroblasts, and monocytes/macrophages, each with distinct features that contribute to the disease.

Overall, our study provides insights into the complex cellular interactions that underlie CLE pathogenesis and may guide the development of novel therapeutic strategies.

021 Multidimensional in situ immune profiling of discoid and subacute cutaneous lupus erythematosus
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We used a multidimensional imaging approach to analyze the immune infiltrate in cutaneous lupus erythematosus (CLE). We performed spatial sequencing and imaging mass cytometry to characterize the immune cell composition and spatial arrangement in healthy and diseased skin. Our findings suggest a complex architecture of immune cells, stromal cells, and extracellular matrix in CLE, with potential implications for disease pathogenesis.

022 UHRF1 downregulation promotes T follicular helper cell differentiation by increasing BCL6 expression in SLE
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In this study, we investigated the role of the epigenetic modifier UHRF1 in T follicular helper (Tfh) cells in systemic lupus erythematosus (SLE). We found that UHRF1 downregulation leads to increased BCL6 expression, which promotes Tfh cell differentiation. This finding reveals the potential for UHRF1 as a therapeutic target for SLE.

023 Single-cell composition and architecture of cutaneous lupus
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In this study, we used single-cell RNA sequencing to characterize the cellular composition of cutaneous lupus. We identified distinct cell populations, including immune cells and keratinocytes, and found evidence of inflammation and fibrosis. These findings provide insights into the pathogenesis of cutaneous lupus and may guide the development of targeted therapies.

024 Immune microenvironment deep profiling of cutaneous lupus erythematosus skin stratified by patient response to antimalarials
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Our study used single-cell RNA sequencing to analyze the immune microenvironment in cutaneous lupus erythematosus (CLE) skin. We found differences in the immune cell populations and gene expression between responders and non-responders to antimalarial treatment. These findings suggest potential targets for personalized therapy in CLE.