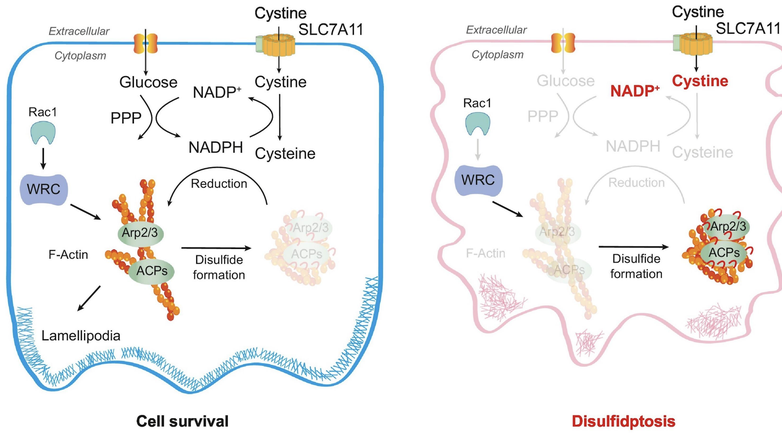
Systematic Review Evaluating Disulfidptosis-Related lncRNAs and Gene Signatures in Acute Myeloid Leukemia

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Background

Acute myeloid leukemia (AML) is an acute and aggressive blood cancer with extensive clonal diversity and poor overall survival. Disulfidptosis, a novel form of programmed cell death associated with disulfide stress and actin cytoskeleton breakdown, illuminates AML pathogenesis. Recent evidence indicates that lncRNAs, such as disulfidptosis-related lncRNAs, could be potential prognostic and therapeutic biomarkers in AML.



Objective

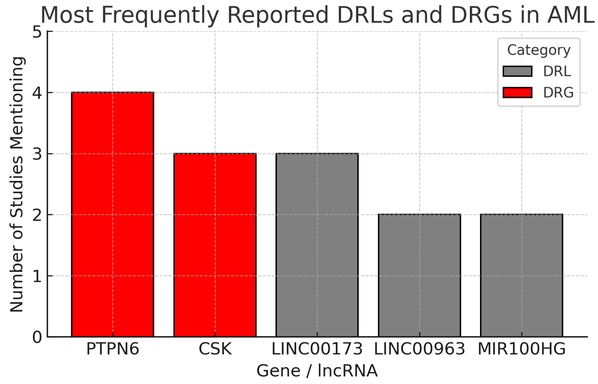
In this systematic review, we summarize the status of disulfidptosis-related lncRNAs (DRLs) and disulfidptosis-related genes (DRGs) in AML, describe the potential of DRLs and DRGs as prognosis markers, explore their relevance with immune microenvironment and elaborate their role in treatment stratification.

Methods

We conducted a literature search following PRISMA guidelines across PubMed, Web of Science and other databases for studies regarding DRLs and DRGs in AML. Eligibility criteria included transcriptomic datasets (bulk or scRNA-seq), prognostic model establishment, identification of immune-related and therapeutic outcomes. The following data were retrieved: study design, cohort characteristics, gene/lncRNA signatures, and validation strategies.
Different bioinformatic techniques, like LASSO regression and univariate and multivariate Cox regression, were employed to identify DRGs and DRLs and establish risk scoring systems, also algorithms like ESTIMATE, CIBERSORT, etc., to assess immune infiltration analysis of the tumour microenvironment.Two reviewers screened titles, abstracts, and assessed outcomes related to efficacy and safety.

Results

Five eligible articles constructed DRL or DRG-based prognostic signatures. The majority of the models stratified the patients into high- and low-risk groups, and higher-risk scores were found to be significantly associated with worse overall survival. A few of the studies had also validated their signatures in independent cohorts and confirmed key DRLs via qPCR. Immune checkpoint was up-regulated in high-risk group, suggesting of immune evasion. Moreover, risk scores were associated with diverse sensitivities of chemotherapy (e.g., cytarabine) and immune checkpoint inhibitors (e.g., anti-PD-1). One report demonstrated the functional importance of DRGs such as PTPN6 and CSK using in vitro knockdown analyses.



Conclusion

lncRNA and gene signatures linked to disulfidptosis would have promising implications as prognostic biomarkers and predictors for AML immunotherapy, thus helping guide personalized therapy for patients with AML. The underlying mechanism and these results should be validated prospectively in more studies.

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