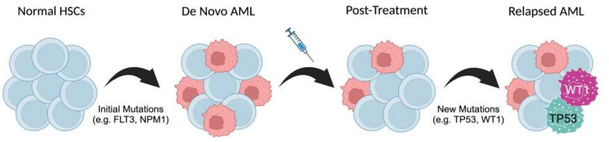
MAPPING RNA SIGNATURES IN ACUTE MYELOID LEUKEMIA (AML): UNVEILING EMERGING GENE MODULATION TARGETS

Ishan Gupta[1], Harsh Goel[2], Anita Chopra[2], Amar Ranjan Singh[2], Jagdish Prasad Meena[3], Aditya Kumar Gupta[3], Ganesh K Viswanathan[4], Sameer Bakhshi[5], Pranay Tanwar[2]*
[1]**MBBS**, [2]Laboratory Oncology, Dr B.R.A.I.R.C.H., [3]Department of Pediatrics, [4]Department of Hematology, [5]Medical Oncology, Dr B.R.A.I.R.C.H., All India Institute of Medical Sciences, New Delhi

AML 504

Introduction

Acute myeloid leukemia (AML) is a genetically diverse malignancy involving multiple molecular alterations, and identification of these changes between de novo and relapsed AML can provide insights into disease progression and highlight potential therapeutic targets.



Aim

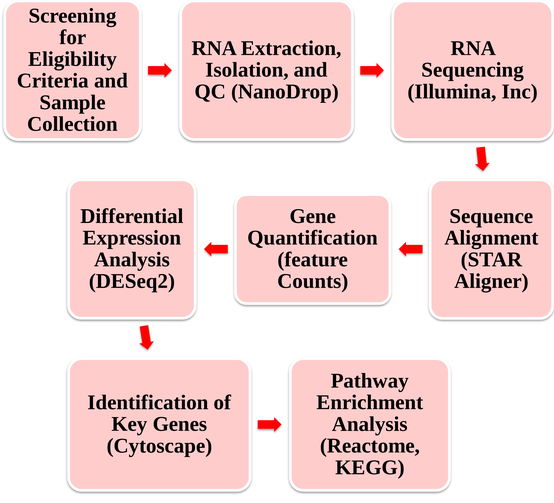
To explore genes with differential expression in de novo compared to relapsed AML cases and the associated dysregulated molecular pathways as well as potential therapeutic targets.

Objectives

✓To identify differentially expressed genes in de novo v/s relapsed AML
✓ To identify key genes involved in relapsed AML and associated dysregulated molecular pathways
✓ To identify potential targets for future CRISPR-based interventions

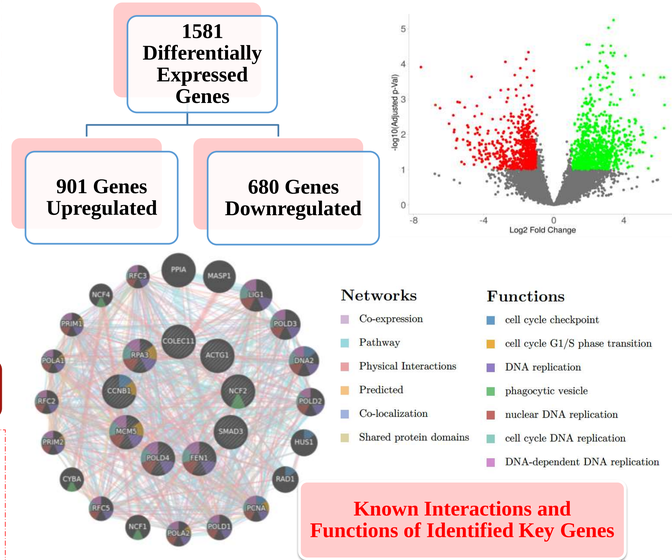
Methods

DESIGN: Basic science research on clinical patient samples and bioinformatics analysis.
SETTING: Tertiary cancer care hospital & academic medical center.
- Paired bone marrow samples were collected from ten AML patients at the time of initial diagnosis of de novo AML as well as relapse

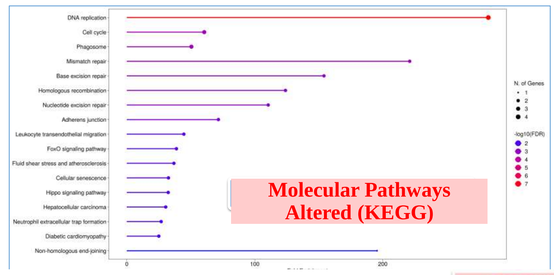


Treatment-naïve patients with a diagnosis of de novo AML were selected continuously from the out-patient clinic (medical oncology), followed up, and subsequently included in the study on disease relapse. Patients not consenting to the collection of either or both the bone marrow samples were excluded.

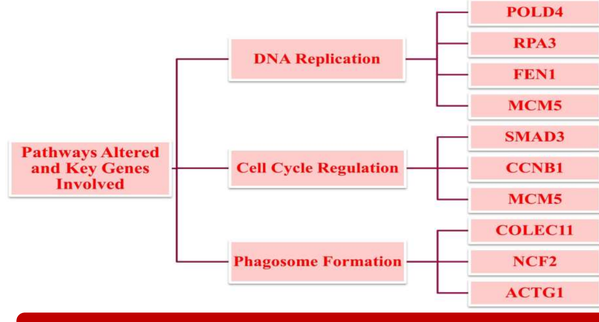
Results



Known Interactions and Functions of Identified Key Genes



Molecular Pathways Altered (KEGG)



Summary

✓Our transcriptomic analysis revealed critical gene expression differences impacting DNA replication and cell cycle regulation pathways
✓ We identified potential therapeutic targets for future CRISPR-based interventions in relapsed AML.

Future Directions

✓Gene Target Validation: Conduct functional studies to confirm the roles of identified genes (e.g., POLD4, SMAD3, CCNB1); Assess significance of genes in AML relapse through CRISPR-Cas9 knockout/activation models
✓ Pre-clinical Studies: Use in vitro AML cell lines and in vivo mouse models to test CRISPR-modified cells
✓ Pathway Analysis Integration: Focus on major molecular pathways impacted by CRISPR interventions and identify synergistic effects with existing therapies
✓ Therapeutic Development

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