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IMPLICATIONS OF CTBP2 GENE FOR DISEASE AND PROGNOSIS IN ACUTE MYELOID LEUKEMIAS (AML): FROM MOLECULAR PROMISES TO CLINICAL CHALLENGES

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INTRODUCTION

- Acute myeloid leukemias (AML) are a group of genetically diverse blood disorders marked by the clonal growth of myeloid precursors with impaired differentiation
- C-terminal binding protein 2 (CTBP2), part of the CTBP transcriptional corepressor family, is known to promote tumor growth in solid cancers. However, its role in AML is not well understood

AIMS & OBJECTIVES

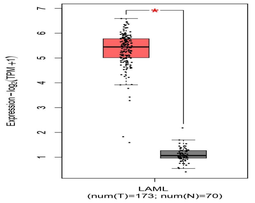
- To explore the molecular functions, clinical significance, and prognostic value of CTBP2 gene in acute myeloid leukemias

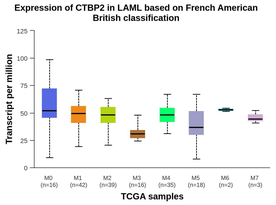
METHODS

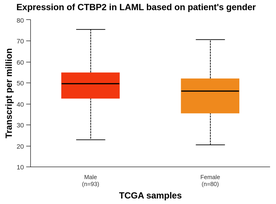
- **Design**: Prospective Clinical Research
- **Setting**: Tertiary Referral Cancer Care Centre
- **Patients**: Patients were selected continuously from the Out-Patient records of the Department of Medical Oncology
- CTBP2 gene expression in AML patients (n=173) and healthy volunteers (n=70) was evaluated
- DNA methylation status of the CTBP2 gene was assessed with UCSC Xena browser and MEXPRESS database
- Molecular mechanisms and biological functions of CTBP2 in AML were explored using Gene Set Enrichment Analysis (GSEA) and the LinkedOmics database
- Relationship between CTBP2 expression and various functional states was investigated using the SANGER Box 3.0 database
- Prognostic significance of CTBP2 - Kaplan-Meier survival analysis

RESULTS

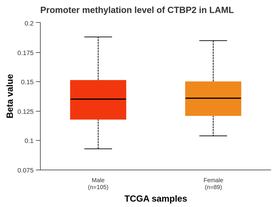
- CTBP2 mRNA was significantly over-expressed in AML patients (n=173) compared to healthy samples (n=70); however, this over-expression was not significantly associated with poorer overall survival (p=0.12)
- Higher CTBP2 expression was particularly noted in the M0 and M6 subtypes of AML, younger group of patients (21-40 years) as well as males compared to females
- Methylation levels were higher in females and in the African-American population cohorts
- GSEA revealed that CTBP2 was seen to be involved in regulation of the immune system, angiogenesis and blood vessel maturation, as well as leukocyte trans-endothelial migration
- Notably, CTBP2 mRNA expression was positively associated with inflammation, as well as differentiation, invasion and metastasis in AML

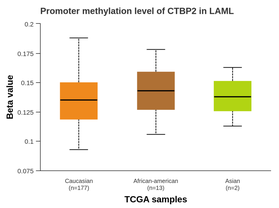


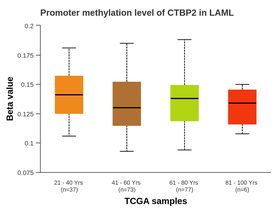




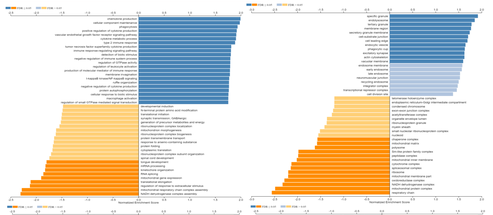
CTBP2 Expression



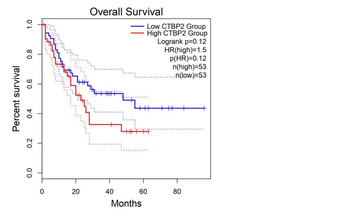




CTBP2 Methylation



Gene Set Enrichment Analysis (GSEA)



Kaplan-Meier Survival Analysis

CONCLUSIONS

- This study demonstrates that CTBP2 expression levels correlate with disease severity
- CTBP2 can serve as a valuable prognostic biomarker
- Due to its involvement in key biological processes and pathways associated with AML progression, CTBP2 presents itself as a promising therapeutic target

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