Same Disease, Different Genes? Uncovering What Sets African American CLL Apart: A Comparative Study With European Cohorts

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Introduction

- CLL is a chronic B-cell malignancy with marked clinical and genetic heterogeneity.
- Cytogenetic and molecular features drive prognosis and treatment decisions.
- African American (AA) patients are underrepresented in genomic studies, limiting understanding of ethnic-specific disease patterns.

Aim

- To characterize the mutational landscape of AA CLL patients and compare it to published European data.

Methods

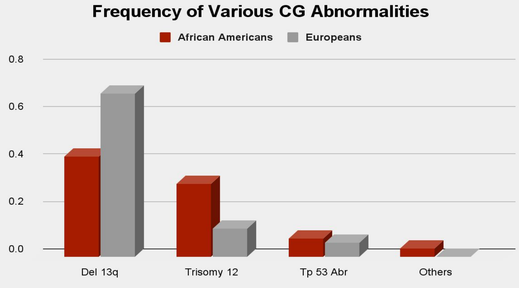
- **Design:** Retrospective cross-sectional study
- **Setting:** Brooklyn Cancer Care
- **Participants:** 26 African-American patients diagnosed with CLL/SLL (2013–2024)
- **Inclusion:**Age ≥18 and availability of lab data, flow cytometry, FISH analysis, imaging, and clinical history.
- **Outcome:** Proportions of patients by clinical stage, cytogenetic and IGHV mutation profiles, and their distribution compared to a European cohort.

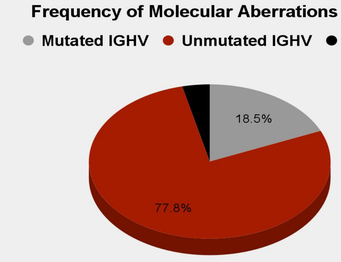
Results

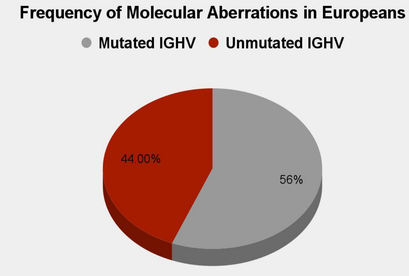
- **Demographics:** 26 AA patients, mean age 69.9 (16M/10F)

Cytogenetics	African Americans	Europeans	Prognosis
Del(13q)	42.3%	69%	Favorable
Trisomy 12	30.8%	12%	Intermediate-risk
Tp53 Aberrations	7.7%	6%	High Risk
Trisomy 15, Trisomy 3, Monosomy 7	3.8%	0%	High Risk with Clonal Evolution Potential

Molecular Abnormalities	African Americans	Europeans	Prognosis
Mutated IGHV	19.2%	56%	Favorable
Unmutated IGHV	80.8%	44%	Poor Prognosis
DNMT3A, NRAS, U2AF1, RUNX1, MYD88, MALT1, t(11,14)	3.8%	0%	High Risk with Clonal Evolution Potential







Discussion

- AA CLL patients display more high-risk features and unique mutations not reported in European cohorts.
- Findings highlight the need for ethnically inclusive genomic research to improve risk models and guide personalized treatment.

References

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