



## The 65th ASH Annual Meeting Abstracts

## ORAL ABSTRACTS

## 613.ACUTE MYELOID LEUKEMIAS: CLINICAL AND EPIDEMIOLOGICAL

**Survival and Prognosis Among 301 Patients with Newly-Diagnosed Acute Myeloid Leukemia Following Venetoclax Plus Hypomethylating Agent Therapy**

Omer Karrar<sup>1</sup>, Moazah Iftikhar<sup>1</sup>, Kristen McCullough, PharmD<sup>2</sup>, Isla Johnson, MD<sup>3</sup>, Maymona Abdelmagid<sup>4</sup>, Aref Al-Kali, MD<sup>1</sup>, Hassan Alkhateeb, MD<sup>1</sup>, Kebede Begna, MD<sup>1</sup>, Abhishek A Mangaonkar, MBBS<sup>1</sup>, Antoine Saliba, MD<sup>1</sup>, Mehrdad Hefazi, MD<sup>1</sup>, Mark R. Litzow, MD<sup>1</sup>, William J. Hogan, MD<sup>1</sup>, Mithun V Shah, MDPhD<sup>1</sup>, Mrinal M. Patnaik, MD MBBS<sup>5</sup>, Animesh D. Pardani, MBBS, PhD<sup>1</sup>, Talha Badar, MD<sup>6</sup>, Hemant S. Murthy, MD<sup>7</sup>, James M. Foran, MD<sup>8</sup>, Jeanne Palmer, MD<sup>9</sup>, Lisa Sproat, MD<sup>10</sup>, Nandita Khera, MD<sup>11</sup>, Cecilia Y. Arana Yi, MD<sup>12</sup>, Ayalew Tefferi, MD<sup>1</sup>, Naseema Gangat, MBBS<sup>1</sup>

<sup>1</sup> Division of Hematology, Mayo Clinic, Rochester, MN

<sup>2</sup> Mayo Clinic, Rochester, MN

<sup>3</sup> Mayo School of Graduate Medical Education, Rochester, MN

<sup>4</sup> Division of Hematology, Mayo Clinic, Rochester, MN, USA., Rochester, MN

<sup>5</sup> Division of Hematology, Department of Medicine, Mayo Clinic, Rochester, MN

<sup>6</sup> Mayo Clinic, Jacksonville, FL

<sup>7</sup> Department of Hematology/Oncology, Mayo Clinic, Jacksonville, FL

<sup>8</sup> Hematology/Oncology, Mayo Clinic, Jacksonville, FL

<sup>9</sup> Mayo Clinic - Arizona, Scottsdale, AZ

<sup>10</sup> Banner Blood & Marrow Transplant Prgm., Phoenix, AZ

<sup>11</sup> Mayo Clinic, Phoenix, AZ

<sup>12</sup> Hematology/Oncology, Mayo Clinic, Scottsdale, AZ

**Background:**

Venetoclax (Ven) in combination with hypomethylating agent (HMA) is the preferred treatment for elderly/unfit patients with newly-diagnosed acute myeloid leukemia (AML). Current prognostication for AML is based on European LeukemiaNet (ELN) genetic risk stratification which has limited applicability in patients treated with Ven-HMA (*Blood*, 2022). Accordingly, our primary objective was to determine predictors of treatment response and survival outcomes in treatment-naïve AML patients receiving Ven-HMA.

**Methods:**

Our study population was recruited from Mayo Clinic (MN, FL, AZ), after institutional review board approval and based on documentation of newly-diagnosed AML treated with Ven-HMA outside of clinical trials between November 2018 and April 2023. Cytogenetic and molecular studies were performed by conventional karyotype, and next-generation sequencing, respectively. Response was assessed according to the 2022 ELN criteria

**Results:***Patient characteristics*

A total of 301 newly-diagnosed AML patients (median age 73 years, 66% male, 62% *de novo*) received a median of 3 cycles (range 1-48) of azacitidine 75 mg/m<sup>2</sup> days 1-7 ( *n*=100) or decitabine 20 mg/m<sup>2</sup> days 1-5 ( *n*=201) with Ven. ELN 2022 cytogenetic risk included favorable (1%, *n*=4), intermediate (61%, *n*=184) or adverse (38%, *n*=113). Mutations involved *TP53* in 77/301 (25%), *ASXL1* in 54/279 (19%), *RUNX1* in 54/296 (18%), *NPM1* in 44/299 (15%), *DNMT3A* in 40/296 (13%), *K/NRAS* in 41/296 (14%), *IDH1* in 20/301 (6%), *IDH2* in 30/301 (10%), *FLT3-ITD* in 25/301 (8%) and *DDX41* in 9/247 (4%) of informative cases.

*Predictors of response*

Complete remission, with (CR) or without (CRi), count recovery, was documented in 182 (60%) patients, including CR in 36% and measurable residual disease (MRD) negative by flow cytometry in 77% of 105 informative cases that achieved CR/CRi. Median time to CR/CRi was 1.4 months. In univariate analysis, CR/CRi was more likely to occur in the presence of *NPM1* mutation, (86% vs. 56%; *p* < .01), *IDH2* mutation, (80% vs. 58%; *p* = .02), *DNMT3A* mutation, (78% vs. 57%; *p* = .01), or *DDX41*

mutation, (100% vs. 58%;  $p < .01$ ), and in the absence of adverse karyotype, (71% vs. 42%;  $p < .01$ ), *TP53* mutation, (67% vs. 40%;  $p < .01$ ), *FLT3-ITD* mutation, (63% vs. 36%;  $p = .01$ ), or *RUNX1* mutation, (64% vs. 44%;  $p = .01$ ); in multivariable analysis, adverse karyotype, ( $p < .01$ ), *FLT3-ITD* ( $p < .01$ ), *RUNX1* ( $p < .01$ ), *NPM1* ( $p = .03$ ), *IDH2* ( $p = .04$ ), and *DDX41*, ( $p = .01$ ) mutations remained significant.

#### Predictors of survival

After a median follow-up of 8.5 months (range 0.5-56), 13.2 months for living patients, 174 (58%) deaths, 73 relapses (40% of those achieving CR/CRi), and 41 (14%; including 35 in CR/CRi) allogeneic hematopoietic stem cell transplants (AHSCT) were documented. In univariate analysis of pre-treatment variables, thrombocytopenia  $< 100 \times 10^9/l$ , (HR 1.5, 95% CI 1.03-2.2;  $p = .03$ ), adverse karyotype, (HR 2.8, 95% CI 2.1-3.8;  $p < .01$ ) *TP53* mutation, (HR 2.5, 95% CI 1.8-3.5;  $p < .01$ ), or absence of *IDH2* mutation, (HR 3.5, 95% CI 1.7-7.6;  $p < .01$ ) predicted inferior survival. Failure to achieve CR/CRi (HR 4.5, 95% CI 3.3-6.1;  $p < .01$ ) was also associated with inferior survival and in multivariable analysis, failure to achieve CR/CRi, (HR 3.4, 95% CI 2.5-4.8;  $p < .01$ ), presence of adverse karyotype, (HR 1.6, 95% CI 1.1-2.6;  $p = .02$ ), *TP53* mutation, (HR 1.6, 95% CI 1.002-2.4;  $p = .04$ ), and absence of *IDH2* mutation (HR 2.2, 95% CI 1.004-4.7;  $p = .04$ ) were identified as risk factors for survival. Subsequent HR-weighted scoring resulted in three-tiered risk stratification: low (0-1 point;  $n = 130$ ), intermediate (2-3 points;  $n = 105$ ), and high (4-5 points;  $n = 66$ ), with respective median survival (3-year rate) of 28.9 (48%), 9.6 (6%), and 3.1 (0%) months ( $p < .01$ ) (Figure). AHSCT had an independent favorable impact on survival (HR 0.3, 95% CI 0.1-0.6;  $p < .01$ ), most apparent in low ( $p = 0.04$ ), and intermediate ( $p < .01$ ), as opposed to high ( $p = .06$ ) risk.

#### Conclusions:

In the current single institutional series of Ven-HMA treated newly-diagnosed AML, response to Ven-HMA was the foremost predictor of survival. Additional risk factors for survival included adverse karyotype, presence of *TP53* and absence of *IDH2* mutations. These observations allowed for a three-tiered genetics-enhanced survival model with CR/CRi as a backbone, and also confirmed survival advantage from AHSCT, regardless of risk category.

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Figure 1. Survival of 301 AML patients receiving frontline Ven-HMA, stratified by HR-weighted scoring system, HR (95% CI), failure to achieve CR/CRi, 3.4 (2.5-4.8), presence of adverse karyotype, 1.6 (1.06-2.5), presence of *TP53* mutation, 1.54 (1.002-2.4), absence of *IDH2* mutation, 2.2 (1.004-4.7), allocating 2 adverse points for not achieving CR/CRi, one adverse point each for adverse karyotype, *TP53* mutation and absence of *IDH2* mutation. OS stratified by low risk (0-1 points), intermediate risk (2-3 points) and high risk (4-5 points) is shown.

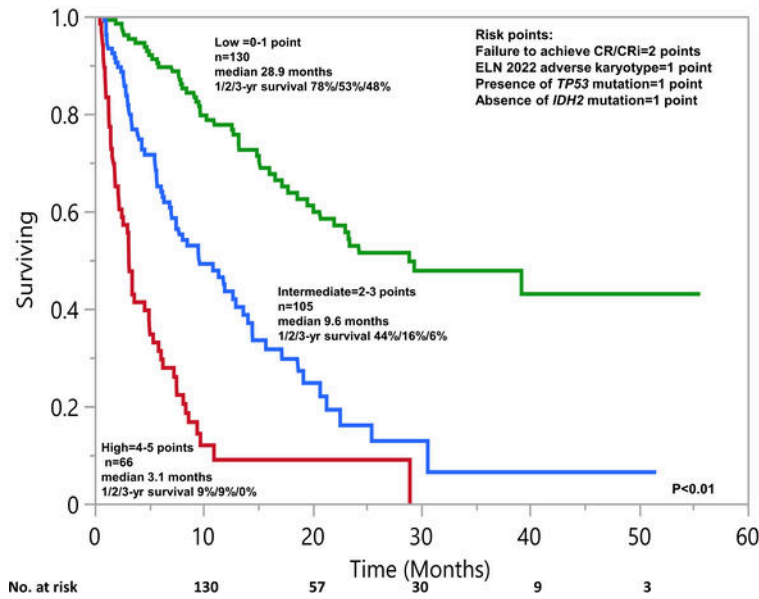
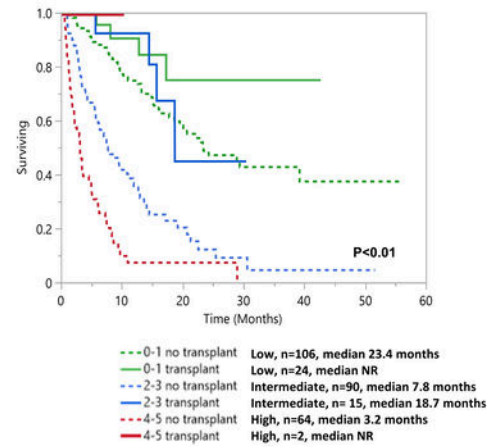


Figure 1

Survival analysis on 301 patients with AML treated with frontline Ven-HMA stratified by low, intermediate and high risk with or without allogeneic transplantation



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