

# 6520 V-RULES: Real-World Effectiveness and Safety of CPX-351 in Patients With Secondary Acute Myeloid Leukemia (AML)

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## Background

- Secondary AML accounts for approximately 25% of all AML cases and is associated with poor outcomes<sup>1-2</sup>
- CPX-351, a dual-drug liposomal encapsulation of daunorubicin and cytarabine in a synergistic 1:5 molar ratio, has demonstrated improved survival in patients with secondary AML when used as frontline therapy<sup>3</sup> and is approved for newly diagnosed, therapy-related AML (t-AML) or AML with myelodysplasia-related changes (AML-MRC) in adult and pediatric (aged ≥1 year) patients in the United States (US) and adults in Europe<sup>4-6</sup>
  - The approval of CPX-351 was based on the pivotal phase 3 trial (ClinicalTrials.gov identifier: NCT01696084), in which CPX-351 demonstrated significantly improved overall survival (OS) and remission rates vs conventional 7+3 chemotherapy, and a comparable safety profile in older adults aged 60-75 years with newly diagnosed, high-risk or secondary AML<sup>3,7</sup>
- Real-world studies complement findings from clinical trials by providing evidence of treatment effectiveness and safety in diverse real-world populations and healthcare settings to support clinical decision-making<sup>8</sup>

## Objective

- To assess real-world effectiveness and safety of CPX-351 in routine clinical practice for US patients with newly diagnosed secondary AML, specifically t-AML or AML-MRC

## Methods

- Vyxeos Real-world US Long-term Effectiveness and Safety (V-RULES) was a retrospective, multicenter, single-arm, observational study conducted at 10 US centers
  - Pseudonymized data were collected from medical records of eligible patients with newly diagnosed t-AML or AML-MRC (according to the World Health Organization [WHO] criteria 2016 or 2022) who received ≥1 infusion of CPX-351 monotherapy since its Food and Drug Administration approval in August 2017 in routine US clinical practice
- Primary outcomes were complete response (CR), CR with partial hematologic recovery (CRh), CR with incomplete platelet or neutrophil recovery (CRi), and OS
- Secondary outcomes included rate of hematopoietic cell transplantation (HCT), OS landmarked from HCT date (to better understand post-transplant prognosis), and safety of CPX-351, and are also reported here
  - Adverse events (AEs) of special interest were defined as duration of myelosuppression, severe infections, and bleeding events; local tissue necrosis; cardiac events; and gastrointestinal toxicity
- The study was designed to be descriptive, without hypothesis testing

## Results

Table 1. Baseline Patient and Disease Characteristics

	Overall (N=161)
Age at AML diagnosis	
Median, years (range)	60 (21, 78)
<60 years, n (%)	78 (48)
≥60 years, n (%)	83 (52)
Male, <sup>a</sup> n (%)	94 (58)
Race, <sup>a</sup> n (%)	
American Indian or Alaska Native	1 (0.6)
Asian	5 (3)
Black or African American	21 (13)
White	116 (73)
Other	15 (9)
Ethnicity, n (%)	
Hispanic or Latino	18 (11)
Not Hispanic or Latino	136 (84)
Unknown	7 (4)
ECOG PS, <sup>c</sup> n (%)	
0	37 (28)
1	78 (60)
2	13 (10)
3	3 (2)
Missing, n	30
AML subtype, n (%)	
t-AML	47 (29)
AML-MRC	114 (71)
Prior MDS <sup>d</sup>	32 (28)
Prior CMML <sup>d</sup>	4 (4)
MDS-related cytogenetic abnormalities <sup>d</sup>	69 (60)
Multilineage dysplasia alone <sup>d</sup>	9 (8)
Grimwade cytogenetic classification, <sup>a</sup> n (%)	
Favorable	9 (6)
Intermediate	57 (37)
Adverse	88 (57)
Molecular abnormalities, n (%)	
<i>TP53</i> mutation <sup>f</sup>	33 (25)
Myelodysplasia-related gene mutations <sup>d</sup>	57 (63)
Charlson comorbidity index, mean (SD)	1.8 (2.1)

Percentages may not add to 100% due to rounding.

<sup>a</sup>Biological sex. <sup>b</sup>WHO response question. <sup>c</sup>5 patients had missing data for race. Percentages were calculated out of total number of patients with non-missing data. <sup>d</sup>Percentages were calculated out of total number of patients with non-missing data. <sup>e</sup>Percentages were calculated out of 114 patients with AML-MRC. <sup>f</sup>Patients had missing data for Grimwade cytogenetic classification. Percentages were calculated out of total number of patients with non-missing data. <sup>g</sup>Percentages were calculated out of 27 patients with missing data for mutated *TP53*. Percentages were calculated out of total number of patients with non-missing data. <sup>h</sup>Myelodysplasia-related mutations were defined as mutations in *ASXL1*, *BCOR*, *EZH2*, *RUNX1*, *SRSF2*, *STAG2*, *UDAF1*, *DNMT3A*, *DNMT3B*, *DNMT3C*, *DNMT3L*, *DNMT3O*, *DNMT3A2*, *DNMT3A3*, *DNMT3A3L*, *DNMT3A3B*, *DNMT3A3C*, *DNMT3A3D*, *DNMT3A3E*, *DNMT3A3F*, *DNMT3A3G*, *DNMT3A3H*, *DNMT3A3I*, *DNMT3A3J*, *DNMT3A3K*, *DNMT3A3L*, *DNMT3A3M*, *DNMT3A3N*, *DNMT3A3O*, *DNMT3A3P*, *DNMT3A3Q*, *DNMT3A3R*, *DNMT3A3S*, *DNMT3A3T*, *DNMT3A3U*, *DNMT3A3V*, *DNMT3A3W*, *DNMT3A3X*, *DNMT3A3Y*, *DNMT3A3Z*, *DNMT3A3AA*, *DNMT3A3AB*, *DNMT3A3AC*, *DNMT3A3AD*, *DNMT3A3AE*, *DNMT3A3AF*, *DNMT3A3AG*, *DNMT3A3AH*, *DNMT3A3AI*, *DNMT3A3AJ*, *DNMT3A3AK*, *DNMT3A3AL*, *DNMT3A3AM*, *DNMT3A3AN*, *DNMT3A3AO*, *DNMT3A3AP*, *DNMT3A3AQ*, *DNMT3A3AR*, *DNMT3A3AS*, *DNMT3A3AT*, *DNMT3A3AU*, *DNMT3A3AV*, *DNMT3A3AW*, *DNMT3A3AX*, *DNMT3A3AY*, *DNMT3A3AZ*, *DNMT3A3BA*, *DNMT3A3BB*, *DNMT3A3BC*, *DNMT3A3BD*, *DNMT3A3BE*, *DNMT3A3BF*, *DNMT3A3BG*, *DNMT3A3BH*, *DNMT3A3BI*, *DNMT3A3BJ*, *DNMT3A3BK*, *DNMT3A3BL*, *DNMT3A3BM*, *DNMT3A3BN*, *DNMT3A3BO*, *DNMT3A3BP*, *DNMT3A3BQ*, *DNMT3A3BR*, *DNMT3A3BS*, *DNMT3A3BT*, *DNMT3A3BU*, *DNMT3A3BV*, *DNMT3A3BW*, *DNMT3A3BX*, *DNMT3A3BY*, *DNMT3A3BZ*, *DNMT3A3CA*, *DNMT3A3CB*, *DNMT3A3CC*, *DNMT3A3CD*, *DNMT3A3CE*, *DNMT3A3CF*, *DNMT3A3CG*, *DNMT3A3CH*, *DNMT3A3CI*, *DNMT3A3CJ*, *DNMT3A3CK*, *DNMT3A3CL*, *DNMT3A3CM*, *DNMT3A3CN*, *DNMT3A3CO*, *DNMT3A3CP*, *DNMT3A3CQ*, *DNMT3A3CR*, *DNMT3A3CS*, *DNMT3A3CT*, *DNMT3A3CU*, *DNMT3A3CV*, *DNMT3A3CW*, *DNMT3A3CX*, *DNMT3A3CY*, *DNMT3A3CZ*, *DNMT3A3DA*, *DNMT3A3DB*, *DNMT3A3DC*, *DNMT3A3DD*, *DNMT3A3DE*, *DNMT3A3DF*, *DNMT3A3DG*, *DNMT3A3DH*, *DNMT3A3DI*, *DNMT3A3DJ*, *DNMT3A3DK*, *DNMT3A3DL*, *DNMT3A3DM*, *DNMT3A3DN*, *DNMT3A3DO*, *DNMT3A3DP*, *DNMT3A3DQ*, *DNMT3A3DR*, *DNMT3A3DS*, *DNMT3A3DT*, *DNMT3A3DU*, *DNMT3A3DV*, *DNMT3A3DW*, *DNMT3A3DX*, *DNMT3A3DY*, *DNMT3A3DZ*, *DNMT3A3EA*, *DNMT3A3EB*, *DNMT3A3EC*, *DNMT3A3ED*, *DNMT3A3EE*, *DNMT3A3EF*, *DNMT3A3EG*, *DNMT3A3EH*, *DNMT3A3EI*, *DNMT3A3EJ*, *DNMT3A3EK*, *DNMT3A3EL*, *DNMT3A3EM*, *DNMT3A3EN*, *DNMT3A3EO*, *DNMT3A3EP*, *DNMT3A3EQ*, *DNMT3A3ER*, *DNMT3A3ES*, *DNMT3A3ET*, *DNMT3A3EU*, *DNMT3A3EV*, *DNMT3A3EW*, *DNMT3A3EX*, *DNMT3A3EY*, *DNMT3A3EZ*, *DNMT3A3FA*, *DNMT3A3FB*, *DNMT3A3FC*, *DNMT3A3FD*, *DNMT3A3FE*, *DNMT3A3FF*, *DNMT3A3FG*, *DNMT3A3FH*, *DNMT3A3FI*, *DNMT3A3FJ*, *DNMT3A3FK*, *DNMT3A3FL*, *DNMT3A3FM*, *DNMT3A3FN*, *DNMT3A3FO*, *DNMT3A3FP*, *DNMT3A3FQ*, *DNMT3A3FR*, *DNMT3A3FS*, *DNMT3A3FT*, *DNMT3A3FU*, *DNMT3A3FV*, *DNMT3A3FW*, *DNMT3A3FX*, *DNMT3A3FY*, *DNMT3A3FZ*, *DNMT3A3GA*, *DNMT3A3GB*, *DNMT3A3GC*, *DNMT3A3GD*, *DNMT3A3GE*, *DNMT3A3GF*, *DNMT3A3GG*, *DNMT3A3GH*, *DNMT3A3GI*, *DNMT3A3GJ*, *DNMT3A3GK*, *DNMT3A3GL*, *DNMT3A3GM*, *DNMT3A3GN*, *DNMT3A3GO*, *DNMT3A3GP*, *DNMT3A3GQ*, *DNMT3A3GR*, *DNMT3A3GS*, *DNMT3A3GT*, *DNMT3A3GU*, *DNMT3A3GV*, *DNMT3A3GW*, *DNMT3A3GX*, *DNMT3A3GY*, *DNMT3A3GZ*, *DNMT3A3HA*, *DNMT3A3HB*, 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*DNMT3A3YZ*, *DNMT3A3ZA*, *DNMT3A3ZB*, *DNMT3A3ZC*, *DNMT3A3ZD*, *DNMT3A3ZE*, *DNMT3A3ZF*, *DNMT3A3ZG*, *DNMT3A3ZH*, *DNMT3A3ZI*, *DNMT3A3ZJ*, *DNMT3A3ZK*, *DNMT3A3ZL*, *DNMT3A3ZM*, *DNMT3A3ZN*, *DNMT3A3ZO*, *DNMT3A3ZP*, *DNMT3A3ZQ*, *DNMT3A3ZR*, *DNMT3A3ZS*, *DNMT3A3ZT*, *DNMT3A3ZU*, *DNMT3A3ZV*, *DNMT3A3ZW*, *DNMT3A3ZX*, *DNMT3A3ZY*, *DNMT3A3ZZ*.

<sup>a</sup>Percentages may not add to 100% due to rounding.

<sup>b</sup>Biological sex. <sup>c</sup>WHO response question. <sup>d</sup>5 patients had missing data for race. Percentages were calculated out of total number of patients with non-missing data. <sup>e</sup>Percentages were calculated out of total number of patients with non-missing data. <sup>f</sup>Percentages were calculated out of 114 patients with AML-MRC. <sup>g</sup>Patients had missing data for Grimwade cytogenetic classification. Percentages were calculated out of total number of patients with non-missing data. <sup>h</sup>Percentages were calculated out of 27 patients with missing data for mutated *TP53*. Percentages were calculated out of total number of patients with non-missing data. <sup>i</sup>Myelodysplasia-related mutations were defined as mutations in *ASXL1*, *BCOR*, *EZH2*, *RUNX1*, *SRSF2*, *STAG2*, *UDAF1*, *DNMT3A*, *DNMT3B*, *DNMT3C*, *DNMT3L*, *DNMT3O*, *DNMT3A2*, *DNMT3A3*, *DNMT3A3L*, *DNMT3A3B*, *DNMT3A3C*, *DNMT3A3D*, *DNMT3A3E*, *DNMT3A3F*, *DNMT3A3G*, *DNMT3A3H*, *DNMT3A3I*, *DNMT3A3J*, *DNMT3A3K*, *DNMT3A3L*, *DNMT3A3M*, *DNMT3A3N*, *DNMT3A3O*, *DNMT3A3P*, *DNMT3A3Q*, *DNMT3A3R*, *DNMT3A3S*, *DNMT3A3T*, *DNMT3A3U*, *DNMT3A3V*, *DNMT3A3W*, *DNMT3A3X*, *DNMT3A3Y*, *DNMT3A3Z*, *DNMT3A3AA*, *DNMT3A3AB*, *DNMT3A3AC*, *DNMT3A3AD*, *DNMT3A3AE*, *DNMT3A3AF*, *DNMT3A3AG*, *DNMT3A3AH*, *DNMT3A3AI*, *DNMT3A3AJ*, *DNMT3A3AK*, *DNMT3A3AL*, *DNMT3A3AM*, *DNMT3A3AN*, *DNMT3A3AO*, *DNMT3A3AP*, *DNMT3A3AQ*, *DNMT3A3AR*, *DNMT3A3AS*, *DNMT3A3AT*, *DNMT3A3AU*, *DNMT3A3AV*, *DNMT3A3AW*, *DNMT3A3AX*, *DNMT3A3AY*, *DNMT3A3AZ*, *DNMT3A3BA*, *DNMT3A3BB*, *DNMT3A3BC*,