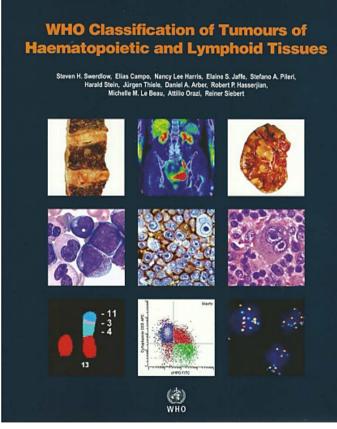
"HIGHLIGHTS" IN EMATOLOGIA II Brutto: Le Leucemie Secondarie

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Agenda

- Biologic considerations
- Therapeutic approach

WHO Classification (2016)



MDS, myelodysplastic syndrome; WHO, World Health Organization

AML categories:

- AML with recurrent genetic abnormalities
- AML with myelodysplasia-related changes (MRC)
- Therapy-related AML/MDS
- AML not otherwise specified (NOS)
- Myeloid sarcoma
- Myeloid proliferations related to Down syndrome

WHO 2016 AML Classification

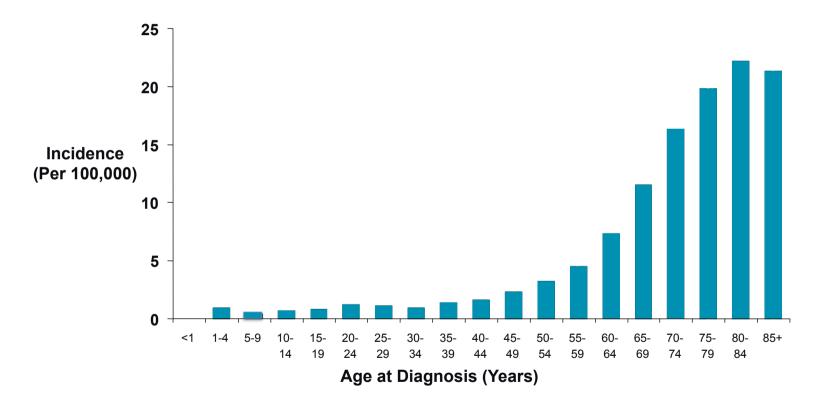
AML with MDS related changes:

- 50% dysplasic cells in 2 lines
- History of MDS
- MDS-related cytogenetics (except del9q)

Cytogenic Abnormalities Complex karyotype (3 or more abnormalities) Unbalanced abnormalities -7/del(7q) del(5q)/t(5q)i(17q)/t(17p) -13/del(13q)del(11q) del(12p)/t(12p)idic(X)(q13) **Balanced Abnormalities** t(11;16)(q23.3;p13.3) t(3;21)(q26.2;q22.1) t(1;3)(p63.3;q21.2) t(2;11)(p21;q23.3) t(5;12)(q32;p13.2) t(5;7)(q32;q11.2) t(5;17)(q32;p13.2) t(5;10)(q32;q21.2) t(3;5)(q25.3;q35.1)

Arber DA, et al. Blood. 2016;127(20):2391-2405..

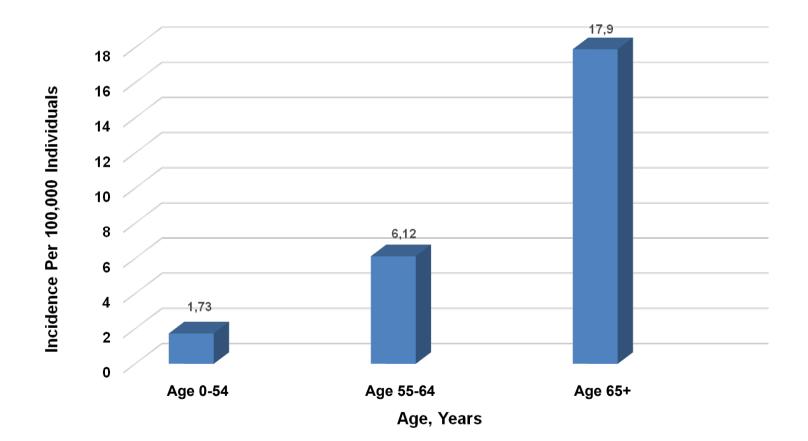
AML is Primarily a Disease of Older Adults



AML, acute myeloid leukemia

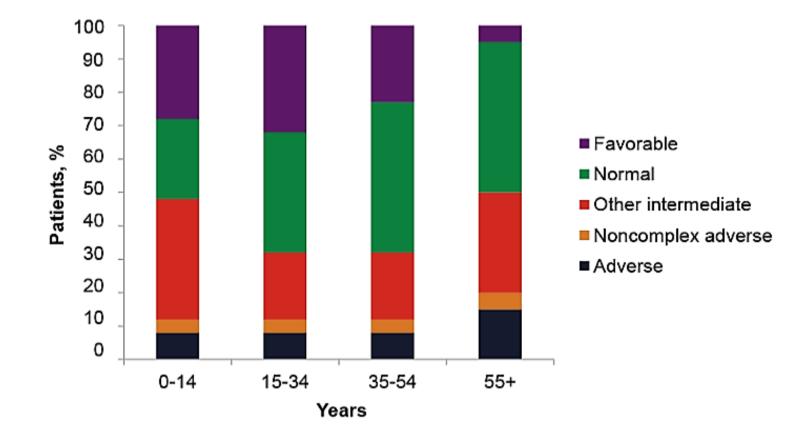
SEER Cancer Statistics Review. 1975-2000. http://seer.cancer.gov/csr/1975_2000/results_merged/sect_13_leukemia.pdf. Accessed 23 May 2018.

Incidence of AML and Age in Italy



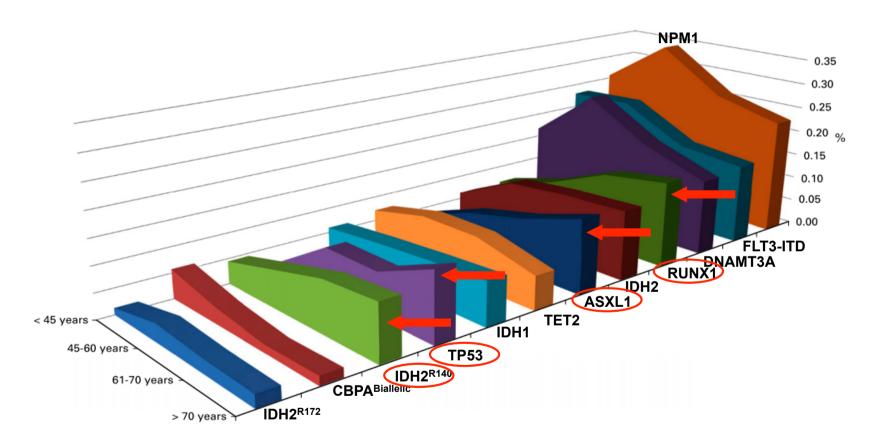
AIRTUM Working Group, et al. Epidemiol Prev. 2016;40(1 Suppl 2):1-20

Cytogenetic Categories and Age in AML



Grimwade D, et al. Blood. 2001;98(5):1312-1320

Age-Related Frequency of Selected Recurring Gene Mutations



Bullinger L, et al. J Clin Oncol. 2017;35(9):934-946

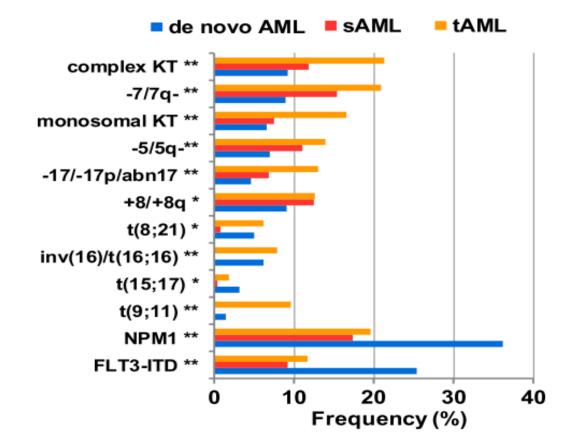
- Can AML ontogeny be mutationally defined?
- Is there any relationship between ontogenic models and age?

Ontogenic Models in AML: 3 Distinct Categories

- <u>De novo AML</u>: Arises in absence of identified exposure or prodromal stem cell disorder
- Secondary AML (sAML): Transformation of AHD
- <u>Therapy-related AML (tAML)</u>: Late complication in individuals with exposure to leukemogenic agents

AHD, antecedent hematologic disorder

Frequency of Cytogenetic Aberrations in De Novo, sAML, and tAML

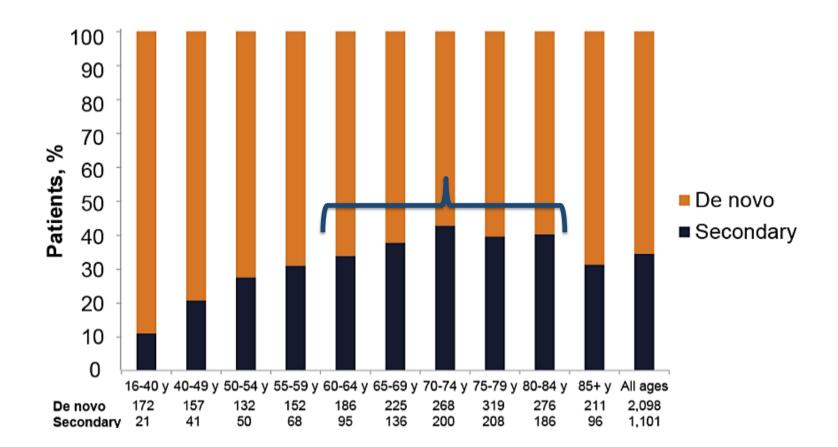


Heuser M. Hematology Am Soc Hematol Educ Program. 2016;2016(1):24-32

AML Ontogeny Can Be Mutationally Defined

	Secondary AML De Novo AML					
			M	Mutated cases, n (%)		P value
	SRSF2 - +		19	(20)	1 (1)	< 0.0001
	ZRSR2		7	(8)	0 (0)	0.0005
Association with sAML	SF3B1 -		10	(11)	1 (1)	0.0001
	ASXL1 -		30	(32)	5 (3)	< 0.0001
with >95% specificity	BCOR -	F → 1	7	(8)	2 (2)	0.035
	EZH2 -	F→→+1	8	(9)	3 (2)	0.009
	U2AF1 -	→ →+ :	15	(16)	8 (4)	0.002
	STAG2 -	→ →+ :	13	(14)	3 (2)	0.07
	NF1 -	⊢ → – į	6	(6)	7 (4)	0.005
	RUNX1 -	→ + + +	29	(31)	9 (11)	< 0.0001
Acception with cAMI	CBL -	<u>⊢ → i</u> i	5	(5)	3 (2)	0.13
Association with sAML	NRAS -	→→	21	(23)	5 (8)	0.002
with <95% specificity	TET2 -	⊢ ⊷-1	19	(20)	7 (9)	0.014
	GATA2 -	H	2	(2)	2 (1)	0.6
	TP53 -	→	14	(15)	6 (9)	0.15
	KRAS -	→ + +	7	(8)	8 (4)	0.4
	PTPN11 -	→	5	(5)	9 (5)	1
	IDH1 -	⊢ ⊷1	10	(11)	20 (11)	1
Neutrality	IDH2 -	— —	10	(11)	9 (11)	1
, to did diffy	SMC1A -	→	3	(3)	7 (4)	1
	RAD21 -		2	(2)	5 (3)	1
Association with de novo AML	FLT3 -	i ⊷-1	18	(19)	0 (28)	0.14
	DNMT3A -	⊢ +-1	18	(19)	51 (28)	0.14
with <95% specificity	SMC3 -		2	(2)	7 (4)	0.7
	CEBPA -		3	(3)	3 (7)	0.28
Association with de novo AML	NPM1 -		5	(5)	4 (30)	< 0.0001
	11g23-rearranged -		- 0	(0)	1 (6)	0.002
with >95% specificity	CBF-rearranged -	· · · · · · · · · · · · · · · · · · ·	- 0	(0)	9 (9)	< 0.0001
•	0.001	0.01 0.1 1 10 100	1000			
	0.001		1000			
		Odds Ratio				

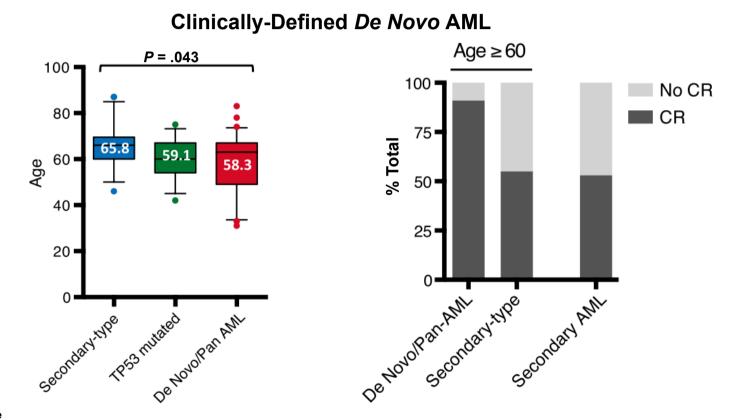
Lindsley RC, et al. Blood. 2015;125(9):1367-1376



Incidence of sAML Increases With Age

Juliusson G, et al. Blood. 2012;119(17):3890-3899

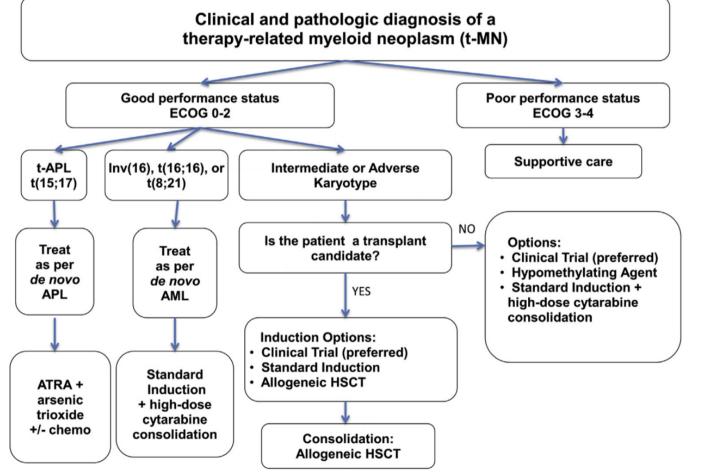
Even in Clinically-Defined *De Novo* AML, sAML-Like Features Are Associated With Age



CR, complete response

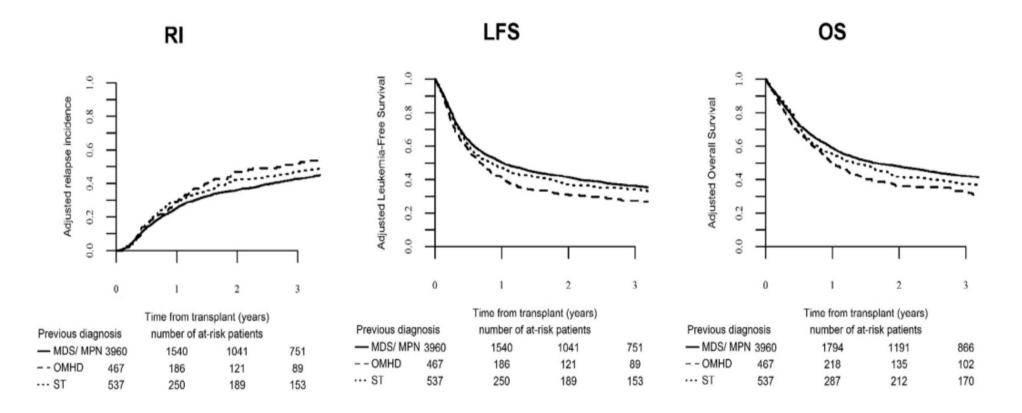
Lindsley RC, et al. Blood. 2015;125(9):1367-1376

Algorithm for the treatment of t-MN



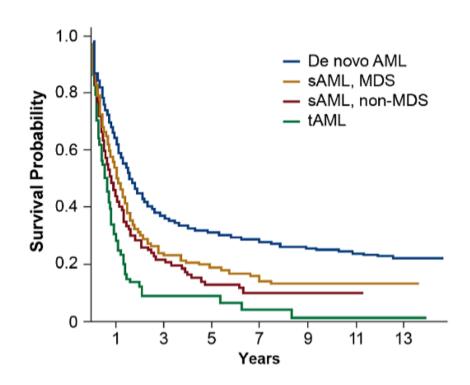
Churpek & Larson, BPRCH 2013

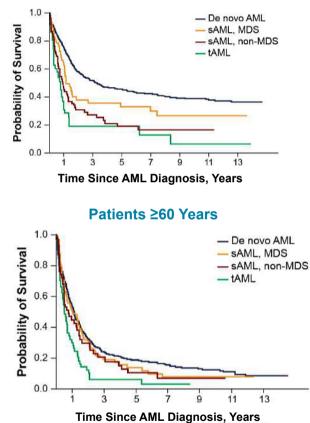
Transplant outcome based on disease type before SAML



S. Sengsayadeth et al. BBMT 24 (2018) 1406-1414

Poor Outcome of sAML and t-AML





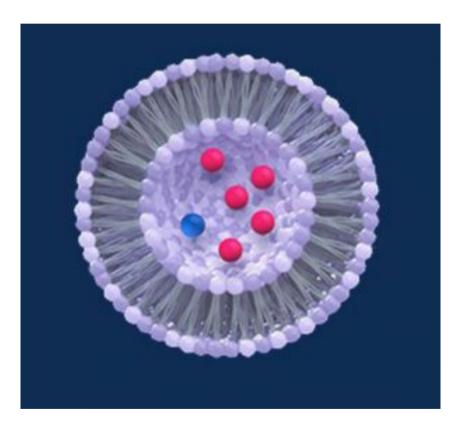
Patients <60 Years

Granfeldt Østgard LS, et al. J Clin Oncol. 2015;33(31):3641-3649

Drug	FDA Approval/ Orphan Drug Designation for AML ¹	FDA Indication for AML ¹	EMA Approval /Orphan Drug Designation for AML ²	EMA Indication for AML ²
GO (fractionated)				
plus 3+7	2017	Newly diagnosed or R/R CD33-positive AML	None	None
single agent		R/R CD33-positive AML	None	None
CPX-351	2017	Newly diagnosed tAML or AML-MRC	2012 (orphan)	None
Midostaurin (plus 3+7)	2017	Newly diagnosed FLT3- mut+	2005 (orphan)	Newly diagnosed FLT3-mut+
Enasidenib	2017	R/R IDH2-mut	2016 (orphan)	None

US Food and Drug Administration. http://www.accessdata.fda.gov/scripts/cder/daf/index.cfm. Accessed May 18, 2017
European Medicines Agency. <u>European Public Assessment Reports.</u> Accessed March 3, 2017. 3. Döhner H, et al. *Blood.* 2017;129:424-447.

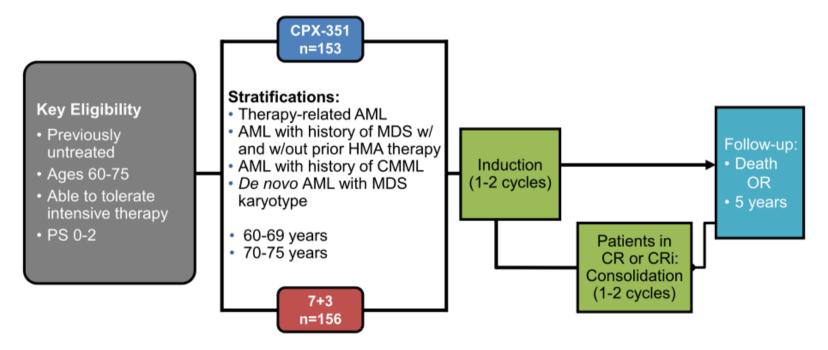
CPX-351 Uses a Nano-Scale Delivery Complex



- ✓ 100-nm bilamellar liposomes
- ✓ 5:1 molar ratio of cytarabine to daunorubicin
- 1 unit = 1.0 mg cytarabine plus 0.44 mg daunorubicin

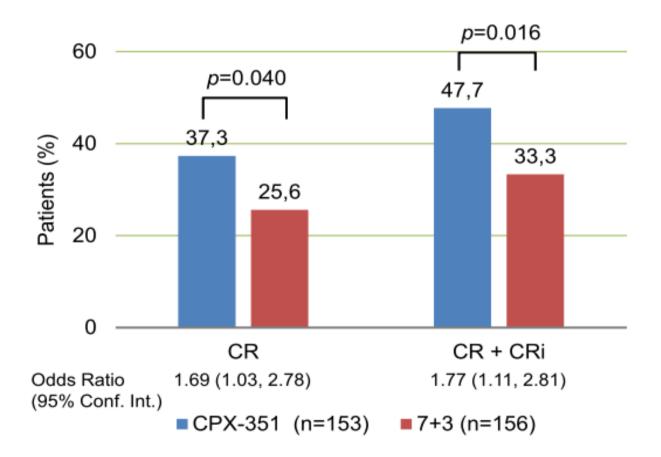
Lancet JE, et al. ASCO 2016. Abstract 7000.

Phase 3 Study of CPX-351 vs Standard Induction in Older Patients w/ Newly Diagnosed Secondary AML (Study 301)

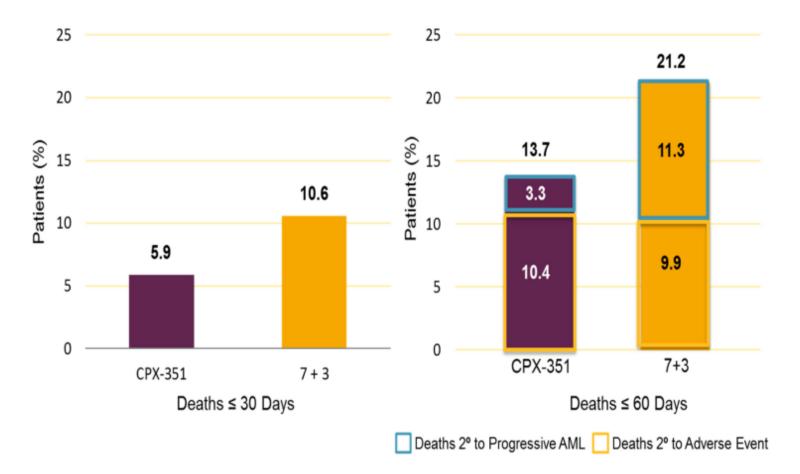


· Primary Endpoint: Overall survival

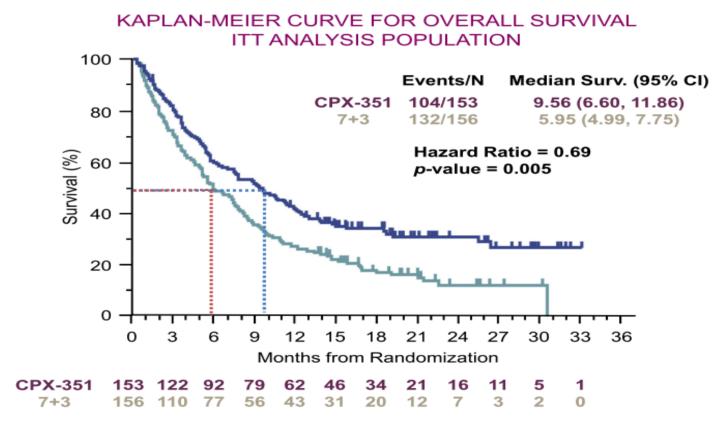
Response Rate



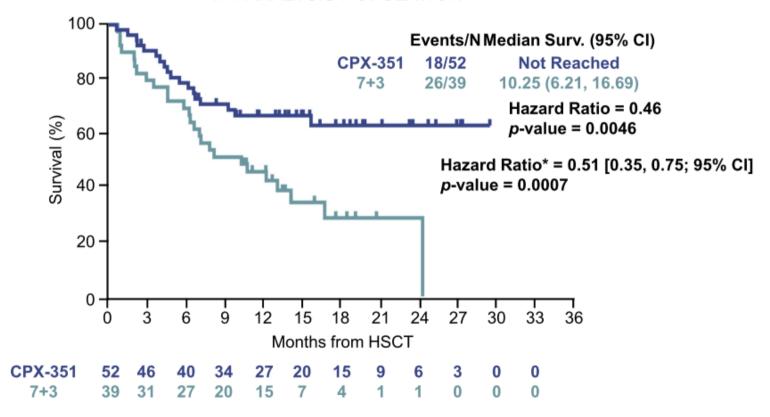
30-Day & 60-Day Mortality Rates



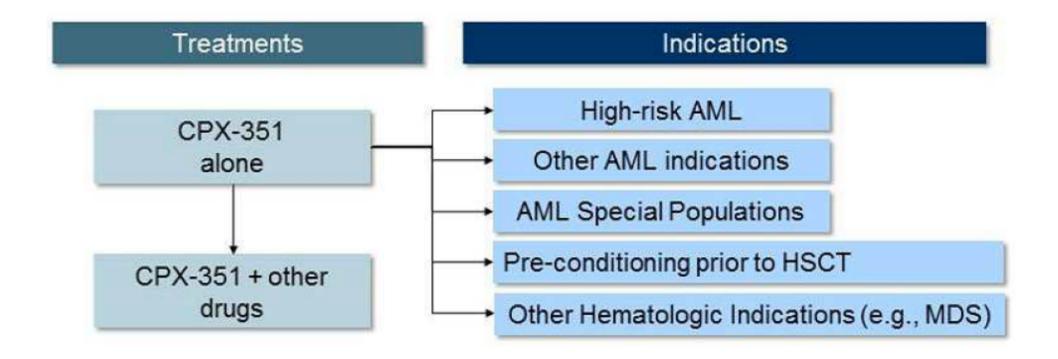
Overall Survival Greater in the CPX-351 Arm Compared to the 7+3 Arm in Phase 3 Study 301



KAPLAN-MEIER CURVE FOR OVERALL SURVIVAL LANDMARKED AT STEM CELL TRANSPLANT ITT ANALYSIS POPULATION



CPX-351 life cycle development Extend use to other AML and hematologic malignancies



Conclusions-1

- sAML among the most difficult disease to treat
- For patients who achieve an initial CR, ASCT represents the best chance for long-term OS
- Need of continued development of novel agents

Conclusions-2

- The current list of disease-relevant genes is likely to expand
- More chances to capture AML heterogeneity at a single-cell level
- Advances in (personalized) treatment
 - Novel therapies

CLINICAL TRIALS IN THE «GENOMIC ERA»

Patients' selection

Relationship between mutations, malignancy and response to novel agents

<u>Basket clinical trials</u>

Pooling together different cancers per their genomic pattern irrespective of their histologic origin (Histology-agnostic randomized trials)

• <u>Umbrella clinical trials</u>

Multiple targeted agents/drugs for a single histology (Beat AML – Master Clinical Trial)

• Adaptive clinical trials

Use of multiple interim analysis to adapt key features based on predefined rules