



Acute myeloid leukemia

Post – ASH meeting 09/01/2015

Ann De Becker

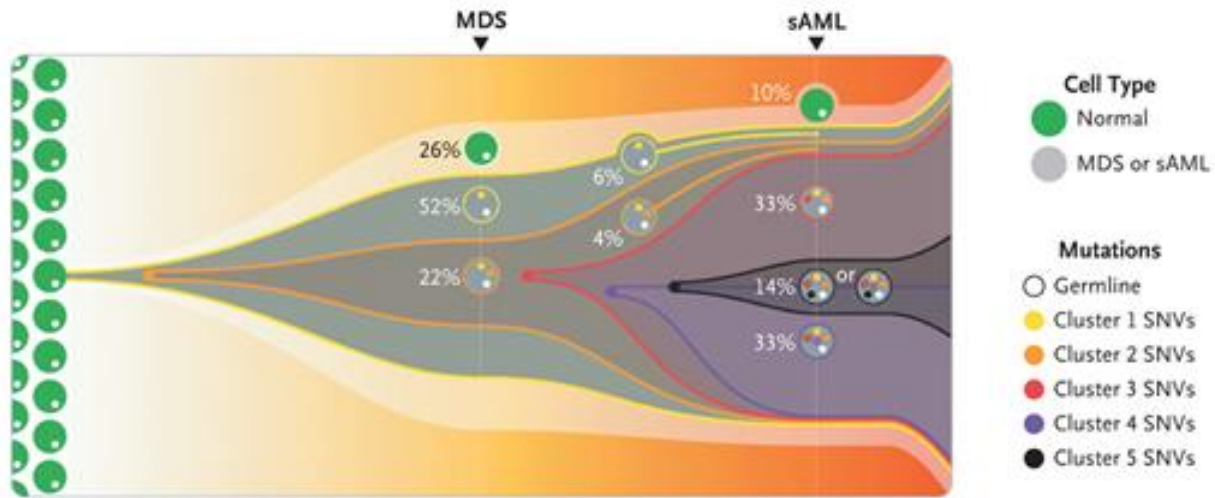
UZ Brussel

AML at ASH 2014

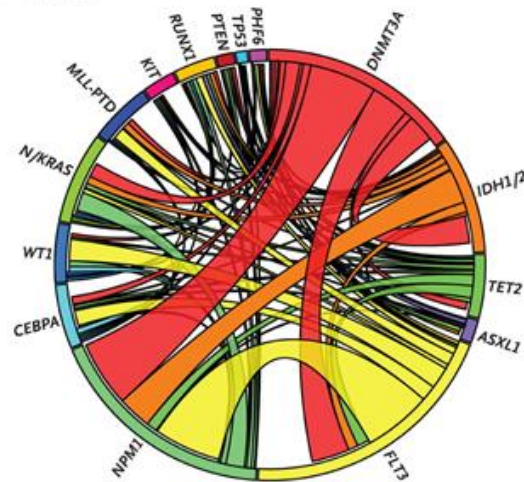
- Biology
- Risk stratification
- Treatment
- MRD assessment
- APL

AML BIOLOGY

AML Biology



A Total Cohort



Gene	Overall Frequency (%)
FLT3 (ITD, TKD)	37 (30, 7)
NPM1	29
DNMT3A	23
NRAS	10
CEBPA	9
TET2	8
WT1	8
IDH2	8
IDH1	7
KIT	6
RUNX1	5
MLL-PTD	5
ASXL1	3
PHF6	3
KRAS	2
PTEN	2
TP53	2
HRAS	0
EZH2	0

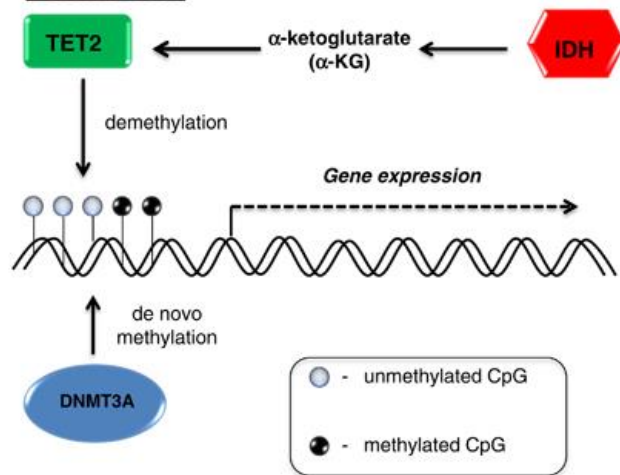
Walter et al NEJM 2012

Patel et al NEJM 2012

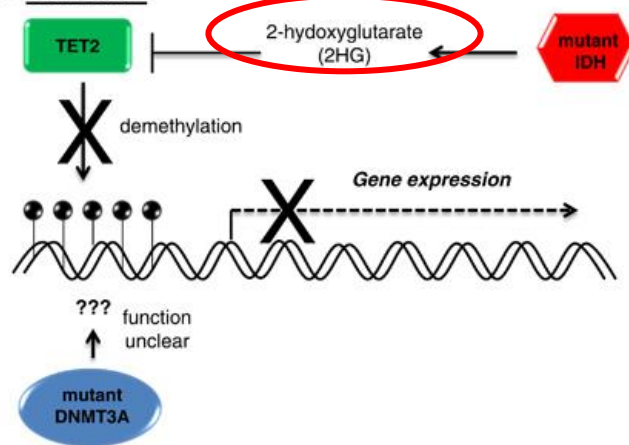
- DNMT3a:
 - Epigenetic regulator
 - Essential for normal HSC differentiation
 - Ablation leads to maturation arrest
 - Additional mutations needed for leukemic transformation:
 - c-KIT
 - Flt3 ITD
 - Mutation arises early in pre-leukemic phase

AML Biology: IDH1/2 mutations:

a Normal cell:



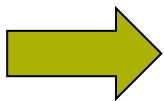
b AML cell:



- Elevated 2-HG levels in IDH1/2 mut vs WT pt in:
 - Serum
 - Urine
 - Marrow aspirate
- Regardless mutation type
- Allows for identification of IDH1/2 mut pt

AML Biology

- Persistence of clonal hematopoiesis in AML patients in CR
 - ALFA 0701:
 - 15pt NPM1mut+/DNMT3a mut+
 - Persistence of DNMT3a mut+ clone in 40% of patients remaining in CR
 - SAL:
 - 48pt NPM1mut+/DNMT3a mut+
 - Persistence of DNMT3a mut+ at CR/FU in 87,5%
 - Associated with inferior outcome?



SURVIVAL OF PRE-LEUKEMIC HSC AFTER CHEMOTHERAPY

- Genetic evolution of (relapsed) AML
 - Significant differences, dependent on cytogenetic risk groups
 - Favorable:
 - Defining aberrations persist at relapse
 - Changes in karyotype 46%
 - Changes in mutational pattern 47%
 - Intermediate:
 - Predominantly instable at molecular level
 - Unfavorable:
 - High karyotype instability

AML RISK STRATIFICATION

Risk stratification

- 2012 revised risk stratification integrating genetic profiling

Cytogenetic Classification	Mutations		Overall Risk Profile
Favorable	Any		Favorable
Normal karyotype or intermediate-risk cytogenetic lesions	<i>FLT3</i> -ITD-negative	Mutant <i>NPM1</i> and <i>IDH1</i> or <i>IDH2</i>	
	<i>FLT3</i> -ITD-negative	Wild-type <i>ASXL1</i> , <i>MLL</i> -PTD, <i>PHF6</i> , and <i>TET2</i>	Intermediate
	<i>FLT3</i> -ITD-negative or positive	Mutant <i>CEBPA</i>	
	<i>FLT3</i> -ITD-positive	Wild-type <i>MLL</i> -PTD, <i>TET2</i> , and <i>DNMT3A</i> and trisomy 8–negative	
	<i>FLT3</i> -ITD-negative	Mutant <i>TET2</i> , <i>MLL</i> -PTD, <i>ASXL1</i> , or <i>PHF6</i>	Unfavorable
	<i>FLT3</i> -ITD-positive	Mutant <i>TET2</i> , <i>MLL</i> -PTD, <i>DNMT3A</i> , or trisomy 8, without mutant <i>CEBPA</i>	
Unfavorable	Any		

Risk stratification

- Development of new scores for CN AML:
 - Marcucci et al: 7 gene score for CN AML
 - NGS to determine demethylated regions
 - Identification of 7 genes with expression associated with OS: lower score = higher CR rate
 - Pastore et al: molecular + clinical markers
 - Clinical: age, PS, wbc count
 - Molecular: NPM1, CEBPA, flt3
 - 3 risk groups (OS, RFS)
 - Thangavelu et al: 8 gene panel
 - Flt3, NPM1, IDH1/2, CEBPA, WT1, RUNX1, TP53

Risk stratification: flt3

- Impact of WT/mutant allelic ratio
 - Cut-off 0,51
 - Higher ratio = low CR rates
- Impact of ITD insertion site in TKD1
 - Low CR rates
- allelic ratio $> 0,51$ after post remission therapy (chemo/autoHCT) = unfavorable RFS (p 0,0008) and OS (p 0,004)
- Multivariate analysis: high allelic ratio predictive for beneficial effect alloHCT, IS in TKD1 remains unfavorable

Risk stratification: TP53

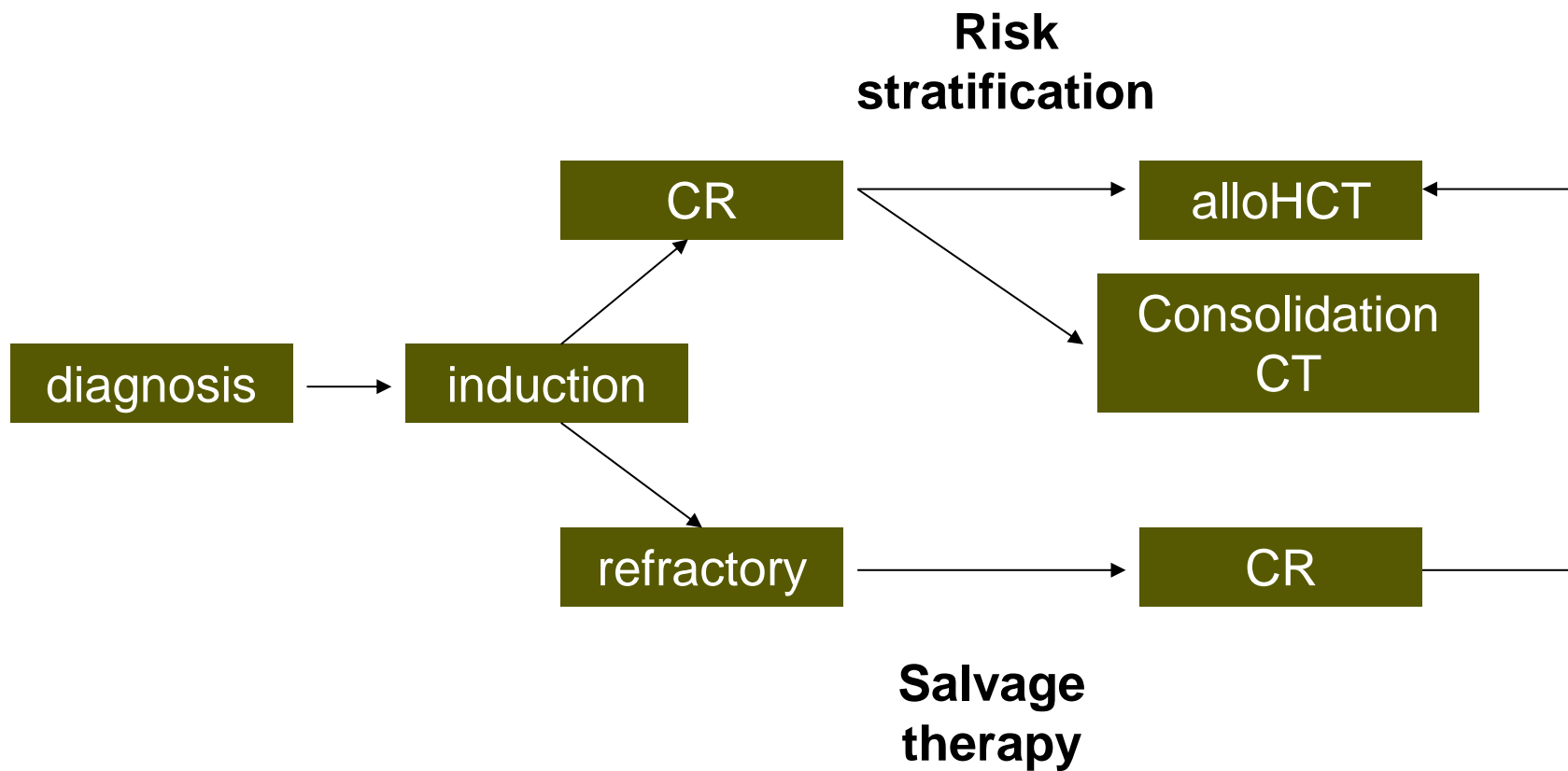
- 172 pt / 886 pt analyzed for TP53mut
- Sanger sequencing 29/172 TP53mut+
 - 36 different types of mutations
 - 7 pt with 2 mutations
- 79% of TP53mut pt also had complex karyotype
- Worse OS
 - Median survival 4,3m vs 31m
- Worse RFS

Risk stratification

- DNMT3a:
 - 30% of CN AML
 - Loss of function mutation
 - Associated with inferior outcome regardless type of mutation
 - Persistence after treatment
- ASXL1
 - Worse OS
- RUNX1 mutation
 - Worse OS

AML TREATMENT

Treatment



Treatment: new cytotoxic agents

- Vosaroxin

- First-in-class anti-cancer quinolone derivative, topo-II-inhibitor

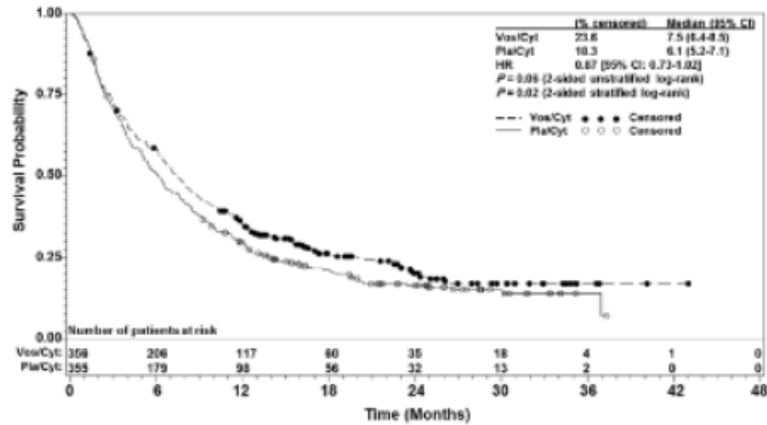
- VALOR:

- Phase III, RCT
 - Cytarabine ± vosaroxin/placebo in R/R AML
 - 711pt
 - Significantly higher CR rate in vosaroxin arm: 30,1% vs 16,3%

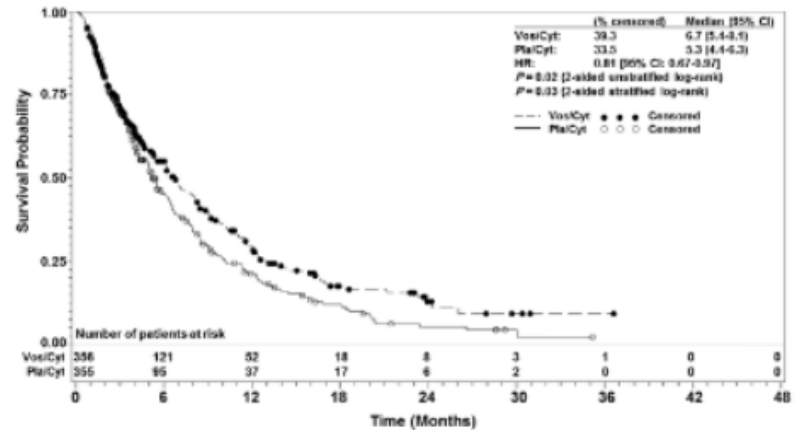
Treatment: VALOR

Figure. OS in patients with R/R AML treated with vosaroxin plus cytarabine vs placebo plus cytarabine

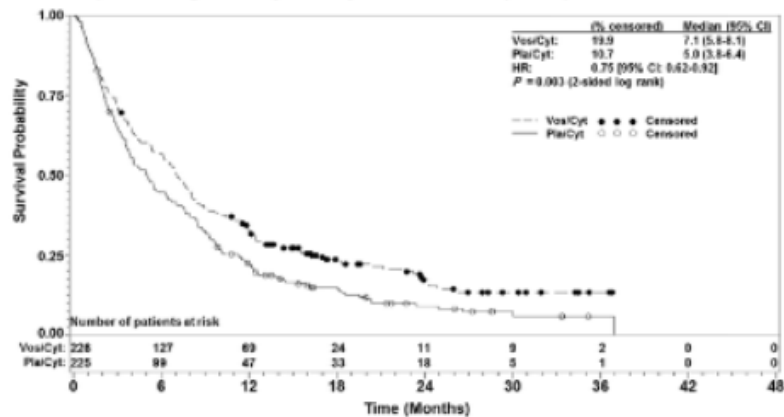
A. OS by treatment arm (N=711)



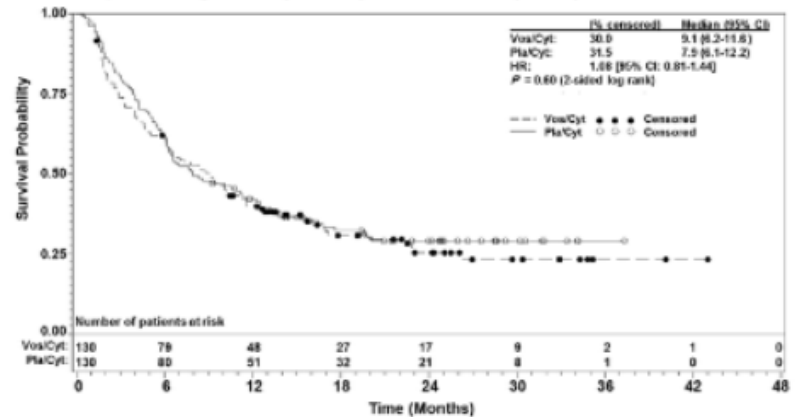
B. OS (censored for ASCT), by treatment arm (N=711)



C. OS in patients aged ≥ 60 years, by treatment arm (n=451)



D. OS in patients aged < 60 years, by treatment arm (n=260)



Treatment: cytotoxic agents

- ECOG E1900: final analysis
 - 657pt, median FU 80m
 - DNR 90 improves survival in AML up to 60y
 - Across all (cyto)genetic risk groups
- ALFA 0701: final analysis
 - 278pt, de novo AML 50-70y
 - standard treatment ± GO
 - No difference in CR+Cri
 - Trend for fewer 1ary refractory pt (30 vs 19)
 - Significantly better EFS, RFS
 - No difference in 3y OS (36 vs 44%)

Targeted therapy: epigenetics: AZA

AML-001:

488 Patients Enrolled

Investigator Preselection

BSC Only
n=89 (18%)

LDAC
n=312 (64%)

IC
n=87 (18%)

1:1 Randomization

AZA
n=44

BSC
n=45

AZA
n=154

LDAC
n=158

AZA
n=43

IC
n=44

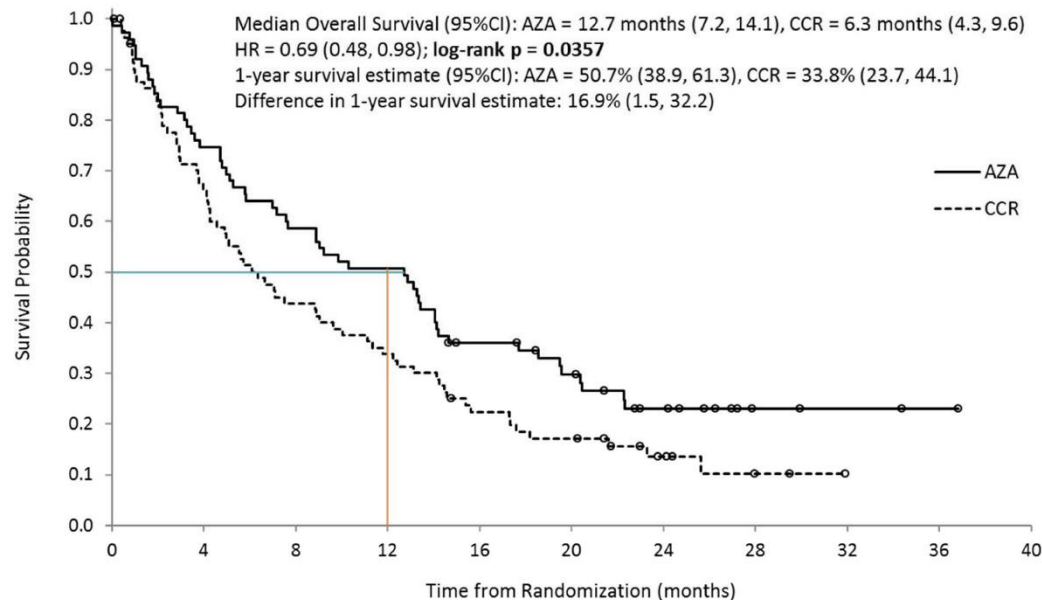
Targeted therapy: epigenetics: AZA

- AML-001
- Vidaza® in newly diagnosed AML with >30% blasts
- Age \geq 65years
- Ineligible for alloHCT
- AZA vs CCR (LDAC, BSC, ICT)
- No significant improvement in OS
- Pre-planned censoring at next treatment: significant better OS for AZA

Targeted therapy: epigenetics: AZA

- AML-001 subgroup analysis:
→ 1/ AML-MRC

Figure. Overall Survival in Patients with AML with Morphologic Dysplastic Changes Treated with AZA vs. CCR



Pts at risk

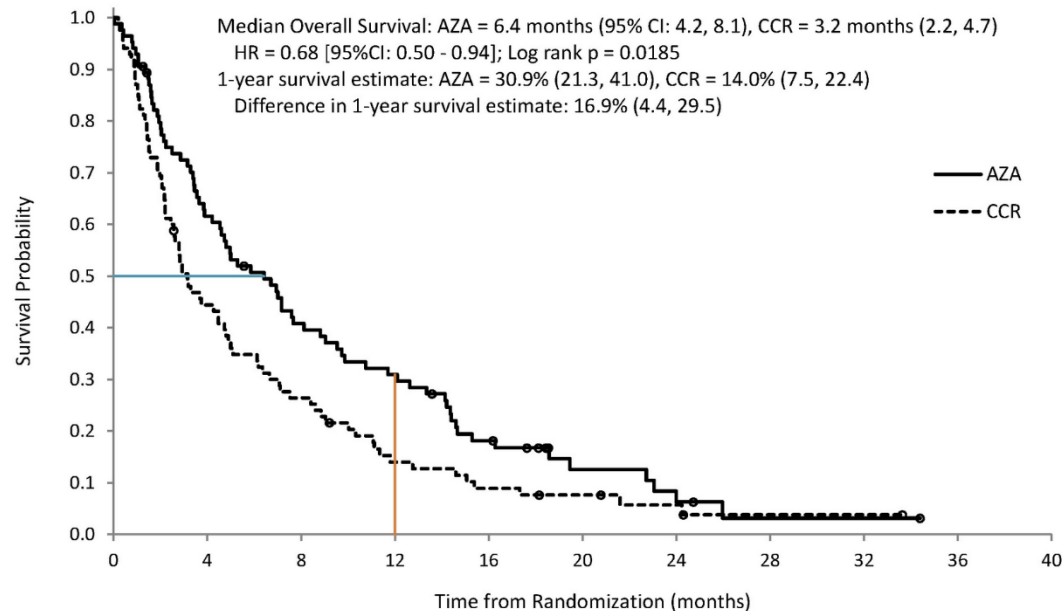
AZA	75	56	44	38	25	19	11	4	3	2	0
CCR	83	53	35	27	17	13	6	2	0		

○ Censored

Targeted therapy: epigenetics: AZA

- AML-001 subgroup analysis:
→ 2/ cytogenetic risk group

Figure. OS in Patients with Poor-risk Cytogenetics



Pts at risk

AZA	85	51	33	25	14	6	3	1	1	0
CCR	85	37	22	11	7	5	3	1	1	0

○ Censored

Targeted therapy: epigenetics

- Decitabine:
 - Priming before ICT
 - Prolonged administration
- New molecules:
 - AG-221: IDH 2 inhibitor
 - EZP5676: DOT1L inhibitor
 - OTX015: BET bromodomain inhibitor
 - SGI-110: 2nd generation hypomethylating agent

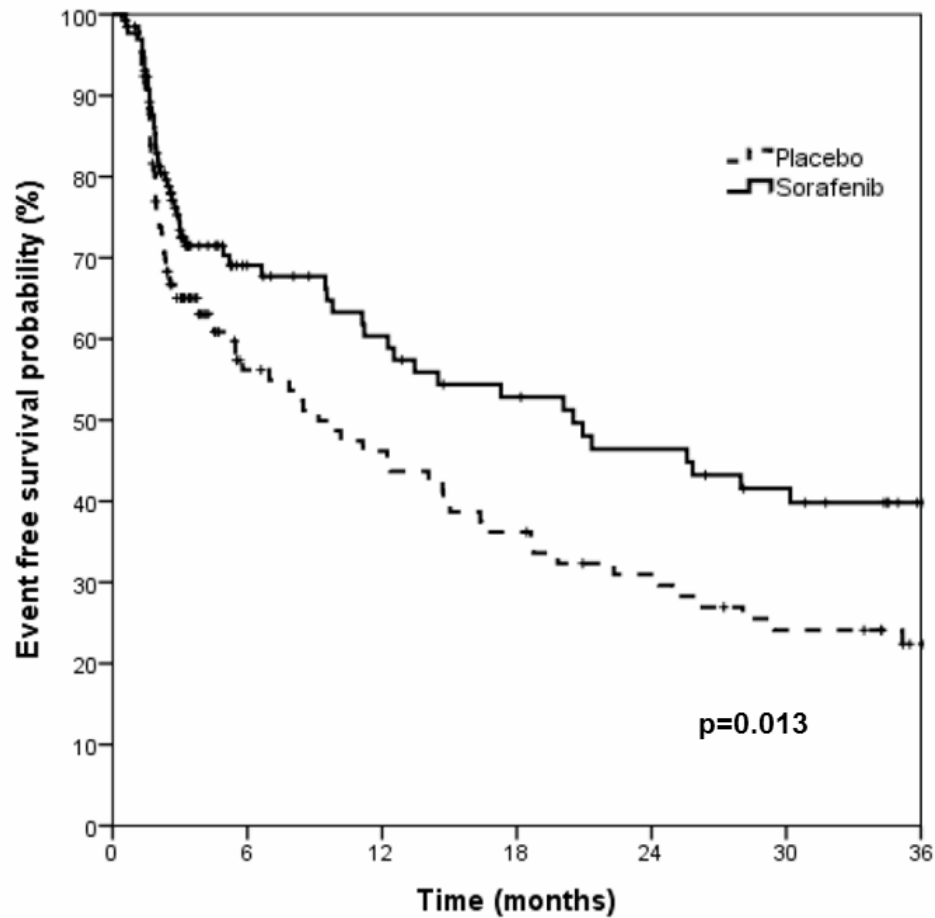
Targeted therapy: flt3

- **SORAML:**

- 276 pt, final analysis, AML < 60y
- chemo + sorafenib/placebo followed by 12m maintenance
- Significantly prolonged 3y EFS, RFS
- No significance for OS
- Flt3 ITD+ pt trend for prolonged OS en RFS in favor of sorafenib

Targeted therapy: flt3

- SORAML:



Targeted therapy: flt3

- Crenolanib:
 - Phase II in R/R AML flt3+
 - Monotherapy
 - Flt3 ITD or flt3 TKD
 - 34 pt evaluable
 - Significantly better response in TKI naive pt
 - Median OS 55w vs 13w
 - On target flt3 inhibition

Targeted therapy: c-KIT

- KIT mutations in ca 30% of CBF-AML
- In general poor prognosis
- Dasatinib:
 - Multikinase-inhibitor
 - Synergism with cytarabine
 - Inhibition of WT and mutant KIT
 - Inhibitor of AML stem/progenitor cell growth & survival

Targeted therapy: c-KIT

- CALGB 10801
- Update, median follow-up 21m

Table. Clinical outcomes

	All (n=59)	Younger (n= 45)	Older (n= 14)	RUNX1/RUNX1T1 (n= 20)	CBFB/MYH11 (n= 38)	<i>KIT</i> -wt (n=46)	<i>KIT</i> -mut (n=10)
CR [*] (%)	90	93	79	90	89	89	90
Relapse ^o (%)	17	13	29	20	16	17	20
2-yr DFS [#] (%)	72	74	65	79	67	72	70
2-yr OS [¶] (%)	87	96	61	85	89	86	90

* CR, complete remission; ^o Relapse rate at any time [#] DFS, disease-free survival, [¶] OS, overall survival

Targeted therapy: cell cycle inhibitors

- Volasertib:

- Polo-like kinase 1 inhibitor

- Phase II

- Median EFS 2,3m vs 5,6m (p0,021) LDAC vs LDAC+volasertib

- Median OS 5,2m vs 8m (p0,047) LDAC vs LDAC+volasertib

Targeted therapy: CXCR-4

- CXCR-4 anchors cells in BM via interaction with CXCL12/SDF-1
- Ulocuplumab = anti-CXCR-4 antibody
- Phase I
- R/R AML, 73pt
- Ulocuplumab + MEC
- CR+CRi 51%, 4pt in CR/CRi after 1 dose of ulocuplumab

Treatment: new agents

- **AMG-330**
→ CD33/CD3 BiTE antibody
- **ABT-199**
→ Selective Bcl-2 inhibitor
- **RG7388**
→ MDM2 antagonist
- **CPX-351**
→ Cytarabine+daunorubicin liposome

MINIMAL RESIDUAL DISEASE

Minimal residual disease

- Discrepancies morphology-flow cytometry
- Heterogeneity of the disease:
 - Mean of 13 mutations in 1 AML pt
- Translocations:
 - Rare breakpoints
 - Comparison to household gene (abl)
 - MRD assessment by RT-qPCR provides independent prognostic info
 - Guidance of treatment regardless flt3/NPM1/... status

Minimal residual disease

- WT1:
 - Not unique
 - Not universal: 46% OK in PB, 13% OK in BM
- NPM1 mutation
 - Off the shelf kits, sensitivity 1/1000000
 - AML17 trial (NCRI):
 - PCR status in PB following 2nd chemotherapy
 - Most potent prognostic factor
 - Present in 98/100 relapses
- New techniques:
 - NGS/digital PCR

ACUTE PROMYELOCYTIC LEUKEMIA

Acute promyelocytic leukemia

- Long term follow-up of patients treated with ATRA-ATO
- 217 pt, treated between 2001-2010
- No late toxicities
- No significant arsenic retention
- Novel agents
 - Next generation retinoids
 - tamibarotene
 - Next generation arsenic:
 - Oral tetra-arsenic-tetra-sulfide

Conclusions

- Further insight in AML biology
- Identification of new targets for treatment
- Efforts to improve risk stratification of intermediate risk AML, CN AML
- Targeted treatment
- MRD assessment
 - complicated by heterogeneity of the disease
- ATRA-ATO gaining ground

Questions?

