Identification of genetic markers as tools for risk stratification and treatment selection in very old acute myeloid leukemia patients

151 Patients with acute myeloid leukemia (AML), median age 76 (75-86 years)

Induction chemotherapy

	Overall	High-dose cytarabine and mitoxantrone (HAM)	Standard-dose cytarabine, daunorubicin and 6-thioguanine (TAD-9)	
Complete remission (CR)	44%			
Median event-free survival (EFS)	1.7 months			
Median relapse-free survival (RFS)	12 months			
Median overall survival (OS)	6 months	7.8 months	3.1 months	p=0.09
Three-year OS	21%			

Analysis of 64 genes recurrently mutated in AML

- Identification of 622 driver mutations
- Median number of 4 mutated genes per patient (range, 1-10 mutations/patient)
- Most frequently mutated genes

TET2	42%	*ASXL1*	21%	*IDH2*	15%
DNMT3A	35%	*RUNX1*	19%	*TP53*	14%
*NPM1**	32%	*FLT3-ITD**	18%	*FLT3-TKD*	12%
SRSF2	25%	*NRAS*	17%	*IDH1*	9%

- The number of mutated genes per patient was not associated with OS
- **Univariate analysis**
  IDH1 was the only gene significantly associated with OS

IDH1 mutations were identified as the strongest genetic predictor of shorter survival

*no significant impact on OS

Prassek *et al.*, Haematologica, 2018