The distribution of cytogenetics abnormalities by FISH and karyotype in AML

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oduction

-random, recurrent cytogenetic abnormalities are common in acute leuken

r recognition has paved the way for the identification of molecular clonal
ns associated with specific subtypes that have therapeutic and prognostic
ications.

t of these abnomalities are currently well established, and important to
ider in the management of patients.

e cytogenetic abnormalities are an important factor for chemotherapy
onse and survival.

oduction

2008 who classification for acute leukemias takes into account the logical aspects, immunophenotypic and cytogenetic (conventional and ecular).

classification establishes a stratification into prognostic groups based on a genetic evaluation

pes of abnormalities are considered as having a favourable prognosis after motherapy : t (15; 17), inv (16) / t (16 ;16), and t (8;21)

er abnormalities such as of inv(3)/t(3;3), t(6;9), monosomy 5/del(5q) or -l(7q) , MLL rearangement, complex karyotype, and recent monosomal otype entity have a worse prognosis.

jective

e aim of our study is to have an approach of molecular cytogeneti
d karyotyping profile of Acute Myeloid Leukaemia (AML) followed
ingle center at Blida to identify a therapeutic strategy.

thods

as a prospective study of 51 months (Oct. 2009 - Dec. 2013) involving 166 c
o acute myeloid leukemia patients.

agnosis, cytogenetic studies were performed preferentially by FISH, and th
onventional cytogenetics wherever possible.

ne marrow specimen were used for an unstimulated 24-hours culture.

yotype :

banding technique was performed. To define a clone, standard criteria we
.

ast 20 metaphases were analysed; karyotypes were classified according to
rnational System for Human Cytogenetic Nomenclature.

thods

H :

stematic panel probes was applied (Kreatech, Cytocell) including : t(8;21)
L/ETO), Inv16/t(16;16)(CBFB/MYH11), MLL(11q23) break-apart. For M0 an
fferenciated , 5q31.1 and 7q22-q31 probes were applied. PML/RARa; RAR
k for AML3.

ast 20 metaphases and 200 nuclei were analyzed, using a fluorescence
oscope with appropriate filters. Cytovision Imaging was used for processin
ges for archives.

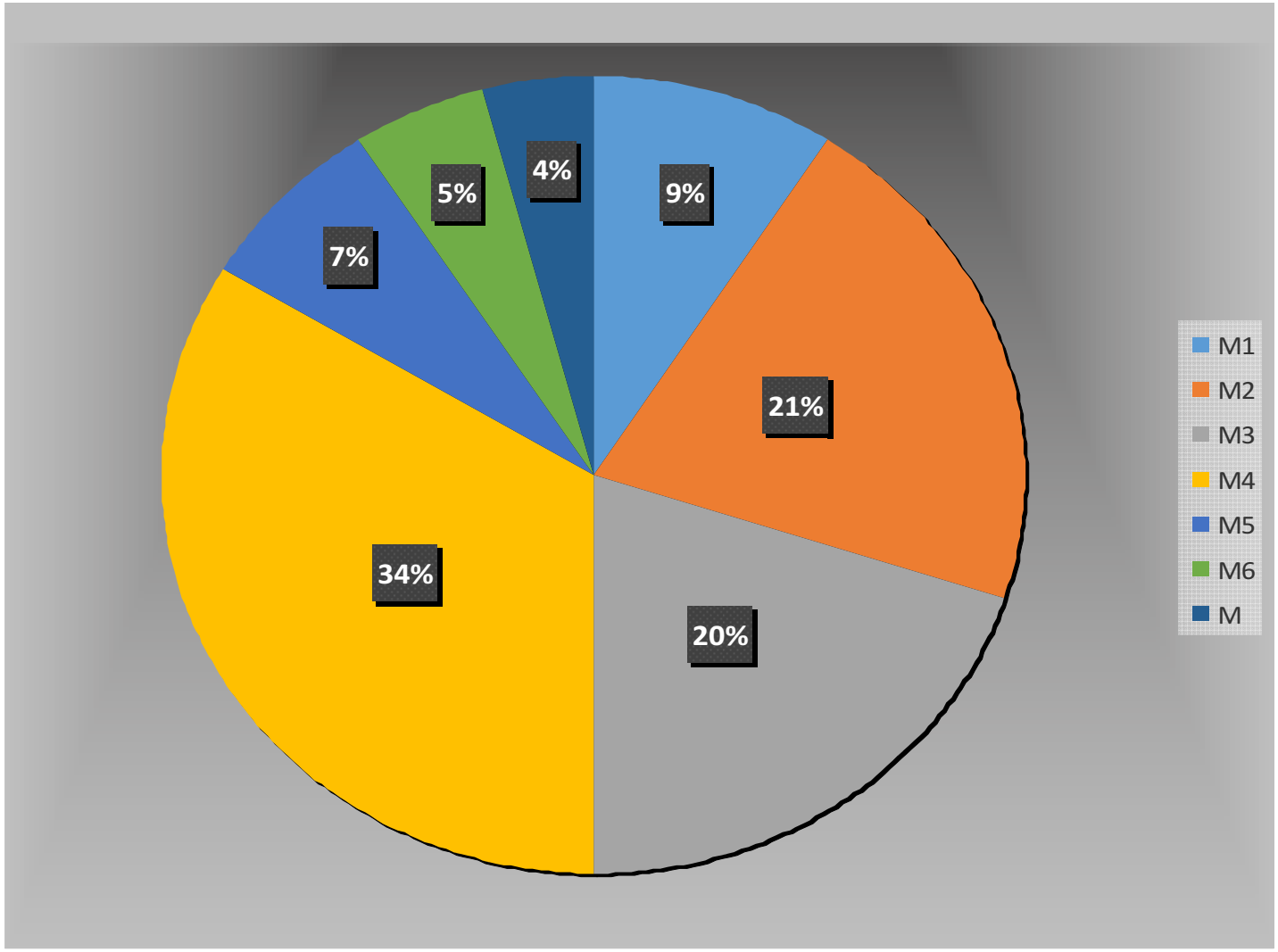
ultats

166 cases fall into adults (M: 80, F: 86). Sex ratio = 0,93

ian age : 42 years (16-87)

subtypes were :

M0 = 2
M1 = 15
M2 = 34
M3 = 33
M4 = 55
M5 = 12
M6 = 8
M = 7



lts : By FISH: 166 cases

Abnormalities	Number of cases	Pourcentage
Inv 16	19	11,5
t(8;21)	12	07,2
t(15;17)	**34**	**20,5**
MLL réarrangé	03	01,8
Del 7q	01	
Mono 5	01	
Dup MLL	01	
Dup21q22/8q	04	
Complexes	04	
Other: del 21q, iso21q, +8q/-8	06	
No abnormalities	82	49,5

ults: By Karyotype: 50 cases

normalities	Number of cases	%
X/46;Y	22	44
X;+4	1	
X;+6	1	
X;+21	1	
erdiploidy: 92;XXXX	2	
Y;-19	2	
Y;iso21q	1	
Y;t(1;14)(p34;q32)	1	
Y;t(4;12)(q12;p13)	1	
mplexe (≥ 3 abnormalities)	4	
onosomal	2	

Abnormalities	Number of cases	
46;XX;t(8;21)	3	
45;X;-Y;t(8;21)	1	
45;XX;-5;-22;+19;del16q22;del17p	1	
46;XX;inv(16)	2	
47;XX;+22;inv(16)	2	
48;XX;+8;+21;inv(16)	2	
50;XX;+8;+9;+21;+mar;inv(16)	1	

ognosis classification

e most common chromosomal abnormalities are grouped as follows

vorable

v(16)(p13q22), t(8;21), t(15;17)

termediate

ormal karyotype, t(9;11) or abnormalities not classified as favorable or favorable.

nfavorable

v(3)(q21q26.2)/t(3;3)(q21;q26.2), t(6;9)(p23;q34), t(v;11)(v;q23), -5/del(5 17p-, complex and monosomal karyotype

ults

Risk	Number of cases	%
Favorable	**65**	**39**
Intermediate	*	48*
Unfavorable	*	13*

sults

21)(q22;q22)/RUNX1-RUNX1T1

nslocation (8;21): was found in 12 pts
of 15 AML1 and 34 AML2

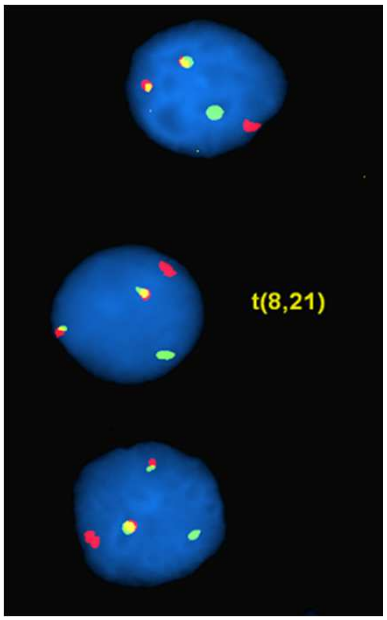
l 7,2% in all AML

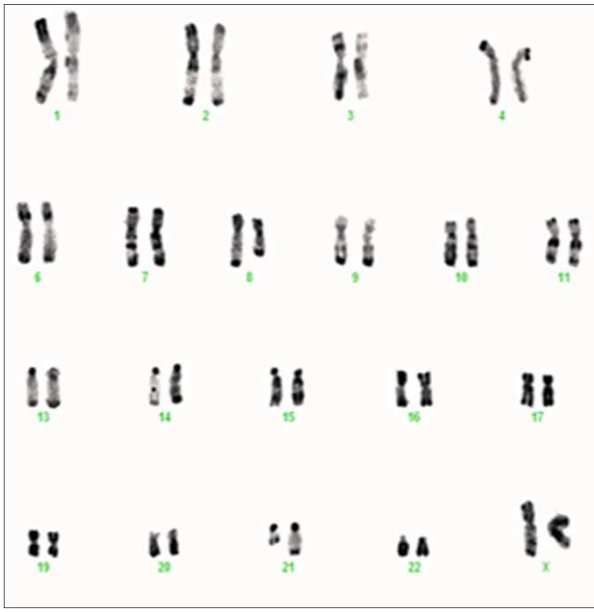
ner 24,5% (M1+M2)

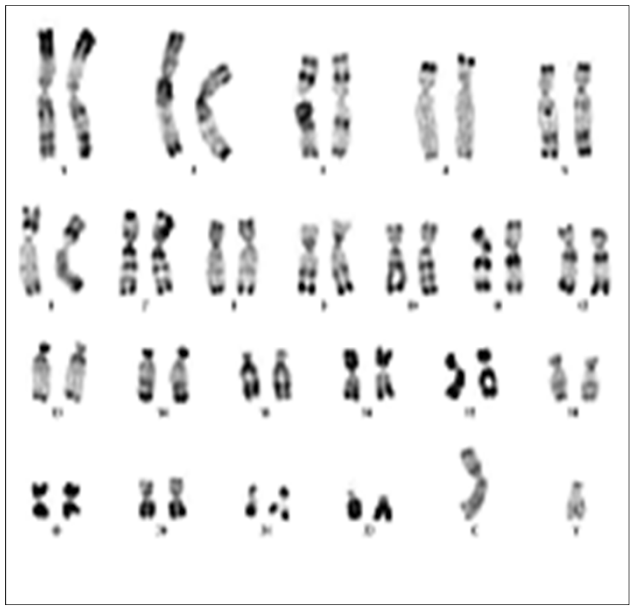
s translocation was exclusively seen
AML2 (11 cases), resulting in 32,3%
AML2 having t(8;21).

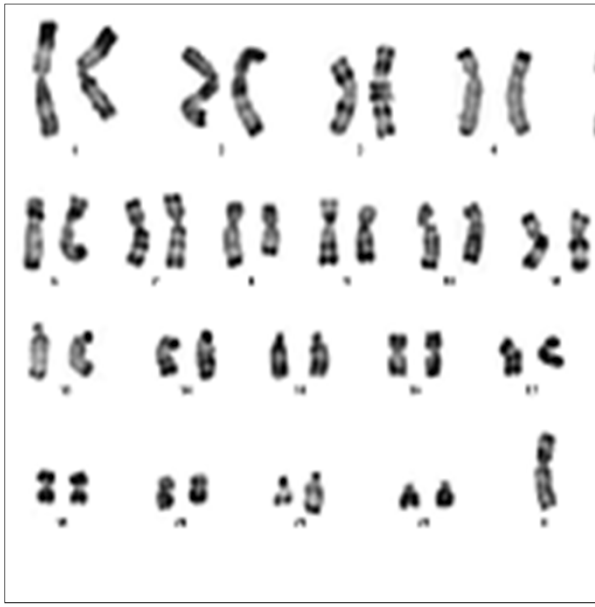
e male / female (M/F) ratio was of 4/8.

an age = 31 years









sults

(16)(p13;q22)/CBFβ-MYH11

ersion (16), t (16; 16) and del 16q22 were
und in 19 pts (8M, 11F), respectively in 16 pts,
ts and 1 pt out of 55 AML4 studied

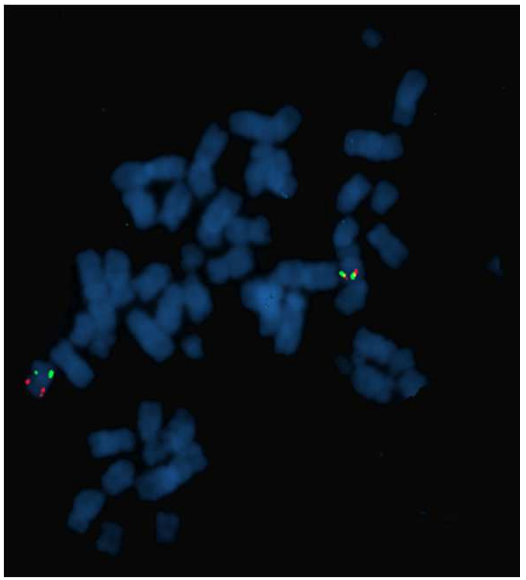
vas shown in 11,4% of all AML

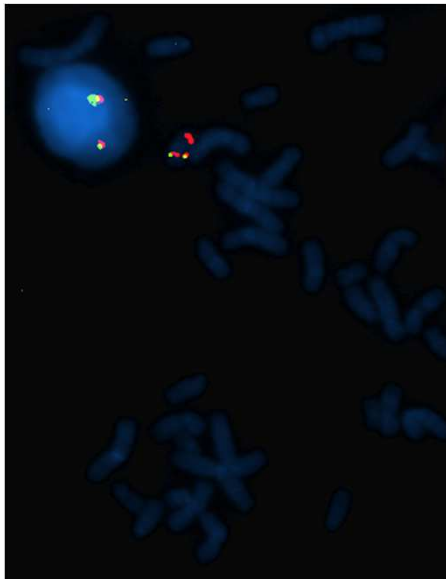
ean age = 40 years

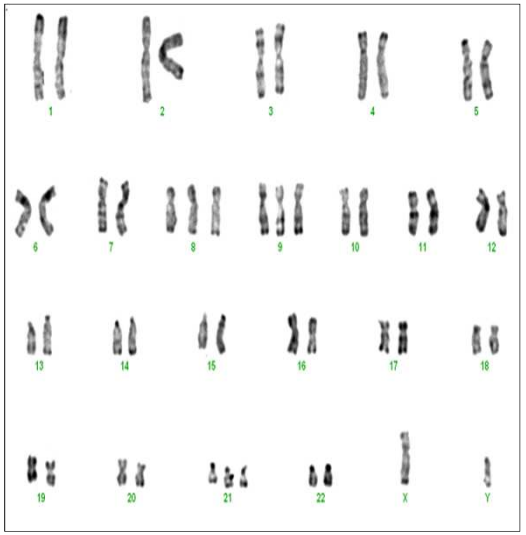
e majority of patients presented abnormal
nophilic precursors in bone marrow smears It
s not been recovered on t (16; 16).

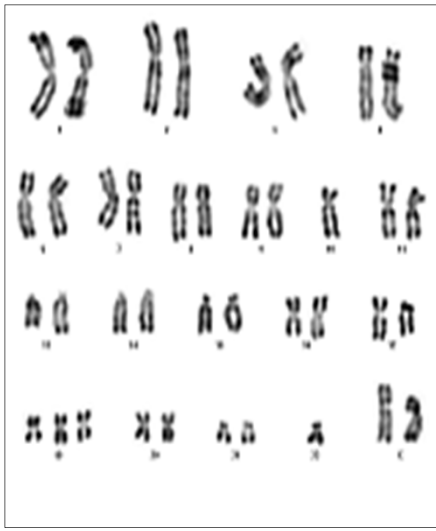
B subtypes were M4 (17), M5 (1) and M2 (1)

(16) was associated with +22 in 3 cases.









ults

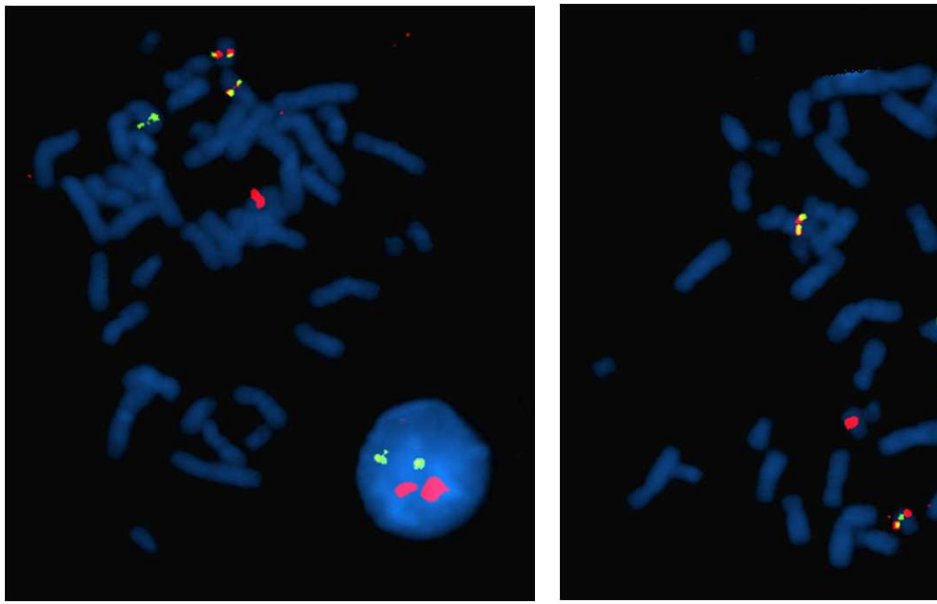
Translocation t (15; 17)(q22;q12)/PML-RARa

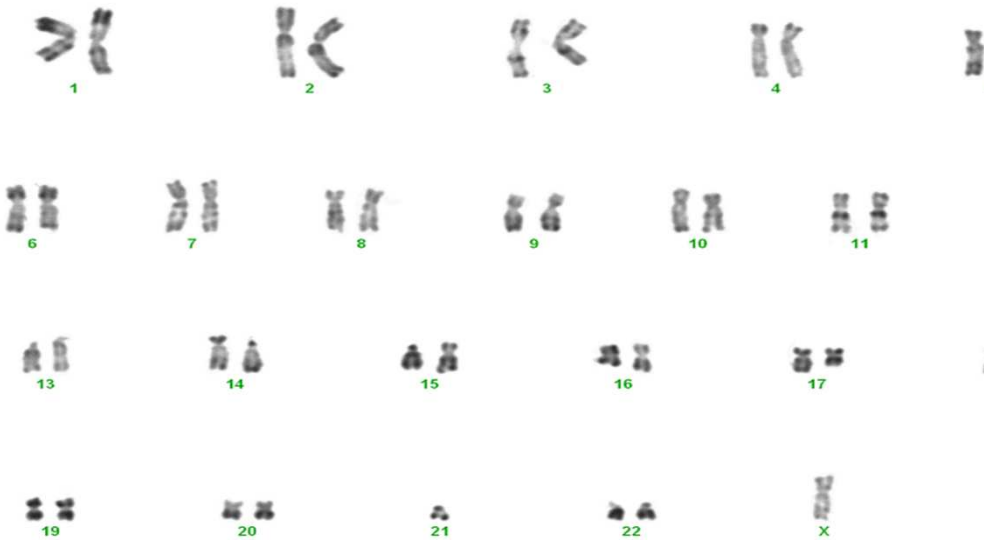
It was found in 34 cases of evoked AML3 (20,4%)

All of them were PML/RARA , no cytogenetic variant was found.

Mean age = 35 years

Sex : 18 M, 16 F Ratio = 1,1





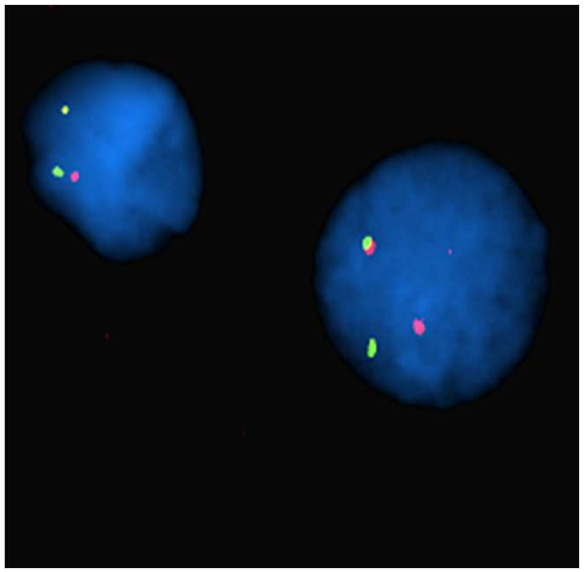
ults

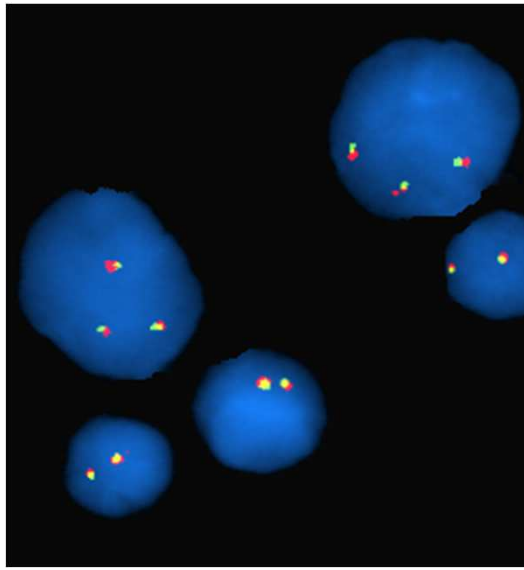
LL rearrangement (11q23)

MLL rearrangement was found in 3 cases (1,8% in all AML) :

1 AML 4 and 2 AML1

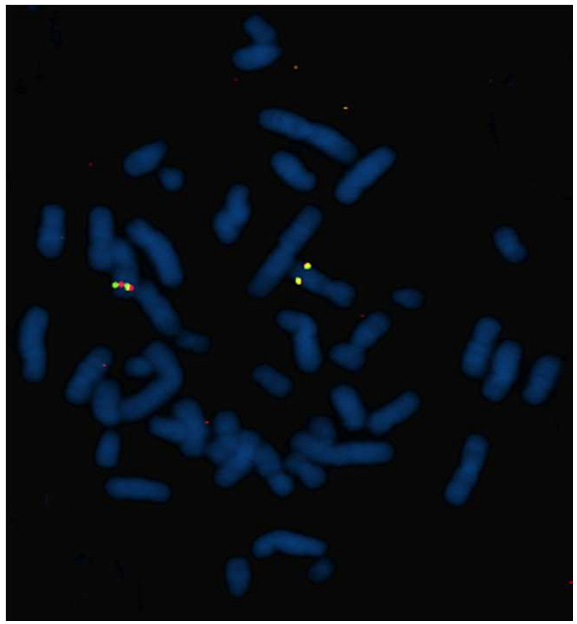
Mean age = 60 years (52-67)



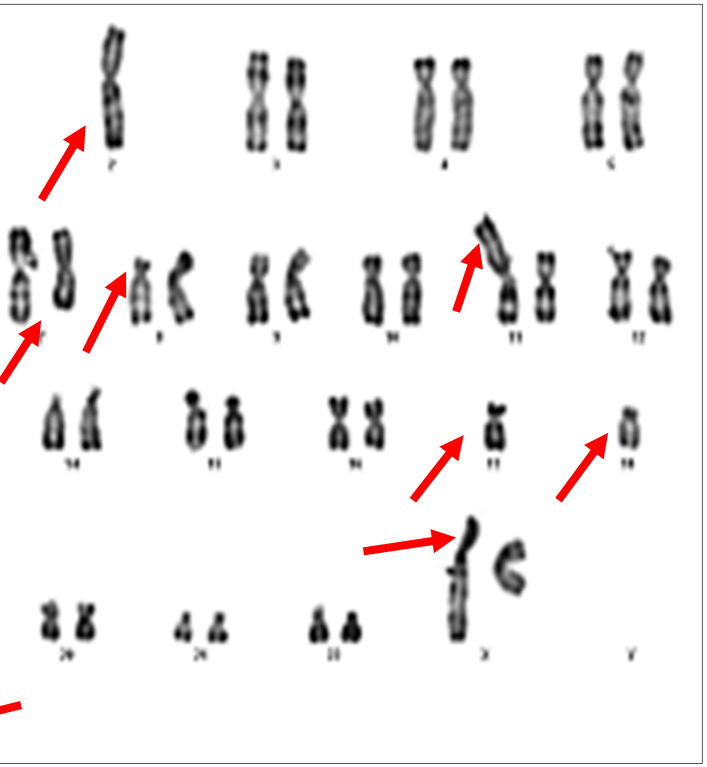


Duplication of MLL was found in 1 case of AML5

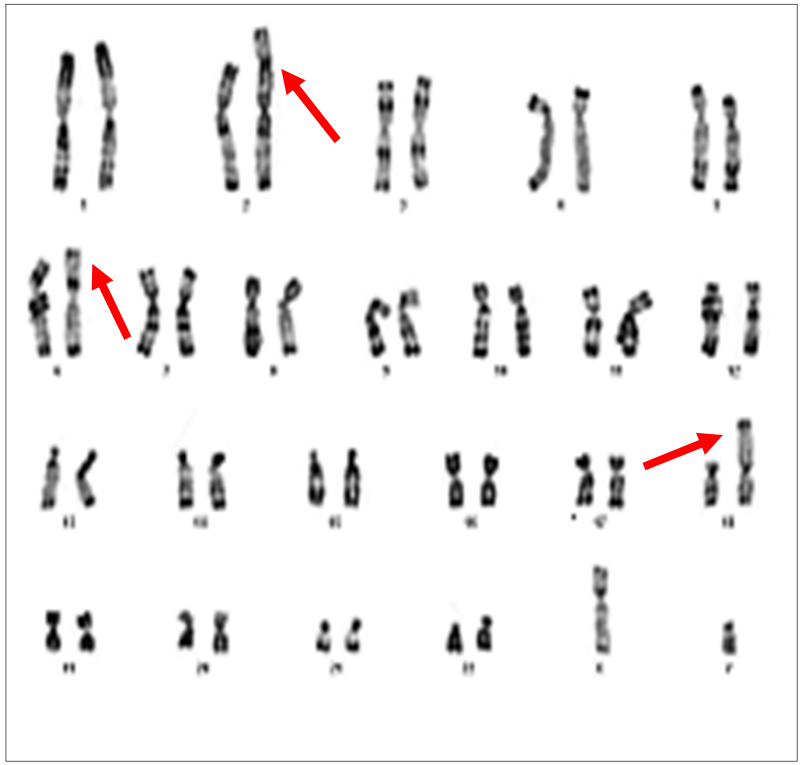
Age = 51 years



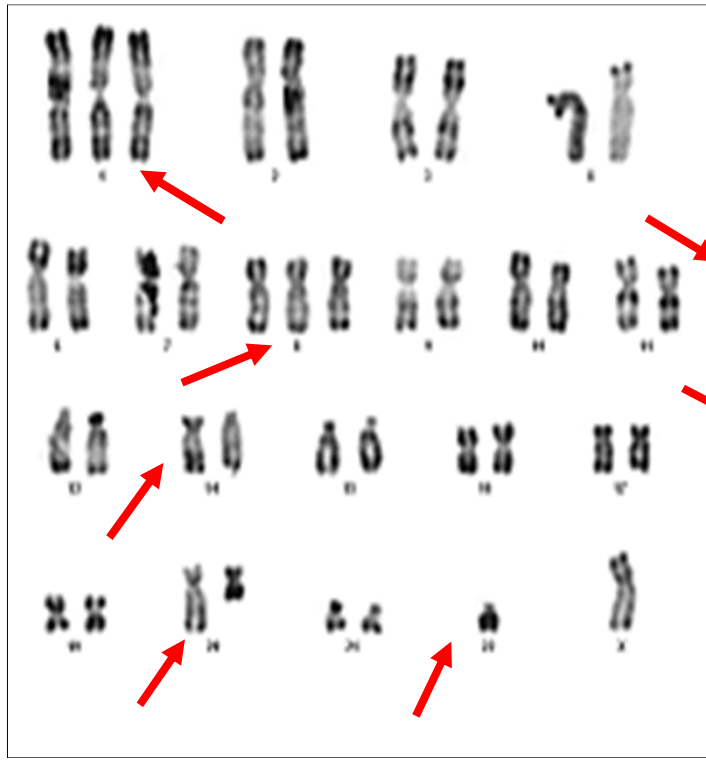
ults
er Aberrations



osomal karyotype



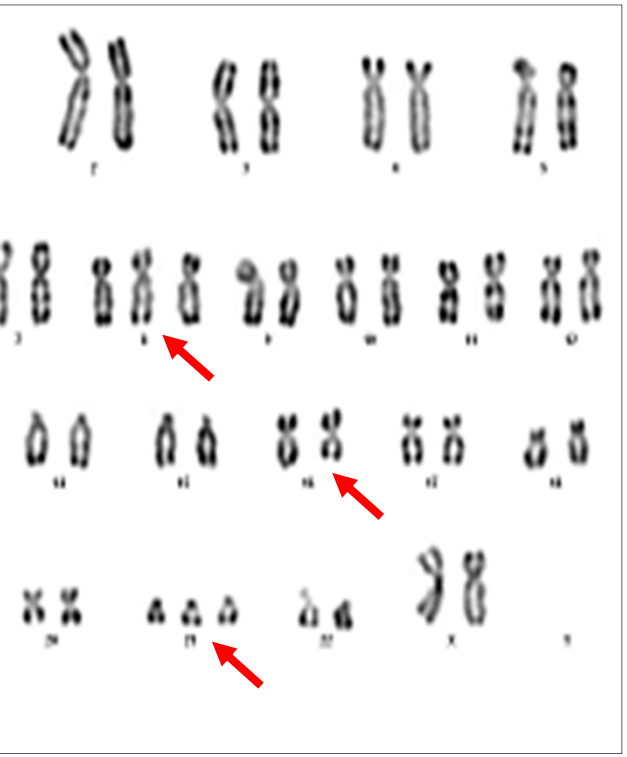
Complex karyotype



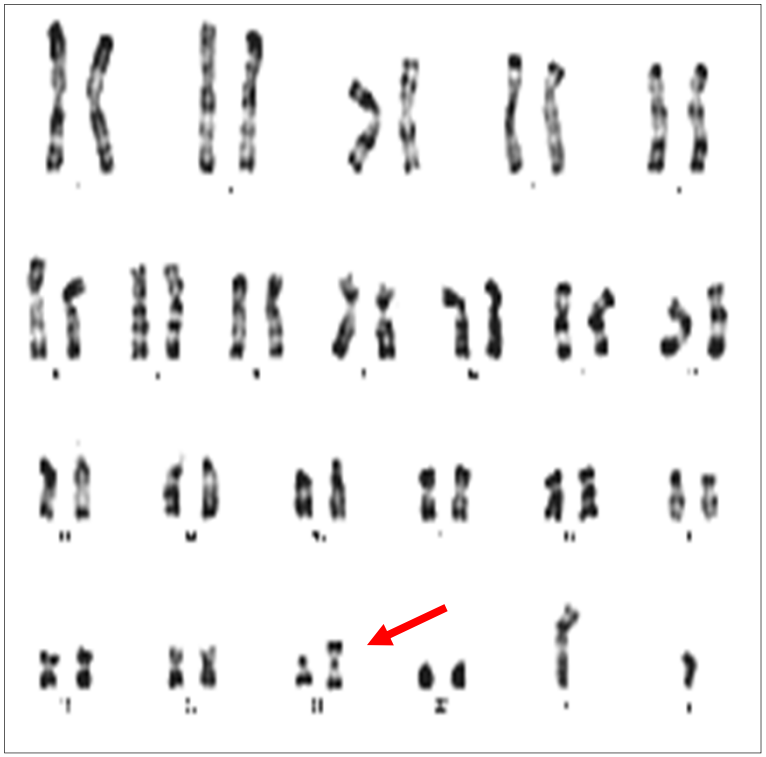
Complex karyotype

ults

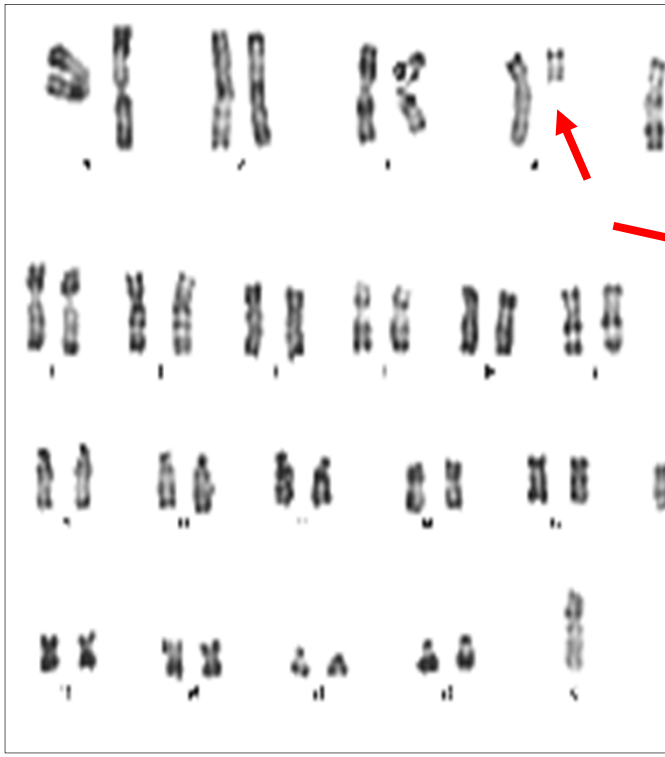
er Aberrations



6);+8;+21



Iso(21q)



t(4;12)(q12;p13)

cussion

nomalie	Iran (2004)	Our results %	Tunisia % 2006	Marocco %	Littérature %
v 16		11,5	1,3	8 (2009)	8 – 12
8;21)		07,2	12 **13,9 (2010)**	12,6 (2009)	5 - 10
15;17)	19,4	20,5	10		5 - 8
LL réarrangé		1,8	2,6		3 - 5
omplexe Karyo		10	14,3		10 - 12
Monosomal Karyo		5			13
o abnormalities		44	43		45

cussion

isk	Our serie	Tunisia 2005(202pts	Marocco* 2009	Littérature Röllig JCO 2011
avorable	39 %	17%	21,2%	10%
ntermediate	48 %*	66%	63,3%	67%
Unfavorable	13%*	17%	15,4%	23%

cussion

ur work, FISH was useful for screening the PML/RARA for the diagnosis AML
abnormalities with favorable prognosis, and to assess MLL rearrangement
uency of AML patient in Blida center.

was rapide and reliable technique (successful in all patients), it was sensitv
cularly to detect inv(16) or variants of t(8;21)/AML/ETO that are usualy
tic.

mains a precious contribution in the event of failure karyotype (failure of
ure or banding of bad quality)

clusion

is a good tool that can be used to detect recurrent abnormalities in mosomes metaphase and in interphase cells . It provids a complementary oach in cases with a normal or failed cytogenetic result.

otype remains the key examination by visualizing all the genome, highlighti plexe and monosomal karyotypes of worse prognosis.

nately these tools are essential and complementary for a reliable diagnosis nostic evaluation of AML.