



Images in Clinical Hematology

Molecular genetic techniques for gains and losses of genomic material in a case of acute myeloid leukemia



Mauren Fernanda Moller dos Santos^{a,*}, Camila Clozato Lara^a,
Elvira Deolinda Rodrigues Pereira Velloso^{a,b}

^a Sociedade Beneficente Israelita Brasileira Albert Einstein (SBIBAE), São Paulo, SP, Brazil

^b Faculdade de Medicina da Universidade de São Paulo (FMUSP), São Paulo, SP, Brazil

ARTICLE INFO

Article history:

Received 30 January 2017

Accepted 26 June 2017

Available online 20 July 2017

A 67-year-old male presented with a four-week history of weakness. The complete blood count showed: hemoglobin: 5.1 g/dL, leukocytes $182.55 \times 10^3/\mu\text{L}$ (23% blasts and 34% monocytes) and platelets: $31 \times 10^9/\text{L}$. A bone marrow aspirate showed 50.4% of myeloid myeloperoxidase (MPO)-blast cells and 42.4% of dysplastic granulocytic-monocytic series, with alpha-naphthyl acetate esterase positivity in 30% of total nucleated cells. Flow cytometry identified two distinct aberrant blasts (CD4-CD7-CD11c-CD13-CD34-CD117-HLA-DR-cMPO⁺) and myeloid/monocytic (CD14-CD33-CD35-HLA-DR-CD11b⁺) populations. Karyotyping showed monosomy 7 and additional material in the long arm of chromosome 2

(Figure 1A). Acute myeloid leukemia (AML)-M4 (FAB classification) or AML with myelodysplasia-related changes (WHO 2008 classification) was diagnosed. Patient died two months after without response to therapy.

Apart from karyotyping, other molecular genetic techniques can detect gains and losses of genomic material.¹⁻³ In this case, the additional material in chromosome 2 was elucidated and chromosome 7 monosomy was confirmed using fluorescence in situ hybridization, multiplex ligation-dependent probe amplification and single nucleotide polymorphism-array methodologies (Figures 1B, 2A and B).

* Corresponding author at: Av. Albert Einstein, 627/701, 05651-901 São Paulo, SP, Brazil.

E-mail address: mauren.santos@einstein.br (M.F. Santos).

<http://dx.doi.org/10.1016/j.bjhh.2017.06.001>

1516-8484/© 2017 Published by Elsevier Editora Ltda. on behalf of Associação Brasileira de Hematologia, Hemoterapia e Terapia Celular. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

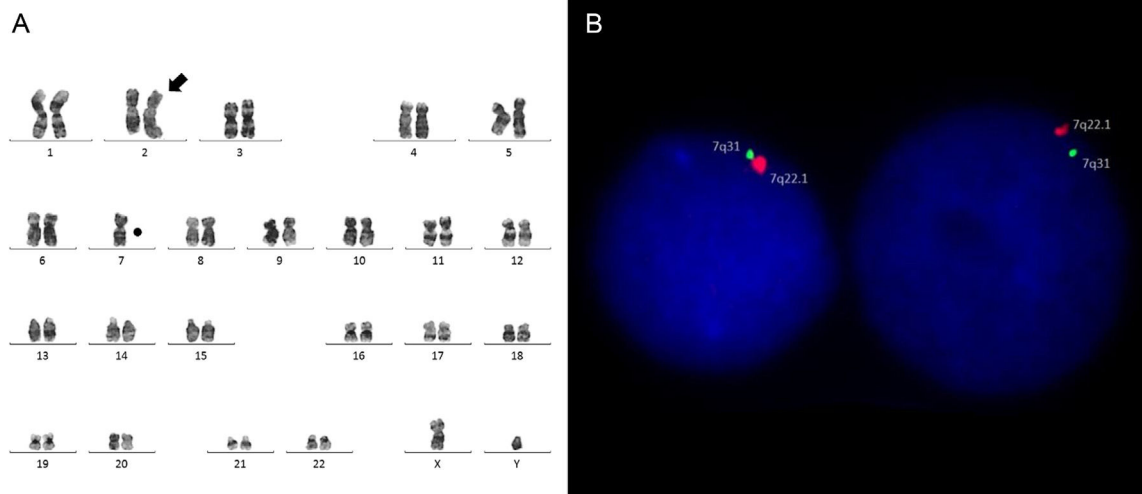


Figure 1 – (A) Karyotype (G-band): 45,XY,add(2)(q35),-7[20]. (B) FISH (Del 7q) Deletion Probe, ref: RU-LPH 025; Cytocell, Cambridge, UK): Deletion of RELN gene (chromosome 7) in 96% of the analyzed nuclei. The absence of a green and a red signal may indicate the monosomy of the chromosome.

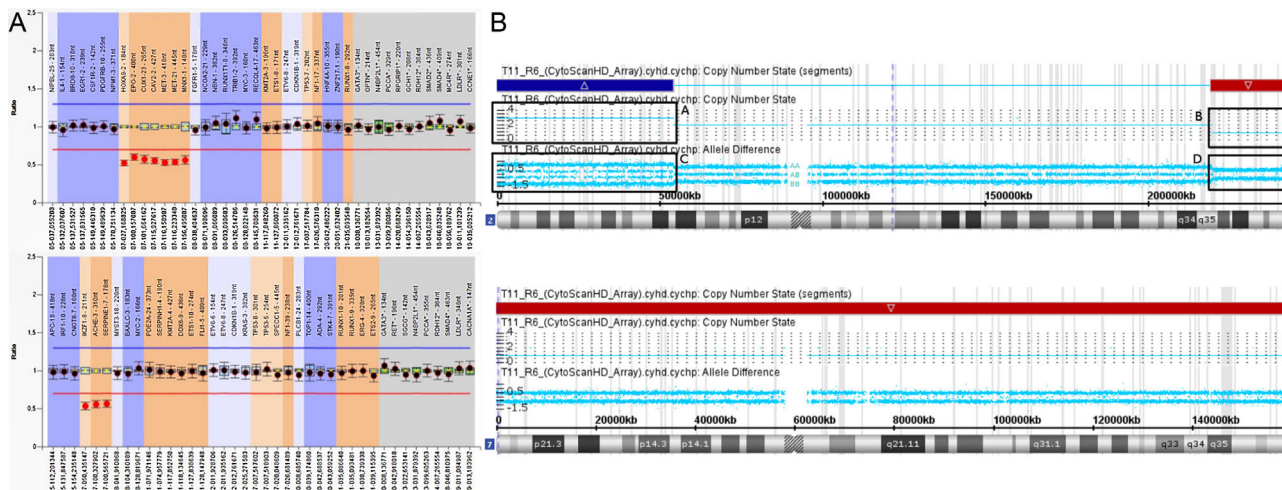


Figure 2 – (A) MLPA with SALSA MLPA probemix P144-A2 (above) and P145-A2 (below) kits (MRC-Holland, Amsterdam, The Netherlands). Dosage quotient of the patients’ probes in relation to a control group. Probes positioned below the 0.65 limit indicate deletion; probes positioned above the 1.35 limit indicate duplication. Probes in red indicate monosomy 7 (deletion of all probes of chromosome 7) and probes in black are normal for the other chromosomes studied in these kits. (B) SNP-A (CytoScanHD Array; Affymetrix, Santa Clara, USA): Diagrams generated by ChAS (Affymetrix) for chromosome 2 (above) and chromosome 7 (below). In “Copy number state”, line in 2.00 indicates a normal copy number (diploid), line in 1.00 indicates a deletion and line in 3.00 indicates a duplication/gain. Lines with intermediate values between 1.00 and 2.00; 2.00 and 3.00 indicate mosaicism. In “Allele Difference”, three lines indicate a normal genotype (AA, AB and BB alleles), two lines indicate deletion (A and B alleles) or loss of heterozygosity (AA and BB alleles) and four lines indicate duplication (AAA, AAB, ABB and BBB alleles). SNP-A revealed the result $arr[hg19] 2p25.3p16.2(12770.54276429)x3[0.8],2q35q37.3(219576639.242783384)x1,(7)x1$ where there was a partial duplication of the short arm of chromosome 2 (A and C), presenting clonal mosaic data of the duplicated region in 80% of the cells, and partial deletion of the long arm of chromosome 2 (B and D). This result can explain add (2) (q35) present in the karyotype, indicating the origin of the additional material. In addition, the monosomy of chromosome 7 was confirmed.

Conflicts of interest

The authors declare no conflicts of interest.

REFERENCES

1. Dutta UR. Precision in chromosome identification with leads in molecular cytogenetics: an illustrated review. *J Pediatr Genet.* 2014;3(1):1–7.
2. Shen Y, Wu BL. Designing a simple multiplex ligation-dependent probe amplification (MLPA) assay for rapid detection of copy number variants in the genome. *J Genet Genomics.* 2009;36(4):257–65.
3. Tiu RV, Gondek LP, O’Keefe CL, Huh J, Sekeres MA, Elson P, et al. New lesions detected by single nucleotide polymorphism array-based chromosomal analysis have important clinical impact in acute myeloid leukemia. *J Clin Oncol.* 2009;27(31):5219–26.