Case Report

Additional information offered by single nucleotide polymorphism array advantages in two myelodysplastic syndromes with excess blasts cases and future perspectives

Thiago Rodrigo de Noronha a,*, Miguel Mitne-Neto b, Maria de Lourdes Chauffaille a,b

a Universidade Federal de São Paulo (Unifesp), São Paulo, SP, Brazil
b Grupo Fleury, Pesquisa e Desenvolvimento, São Paulo, SP, Brazil

A R T I C L E   I N F O

Article history:
Received 22 March 2018
Accepted 26 June 2018
Available online 29 December 2018

Introduction

The myelodysplastic syndromes (MDS) are clonal stem-cell disorders characterized by ineffective haemopoiesis leading to blood cytopenias and by progression to acute myeloid leukemia (AML) in a third of patients.1 Diagnosis of MDS is based on examination of the blood and bone marrow (BM), which shows blood cytopenias and hypercellular marrow with dysplasia, with or without an excess of marrow blasts.2 The detection of chromosomal abnormalities in MDS supports the diagnosis, classification, prognostic stratification, therapy option, treatment monitoring and better understanding of the biology of the disease. The main chromosomal abnormalities of MDS are losses and gains of genetic material, and these changes are among the most important prognostic parameters in IPSS-R.3 As a consequence, major advances have been achieved in the treatment and survival of patients. However, nearly half of the patients present a normal karyotype, which prevents their further characterization.1 Therefore, there is the desire to increase the abnormalities detection rate by other methods.

The single nucleotide polymorphism (SNP) array method is a sensitive technology used to perform high-resolution genome-wide DNA copy number analysis and to detect the copy-neutral loss of heterozygosity (CN-LOH).4 The SNP array method uses millions of markers (probes comprised by 25-mer oligonucleotides) across the entire human genome. There are two types of probes: non-polymorphic probes, used only for assessing copy number, and polymorphic probes, used to assess genotypes. For copy number analysis, patient DNA labeled with a fluorochrome provides signal intensity that, when compared to a set of reference DNAs, indicates whether...
there is a gain or loss of genetic material. For genotype analysis, the SNP has a single base pair substitution (A, T, C, or G) of one nucleotide to another, following which the alleles are arbitrarily designated as A for one SNP and B for the other SNP and reveal which of the genotypes (example, AA, BB or AB) is present along the entire chromosome.5

Previous studies have shown that the addition of the SNP array to karyotype (KT) increases by 28% the detection rate of cytogenetic abnormalities. To substantiate this idea, we describe two cases of MDS to which the SNP array added valuable information to the karyotype.5

Methods

Patients

Patients described in this report were accompanied at the Hospital São Paulo of the Federal University of São Paulo, São
Paulo, Brazil. The Ethics Committee of the institution approved the study, and written informed consent was obtained (CAAE 00547512.5.0000.5505).

**Metaphase cytogenetics**

G banding karyotyping (KT) or metaphase cytogenetics was performed on BM samples at the time of initial diagnosis using standard methods and the karyotype was described according to the International System for Human Cytogenetic Nomenclature (ISCN) 2016.

**Single nucleotide polymorphism array**

The SNP array was performed on BM and buccal cells samples. Two hundred and fifty nanograms of DNA was extracted and digested, amplified, purified, fragmented, labeled and hybridized using the Affymetrix CytoScan® HD Array; CEL files were created using the GeneChip System 3000 7G according to the manufacturer’s instructions. The CEL files were analyzed using the Chromosome Analysis Suite v3.0 (ChAS) software. Regions of copy number variations (CNVs) larger than 1 Mb and CN-LOH larger than 10 Mb, identified by the ChAS Software or detected by visual inspection, regardless of gene content, are denoted as true aberrations, with the exception of those known to be normal genomic variants (present in the Genomic Variants Database [http://projects.tcag.ca/variation]) or found in constitutional (buccal cells) SNP array analysis. Aberrations that were identified by the SNP array were described according to the ISCN 2016.

**Discussion**

The SNP array has the advantage of detecting genomic alterations regardless of the cell cycle, even when the cell is quiescent or has defective growth. It also enables the identification of CN-LOH (these regions are without heterozygosity, i.e. all the genetic variations within the regions have two identical alleles), submicroscopic amplifications and deletions that are not detected by KT. On the other hand, the SNP array does

---

**Cases report**

Case 1: a 64yo male patient, classified according to the WHO 2016 as myelodysplastic syndromes with excess blasts (MDS-EB), bone marrow histology showed grade II fibrosis.

Karyotype: 46,XY,del(5)(q15q33),del(17)(p11.2)(16)/46,XY[4].

SNP array: arr[hg19] 5q21.1q35.3(99,749,120-180,719,789)x1; arr[hg19] (7)x1; arr[hg19] (8)x3; arr[hg19] 12p13.3p12.3(173,786-19,670,207)x1; arr[hg19] 12p12.1p11.22(25,285,957-28,222,696)x1; arr[hg19] 12q22q23.3(93,071,445-104,654,711)x1; arr[hg19] (16)x1; arr[hg19] 17p13.3p11.2(525-22,125,370)x1-2; arr[hg19] [Y]x1 (Figure 1).

Case 2: a 74yo male patient, classified according to the WHO 2016 as myelodysplastic syndromes with excess blasts (MDS-EB), bone marrow histology showed grade II/III fibrosis.

Karyotype: 46,XY[20].

SNP array: arr[hg19] 21q21.1q22.3(22,88,454-48,084,820)hmz (Figure 2).

The SNP array detailed graphical results of all chromosomes (cases 1 and 2) can be seen in the Supplementary File.

---

**Figure 2** – Genomic alterations detected by SNP array in case 2. a. Karyoview of bone marrow (first line) and buccal cells (second line). b. Constitutional CN-LOH in 6q13q14.3 present in buccal cells and bone marrow SNP array analysis. c. Acquired CN-LOH in 21q21.1q22.3 present only in bone marrow SNP array analysis.
The authors declare no conflicts of interest.