

# Leukaemia Section

## Mini Review

### t(5;11)(q35;p15.5)

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## Clinics and pathology

### Disease

De novo acute non lymphocytic leukemia (ANLL).

### Phenotype/cell stem origin

No specific subtype. Only 5 cases reported to date (1 ANLL-M1, 2 ANLL-M2, 2 ANLL-M4).

### Epidemiology

All 5 reported cases were children or young adults (age range 3-18 years). Male: female ratio 1.5:1.

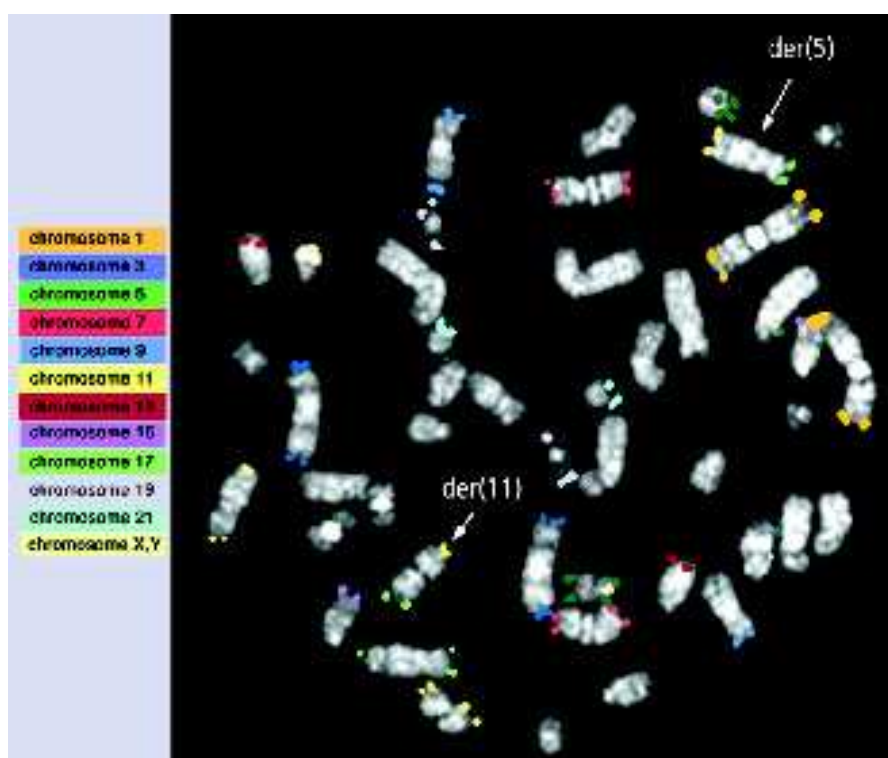


Fig 1. Identification of a cryptic t(5;11) using the M-TEL assay. Bone marrow metaphase from a normal karyotype ANLL child hybridized with the M-TEL1 probe set. Chromosomes 1, 3, 7, 9, 13, 15, 17, 19, 21 and X and Y probes were all correctly hybridized. However, one homologue of chromosome 5 has chromosome 11 material on the q arm (yellow), and the corresponding chromosome 11 homologue has chromosome 5 material on the p arm (green). This corresponds to a balanced translocation, t(5q;11p). The der(5) and der(11) are indicated by arrows.

## Cytogenetics

### Cytogenetics morphological

The t(5;11)(q35;p15.5) is not detectable by G-banding. Three cases were reported as cryptic t(5;11) associated with del(5q); a further two cases were identified in apparently normal karyotypes.

### Cytogenetics molecular

In one FISH study using whole chromosome paints, three out of four cases of childhood ANLL with del(5q) as the sole cytogenetic abnormality were found to have a cryptic t(5;11). In a second study using chromosome-specific subtelomeric probes, two out of 31 children and young adults (19 years) with a normal G-banded karyotype were found to have a cryptic t(5;11).

Note: while the der(11) is detectable by single colour painting using chromosome 5 whole chromosome paint (WCP), the der(5) is not detectable using chromosome 11 WCP. Neither M-FISH or SKY can reliably detect the t(5;11).

### Probes

Subtelomeric probes: PAC GS-240-G13 (5q), PAC GS-908-H22 (11p), both from Incyte Genomics NSD1 BAC: CTC HSP 2301A4 (available from Incyte Genomics); NUP98: PAC1173 K1, p9R1 (exons 10-12 of NUP98 gene), p6G2 (exons 13-14 of NUP98 gene).

## Genes involved and proteins

### NUP98

#### Location

11p15.5

#### Note

At least 8 different fusion partners for NUP98 in leukaemia.

#### DNA/RNA

Two major transcripts: 4.0 and 7.0 kb. The 4.0 kb transcript consists of 20 exons.

### Protein

98 kD protein. Component of the nuclear pore complex, which regulates nucleocytoplasmic transport of protein and RNA. Contains multiple phenylalanine-glycine (FG) repeats which act as 'docking' sites for transport receptors.

### NSD1 (nuclear receptor-binding, SET domain-containing protein 1)

#### Location

5q35

#### DNA/RNA

At least 21 exons, cDNA is 8552 bp, open reading frame of 8088 bp.

#### Protein

Predicted protein of 2696 amino acids. Contains at least 6 functional domains: su(var)3-9, enhancer-of-zeste, trithorax (SET), proline-tryptophan-tryptophan-proline (PWWP-I, PWWP-II), plant homeodomain protein-finger domains (PHD-I, PHD-II, PHD-III) and ten putative nuclear localization signals.

## Result of the chromosomal anomaly

### Hybrid gene

#### Note

Reciprocal NSD1-NUP98 fusion also present in all cases tested.

#### Description

The NUP98 and NSD1 mRNA are fused in-frame joining nucleotides 1552 of NUP98 to nucleotide 3506 of NSD1. The reciprocal transcript fuses NSD1 and NUP98 mRNA in-frame joining nucleotide 3505 of NSD1 to nucleotide 1553 of NUP98.

#### Detection

RT-PCR with sense NUP98-5' (5'-TCTTGGTACAGGAGCCTTTG-3'), and antisense NSD1-1 (5'TCCAAAAGCCACTTGCTTGGC-3') primers.

## Fusion protein

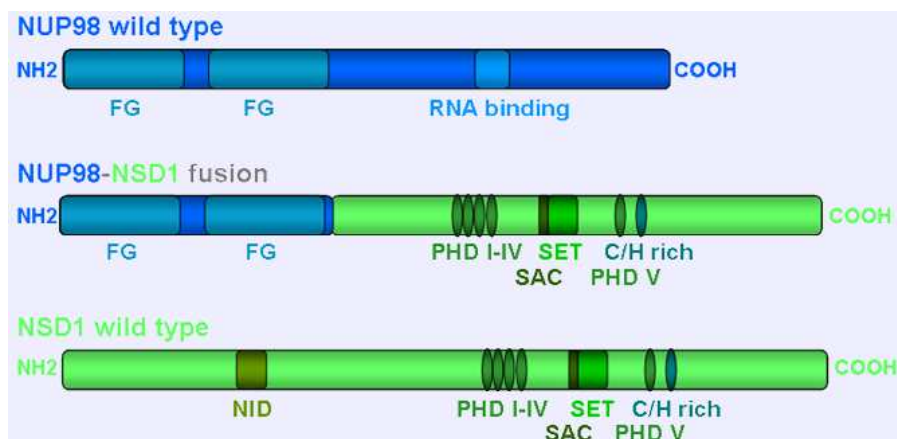


Fig 2. Schematic representation of the NUP98-NSD1 fusion protein. The wild type NUP98 and NSD1 proteins are also shown. The putative NUP98-NSD1 fusion protein would retain the NH2 terminal region of NUP98 containing the phenylalanine-glycine (FG) repeat domains and the COOH terminal region of NSD1 containing the SET, SET domain associated cysteine-rich (SAC) and PHD finger domains.

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*This article should be referenced as such:*

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