Leukaemia Section

Short Communication

ider(20q) in Myeloid Malignancies

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Identity

Partial karyotypes for ider(20q) in G-banding (left) and R-banding (right).

Clinics and pathology

Disease
Myelodysplastic syndrome (21 cases), Acute Myeloid Leukemia (5 cases), Chronic Myelomonocytic Leukemia (1 case).

Phenotype/cell stem origin
Thrombopenia (90%) with anemia (60%). Dysplastic changes in bone marrow: dyserythropoiesis associated with dysgranulopoiesis and/or dysmegakaryocytepoiesis.

Epidemiology
The frequency of ider(20q) is estimated at 0.49% in myelodysplastic syndrome and 0.26% in acute myeloid leukemia according to one study. They are found in older patients (average age: 68 years; range: 38-91).

Prognosis
Prognosis of patients with ider(20q) seems to be poor compared to patients with del(20q), but it is unclear due to the small number of cases.
Cytogenetics

Cytogenetics morphological
A monosomy of chromosome 20 with small metacentric marker chromosome: 46,XX or XY,-20,+mar is most likely an isoderivative of chromosome 20.
The ider(20)(q10)del(20)(q11q13) is a variant of del(20)(q11q13).

Cytogenetics molecular
The ider(20q) is monocentric or dicentric.
The proximal breakpoints are consistently located in 20q11.21 band. The distal breakpoints span from band 20q13.13 to band 20q13.33.
The commonly deleted region include the short arm of chromosome 20 and a large region on the long arm of chromosome 20 spanning from 20q11.21 to 20q13.13. A commonly proximal retained region (from centromere to 20q11.21) and commonly distal retained region (from 20q13.33 to telomere 20qter) of the long arm of chromosome 20 were determined. These retained regions are duplicated.

FISH with subtelomeric probes 20p (Green signal) and 20q (Red signals). The ider(20q) contains two red signals and no green signal.

Additional anomalies
Additional anomalies in decreasing frequency: - del(20q) detected by conventional cytogenetics and/or by FISH,
- 2 copies of ider(20q),
- monosomy 7,
- complex karyotypes in acute myeloid leukemia.

**Genes involved and proteins**

**Note**
To explain specific phenotype, loss of tumor suppressor genes in deleted region (ADA, L3MBTL) and gene dosage effect of genes located on the retained region of chromosome 20 are suggested.

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