Solid Tumour Section
Short Communication

t(11;22)(q24;q12) in rhabdomyosarcomas (RMS)

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Disease
Rhabdomyosarcomas, the most common pediatric soft tissue sarcomas, are tumours related to the skeletal muscle lineage. The 2 major subtypes are alveolar rhabdomyosarcoma (ARMS) and embryonal rhabdomyosarcoma (ERMS). Other subtypes are botryoid, spindle cell, anaplastic, pleomorphic, and undifferentiated RMS.

Note
Most ARMS cases are characterised by either a t(2;13)(q35;q14), resulting in a PAX3/FOXO1 hybrid gene, or a t(1;13)(p36;q14) resulting in a PAX7/FOXO1 hybrid gene. Most ERMS are characterized by chromosome gains and a loss of heterozygocity in 11p15.

Epidemiology
Three cases of RMS with t(11;22)(q24;q12) have been described to date, including a two-years-old girl with a mixed embryonal and alveolar RMS, who died 14 months after diagnosis, a 4.5-year-old girl, also with a mixed embryonal and alveolar RMS, who was alive and well 9 months after diagnosis (Sorensen et al., 1993; Thorner et al., 1996).

Genetics
Note
A t(2;13) hybrid transcript was excluded in the two cases described by Thorner et al., 1996. In the 4.5-year-old girl case, a highly abnormal karyotype was found, with 85 to 200 chromosomes per mitosis, and MDM2 was amplified more than a hundred times.

Hybrid Gene
Description
5' EWSR1 - 3' FLI1. EWSR1 exon 7 is fused in frame to FLI1 exon 6.

Fusion Protein
Description
Fusion of the N terminal transactivation domain of EWSR1 to the ETS type DNA binding domain of FLI1.

Genes involved and proteins

<table>
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<tr>
<th>Genes</th>
<th>Location</th>
<th>Protein</th>
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<tr>
<td>FLI1</td>
<td>11q24</td>
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<tr>
<td>EWSR1</td>
<td>22q12</td>
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Gene involved and proteins

FLI1
Location
11q24

Protein
From N-term to C-term: a 5’ ETS domain, a Fli-1-specific transcriptional activation domain, and a 3’ ETS transcriptional activation domain. Member of ETS transcription factor gene family. FLI1 binds to DNA in a sequence-specific manner.

EWSR1
Location
22q12

Protein
From N-term to C-term: a transactivation domain (TAD) containing multiple degenerate hexapeptide repeats, 3 arginine/glycine rich domains (RGG regions), a RNA recognition motif, and a RanBP2 type Zinc finger. Role in transcriptional regulation for specific genes and in mRNA splicing.

Result of the chromosomal anomaly

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References


This article should be referenced as such: