

Solid Tumour Section

Mini Review

Soft tissue tumors: Rhabdomyosarcoma

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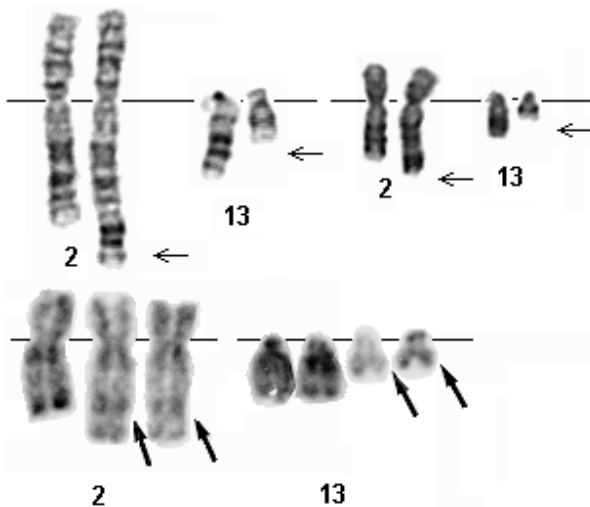
Published in Atlas Database: March 1998

Online updated version is available from: <http://AtlasGeneticsOncology.org/Tumors/rhab5004.html>
DOI: 10.4267/2042/37445

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Identity

Note: Rhabdomyosarcoma (RMS) are mesenchymal tumours belonging to the group of small round-cell tumors, displaying various degrees of striated muscular differentiation.



t(2;13)(q35;q14) G-banding (above) - Courtesy G. Reza Hafez, Eric B. Johnson, and Sara Morrison-Delap, - Cytogenetics at the Waisman Center ; R-banding (below) - Courtesy Jean-Luc Lai.

Classification

Rhabdomyosarcoma covers two distinct entities:

- Embryonal rhabdosarcoma (E-RMS)
- Alveolar rhabdomyosarcoma (A-RMS)

Clinics and pathology

Embryonic origin

Mesoderm.

Epidemiology

The most common pediatric soft tissue sarcoma (5 to 8% of all malignancies in childhood); annual incidence is 4/10⁶; E-RMS accounts for 75% of all RMS, and is observed in young children (3-12 yrs); A-RMS is found in the remaining 25%, and is observed in older children and young adults (6-21 yrs).

Clinics

E-RMS occurs predominantly in the head and neck region, the genito-urinary tract, and the retroperitoneum; A-RMS occurs predominantly in the extremities and the trunk; RMS often present as a tumour mass, or may be discovered from symptoms according.

Pathology

In E-RMS, tumor cells are round or spindle-shaped and may exhibit various degrees of muscular differentiation; they are often dispersed in an abundant myxoid stroma; the botryoid type, observed in tumors developed in mucosa-lined organs (vagina, bladder), exhibits a polypoid grape-like pattern.

In A-RMS, tumor cells are round and more dense than in E-RMS and, typically, they are arranged according a pattern reminiscent of lung alveoli.

Prognosis

Dependent on the extent of disease at time of diagnosis, and on the type of RMS; patients with A-RMS have a poorer survival than those with E-RMS.

Genetics

Note: E-RMS and A-RMS are two distinct entities also from the genetic point of view.

Cytogenetics

Morphological cytogenetics

E-RMS do not show recurrent structural chromosome rearrangement; the majority of the tumors are hyperdiploid, with an increased copy number for chromosomes 2, 7, 8, 12, and 13, in particular; comparative genomic hybridization (CGH) confirms these findings, showing gains of a variety of whole chromosomes, 2, 13, 12, 8, and 7 (in 50-60% of the cases), 17, 18, and 19 (40%), and the loss of chromosomes 16 and 10 (in 30-40%), and 15 and 14 (20%); polymorphism studies shows that E-RMS is associated with the loss of heterozygosity at 11p13.

A-RMS is characterized by two pathognomonic translocations: t(2;13)(q35;q14) and t(1;13)(p36;q14), found in 80 and 15% of the cases respectively, leading to the formation of gene fusions, namely PAX3-FKHR, in the t(2;13), and PAX7-FKHR in the t(1;13), generating fusion transcripts; double-minute chromosomes have been reported in some RMS, and CGH has showed a high frequency of genomic amplifications; the amplicons are located in 12q13-15 (50% of the cases), 2p24 (36%), 13q14, 13q32, and 1q36 (14%), 1q21 and 8q13-q21 (7%); the 12q13-15 amplicon could involve genes: CHOP, MDM2, and SAS; MYCN gene is amplified in cases with the amplicon at 2p24, but unlike in neuroblastoma, no correlation with prognosis seems to exist in RMS; cases with the fusion PAX7-FKHR often show an amplification of the fusion gene (and more frequently than cases with the PAX3-FKHR gene do).

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This article should be referenced as such:

Couturier J. Soft tissue tumors: Rhabdomyosarcoma. *Atlas Genet Cytogenet Oncol Haematol.*1998;2(3):105-106.
