Bone and Soft Tissue: Ewing-like sarcoma

Kelly M Bailey

University of Pittsburgh School of Medicine, Department of Pediatrics, Division of Pediatric Hematology/Oncology, Kelly.Bailey@chp.edu

Published in Atlas Database: July 2019

Online updated version : http://AtlasGeneticsOncology.org/Tumors/EwinglikeID6988.html
DOI: 10.4267/2042/70727

This work is licensed under a Creative Commons Attribution-Noncommercial-No Derivative Works 2.0 France Licence.
© 2020 Atlas of Genetics and Cytogenetics in Oncology and Haematology

Abstract

Ewing-like sarcoma is a recently defined subset of bone or soft tissue sarcomas. It is one of the pediatric small, round, blue cell tumors and is fusion gene-driven cancer. However, the driving fusions are distinct from that of the FET-ETS family rearrangements that define Ewing sarcoma (see separate entry for Ewing sarcoma).

Keywords

Ewing-like sarcoma

Identity

Previously classified as Ewing tumors.

Classification

Ewing-like sarcoma can arise in the bone or soft tissue.

Clinics and pathology

Disease

Ewing-like sarcoma

Etiology

Ewing-like sarcomas are characterized by EWSR1/NFATC2 fusions, CIC fusions, or BCOR rearrangements.

Clinics

Ewing-like sarcoma is a very rare subtype of bone, soft tissue or visceral sarcoma.

Pathology

Small, round blue cells, with variable CD99 staining.

Treatment

Patients with Ewing-like sarcoma are currently treated following Ewing sarcoma therapy protocols. This may change over time as more is understood about the individual fusions driving Ewing-like sarcomas.

Prognosis

Survival is generally poorer for Ewing-like sarcomas compared to that of Ewing sarcoma. The exact prognoses for individual Ewing-like fusions types is still under investigation. In general, CIC-fused Ewing-like sarcomas have a very poor prognosis (<50%).

Cytogenetics

Ewing-like sarcomas harbor distinct fusions from that of Ewing sarcoma:

- t(X;4)(p11.4; q31.1) BCOR/MALM3
- t(X;22)(p11.4;q13.2) ZC3H7B/BCOR
- t(X;4)(q13.1; q35.2) CIC/FOXO4
- t(4;15)(q35.2; q14)CIC/NUTM1
- t(4;19)(q35.2; q13.2)CIC/DUX4
- t(20;22)(q13.2;q12.2) EWSR1/NFATC2
- and fusion BCOR/CCNB3 (Xp11.4-Xp11.22)

Genes involved and proteins

The following genes have been identified in Ewing-like sarcomas: EWSR1, NFATC2, BCOR, CCNB3, MAML3, CIC, DUX4, ZC3H7B, FOXO4, NUTM1.
EWSR1 (Ewing sarcoma breakpoint region 1)
Location 22q12.2
Protein Contains both a transcriptional activation domain and an RNA-binding domain.

NFATC2 (Nuclear factor of activated T cells 2)
Location 20q13.2
Protein DNA binding protein, responsive to T-cell receptor signaling.

BCOR (BCL6 corepressor)
Location Xp11.4
Protein Suppresses some genes by interacting with proteins comprising DNA binding complexes.

MAML3 (Mastermind like transcriptional coactivator 3)
Location 4q31.1
Protein Involved in the NOTCH pathway.

CCNB3 (Cyclin B3)
Location Xp11.22
Protein Cyclin family member; involved in cell cycle regulation.

CIC (Capicua transcriptional repressor)
Location 19q13.2
Protein HMG-box family member.

DUX4 (Double homeobox 4)
Location 4q35.2
Protein Associated with various forms of muscular dystrophy.

ZC3H7B (Zinc Finger CCCH-type containing 7B)
Location 22q13.2
Protein Nuclear protein; Contains domains involved in protein-protein and protein-nucleic acid interactions.

FOXO4 (Forkhead Box O4)
Location Xq13.1
Protein Involved in cell growth and differentiation.

NUTM1 (NUT midline carcinoma family member 1)
Location 15q14
Protein TERT expression regulation.

Result of the chromosomal anomaly

Fusion Protein
EWSR1/NFATC2
BCOR/MALM3
BCOR/CCNB3
ZC3H7B/BCOR
CIC/DUX4
CIC/NUTM1
CIC/FOXO4

References

This article should be referenced as such: