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Gene Section
Review

ETV6 (ets variant 6)

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Romana SP. ETV6 (ETS variant gene 6 (TEL oncogene)). Atlas Genet Cytogenet Oncol Haematol 1999;3(4):181-182.

Abstract

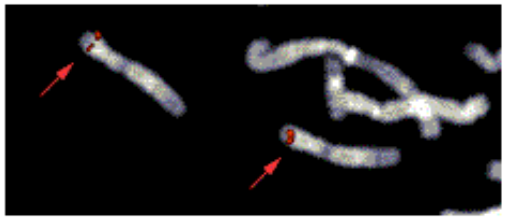
The ETV6 gene located at band 12p13 encodes a protein containing two major domains, the HLH (helix-loop-helix) domain, encoded by exons 3 and 4, and the ETS domain, encoded by exons 6 through 8, with in between the internal domain encoded by exon 5. ETV6 is a strong transcriptional repressor, acting through its HLH and internal domains. Five potential mechanisms of ETV6-mediated carcinogenesis have been identified: constitutive activation of the kinase activity of the partner protein, modification of the original functions of a transcription factor, loss of function of the fusion gene, affecting ETV6 and the partner gene, activation of a proto-oncogene in the vicinity of a chromosomal translocation and dominant negative effect of the fusion protein over transcriptional repression mediated by wild-type ETV6. Thirty-three ETV6 partner genes have been identified.

Identity

Other names: TEL, TEL1

HGNC (Hugo): ETV6

Location: 12p13.2



ETV6 (12p13.2) in normal cells: clone dJ852F10 - Courtesy Mariano Rocchi, Resources for Molecular Cytogenetics.

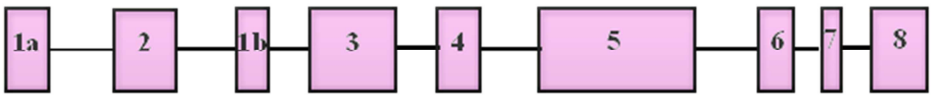
DNA/RNA

Description

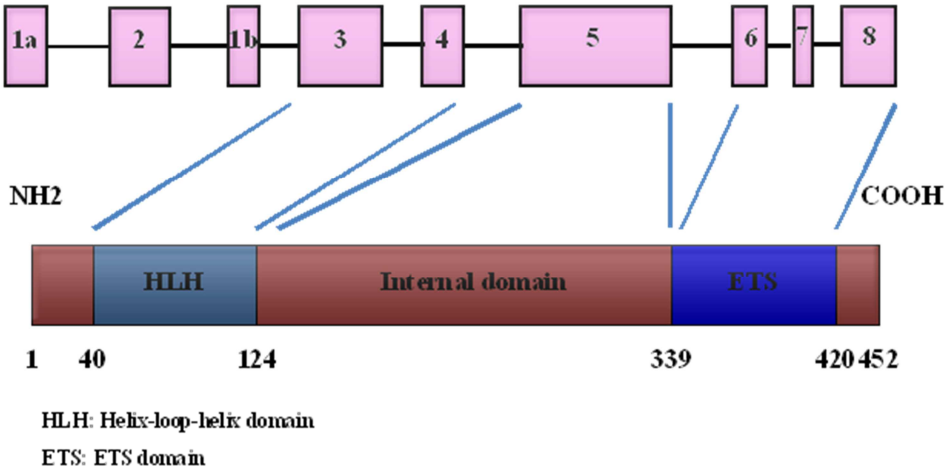
A member of the ets (E-26 transforming specific) family of transcription factors; the gene spans a region of 240 kb and consists of 8 exons. There are two start codons, one (exon 1a starting at codon 1) located at the beginning of the gene and another alternative (exon 1b starting at codon 43) upstream of exon 3.

Transcription

Transcription is from telomere to centromere; there are three species of transcripts : 2400 kb, 4300 kb and 6200 kb; the gene encodes for a 1356 kb cDNA.



Schematic diagram of the ETV6 gene showing the 8 exons. Exon 1b is an alternative exon located in intron 2. Reprinted from Leukemia Research, vol 36, De Braekeleer E et al. ETV6 fusion genes in hematological malignancies: A review. Pages 945-961, 2012. With permission from Elsevier.



Schematic diagram of the ETV6 protein showing the major domains. Reprinted from Leukemia Research, vol 36, De Braekeleer E et al. ETV6 fusion genes in hematological malignancies: A review. Pages 945-961, 2012. With permission from Elsevier.

Protein

Description

The ETV6 protein is a 452 amino acid polypeptide that shares homology at the 5' and 3' ends with other ETS family members. ETS proteins form one of the largest families of signal-dependent transcriptional regulators, mediating cell proliferation, differentiation and tumorigenesis.
The ETV6 protein contains two major domains, the HLH (helix-loop-helix) and ETS domains.
The HLH domain, also referred to as the pointed or sterile alpha motif domain, is encoded by exons 3 and 4 and is responsible for hetero- and homodimerization with other ETV6 proteins and possibly other ets family members.
The ETS domain, encoded by exons 6 through 8, is responsible for sequence specific DNA-binding and protein-protein interaction. A central domain, called internal domain, is encoded by exon 5 and is involved in the recruitment of a repression complex including N-Cor, mSin3 and SMRT.

Expression

Expression arrays and Northern analysis have shown ubiquitous expression with greater expression in bone marrow, spleen and thymus.

Localisation

Immunofluorescence has shown a nuclear localization.

Function

The ETV6 protein plays a crucial role in the embryonic development and hematopoietic regulation.
ETV6 is essential for normal development and is specifically required for maintaining blood vessel integrity within the developing yolk sac and survival of different cell types in the developing embryo.
ETV6 is essential for the establishment of hematopoiesis of all lineages in the bone marrow.
ETV6 is a strong transcriptional repressor. Repression is mediated by the HLH domain and the internal domain.
Repression by the HLH domain is mediated through interaction with the HLH domain of L3MBTL1, a member of the polycomb group of chromatin-associated proteins, that can maintain long term repression of genes through a histone deacetylase-independent mechanism.
Repression by the internal domain is mediated through interaction with corepressors such as N-Cor, mSin3 and SMRT, which in turn can recruit histone deacetylases.

Mutations

Note

ETV6 is implicated in leukemia, myelodysplastic syndromes and sarcoma.
Deletions: ETV6 is frequently deleted in hematological malignancies.
The deletion of the normal (untranslocated) ETV6 allele in the presence of a translocation affecting ETV6 is quite frequent, notably in patients with ETV6-RUNX1, ETV6-NTRK3, ETV6-ABL1, ETV6-ACSL6 and ETV6-STL fusion.
Deletion of an ETV6 allele has also been observed in the absence of rearrangement of the second allele.

Implicated in

t(1;12)(p36;p13) MDS2/ETV6

Disease
One CML with t(9;22) (no molecular analysis) and one refractory anemia with excess of blasts in transformation.

Abnormal protein
Truncated ETV6 protein lacking critical functional domains and suggesting a loss of function of ETV6.

Oncogenesis
Loss of function of ETV6? Expression of RPL11, centromeric to MDS2 (63.5 kb) much higher in the patient than in controls.

t(1;12)(q21;p13) ARNT/ETV6

Disease
One AML-M2 and one T-cell acute lymphoblastic leukemia.

Hybrid/Mutated gene
The ETV6-ARNT transcript contains the first 4 exons of ETV6 fused in frame with exon 1 or 2 of ARNT.

Abnormal protein
The ETV6-ARNT protein contains the oligomerization domain of ETV6 and almost all of the ARNT protein, including its major domains.

Oncogenesis
Given the presence of the oligomerization domain of ETV6 in the ETV6-ARNT protein, it is expected that the HLH domain of ETV6 convert ARNT from a transcriptional activator into a repressor. Furthermore, the ETV6-ARNT fusion protein retaining the HLH domain of ETV6 could interact with the other ETV6 protein.

t(1;12)(q25;p13) ABL2/ETV6

Disease
AML-M3, AML-M4, T-cell ALL, B-cell ALL.

Hybrid/Mutated gene
Breakpoint in intron 5 of ETV6 in all three cases.

Abnormal protein
Fusion protein contains the HLH oligomerization domain of ETV6 and the SH2, SH3, and protein tyrosine kinase domains of ABL2.

Oncogenesis
Constitutive activation of the kinase activity of ABL2.

t(3;12)(q26;p13) MDS1-EVI1 (MECOM)/ETV6

Note
Rare, but recurrent, chromosomal aberration (more than 30 cases). Few patients studied on a molecular level.

Disease
Myeloproliferative disorders, myelodysplastic syndromes and acute myelogenous leukemia.

Hybrid/Mutated gene
Two different mechanisms for generating the fusion gene.
First mechanism: in-frame chimeric transcript consisting of the first two exons of ETV6 fused to MDS1 sequences, which in turn is fused to the second exon of the EVI1 gene.
Second mechanism: direct fusion between ETV6 and EVI1, in which case an out-of-frame fusion between exon 2 of ETV6 and exon 2 of EVI1 is generated but the open reading frame of EVI1 is not disrupted.

Abnormal protein
In both fusion types, ETV6 contributes no known functional domain to the predicted chimeric protein.

Oncogenesis
Oncogenic potential of the translocation could be the result of the ETV6 promoter driving the transcription of EVI1, resulting in activation of the transcription factor EVI1, which is not normally expressed in hematopoietic cells.

t(4;12) (p16;p13) FGFR3/ETV6

Disease
Peripheral T-cell lymphoma

Hybrid/Mutated gene
Fusion of exon 5 of ETV6 to exon 10 of FGFR3.

Abnormal protein
Protein consists of the HLH domain of ETV6 and the tyrosine kinase domain of FGFR3.

Oncogenesis
Constitutive activation of the kinase activity of FGFR3.

t(4;12)(q11;p13) CHIC2 (BTL)/ETV6

Note
Rare but recurrent chromosomal abnormality. Ten cases with molecular analysis showed a CHIC2/ETV6 fusion gene.

Disease
AML (FAB type M0, M1, M2, therapy-related), RAEB.

Hybrid/Mutated gene
At least two different mechanisms.
First mechanism: In-frame fusion between CHIC2 exons 1-3 and exons 2-8 of the ETV6 gene.
Second mechanism: Breakpoints located in introns 1 and 2 of ETV6 but outside the CHIC2 gene, with no detectable CHIC2-ETV6 fusion gene.

Abnormal protein
Fusion protein contains both the HLH and ETS domains of ETV6 but no specific domain of CHIC2.

Oncogenesis
Ectopic expression of GSX2 detected in all cases studied, with or without the CHIC2-ETV6 fusion. GSX2 contains a homeobox domain very similar to the homeobox of the clustered HOX genes, which are involved in both normal and abnormal hematopoiesis. Overexpression of GSX2, but not CHIC2-ETV6 has transforming properties.

t(5;12)(q31;p13) ACSL6/ETV6

Note
Recurrent translocation occurring in various myeloid malignancies, often associated with eosinophilia. Only seven cases with molecular analysis.

Disease
Myelodysplastic syndrome (RAEB), AML, AEL, atypical CML, Polycythemia Vera.

Hybrid/Mutated gene
Different fusion genes are generated in four patients:
- in-frame fusion of exon 1 of ETV6 to the 3'UTR of ACSL6
- out-of-frame fusion of exon 2 of ETV6 to exon 11 of ACSL6
- out-of-frame fusion of exon 1 of ETV6 to exon 1 of ACSL6
- in-frame fusion of exon 1 of ETV6 to almost the complete ACSL6 (breakpoint at the 5' end of the ACSL6 gene).

Oncogenesis
Given the absence of a common in-frame fusion gene generated by the t(5;12)(q31;p13) and the heterogeneity in the localization of the ACSL6 breakpoints, no common fusion protein can explain the pathogenic character of the translocation. IL3, located near the breakpoint at 5q31, is ectopically expressed in the leukemic cells, leading to a proliferative defect.

t(5;12)(q33;p13) PDGFRB/ETV6

Note
Recurrent chromosomal abnormality (dozens of cases).

Disease
Myeloproliferative/myelodysplastic syndrome (usually referred as atypical Philadelphia-negative CML and CMML) with eosinophilia.

Hybrid/Mutated gene
Exon 4 of the ETV6 gene is generally fused in-frame to exon 11 of the PDGFRB gene.
Two cases showing a different fusion gene with the ETV6 breakpoint in intron 7.

Abnormal protein
Protein includes the HLH domain of ETV6 and the tyrosine kinase domain of PDGFRB.
In both cases showing a different fusion gene, the fusion protein retains the internal domain of ETV6 which has the ability to bind to corepressors and induce the transcription-repressive activity of ETV6.

Oncogenesis
Constitutive activation of the kinase activity of PDGFRB.
In both cases showing a different fusion gene, it is likely that the fusion protein acts differently from that observed in the other cases.

t(6;12)(q23;p13) STL/ETV6

Note
Only one case reported.

Disease
B-cell ALL.

Hybrid/Mutated gene
Fusion gene only retains the first two exons of ETV6.

Abnormal protein
Fusion protein contains no important domains (HLH or ETS) of ETV6.

Oncogenesis
It is likely that the truncated ETV6 contributes to leukemogenesis through ETV6 haploinsufficiency.

t(7;12)(q36;p13) MNX1(HLXB9)/ETV6

Note
Recurrent translocation found in 20 to 30% of AML children less than 18 months of age. The 7q36 breakpoint heterogeneity suggests that this translocation does not lead to the formation of a unique fusion gene. Six cases with molecular analysis showing a MNX1/ETV6 fusion.

Disease
AML

Hybrid/Mutated gene
5' MNX1-3' ETV6 resulting in a transcript in which MNX1 exon 1 is joined with ETV6 exon 3.

Abnormal protein
Protein contains the HLH and ETS domains of ETV6 but not the homeobox domain of MNX1.

Oncogenesis
It is thought that the chimeric protein acts as an aberrant transcription factor, which could affect both MNX1 and ETV6 pathways of transcription modulation.

dic(9;12)(p13;p13) PAX5/ETV6

Note
Nonrandom chromosome abnormality found in about 1% of childhood B-cell ALL.

Disease
ALL.

Hybrid/Mutated gene
5'PAX5-3'ETV6 transcript with fusion of exon 4 of PAX5 to exon 3 of ETV6.

Abnormal protein
The PAX5-ETV6 protein contains the "paired box" (DNA binding) domain of PAX5 fused to the HLH and ETS-binding domains of ETV6.

Oncogenesis
It is thought that the chimeric protein could act as an aberrant transcription factor, which could affect both PAX5 and ETV6 pathways of transcription modulation.

t(9;12) (p24;p13) JAK2/ETV6

Note
Only six cases described with ETV6/JAK2 fusion.

Disease
Pre-B ALL, atypical CML, T-cell ALL.

Hybrid/Mutated gene
Breakpoint variability: introns 4 and 5 of ETV6 and introns 12 and 17 of JAK2.

Abnormal protein
Protein retains the HLH domain of ETV6 but different domains of JAK2 (complete JH2 and JH1 in one case, only part of JH2 in the other).

Oncogenesis
Constitutive activation of the kinase activity of JAK2.

t(9;12)(q22;p13) SYK/ETV6

Note
Only two cases reported.

Disease
MDS.

Hybrid/Mutated gene
Chimeric gene fuses the first 5 exons of ETV6 with SYK starting with exon 5.

Abnormal protein
Fusion protein contains the HLH domain of ETV6 with part of the C-terminal SH2 and the complete protein kinase domain of SYK.

Oncogenesis
Constitutive activation of SYK kinase activity.

t(9;12)(q34;p13) ABL1/ETV6

Note
26 cases described with different hemopathies but eosinophilia is a common feature.

Disease
Acute myeloblastic leukemia (AML), chronic myelogenous leukemia (CML), B-cell acute lymphocytic leukemia (ALL), T-cell ALL, MDS (RAEB), chronic myeloproliferative neoplasm, Philadelphia chromosome-negative CML.

Hybrid/Mutated gene
Two ETV6-ABL1 transcripts are usually identified: one joining exon 5 of ETV6 to exon 2 of ABL1 and one joining ETV6 exon 4 to ABL1 exon 2.

Abnormal protein
The protein retains all three SH domains, including the tyrosine kinase domain, of ABL1 and the HLH domain of ETV6.

Oncogenesis
Tyrosine kinase activation of ABL1.

t(10;12)(q24;p13) GOT1/ETV6

Note
Two cases of MDS described.

Disease
MDS (RA and RAEB).

Hybrid/Mutated gene
Transcript containing exon 2 to exon 9 of GOT1 and the first 2 or 3 exons of ETV6.

Abnormal protein
Absence or truncation of the HLH domain of ETV6 in the protein.

Oncogenesis
Possibly inactivation of the wild type ETV6.

t(12;13)(p13;q12) ETV6/CDX2

Note
The t(12;13)(p13;q12-14) is a rare, but recurrent, translocation reported in a range of malignant hemopathies. However, it is evident from FISH studies that they are heterogeneous at the molecular level.

Disease
CML in transformation, myelodysplastic syndrome (MDS), acute non lymphocytic leukemia (ANLL), B and T- ALL. A sole case with ETV6/CDX2 fusion in a AML-M1.

Hybrid/Mutated gene
One in-frame fusion between exon 2 of ETV6 and exon 2 of CDX2; one fusion introducing an in-frame stop codon.

Abnormal protein
ETV6 contributes no functional domain to the fusion protein.

Oncogenesis
It is likely that the ETV6 promoter drives the transcription and ectopic activation of CDX2, which has leukemogenesis properties.

t(12;13)(p13;q14) ETV6/TTL [not annotated gene in HGNC]

Note
Identified in several cases of ALL and less frequently in acute or chronic myeloid malignancies.

Disease
A sole case with TTL/ETV6 fusion in a ALL.

Hybrid/Mutated gene
ETV6/TTL fusion transcript: 3' TTL sequence introduces an in-frame stop codon after the end of ETV6 exon 1.
TTL-ETV6 transcript is a direct in-frame fusion between TTL exon 5 and ETV6 exon 2.

Abnormal protein
No ETV6 functional domains in the ETV6/TTL protein; HLH and ETS domains conserved in TTL-ETV6 protein.

Oncogenesis
Chimeric protein could act as an aberrant transcription factor, affecting the ETV6 pathway of transcription modulation, or there could be a loss of function of ETV6 and/or TTL.

t(12;15)(p13;q25) ETV6/NTRK3

Disease
Congenital Fibrosarcoma, Congenital Mesoblastic Nephroma (cellular and mixed variants), Secretory Ductal Carcinoma of Breast, rarely in AML (M0, M2) and chronic eosinophilia leukemia (1 case).

Hybrid/Mutated gene
5' ETV6-3' NTRK3.

Abnormal protein
Fusion protein retains the HLH domain of ETV6 and the protein tyrosine kinase (PTK) domain of NTRK3.

Oncogenesis
Constitutive active tyrosine kinase.

t(12;17)(p13;p13) ETV6/PER1

Disease
Only one case of AML evolving from CMML.

Hybrid/Mutated gene
Fusion between exon 1 of the ETV6 gene and exon 22 and part of intron 21 of PER1.

Abnormal protein
No protein as PER1 has an antisense orientation.

Oncogenesis
It is proposed that PER1 inactivation or deregulated expression of genes located close to the breakpoint, such as HES7 or STK12, could contribute to leukemogenesis.

t(12;21)(p13;q22) ETV6/RUNX1

Note
Most common structural chromosomal abnormality in pediatric common or B-cell acute lymphoblastic leukemia, accounting for about 20-25% of the cases.

Disease
Childhood B-cell (ALL).

Hybrid/Mutated gene
Fusion of the 5' region of ETV6 (from exon 1 to 5) with almost the entire coding region of RUNX1.

Abnormal protein
The fusion protein retains the HLH domain and the central repression domain of ETV6 as well as the RHD (Runt homology domain) and the transcription activation domain of RUNX1.

Oncogenesis
The ETV6-RUNX1 fusion protein retains the ability to bind the RUNX1 target sequences and functions as a histone deacetylase (HDAC)-dependent repressor, causing deregulation of the RUNX1 target genes. ETV6-RUNX1 is also likely to disrupt normal ETV6 functions through HLH-mediated heterodimerization.

t(12;22)(p13;q11) MN1/ETV6

Note
Rare anomaly in myeloid hemopathies (6 cases with molecular analysis).

Disease
Myeloproliferative disorder, myelodysplastic syndrome, AML.

Hybrid/Mutated gene
Two different types of MN1/ETV6 fusion (types I and II).

Abnormal protein
Type I fusion protein contains almost the entire MN1 fused to ETV6 at a position N terminal to the HLH domain whereas type II fusion protein has only part of the HLH domain, making it nonfunctional. Both fusion types retain the ETS domain.

Oncogenesis
Could act as an altered transcription factor by activating ETV6-responsive transcription and/or inhibiting RAR-mediated transcription and/or being a dominant-negative suppressor of MN1.

t(4;12)(q23;p13) ETV6/PDGFRA

Note
PDGFRA is a gene found to be fused with several partners in chronic eosinophilic leukemia.

Disease
Only one case of myeloproliferative neoplasm associated with hypereosinophilia and ETV6/PDGFRA fusion.

Hybrid/Mutated gene
In-frame fusion gene between ETV6 exon 6 and PDGFRA exon 11.

Abnormal protein
Protein retains most of ETV6, including the HLH domain and part of the ETS domain, fused to the WW-like domain and the kinase domain of PDGFRA.

Oncogenesis
Constitutive protein kinase activation.

t(12;13)(p13;q12) ETV6/FLT3

Note
FLT3 is one of the most frequently mutated genes in hematological malignancies, being found in about 30% of AML patients and rarely in ALL patients.

Disease
Three cases of myeloproliferative neoplasm with hypereosinophilia associated with ETV6/FLT3 fusion.

Hybrid/Mutated gene
In-frame fusion gene between ETV6 exon 4 or exon 5 and FLT3 exon 14.

Abnormal protein
Protein retains the HLH domain of ETV6 and the tyrosine kinase domains of FLT3.

Oncogenesis
Constitutively tyrosine kinase activation.

t(6;12)(q21;p13) ETV6/FRK

Disease
Only one case of AML-M4.

Hybrid/Mutated gene
ETV6 exon 4 fused in frame to exon 3 of FRK.

Abnormal protein
Chimeric protein composed of the HLH domain of ETV6 and most of the SH2 (likely to be nonfunctional) and the kinase domains of FRK.

Oncogenesis
Dual action of constitutively tyrosine kinase activation and dominant-negative effect on ETV6-mediated transcriptional repression.

ins(12;8)(p13;q11q21) ETV6/LYN

Disease
Only one case of primary myelofibrosis associated with ETV6/LYN.

Hybrid/Mutated gene
Chimeric gene consists of the 5' region of ETV6 (breakpoint in intron 5) and the 3' region of LYN.

Abnormal protein
Protein retains the HLH domain of ETV6 and the tyrosine kinase domain of LYN.

Oncogenesis
Constitutively tyrosine kinase activation.

inv(12)(p13q13) ETV6/PTPRR

Disease
Only one case of AML-M2 associated with ETV6/PTPRR.

Hybrid/Mutated gene
ETV6 exon 4 is fused to exon 7 of the PTPRR; 10 isoforms through alternative splicing.

Abnormal protein
A truncated ETV6 including the HLH domain but no functional domains of PTPRR due to frameshift and a chimeric ETV6-PTPRR protein that includes the HLH domain of ETV6 and the protein tyrosine phosphatase domain of PTPRR among others.

Oncogenesis
Dominant negative effect over transcriptional repression mediated by wild-type ETV6.

t(8;12)(q13;p13) ETV6/NCOA2

Disease
Pediatric acute biphenotypic leukemia (6 cases with ETV6/NCOA2), adult T-ALL (1 case).

Hybrid/Mutated gene
Two different in-frame fusions are known:
- one between ETV6 exon 4 and NCOA2 exon 15 (five cases)
- one between ETV6 exon 5 and NCOA2 exon 14 (one case).

Abnormal protein
Protein consists of the HLH domain of ETV6 and the CBP interaction and the AD2 (transactivation domain 2) acetyltransferase domains of NCOA2.

Oncogenesis
It is hypothesized that the ETV6-NCOA2 protein acts as a modulator of the transcriptional activity of CBP-dependent activators or can recruit CBP to ETV6 target genes resulting in their constitutive activation.

Cryptic rearrangement shown by FISH between 12p13 and 12q24 ETV6/BAZ2A in a t(?1;12)(q42;p13)

Disease
Only one case of pre-B ALL.

Hybrid/Mutated gene
Fusion of ETV6 and BAZ2A consisting of exons 1 and 2 of ETV6 and a sequence from intron 1 of BAZ2A.

Abnormal protein
No chimeric protein expected to be produced, but, maybe, a truncated ETV6.

Oncogenesis
It is likely that the truncated ETV6 contributes to leukemogenesis through ETV6 haploinsufficiency.

t(5;12;22)(q13;p13;q11) ETV6/FCHO2

Disease
Only one case of AML-M1.

Hybrid/Mutated gene
Transcript consisting of ETV6 exons 1 and 2 with sequences of FCHO2.

Abnormal protein
No chimeric protein expected to be produced (genes in opposite orientations following the translocation), but, maybe, a truncated ETV6.

Oncogenesis
It is likely that the truncated ETV6 contributes to leukemogenesis through ETV6 haploinsufficiency.

t(12;14)(p13;q32) ETV6/IGH co-localization

Disease
One case of pediatric pre-B ALL.

Cytogenetics
Co-localization of both ETV6 and IGH signals by FISH (no molecular analysis).

t(12;22)(p13;q12) ETV6/EMID1

Disease
Only one case of AML-M2.

Cytogenetics
Co-localization of both ETV6 and EMID1 signals by FISH (no molecular analysis).

Abnormal protein
No chimeric protein expected to be produced (genes in opposite orientations following the translocation), but, maybe, a truncated ETV6.

t(12;17)(p13;q21) ETV6/RARA

Disease
Only one case of myelofibrosis evolved in AML.

Cytogenetics
Co-localization of both ETV6 and RARA signals by FISH (no molecular analysis).

Abnormal protein
No chimeric protein expected to be produced (genes in opposite orientations following the translocation), but, maybe, a truncated ETV6.

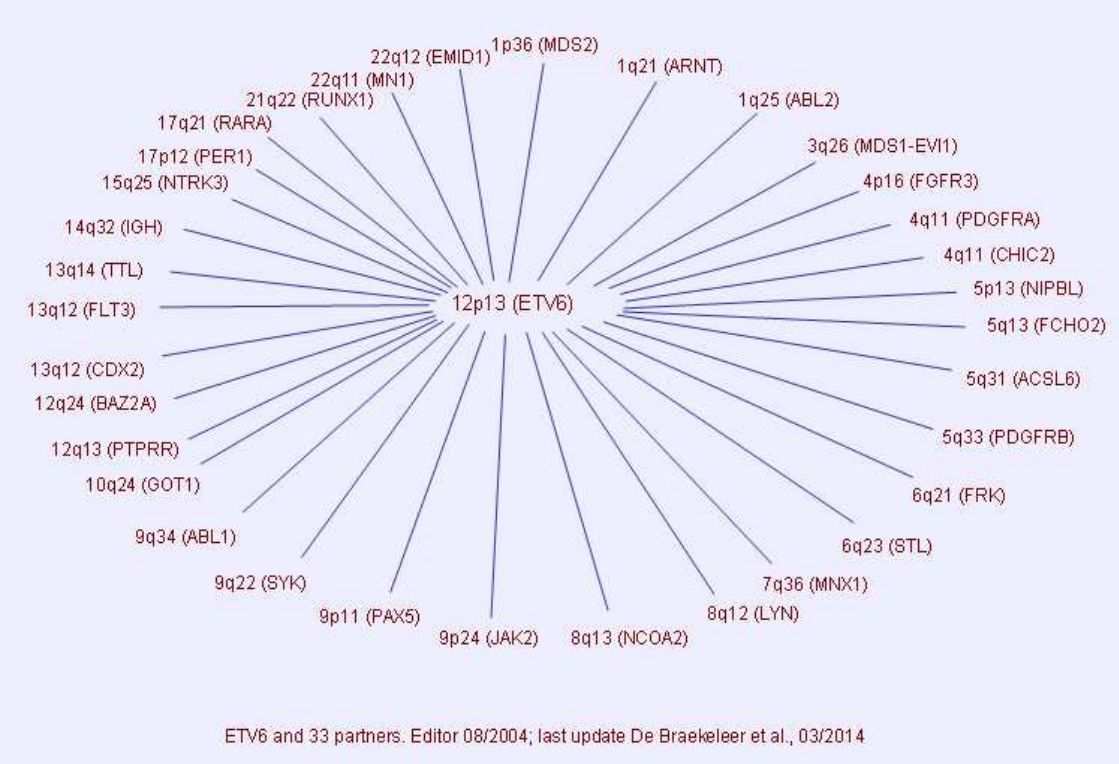
t(5;12)(p13;p13) NIPBL/ETV6

Disease
Only one case of acute megakaryoblastic leukemia (AML-M7).

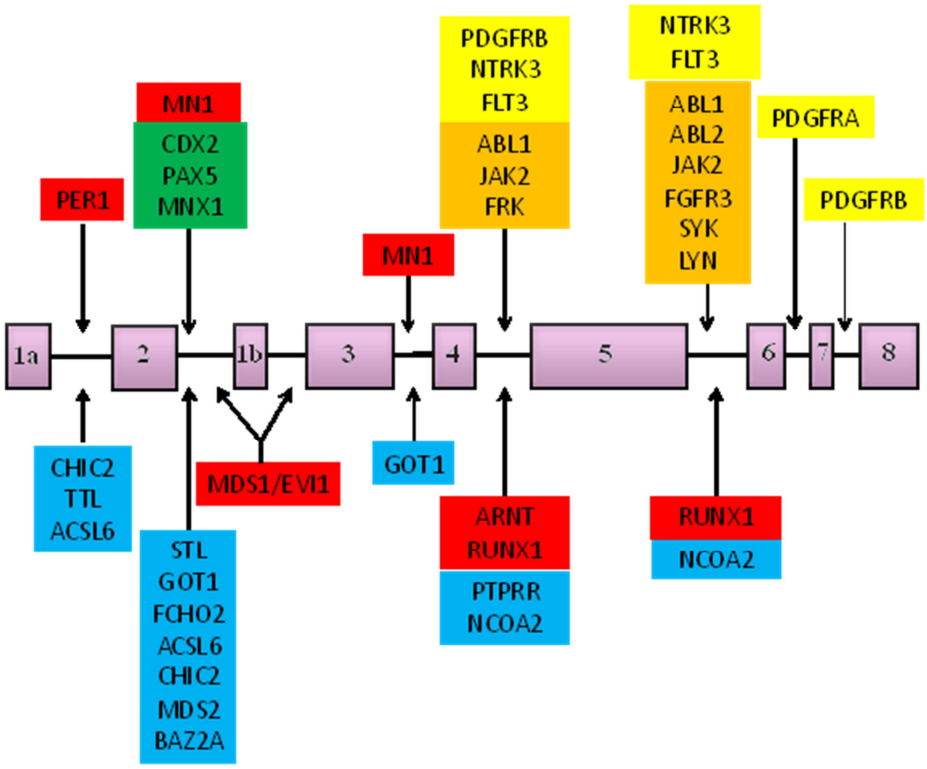
Cytogenetics
Co-localization of both ETV6 and NIPBL signals by FISH (no molecular analysis).

Breakpoints

See figures below.



Chromosomal distribution of the 33 ETV6 partners thus far identified.



Physical map of the breakpoint distribution in the ETV6 gene. Yellow boxes: receptor tyrosine kinase genes; orange boxes: non-receptor tyrosine kinase genes; red boxes: transcription factor genes; green boxes: homeobox genes; blue boxes: other genes. Reprinted from Leukemia Research, vol 36, De Braekeleer E. et al. ETV6 fusion genes in hematological malignancies: A review. Pages 945-961, 2012. With permission from Elsevier.

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