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Gene Section
Mini Review

MYST3 (MYST histone acetyltransferase (monocytic leukemia) 3

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Identity

Hugo: MYST3
Other names: MOZ (monocytic leukemia zinc finger); ZNF220; RUNXBP2
Location: 8p11

DNA/RNA

Description

The gene spans121 kb on minus strand; 17 exons.

Transcription

7.85 kb.

Protein

Description

2004 amino acids; 225 kDa; composed from N-term of: a NEMM domain (N-term region of ENOK, MOZ or MORF) including a H15 (linker H1 and H5 like) nuclear localization domain, 2 PHD (plant homeodomain, also known as LAP (leukemia associated protein)) Zn fingers (C4HC3), a C2HC Zn finger, essential part of the histone acyl transferase domain (HAT MOZ-SAS), an acidic (Glu-Asp) domain, localisation of breakpoints in the inv(8) and in the t(8;22) in 1118, and a Ser-(Pro-Glu)-Met rich domain, localisation of the t(8;16) breakpoint in 1547.

Localisation

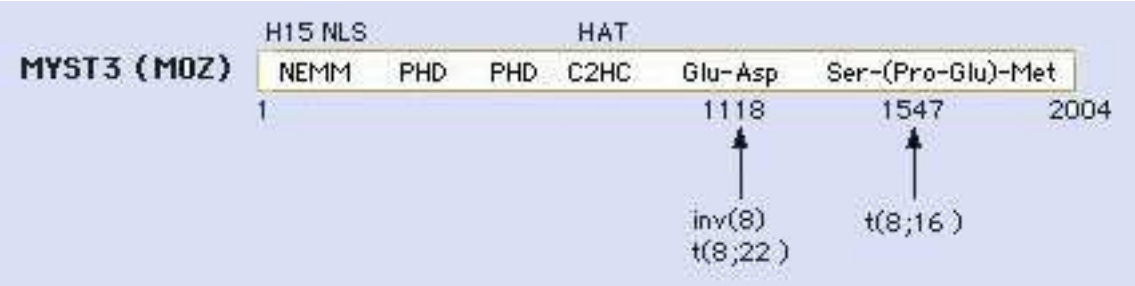
Nucleus.

Function

Lysine acetyltransferase activity (histone acyl transferase); MYST3 (MOZ) and MYST4 (MORF) possess both transcription activation and transcription repression domains; transcriptional regulators; interact with RUNX1 and RUNX2; Moz, the zebrafish ortholog of MYST3, was also found to regulate Hox expression; Moz behaves like a trithorax group factor.

Homology

With MYST4 (MORF) (monocytic leukemia zinc finger protein-related factor), a transcription regulator with positive and negative domains and activities.



Implicated in

t(2;8)(p23;p11) in therapy related myelodysplastic syndrom ⟶ MYST3 / ?

Disease

Only 1 case to date, a boy aged 6 years.

inv(8)(p11q13) in acute myelomonocytic or monocytic leukaemia (M4 or M5 AML) ⟶ MYST3 / NCOA2

Disease

Erythrophagocytosis; very rare: less than 10 cases; young age, and female sex.

Prognosis

Likely to be poor.

Hybrid/Mutated Gene

5' MYST3 - 3' NCOA2.

Abnormal Protein

The fusion product retains the zinc fingers, the the histone acetyl transferase (HAT) domain of MYST3 and the HAT domains and CREBBP interacting domain of NCOA2.

t(8;16)(p11;p13) in acute myelomonocytic or monocytic leukaemia (M4 or M5 AML) and therapy related AML (t-AML) ⟶ MYST3 / CREBBP

Disease

Erythrophagocytosis; rare: less than 1% of AML; found in children and young adults of both sex.

Prognosis

Poor.

Hybrid/Mutated Gene

5’ MYST3 - 3’ CREBBP.

Abnormal Protein

The fusion product retains the zinc fingers, the HAT domain of MYST3 and most of CREBBP, including the CREBBP interacting domain and the HAT domain; the fusion protein may repress RUNX1-dependant gene expression.

t(8;22)(p11; q13) in acute myelomonocytic or monocytic leukaemia (M4 or M5 AML) ⟶ MYST3 / EP300

Disease

Erythrophagocytosis; very rare: less than 5 cases.

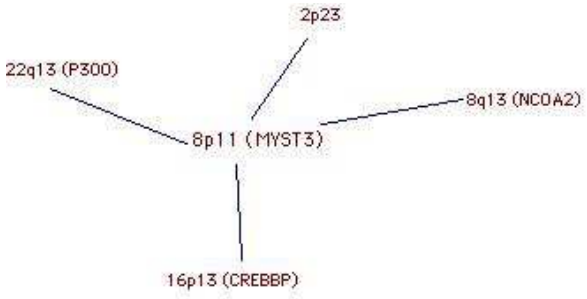
Prognosis

Likely to be poor.

Oncogenesis

EP300 is very similar to CRBBP (see above), the breakpoints on these 2 genes are on homologous regions; the breakpoint on MYST3 is more proximal in the t(8;22).

Breakpoints



MYST3 (MOZ) and partners. Editor 08/2004; last update 08/2005.

To be noted

Note: MYST3 and MLL share: a common dual transcription activation / repression activity; probable or certain HOX genes expression regulation; 2 common translocation partners: CREBBP and EP300 giving rise to AML and t-AML with poor prognoses.

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