

Gene Section

Mini Review

MAML2 (mastermind-like 2)

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Identity

Hugo: MAML2

Other names: hMam-3; KIAA1819

Location: 11q21

DNA/RNA

Description

Spans 365 kb; 5 exons.

Transcription

A major transcript of 7.5 kb.

Protein

Description

1153 aa, 125 kDa; conserved N-terminal basic domain (aa 29-92) which binds to the ankyrin repeat domain of Notch receptors; two acidic domains (aa 263-360 and 1124-1153) and a C-terminal transcriptional activation domain.

Expression

Widely expressed.

Localisation

Nuclear granules.

Function

Mastermind-like coactivator for all four Notch receptors; forms a complex with the Notch intracellular domain (Notch ICD) and the CSL family of transcription factors (CSL: CBF1/RBP-jk, Suppressor of Hairless, LAG1), resulting in activation of the Notch

target genes HES1 and HES5; functions as a CSL-dependent transcriptional coactivator for ligand-stimulated Notch.

Homology

MAML1 and MAML3.

Implicated in

Mucoepidermoid carcinoma with t(11;19)(q21-22;p13)

Disease

- Most common type of malignant salivary gland tumor:
- Second most frequent lung tumor of bronchial gland origin;
- Rare tumour in the thyroid.

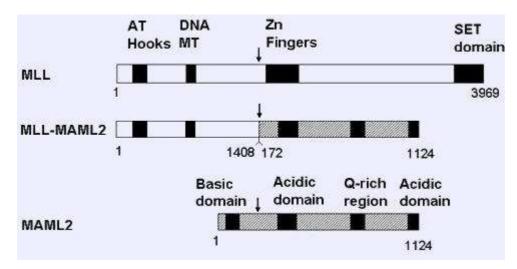
The t(11;19) was found in samples from the three different sites.

Prognosis

- Mucoepidermoid carcinomas have an unpredictable behaviour.
- The CRTC1-MAML2 fusion transcript was found equally in low, intermediate and high grade tumours; however, tumours lacking the fusion transcript were significantly associated with metastases; they may represent a subset of aggressive tumours.
- In another study, the median survival for fusion-positive patients was greater than 10 years compared to 1.6 years for fusion-negative patients.

Hybrid/Mutated Gene

CRTC1-MAML2; exon 1 of CRTC1 fused to exons 2-5 of MAML2. Note: CRTC1 is also known as MECT1, or WAMTP1.



Abnormal Protein

CRTC1-MAML2. In the fusion protein, the first 171 aa including the basic domain of MAML2 are replaced by 42 aa of CRTC1; there are no sequence similarities in the N-terminal domains of MAML2 and CRTC1. The fusion protein activates transcription of the Notch target gene HES1 independently of both Notch ligand and CSL.

Transforming activity of CRTC1-MAML2 fusion oncoprotein is mediated by mimicking constitutive activation of cAMP signaling, by activating CREB directly.

Warthin's tumor with t(11;19)(q21-22:p13)

Note: In rare instances mucoepidermoid carcinoma may arise from or coexist with Warthin's tumors.

Disease

Warthin's tumor is a salivary gland neoplasm consisting of benign epithelial and lymphoid components; malignant transformation is extremely rare.

Hybrid/Mutated Gene

CRTC1-MAML2

Clear cell hidradenomas of the skin with t(11;19)(q21-22;p13)

Disease

Clear cell hidradenomas of the skin are benign sweat gland tumors of eccrine duct origin.

Hybrid/Mutated Gene

CRTC1-MAML2; exon 1 of CRTC1 fused to exons 2 of MAML2.

inv(11)(q21q23) in therapy related leukemias

Disease

Therapy-related acute leukemia and MDS.

Hybrid/Mutated Gene

MLL-MAML2; exon 1-7 of MLL fused to exons 2-5 of MAML2.

Abnormal Protein

Hybrid transcript MLL/MAML2 contains the following domains: from MLL: AT-hook, DNA-Methyltransferase; from MAML2: Q rich domain, acidic domain.

To be noted

Note: It is amazing that a similar fusion transcript (CRTC1-MAML2) can be seen both in a benign and in a malignant tumour of the same organ: Warthin's tumor, a benign salivary gland neoplasm, and mucoepidermoid carcinoma of the salivary gland: either another event differentiate the two, or the genetic event takes place in different cell types or in a given cell type at different states of differenciation.

It has been hypothezised that CRTC1-MAML2 fusion is etiologically linked to benign and low-grade malignant tumors originating from diverse exocrine glands rather than being linked to a separate tumor entity.

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