

Gene Section

Mini Review

HMGIC (High mobility group protein isoform I-C)

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Identity

HGNC (Hugo): HMGIC

Location: 12q15

Local order: Telomeric to CDK4, centromeric to MDM2.



Probe(s) - Courtesy Mariano Rocchi.

DNA/RNA

Description

5 exons, spans approximately 160 kb; the size of intron 3 is 140 kb.

Transcription

RNA: 4.1 kb.

Protein

Description

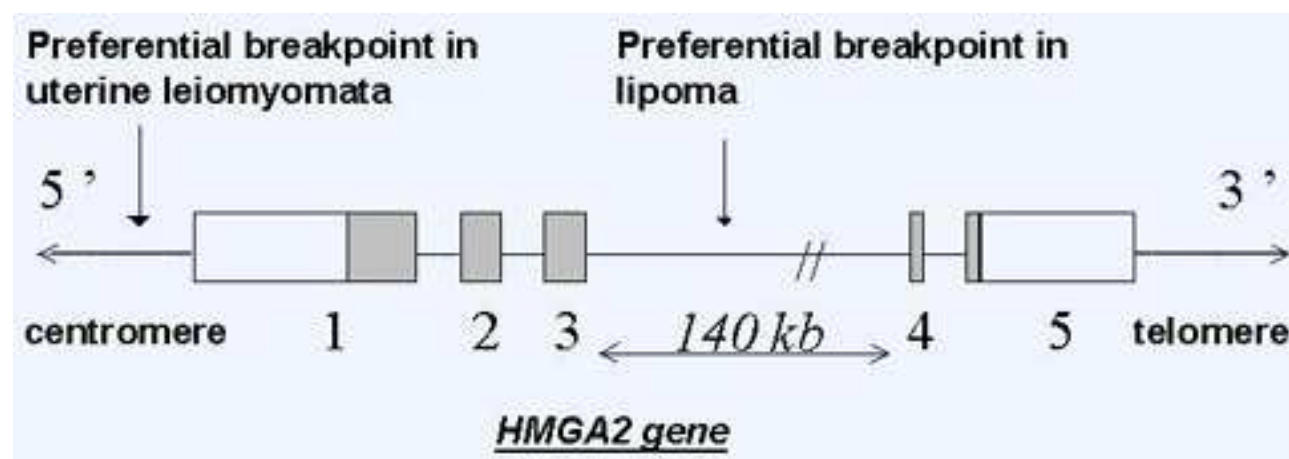
109 amino acids; three DNA binding domains (AT hooks) linked to the carboxy-terminal acidic domain that does not activate transcription.

Expression

Fetal tissues: expression in various tissues, prominent in kidney, liver and uterus; adult tissues: no expression except in lung and kidney; tumors: expression in benign mesenchymal tumor tissues correlated to 12q15 rearrangements.

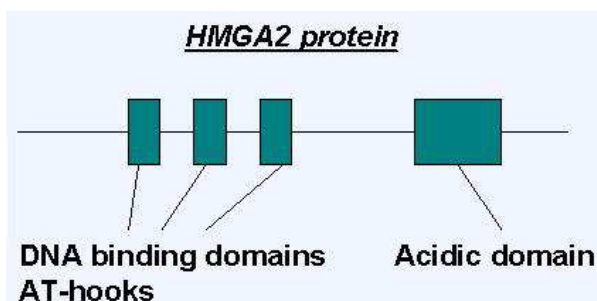
Localisation

Nuclear.



Function

Architectural factor, non histone, preferential binding to AT rich sequences in the minor groove of DNA helix; the precise function remains to be elucidated; probable role in regulation of cell proliferation.



Homology

Member of the HMGI protein family.

Mutations

Germinal

Deletion of HMGIC in mutant mice or transgenic 'knock out' mice for the first two exons of HMGIC have the 'pigmy' phenotype: low birth weight, craniofacial defects, adipocyte hypoplasia adult body weight about 40% of normal.

Implicated in

Mesenchymal benign tumors as follows:

Lipoma

Disease

Benign adipocyte tumor.

Prognosis

Good.

Cytogenetics

Various rearrangements involving 12q15 (translocations, inversions, deletions...); reciprocal translocations involve 12q15 with different partners such as chromosomes 1, 3, 7, 10, 11, 13, 15, 17, 21, X; the most frequent anomaly is t(3;12)(q27-28;q15); cryptic rearrangements, such as paracentric inversions not detectable by conventional cytogenetics but detectable by FISH, have been described.

Hybrid/Mutated gene

For t(3;12): HMGIC-LPP (LPP: lipoma preferred partner; 3q27-28); a gene located in 13q, LHPF (lipoma HMGIC fusion partner) was found to be fused with HMGIC in one case of lipoma.

Abnormal protein

HMGIC-LPP; the three AT hook domains at the aminoterminal of HMGIC are fused to the LIM domain

of LPP; another fusion protein due to the fusion of HMGIC with a putative gene located at 15q24 predicted to encode a protein with a serine/threonine-rich domain has also been described.

Oncogenesis

The relevance of the exact role LPP in the HMGIC-LPP fusion is not established yet; the truncation of HMGIC may have a role in the tumorigenesis.

Uterine leiomyoma (uterine fibroids)

Disease

Benign mesenchymal tumors.

Prognosis

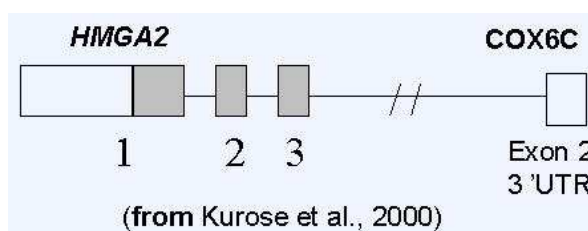
Good.

Cytogenetics

Approximately 40% of uterine leiomyomas have structural chromosomal rearrangements, about 10% of which involve 12q15 (translocations, inversions, deletions...); the most frequent anomaly is t(12;14)(q15;q23-24).

Hybrid/Mutated gene

In a majority of cases, there is no fusion gene: the breakpoint is located 10 kb up to 100 kb 5' to HMGIC; the recombinational repair gene RAD51B is a candidate to be the partner gene of HMGIC in t(12;14); in one case with paracentric inversion, HMGIC exon 3 was fused to ALDH2 exon 13 (12q24.1); in one case (no cytogenetic analysis) HMGIC exon 3 was fused to COX6C 3' UTR (8q22-23); in one case, with apparently normal karyotype, exon 3 of HMGIC was fused to retrotransposon-like sequences RTVLH 3' LTRs.



Abnormal protein

HMGIC-ALDH2: ALDH2 contribution was only 10 amino acids.

Oncogenesis

HMGIC-ALDH2: it is suggested that the truncation of HMGIC, rather than fusion may be responsible for tumorigenesis; the 3' untranslated region may stabilize the HMGIC messenger RNA.

Pleomorphic adenoma of the salivary gland (or mixed salivary gland tumor)

Disease

Benign tumors from the major or minor salivary glands.

Prognosis

Good.

Cytogenetics

Approximately 12% of pleomorphic adenomas of salivary glands show abnormalities involving HMGIC in 12q15; the most frequent aberration is t(9;12)(p24.1;q15).

Hybrid/Mutated gene

In t(9;12): HMGIC-NFIB fusion; another type of fusion HMGIC-FHIT (3p14.2) has also been described.

Pulmonary chondroid hamartoma of the lung**Disease**

Benign mesenchymal tumors of the lung.

Prognosis

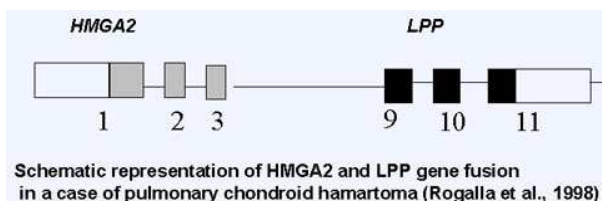
Good.

Cytogenetics

Various rearrangements involving 12q15 leading to HMGIC dysregulation; cryptic rearrangements such as paracentric inversions not detectable by conventional cytogenetics but detectable by FISH have been described.

Hybrid/Mutated gene

In two cases with apparently normal karyotypes, exon 3 of HMGIC was fused to retrotransposon-like sequences RTVLH 3' LTRs; in five cases with t(3;12)(q27;q15) (see lipomas), a fusion HMGIC-LPP was described.

**Endometrial polyps****Disease**

Uterine benign tumors.

Prognosis

Good.

Cytogenetics

Various rearrangements involving 12q15 leading to HMGIC dysregulation; cryptic rearrangements such as paracentric inversions not detectable by conventional cytogenetics but detectable by FISH have been described; in one case, HMGIC was amplified and overexpressed.

Myofibroblastic inflammatory tumor**Disease**

Benign mesenchymal tumors.

Prognosis

Good.

Cytogenetics

In one case, a complex rearrangement involving chromosomes 12 (in 12q15), 4 and 21 was described.

Hybrid/Mutated gene

An aberrant transcript was produced by the fusion of HMGIC exon 3 to an ectopic sequence originating from the third intron of HMGIC.

Malignant tumors as follows:**Well-differentiated liposarcoma****Disease**

Malignant adipocyte tumor; peripheral or retroperitoneal location.

Prognosis

Rather good; borderline malignancy; locally aggressive, rarely metastasizes.

Cytogenetics

Supernumerary ring or giant marker chromosomes containing 12q14-15 amplification (surrounding MDM2); HMGIC is frequently amplified together with MDM2; in two cases, a rearrangement of HMGIC, in addition to amplification has been described.

Hybrid/Mutated gene

In one case an ectopic sequence from unknown origin was shown to be fused to HMGIC exon 3.

Osteosarcoma**Disease**

Malignant tumor.

Hybrid/Mutated gene

In one osteosarcoma cell line (OsA-CI) the three DNA binding domains of HMGIC fused to the keratan sulfate protein glycan gene LUM (12q22-23); LUM was fused out of frame, and only 3 amino acids were fused to HMGIC; in addition, the rearranged gene was amplified.

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