

Gene Section

Short Communication

MIR211 (microRNA 211)

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Identity

Other names: MIRN211, mir-211

HGNC (Hugo): MIR211

Location: 15q13.3

Local order: Based on Mapviewer, gene flanking miR-211 oriented on 15q13 are:

- FAN1 (FANCD2/FANCI-associated nuclease 1); 15q13.2-q13.3
- MTMR10 (myotubularin related protein 10); 15q13.3
- **miR-211 (microRNA 211); 15q13.3**
- TRPM1 (transient receptor potential cation channel, subfamily M, member 1); 15q13.3
- LOC283710; 15q13.3.

DNA/RNA

Description

miR-211 is located in the intron 6 of TRPM1 gene at 15q13, which is transcribed by RNA polymerase II.

Transcription

The primary transcript contains of 110 nucleotides (TCACCTGGCC ATGTGACTTG TGGGCTTCCC TTTGTCATCC TTCGCCTAGG GCTCTGAGCA GGGCAGGGAC

AGCAAAGGGG TGCTCAGTTG TCACTTCCCA CAGCACGGAG) which is cleaved by the Drosha ribonuclease III enzyme into 2 products, hsa-miR-211-5p (26-47 bp) and hsa-miR-211-3p (63-83 bp).

This miRNA is further cleaved by the cytoplasmic Dicer ribonuclease to the mature miR-211 sequence (5'-UUCCCUUUGUCAUCCUUCGCCU-3') with stem-loop shape.

In general, the mature miRNA is incorporated into a RNA-induced silencing complex (RISC), that can target mRNA through imperfect base pairing, leading to translational inhibition or destabilization of the target mRNA.

Pseudogene

No reported pseudogenes.

Protein

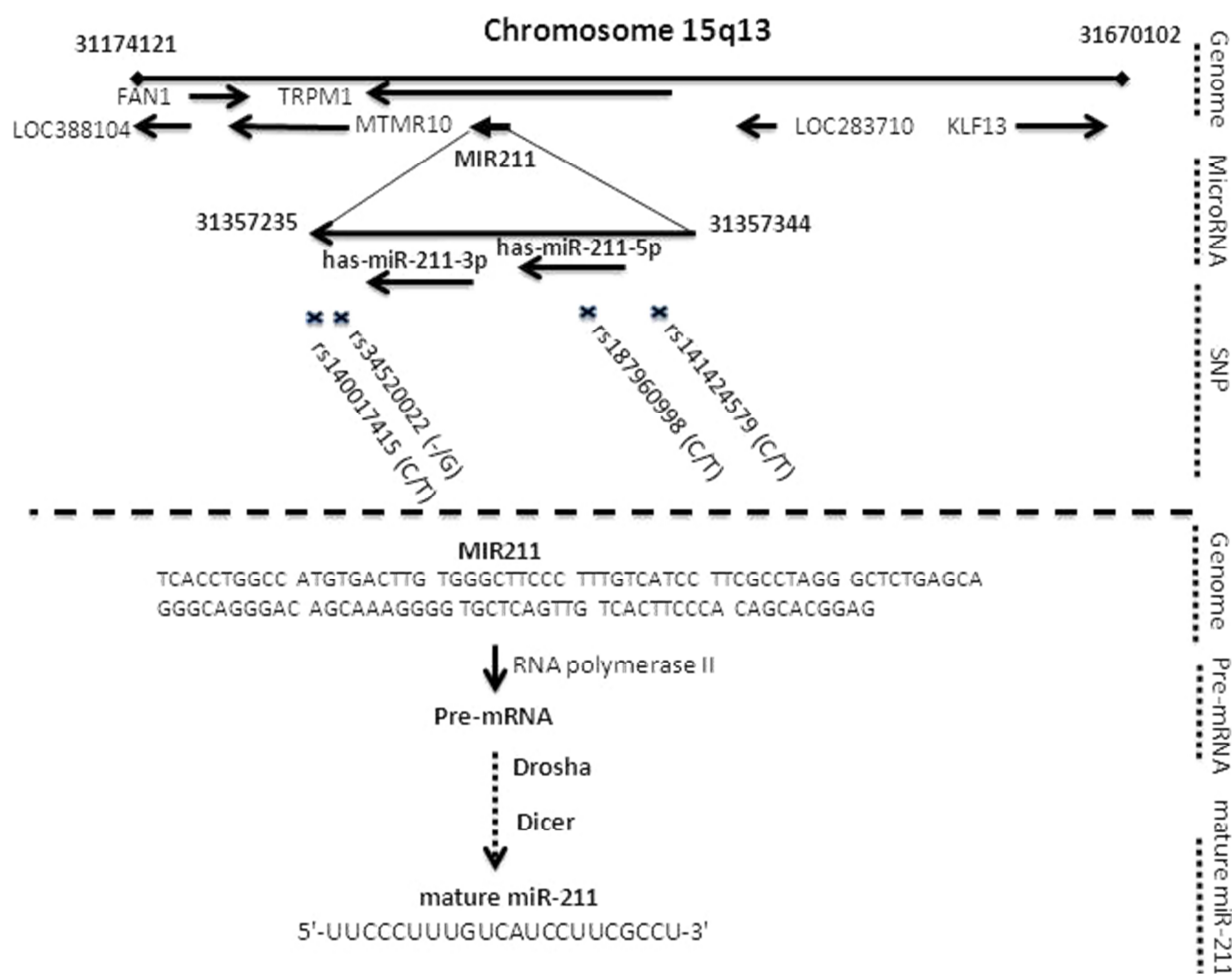
Note

This miRNA is not translated into amino acids.

Mutations

Note

No mutations have been reported, while single nucleotide variations (SNPs) include: rs141424579, rs187960998, rs34520022 and rs140017415.



Location of miR-211 in chromosome 15q13. This gene is located in the intron 6 of the TRPM1 gene within 31357235-31357344 bp. The mature miR-211 is 22 nucleotides long.

Implicated in

Pancreatic cancer

Note

Giovannetti and collaborators, recently identified miR-211 as a prognostic factor in resected pancreatic ductal adenocarcinoma (PDAC) patients using high-throughput microarray analysis of more than 1200 human miRNAs in PDAC patients classified in short-term overall survivors versus long-term survivors (Giovannetti et al., 2012). This study evaluated 26 PDAC patients with homogeneous clinicopathological characteristics that underwent resection with curative intent and were treated with standard gemcitabine adjuvant regimen. The miRNA microarray analysis was carried out in 19 samples that passed the RNA quality criterion, including 13 patients with short survival and 6 patients with long survival. These results illustrated that patients with low miR-211 expression according to median value had a significantly shorter median overall survival compared to patients with high miR-211 expression (OS, 14.8, 95%CI = 13.1-16.5, vs. 25.7 months, 95%CI = 16.2-35.1, log-rank-P = 0.004).

Multivariate analysis revealed that low miR-211 expression was an independent factor of poor prognosis (hazard ratio 2.3, P = 0.03). The expression of this miRNA was also assessed by quantitative-PCR in an independent cohort of laser-microdissected PDACs from 60 resected patients treated with the same gemcitabine regimen, showing the significant association of miR-211 expression status with both OS and disease-free-survival (DFS).

Colorectal cancer

Note

miR-211 has been found to be expressed in colorectal cancer and a recent study showed that over-expression of miR-211 in the colorectal cancer cell line HCT-116 promotes cellular growth in vitro and in vivo by downregulating the expression level of the CHD5 tumor suppressor gene (Cai et al., 2012).

Glioblastoma

Note

Glioblastoma multiforme (GBM) is the most aggressive brain tumor with less than one year survival time. Thus, there is an urgent need to identify new

predictive/prognostic biomarkers that can predict/manage the patients at earlier stages. A recent study showed that miRNA-211 is downregulated in GBM, which might be due to aberrant methylation-mediated epigenetic silencing of the miR-211 promoter. Asuthkar and collaborators showed that miR-211 has an inhibitory effect on glioma cell invasion and migration via suppression of MMP-9 and demethylation of miR-211 promoter-associated CpG islands, which results in insensitivity of some GBMs to radiation and chemotherapy (Asuthkar et al., 2012).

Oral carcinoma

Note

High expression of miR-211 has been shown to be associated with the advanced nodal metastasis, vascular invasion, and poor prognosis of oral carcinoma.

Chang and colleagues demonstrated that enforced miR-211 expression significantly increased the proliferation, migration, and anchorage-independent colony formation of oral carcinoma cells, while it enhanced the tumorigenicity (Chang et al., 2008).

Breast cancer

Note

Expression of 455 miRNAs was evaluated in a highly bone metastatic MDA-MB-231 variant, compared to the parental MDA-MB-231 breast cancer cell line. 16 miRNAs (3.5%) were found to have >3-fold expression difference between the two cell types. This study showed that miRNA-211 inhibits TGF- β -induced IL-11 production by binding to its 3' UTR in bone metastatic breast cancer cells (Pollari et al., 2012).

Melanoma

Note

Several studies showed that miR-211 is downregulated in melanoma and has been found to act as a tumour suppressor. In particular, Xu and collaborators performed miRNA microarray expression in 52 formalin-fixed and paraffin-embedded specimens from different stages of melanomagenesis and 15 cell lines. They showed that expression of miR-211 was downregulated in melanoma cells and melanoblasts compared to melanocytes, and upregulation of miR-211 could lead to suppression of tumor invasion in melanoma (Levy et al., 2010; Mazar et al., 2010; Xu et al., 2012).

Cervical cancer

Note

In cervical cancer, miR-211 has been shown to be upregulated, while inhibition of this miRNA decreased the growth of Hela cells (Cheng et al., 2005).

Stroke risk

Note

Brain vascular leaking and inflammation has been reported as two important pathological processes of

stroke. Angiopoietin-1 is a vascular strengthening factor which acts a protective factor for pathological vascular inflammation and leakage. The rs2507800 variant is located in the miR-211-binding site of angiopoietin-1, Cheng and colleagues evaluated the effect of the variant on angiopoietin-1 translation. They showed that the A allele of rs2507800 inhibited angiopoietin-1 translation by facilitating miR-211 binding. Furthermore they assessed the association of the variant with stroke in 438 stroke patients and 890 controls, and replicated in an independent population of 1791 stroke patients and 1843 controls. These results illustrated that the TT genotype (rs2507800) in the 3'-UTR of angiopoietin-1 could reduce the risk of stroke by interacting with miR-211 binding (Chen et al., 2010).

Human retinal pigment epithelium

Note

Wang and collaborators identified the critical role of miR-211 in maintaining epithelial barrier function and cell physiology in human retinal pigment epithelium. Moreover they found that miR-211 is one of the most highly expressed microRNAs in human retinal pigment epithelium. Expression of this miRNA was significantly lower in the NCI60 tumor cell line panel compared with 13 normal tissues (Wang et al., 2010).

To be noted

Note

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