Atlas of Genetics and Cytogenetics in Oncology and Haematology

OPEN ACCESS JOURNAL INIST-CNRS

Gene Section

Review

MIR143 (MicroRNA 143)

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Published in Atlas Database: February 2014

Online updated version : http://AtlasGeneticsOncology.org/Genes/MIR143ID50848ch5q32.html
DOI: 10.4267/2042/54133

Abstract

Review on MIR143, with data on DNA/RNA and where the gene is implicated.

Identity

Other names: MIRN143

HGNC (Hugo): MIR143

Location: 5q32

Local order: According to RefSeq, hsa-miR-143 is clustered together with hsa-miR-145, and this microRNA-143/145 cluster is located in the non-protein coding MIR143 host gene (MIR143HG). Genes flanking hsa-miR-143 are: PCYOX1L (prenylcysteine oxidase 1 like; + strand), IL17B (interleukin 17B; - strand), MIR143 host gene (+ strand), CSNK1A1 (casein kinase 1 alpha 1; - strand), and RPL29P14 (ribosomal protein L29 pseudogene 14; - strand).

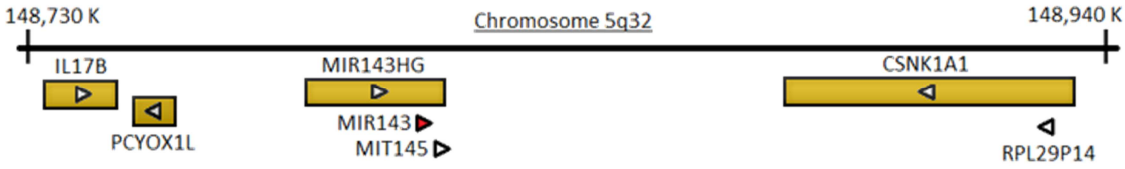
DNA/RNA

Description

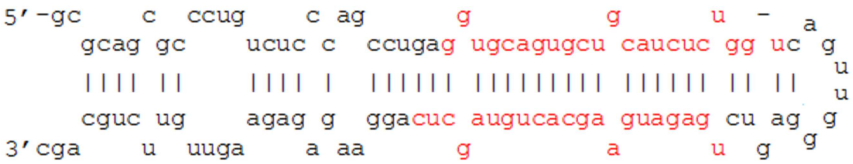
hsa-miR-143 is clustered with miR-145, which are separated by approximately 1.6 kb, and are located within an intergenic region on chromosome 5 (5q32). Positions of the clustered miRNAs are:
- hsa-mir-143: chr5: 148808481-148808586 [+]
- hsa-mir-145: chr5: 148810209-148810296 [+].

Transcription

The miR-143/145 cluster was demonstrated to be transcribed from a non-protein coding host gene (MIR143HG; GenBank: NR_027180) into an 11 kb primary miRNA transcript (pri-miRNA), which was then processed into the mature microRNAs (Iio et al., 2010). Expression of the cluster host gene and mature miR-143 were found to be reduced in various human cancer tissues and cell lines (Iio et al., 2010).



Genes flanking hsa-miR-143 on chromosome 5q32. The red arrow indicates the position and orientation of miR-143.



The stem-loop structure of hsa-miR-143, with sequences of mature miR-143-5p and miR-143-3p highlighted in red.

DEAD-box RNA helicase 6 (DDX6) was reported to post-transcriptionally down-regulate miR-143/145 levels by increasing the instability of MIR143 host gene RNA product (Iio et al., 2013).
Moreover, tumour suppressor protein p53 was reported to enhance the miR-143 maturation in a transcription-independent manner (Suzuki et al., 2009).

Pre-mir-143:
- Accession no.: MI0000459
- Length: 106 nt
- Sequence:
GCGCAGCGCCCUGUCUCCCAGCCUGAGGU GCAGUGCUGCAUCUCUGGUCAGUUGGGAG UCUGAGAUGAAGCACUGUAGCUCAGGAAG AGAGAAGUUGUUCUGCAGC

Mature hsa-miR-143-5p:
- Accession no.: MIMAT0004599
- Length: 22 nt
- Sequence:
27- GGUGCAGUGCUGCAUCUCUGGU -48

Mature hsa-miR-143-3p:
- Accession no.: MIMAT0000435
- Length: 21 nt
- Sequence:
61- UGAGAUGAAGCACUGUAGCUC -81

Pseudogene

No pseudogenes were reported for miR-143.

Protein

Note
miRNAs are not translated into amino acids.

Mutations

Note
No mutations have been reported within the precursor or mature miR143 sequences.
However, several single nucleotide variations (SNVs), including rs41291957, rs4705343, rs353292, rs353293, rs17796757, rs4705341, rs3733845, rs3733846, rs353286 and rs17796714, have been reported within the MIR143 host gene sequence, upstream of the miR-143/145 cluster.

Implicated in

Non-small cell lung cancer

Note
miR-143 has been found to be down-regulated in non-small cell lung cancer (NSCLC) tissues and was negatively correlated with PKCε expression.
It was shown to regulate PKCε expression and was associated with apoptosis in NSCLC cells (Zhang et al., 2013b).

Colorectal cancer

Note
miR-143 level was found to be down-regulated in colorectal cancer patients' blood and tumour tissues. Over-expression of miR-143 inhibited tumour growth and angiogenesis, and increased the chemosensitivity to oxaliplatin treatment (Qian et al., 2013).
miR-143 was also reported to reduce the invasion and migration of colorectal carcinoma cells by targeting the Toll-like receptor 2 (TLR2) signalling pathway (Guo et al., 2013).

Pancreatic cancer

Note
miR-143 was reported to modulate the prostaglandin E_2 (PGE_2) production and PGE_2-mediated cellular proliferation, in pancreatic cancer cells, by targeting the COX-2 mRNA stability and expression (Pham et al., 2013).

Esophageal squamous cell carcinoma

Note
miR-143 expression was reduced in esophageal squamous cell carcinoma (ESCC) tissues as compared with the adjacent normal tissues. Restoration of the miR-143 expression was demonstrated to induce ESCC cells apoptosis and suppress the cell migration and invasion (Ni et al., 2013).

Prostate cancer cells

Note
miR-143 and miR-145 were reported to inhibit the cell viability and tumorigenicity of the bone metastatic prostate cancer cells, PC-3.
They were suggested to play an important role in the bone metastasis of prostate cancer by regulating the cancer stem cell characteristics (Huang et al., 2012).

Cervical cancer

Note
miR-143 level was deregulated in cervical cancer tissues, as demonstrated by miRNA microarray (Liu et al., 2012).
Over-expression of miR-143 in HeLa cells was reported to promote apoptosis and suppress xenograft tumour formation, by targeting the Bcl-2 gene.

Bladder cancer cells

Note
miR-143 and miR-145 co-treatment on bladder cancer cell lines, T24 and NKB1, was showed to

synergistically inhibit cell growth by suppressing the PI3K/Akt and MAPK signalling pathways (Noguchi et al., 2013).

Liposarcoma

Note

miR-143 expression was found to be reduced in both well-differentiated (WDLS) and dedifferentiated liposarcomas (DDLS). Re-expression of miR-143 inhibited DDLS cell proliferation, induced apoptosis, and suppressed the expression of a module of genes including Bcl-2, topoisomerase 2A (TOP2A), polo-like kinase 1(PLK1), and protein regulator of cytokinesis 1 (PRC1) (Ugras et al., 2011).

Breast cancer

Note

Reduced levels of miR-143 was demonstrated in different breast cancer cell lines and primary tumours. Restoration of the miR-143 expression in breast cancer cells was found to inhibit cell proliferation and the formation of soft agar colonies. DNA methyltransferase 3A (DNMT3A) was validated as a direct target of miR-143, which resulted in the regulation of phosphatase and tensin homolog (PTEN) and TNFRSF10C promoter methylation (Ng et al., 2013).

Ulcerative oesophagitis

Note

Up-regulation of miR-143 expression was reported in the oesophageal mucosa of ulcerative oesophagitis patients. It was suggested to induce apoptosis, and regulate the cell proliferation of oesophageal epithelium in response to gastro-oesophageal reflux (Smith et al., 2013).

Glucose Metabolism

Note

miR-143 was reported to inhibit glycolysis in a variety of cancer cells, including breast cancer, glioblastoma, colon cancer, head and neck squamous cell carcinoma, and lung cancer (Fang et al., 2012; Gregersen et al., 2012; Jiang et al., 2012; Peschiaroli et al., 2013; Zhao et al., 2013). Hexokinase 2 (HK2) was validated as a direct target of miR-143, in which their interaction was hypothesized to be an important regulator of glucose metabolism in cancer cells.

MDM2-p53 pathway

Note

miR-143 and miR-145 were reported to negatively modulate MDM2 expression and were post-transcriptionally activated by tumour suppressor protein p53. Together, miR-143/145, MDM2 and p53 form a regulatory feedback loop that was shown to modulate cell proliferation and apoptosis in the head and neck squamous cell carcinomas (Zhang et al., 2013a).

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This article should be referenced as such:

Kwong A, Shin VY, Ho JCW. MIR143 (MicroRNA 143). Atlas Genet Cytogenet Oncol Haematol. 2014; 18(10):724-727.