

SNHG8/mir-335-5p/PYGO2 Axis: A New Targets of Triple Negative Breast Cancer

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Abstract...

The relationship between long non-coding RNAs (lncRNAs) and human diseases has been widely studied. lncRNAs are considered to be an important participant in cancer. Small Nucleolar RNA Host Gene 8 (SNHG8) is a newly discovered lncRNA belonging to the Small Nucleolar RNA Host Gene (SNHG) family. Firstly, this study introduces the carcinogenicity of SNHG8 and discusses its mechanism in many types of cancer. Previous studies have shown that SNHG8 promotes cancer through mir-335-5p/PYGO2 axis in triple negative breast cancer (TNBC). Therefore, we further analyzed the role of PYGO2 protein in tumor progression in various cancers. SNHG8, mir-335-5p and PYGO2 can be used as biomarkers for TNBC evaluation and potential targets for treatment. We hoped to provide new insights for cancer diagnosis, prognosis and treatment.

Key words: SNHG8; PYGO2; Triple negative breast cancer.

Introduction

In the worldwide, breast cancer is the most common malignancy in women. According to GLOBOCAN data in 2020, there were 230 new cases of breast cancer, accounting for 11.7% of all new cancer cases. Breast cancer is the fifth leading cause of cancer death worldwide [1]. Among them, TNBC accounts for 15-20% in invasive breast cancer, and is significantly different

from Estrogen Receptor (ER), Progesterone Receptor (PR) and human epidermal growth factor receptor 2 (HER-2) in molecular genetics, histopathology and clinical features. Compared with other molecular typing of breast cancer, TNBC has a higher malignancy and worse prognosis. Although there are many ways to treat TNBC, such as surgery, chemotherapy and radiotherapy, TNBC still has a high risk of death and recurrence. Therefore, it is urgent to explore new therapeutic targets for TNBC.

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With the development of high-throughput RNA sequencing technology, only 1.2-2% of the human genome have protein-coding function. Most of the rest have been transcribed into non-coding RNA. LncRNA is a long chain non-coding RNA with a length of 200 nt-100 KB [2]. LncRNA does not translate proteins, but can be used as a molecular sponge of miRNA to regulate the stability, translation and post transcriptional modification of mRNA. So that LncRNA participate in many processes such as embryonic development, cell proliferation, cell differentiation and tumor progression [2]. Many studies have revealed the key role of LncRNA in tumor progression. LncRNA can pass through many signaling pathways, such as p53, NF- κ B and PI3K / Akt. LncRNA can affect the expression of tumor genes and have great potential as tumor biomarkers or therapeutic targets [3].

SNHG8s are a group of small nucleolar host lncRNAs, which are located in the cytoplasm and nucleus. Small nucleolar RNA is produced by selective splicing [4]. LncRNA SNHG8 belongs to SNHG family, with a total length of 1062nt and located on chromosome 4q26 [5]. SNHG8 is a research hotspot of SNHG family, which was found to be related to the malignant proliferation

and differentiation of many tumors. However, few studies have further explored the expression and regulation mechanism of SNHG8 in breast cancer. High expression was detected in tissues and cells of a variety of malignant tumors, including breast cancer [6], gastric cancer [7], osteosarcoma [8], hepatocellular carcinoma [9] and non-small cell lung cancer (NSCLC) [10]. In addition, SNHG8 has been shown to be carcinogenic by targeting MicroRNAs (miRNAs) in a variety of cancers (Table 1). For example, in colorectal cancer, SNHG8 can promote the proliferation and invasion of tumor cells by sponging mir-663 and mir-588 [11,12]. SNHG8 negatively regulates mir-542-3p in the progression of NSCLC by regulating downstream effectors such as CCND1 and CDK6, which has shown great potential in the treatment of NSCLC [10]. SNHG8 can also regulate different miRNAs and affect the expression of downstream factors, so as to promote the occurrence and development of tumors. In addition, recent studies have found that SNHG8 passes Wnt/ β -Catenin pathway to promote the proliferation, migration and epithelial mesenchymal transformation (EMT) of tumor cells in ovarian cancer [13].

Table 1: The relationship between SNHG8 and target genes and downstream effectors.

Cancer type	Target gene	Downstream effect factor	Reference
Non-small-cell Lung Cancer	miR-542-3p	CCND1/CDK6	[1]
Hepatocellular Carcinoma	miR-149-5p		[2]
Breast Cancer	miR-634/	ZBTB20	[3]
Triple-negative Breast Cancer	miR-335-5p	PYGO2	[4]
Osteosarcoma	miR-876-5p		[5]
Osteosarcoma	miR-542-3p		[6]
Colorectal Cancer	miR-588	ATG7	[7]
Prostate Cancer	miR-384	HOXB7	[8]
Esophageal Squamous Cell Carcinoma	miR-411	KPNA2	[9]
Nasopharyngeal Carcinoma	miR-656-3p	SATB1	[10]
Ovarian Cancer	miR-1270	S100A11	[11]
Endometrial Carcinoma	miR-152	c-MET	[12]
Diffuse Large B-Cell Lymphoma	miR-335-5p		[13]
Gastric Cancer	miR-491	PDGFRA	[14]
Epstein-Barr Virus-Associated Gastric Cancer	miR-512-5p	TRIM28	[15]
Colorectal Cancer	miR-663		[16]

The above results reveal the important role of SNHG8 in the development of malignant tumors. Our previous studies have shown that SNHG8 is highly expressed in TNBC cells and promotes the growth, proliferation, migration and EMT progress of tumor cells. In depth studies on the downstream pathway of SNHG8 show that SNHG8 regulates TNBC cells through mir-335-5p/ PYGO2 axis [14-24].

PYGO2 protein is located on chromosome 1q213 position, with a total length of 233 amino acids, which include two important structures: N-terminal NHD domain and C-terminal PhD domain [25]. PYGO2 is involved in the morphogenesis and development of many tissues, including the brain, eyes, hair follicles, lungs, kidneys and pancreas [26]. PYGO2 is an important functional protein of Wnt/ β - Catenin signaling pathway.

Wnt/ β -Catenin signal transduction pathway is involved in embryonic development, cell growth, stem cell proliferation and tumorigenesis, and is related to a variety of female reproductive system diseases and plays an important role in the occurrence and development of tumors [27]. PYGO2 is highly expressed in human glioma. Inhibiting PYGO2 expression can inhibit the growth and proliferation of human glioma cells [28]. PYGO2 has tumor promoting function. The number and size of chemically induced tumors were significantly reduced in PYGO2 deficient internal tumor mice [29]. Studies have shown that pygopus 2 promotes the proliferation and invasion of renal cell carcinoma cells both in vivo and in vitro [30]. PYGO2 was up-regulated by, which promoted the resistance of pancreatic cancer to gemcitabine [31].

It is worth noting that PYGO2 has been proved to be up-regulated in breast cancer. PYGO2 via Wnt/ β -Catenin pathway activates MDR1 expression and mediates chemo resistance in breast cancer. Its high expression inhibits the sensitivity of breast cancer cells to chemotherapeutic agents [32]. Mir-516a-3p blocks the Wnt/ β -Catenin pathway by inhibiting PYGO2, and further inhibits the growth, metastasis and EMT of tumor cells in breast cancer [33].

Knockdown of PYGO2 in glioma U251 Cell line can inhibit the growth of tumor cells [28]. PYGO2 plays a role as a driving oncogene in metastatic prostate cancer and may become a potential prognostic biomarker and therapeutic target [34].

Signal transduction plays an important role in the development of tumor. SNHG8 affects the level of PYGO2 downstream by regulating mir-335-5p, and plays an important role in tumor cell proliferation, invasion and migration. Although there are many kinds of research on SNHG8 and cancer, it is mainly in the basic research stage. More clinical application researches are needed in the future.

Conclusion

In conclusion, SNHG8 is a new target for disease diagnosis, treatment and prognosis evaluation in TNBC. In the future, the specific pathways and signaling molecules of lncRNAs including SNHG8 in cancer will be further explored and applied to cancer prevention, diagnosis and treatment.

Declarations

Author disclosure statement: The author declares that there is no conflict of interest related to the content of this article. Abide by the code of ethics. This paper is based on previous research. The authors did not involve any new studies (on human or animal subjects).

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