Introduction

As the third most prevalent cancer type, colon cancer is also the fourth leading cause of cancer-related deaths worldwide. More than 1.2 million people are diagnosed with colon cancer, and >600,000 die from the disease every year (1-3). Additionally, colon cancer is the fifth leading cause of death in China, constituting a major health problem (4). Advanced age, alcohol consumption, obesity, smoking, lack of physical activity, high consumption of red or processed meat, low calcium intake, and very low consumption of fruits and vegetables may contribute to colon cancer (5). In terms of genes, activation of proto-oncogenes and inactivation...
of tumor suppressor genes may lead to colon cancer (6). Several oncogenes and tumor suppressor genes, such as Adenomatous polyposis coli, Tumor protein 53, and KRAS proto-oncogene GTPase have been identified as the key factors in tumor formation years ago (7-10). However, although we have an improved understanding of the development and progression of colon cancer, a cure is yet to be found.

Nucleolar protein p120 (NOP2) expression has been shown to be significantly upregulated in most types of human malignant tumor cells, such as breast cancer cells, but not in healthy, resting cells (11-13). NOP2 has been identified as a “telomerase RNA component” (TERC)-binding protein, and it can also bind to the “T-cell factor” (TCF)-binding element of the Cyclin D1 promoter, activating the transcription of Cyclin D1 (14). Although NOP2 could be implicated as a tumor cell maker, it has not been specifically studied in colon cancer.

In the study presented herein, we knocked down NOP2 in the human colon cancer cell lines, LOVO and HCT116, via siRNA transfection to determine the role of NOP2 in colon cancer. The effects of NOP2 silencing on the colon cancer cells were evaluated by CCK-8 and transwell assays as well as transcriptome sequencing.

**Methods**

**Cell culture**

Colon cancer cells (HCT116 and LOVO) were obtained from Sangon Biotech (Shanghai, China). HCT116 cell lines were cultured in F12K medium (GIBCO, CA, USA) supplemented with 10% FBS and 1% Penicillin/Streptomycin (Sangon Biotech, Shanghai, China). Cells were grown at 37 °C in a humidified atmosphere with 5% CO₂.

**Fluorescence quantitative PCR**

Total RNA was extracted from cultured cells using the TRIZOL reagent (Invitrogen, CA, USA) according to the manufacturer’s protocol. The RNA concentration and quality were determined by OD260/OD280 and agarose gel electrophoresis. Total RNA (1 µg) was then reverse-transcribed with a commercial reverse transcription kit (Thermo Bio.), and then PCR was performed with the 2× Master Mix kit (Roche) according to the manufacturer’s instructions. FastStart Universal SYBR Green Master mix was used to amplify cDNA on a QuantStudio 6 Flex Real-Time PCR System (ThermoFisher, Shanghai, China). The primers used for RT-PCR were as follows:

 NOP2-1 forward, 5'-TGTCTGAGCTGGTGGAGT TCTTAG-3' and reverse, 5'-ACCCCACGATTGATTA GAGCC-3'; GAPDH forward, 5'-AGAAGGCTGGG CATT-3' and reverse, 5'- TGCTAAGCAGTTGG TGTTG-3'.

The relative expression levels were evaluated by the 2^−ΔΔct method using GAPDH as the internal control for normalization of the values.

**siRNA transfection**

LOVO cell lines were cultured in RPMI-1640 medium (CORNING, NY, USA) supplemented with 10% FBS and 1% Penicillin/Streptomycin (Sangon Biotech, Shanghai, China). Cells were grown at 37 °C in a humidified atmosphere with 5% CO₂.

**Western blot analysis**

After analyzing the cells in RIPA buffer (Thermo Fisher Scientific, Waltham, MA), total protein concentration was measured using the BCA assay kit (Pierce Biotechnology, Inc., Rockford, IL, USA). The same quantity of total proteins from each sample was resolved by 10% SDS-PAGE and then electrophoretically transferred onto polyvinylidene fluoride
(Sangon Biotech, Shanghai, China) membranes at 80 V for 2 h. The membranes were blocked with TBST solution (0.1% Tween20) containing 5% skim milk and incubated with the primary antibodies anti-NOP2 (1:500; 10448-1-AP, Proteintech, Wuhan, China) and anti-GAPDH (1:1,000; 60004-1-lg, Proteintech, Wuhan, China) at 4 °C overnight. The membranes were washed with TBST and incubated with the HRP-conjugated goat anti-mouse IgG (1:1,000, A0216, Beyotime, Shanghai, China) or goat anti-rabbit IgG (1:5,000, Ab721, Abcam) for 2 h. The membranes were then washed with 1% TBST for 3 times, and the protein bands were visualized using ECL (Thermo Fisher Scientific, Waltham, MA, USA) and a ChemiDoc MP system.

**CCK-8 assay**

Cells were seeded in a 96-well plate (3599, CORNING, NY, USA) at a density of 2×10³ per well. Each plate contained 6 replicates, and the marginal wells were added sterile water for the contrast. After culturing for 0, 24, 48, 72, or 96 h, CCK-8 (Beyotime, Shanghai, China) was added and OD₄₅₀ of the culture was measured.

**Transwell assay**

Cells were washed with an appropriate amount of 1× PBS, and then an appropriate amount of 0.25% Trypsin-EDTA (25200072, GIBCO, CA, USA) was added. The culture vessel was gently shaken to submerge all the cells and returned to the incubator for 3 min. After the cells retracted and rounded up, complete medium at the same amount used for the culture was added to terminate the trypic digestion. The plates were then centrifuged and the supernatant was removed. The cells were resuspended in serum-free RPMI-1640 medium (CORNING, NY, USA) and counted. Their concentration was adjusted to 2×10⁵/mL. Then, 500 µL of the cell suspension was loaded into the upper chambers (CORNING, NY, USA) of the transwell device, and 700 µL complete medium with 10% FBS was added into the lower chamber. After 24 h of culture, the cells underneath the transwell membrane were stained and counted under a microscope by evaluating three random high-power fields. For the transwell and invasion experiments, 24-well plates with 8.0-µm transparent PET membrane (353097, BD Falcon, NY, USA), and Corning BioCoat™ Matrigel® invasion chambers with 8.0-µm PET membrane in 24-well plates were used, respectively.

**Transcriptome sequencing**

Total RNA was extracted from cultured cells using the TRIzol reagent (Invitrogen, CA, USA) according to the manufacturer’s protocol. Oligo-dT magnetic beads were used for mRNA isolation. The isolated mRNA was subjected to mRNA fragmentation in a fragmentation buffer by divalent cations and under high-temperature conditions. Single-strand cDNAs from the fragmented mRNAs were synthesized using reverse transcriptase and random hexamer primers. The mRNA strands of the heteroduplexes were digested by RNase H to synthesize the complementary strands of the cDNAs, thereby realizing cDNA second strand synthesis. The sticky ends of the double-stranded cDNAs are blunted by the addition of End Repair Mix. An Adenosine monophosphate was added to the 3’ ends of the double-stranded cDNAs for ligation of the cDNAs to the Y-shaped linker. The adaptor-ligated library was size-selected using Ampure Beads (Beckman, Brea, California, USA). The library was PCR-amplified for 15 cycles, and then purified using Ampure Beads (Beckman, Brea, CA, USA) and quantified with the Quant-iT™ PicoGreen® dsDNA Assay Kit (Life, Carlsbad, CA, USA) following the manufacturer’s protocol. The sizes of the DNA fragments were determined using Agilent 2200 (Agilent, Santa Rosa, CA, USA). Sequencing was performed on the Illumina sequencing platform (Illumina, San Diego, CA, USA). All the raw data was converted to the Fastq format. The differentially expressed genes were analyzed by DESeq algorithm, and Gene Ontology (GO) and pathway analysis of significant differential genes were performed by Fisher.

**Statistical analysis**

Statistical analysis was performed using GraphPad Prism 6. Significance of differences between two groups was determined using the Student’s t-test. Correlation between the NOP2 expression and characteristics of the colon cancer patients was evaluated by using the Chi-square test. P<0.05 was defined as the significance level.

**Results**

**NOP2 expression was significantly upregulated in colon cancer cells**

Fluorescence quantitative PCR was used to investigate the expression of NOP2 in colon cancer tissues and cell
lines. As shown in Figure 1A,B, mRNA and protein levels of NOP2 were significantly upregulated in colon tumor samples compared with those in the healthy controls. Similarly, NOP2 was upregulated in the colon cancer cell lines examined relative to the non-transformed cells (Figure 1C,D). Moreover, expression of NOP2 significantly showed a positive correlation with lymphatic metastasis and high TNM stage (Table 2).

NOP2 was efficiently silenced in colon cancer cell lines

After siRNA infection, we used fluorescence quantitative PCR and western blot analysis to examine the expression of NOP2 in both HCT116 and LOVO cell lines. Fluorescence quantitative PCR results in Figure 2A,B showed that all the three siRNAs efficiently knocked down NOP2 in both HCT116 and LOVO cell lines. Western blot analysis demonstrated that NOP2 protein levels were also reduced (Figure 2C). The results indicated that the most effective siRNA among the three tested siRNAs was si2215, and thus the subsequent experiments were performed with this siRNA.

Silencing NOP2 inhibited colon cancer cell proliferation, invasion, and migration

The effect of NOP2 silencing on colon cancer cells was explored by CCK-8 and Transwell assays. As indicated in Figure 3A,B,C,D,E,F,G,H,I,J, the proliferation (P<0.05, P<0.05), invasion (P<0.0005, P<0.05), and migration (P<0.005, P<0.05) of the colon cancer cells (HCT116 and LOVO, respectively) were significantly suppressed in the NOP2 knockdown groups compared with those in the negative control (NC) groups.

Differentially expressed genes between the NOP2 knockdown and NC groups

As shown in Figure 4A,B, 88 and 94 genes were significantly down- and upregulated, respectively, in LOVO cells upon NOP2 knockdown, relative to those in the control group (1log2 Fold Change>1, FDR <0.05). In the NOP2-knockdown HCT116 cells, 95 and 175 genes were down- and upregulated, respectively, relative to those in the control group (1log2 Fold Change>1, FDR
<0.05). Among all these genes, ASMTL and C6orf52 were significantly downregulated in both the cell lines with NOP2 knockdown, while MUC19, TXK, APOBEC2, and RBM44 were significantly upregulated.

**GO and pathway analysis of the NOP2-knockdown colon cancer cell lines**

To study the function of NOP2 in colon cancer and the molecular mechanisms involved, GO and pathway analysis were performed for differentially expressed genes induced by NOP2 knockdown. The roles of NOP1 were investigated by GO analysis within three different domains (BP, CC, and MF). All the terms that showed significant differences, ranked by −log10 (P value), are displayed in Figure 5A (HCT116) and 5B (LOVO). Top terms for HCT116 cell line included positive regulation of T cell-

mediated cytotoxicity, negative regulation of interleukin-6 biosynthetic process, and multicellular organismal development. For the LOVO cell line, top terms included collagen catabolic process, thiamine metabolism, and negative regulation of cytosis. The top 20 significantly enriched KEGG pathways, ranked by −log10 (P value), are...
Figure 3 Silencing NOP2 inhibited colon cancer cell proliferation, invasion, and migration. N=6; P<0.05; *, P<0.01 (calculated by T-test). (A,B,C,D) Transwell invasion and migration results for LOVO cell line. Invasion and migration of the NOP2-siRNA group were significantly inhibited compared with those of the NC group. The results were derived from three random microscope fields; (E,F,G,H) transwell invasion and migration results for HCT116 cell line. Invasion and migration of the NOP2-siRNA group were significantly inhibited compared with those of the NC group. The results were derived from three random microscope fields; (I) CCK-8 analysis of HCT116 cell line showed that the cell proliferation of the NOP2-siRNA group was significantly inhibited compared with that of the NC group. Samples were taken after (0, 24, 48, 72, and 96) hours; (J) CCK-8 analysis of LOVO cell line showed that the cell proliferation of the NOP2-siRNA group was significantly inhibited compared with that of the NC group. Samples were taken after (0, 24, 48, 72, and 96) hours. NOP2, nucleolar protein p120; NC, negative control.
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Figure 4 Differentially expressed genes between the NOP2 knockdown and NC groups. (A) Downregulated genes in the NOP2-siRNA groups in comparison with the NC groups. A total of 93 and 86 genes were downregulated in HCT116 and LOVO cell lines, and 2 genes were downregulated in both the cell lines; (B) upregulated genes in siRNA groups in comparison with the NC groups. A total of 171 and 90 genes were upregulated in HCT116 and LOVO cell lines, and 4 genes were up-regulated in both the cell lines. NOP2, nucleolar protein p120; NC, negative control.

displayed in Figure 5C (LOVO) and 5D (HCT116). The identified pathways in both the cell lines were Cytokine-cytokine receptor interaction, type I diabetes mellitus, taste transduction, and systemic lupus erythematosus.

Discussion

Colon cancer is one of the leading causes of cancer-related death, and the incidence of colon cancer has recently been increasing (15,16). There are more than one million new colon cancer cases and approximately 700,000 people die from colon cancer each year (17). The etiology of colon cancer is multifactorial and has remained poorly defined (18). NOP2, as an important regulator of the cell cycle, has been shown to be associated with a non-canonical mechanism by which telomerase promotes cell proliferation in breast cancer cells (14). However, the role of NOP2 in colon cancer remains unclear. We were stimulated to investigate this role by the current lack of clarity. Our results demonstrated that silencing NOP2 suppressed colon cancer cell proliferation, invasion, and migration. Furthermore, we also found that the levels of several genes were significantly different between the experimental and control groups.

NOP2 is a nucleolar antigen expressed in proliferating cells and many human tumors (19). Translational repression of NOP2 has been shown to suppress breast cancer proliferation (20). NOP2 also plays an important role in the proliferation of gliomas, and the ribozyme against NOP2 mRNA can suppress glioma cell growth (21). Similar conclusions have also been drawn in the prostate (22) and lung cancer (23). Our results here showed that NOP2 was significantly overexpressed in neoplastic cells, in line with the results of a previous study (24). To further understand the role of NOP2 in colon cancer, we transfected colon cancer cells with NOP2-siRNAs and found that, in addition to cell proliferation, NOP2 also had a role in cell migration and invasion. We demonstrated that silencing NOP2 significantly suppressed colon cancer cell proliferation, migration, and invasion.

Furthermore, we performed transcriptome sequencing to explore the action mechanism of NOP2. We thereby found that TXK tyrosine kinase was significantly upregulated in the NOP2 knockdown groups. As a member of the Tec family of tyrosine kinases, TXK is the most commonly found growth factor receptor in many tumors and has a key signal-transducing role (25,26). It has been shown to have anti-cancer/immunomodulatory effects (27). Accordingly, our results show a plausible action mechanism of NOP2 in colon cancer, requiring further research.

Conclusions

In conclusion, our study demonstrates that lack of NOP2 significantly downregulates ASMTL and C6orf52, while upregulating MUC19, TXK, APOBEC2, and RBM44. Reducing NOP2 levels significantly suppresses colon cancer
Figure 5 GO and pathway analysis results. (A) Top 20 results of the GO enrichment analysis for significantly differentially expressed genes between the NOP2-siRNA groups and NC groups in the HCT116 cell line; (B) top 20 results of the GO enrichment analysis for significantly differentially expressed genes between the NOP2-siRNA groups and NC groups in LOVO cell line; (C) top 20 results of the KEGG pathway enrichment analysis for significantly differentially expressed genes between the NOP2-siRNA groups and NC groups in LOVO cell line; (D) top 20 results of the KEGG pathway enrichment analysis for significantly differentially expressed genes between the NOP2-siRNA groups and NC groups in the HCT116 cell line. GO, gene ontology; NOP2, nucleolar protein p120; NC, negative control.
cell proliferation, migration, and invasion. This effect may be related to differential expression of other genes, such as TXK, and this correlation needs to be elaborated in future research.

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**Footnote**

**Conflicts of Interest:** All authors have completed the ICMJE uniform disclosure form (available at [http://dx.doi.org/10.21037/tcr.2019.09.46](http://dx.doi.org/10.21037/tcr.2019.09.46)). The authors have no conflicts of interest to declare.

**Ethical Statement:** The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). The institutional ethical approval and individual informed consent were waived due to the nature of the study.

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