

## LEF1 Promotes Colorectal Cancer Progression by Activating Wnt/ $\beta$ -Catenin Signaling and Stemness-Associated Genes

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**Citation:** Liu X. LEF1 Promotes Colorectal Cancer Progression by Activating Wnt/ $\beta$ -Catenin Signaling and Stemness-Associated Genes. *Medi Clin Case Rep J* 2025;3(3):1321-1323. DOI: doi.org/10.51219/MCCRJ/Xing-Liu/367

**Received:** 16 January, 2025; **Accepted:** 19 February, 2025; **Published:** 24 March, 2025

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### ABSTRACT

**Objective:** To investigate the role of LEF1 (lymphoid enhancer-binding factor 1, a key transcription factor of Wnt/ $\beta$ -catenin pathway) in colorectal cancer (CRC) cell proliferation, migration, invasion and its regulatory effect on Wnt signaling.

**Methods:** LEF1 expression (total and nuclear) was detected in CRC cell lines (HCT116, SW480) and normal colonic epithelial cell line (NCM460) by Western blot and qRT-PCR. LEF1 was overexpressed via plasmid (pcDNA3.1-LEF1) or knocked down via siRNA in HCT116 cells. Cell proliferation (CCK-8), migration (scratch assay), invasion (Transwell), sphere formation (stemness assay) and Wnt/ $\beta$ -catenin-related proteins (nuclear  $\beta$ -catenin, c-Myc, CD44) were analyzed.

**Results:** LEF1 was upregulated in CRC cells compared with NCM460 ( $P < 0.01$ ), with higher nuclear LEF1 and  $\beta$ -catenin levels in metastatic SW480. LEF1 overexpression increased HCT116 cell proliferation (OD<sub>450</sub> at 72h:  $1.45 \pm 0.14$  vs.  $0.96 \pm 0.10$ ,  $P < 0.05$ ), migration rate ( $74.5 \pm 6.2\%$  vs.  $46.8 \pm 4.7\%$ ,  $P < 0.01$ ), invasive cell number ( $138 \pm 12$  vs.  $61 \pm 7$ ,  $P < 0.01$ ) and sphere formation efficiency ( $2.8 \pm 0.3$  folds vs. control,  $P < 0.01$ ), while enhancing nuclear LEF1- $\beta$ -catenin complex formation and c-Myc/CD44 expression ( $P < 0.05$ ). LEF1 knockdown showed opposite effects.

**Conclusion:** LEF1 promotes CRC progression by activating Wnt/ $\beta$ -catenin signaling and regulating stemness-associated genes, serving as a potential therapeutic target.

**Keywords:** Colorectal Cancer; Cell Proliferation; Transwell; Lymphoid Enhancer-Binding Factor 1

### Introduction

Colorectal cancer (CRC) is a leading cause of cancer-related deaths globally, with ~935,000 annual fatalities<sup>1</sup>. The Wnt/ $\beta$ -catenin pathway is constitutively activated in over 80% of CRC cases, driving tumor initiation, progression and metastasis<sup>2</sup>. LEF1, a member of the TCF/LEF transcription factor family, is the key effector of Wnt signaling: in the presence of Wnt ligands, LEF1 dissociates from inhibitory complexes,

translocates to the nucleus and forms a complex with  $\beta$ -catenin to transcribe downstream target genes (e.g., c-Myc, Cyclin D1, CD44) involved in cell cycle progression, stem cell maintenance and invasion<sup>3,4</sup>. Clinical studies have shown elevated LEF1 expression in CRC tissues, correlating with tumor stage, lymph node metastasis and poor 5-year survival<sup>5,6</sup>. However, LEF1's functional role in CRC cell behaviors and its mechanism of regulating Wnt/ $\beta$ -catenin activation remain to be fully clarified.

This study uses CRC cell lines to verify LEF1's effect on tumor progression and its association with Wnt signaling.

## Materials and Methods

### Cell culture

HCT116 (low-metastatic CRC), SW480 (high-metastatic CRC) and NCM460 (normal colonic epithelial) cells were purchased from ATCC (Manassas, VA, USA). Cells were cultured in RPMI-1640 medium (Gibco, Grand Island, NY, USA) with 10% fetal bovine serum (FBS) and 1% penicillin-streptomycin at 37°C, 5% CO<sub>2</sub>. For Wnt signaling stimulation, cells were treated with 200 ng/mL Wnt3a (R&D Systems, Minneapolis, MN, USA) for 24h.

### Transfection

LEF1 overexpression plasmid (pcDNA3.1-LEF1) and empty vector were from Addgene (Cambridge, MA, USA). LEF1 siRNA (si-LEF1) and negative control siRNA (si-NC) were from Thermo Fisher Scientific (Waltham, MA, USA). HCT116 cells (5×10<sup>5</sup> cells/well) were transfected with plasmids/siRNA using Lipofectamine 3000 (Invitrogen, Carlsbad, CA, USA) at 60-70% confluency. LEF1 expression was verified by Western blot/qRT-PCR 48h post-transfection.

### qRT-PCR and western blot

**qRT-PCR:** Total RNA was extracted with TRIzol (Thermo Fisher Scientific). cDNA was synthesized with PrimeScript RT Kit (Takara, Kyoto, Japan). LEF1 primers: Forward 5'-ATGACCGAGTACGAGAAGCC-3', Reverse 5'-TCAGCTGCTTCTCGTTGCTC-3'; target genes (c-Myc, CD44) and GAPDH (internal control) primers were designed according to NCBI sequences. Relative expression via 2<sup>-ΔΔCt</sup> method.

**Western Blot:** Cytoplasmic/nuclear proteins were extracted using Nuclear Extraction Kit (Beyotime, Shanghai, China). Equal amounts of protein (30μg) were separated by 10% SDS-PAGE, transferred to PVDF membranes (Millipore, Billerica, MA, USA) and probed with antibodies against LEF1 (total/nuclear), β-catenin (total/nuclear), c-Myc, CD44 (Cell Signaling Technology, Danvers, MA, USA), Lamin B1 (nuclear loading control) and GAPDH (cytoplasmic control, Beyotime) at 4°C overnight. Co-immunoprecipitation (Co-IP) was used to detect LEF1-β-catenin complex (nuclear protein incubated with anti-LEF1 antibody, then probed with anti-β-catenin). Bands were visualized with ECL kit and quantified by ImageJ.

### Functional assays

- **CCK-8 Assay:** Transfected cells (2×10<sup>3</sup> cells/well) were seeded in 96-well plates. OD450 was measured at 24h, 48h, 72h after adding 10μL CCK-8 solution (Dojindo, Kumamoto, Japan).
- **Scratch Assay:** Confluent cells were scratched; migration rate was calculated at 0h/24h.
- **Transwell invasion assay:** Matrigel-coated chambers (8μm pore size, Corning, NY, USA) were used. Invasive cells were counted at 24h.
- **Sphere formation assay:** Cells (1×10<sup>3</sup> cells/well) were seeded in ultra-low attachment 6-well plates with stem cell medium (DMEM/F12 + 20 ng/mL EGF + 20 ng/mL bFGF + 1× B27). Spheres (>50 μm) were counted after 7 days.

### Statistical analysis

Data were presented as mean ± SD (n=3). Statistical analysis was performed using SPSS 26.0 (IBM, Armonk, NY, USA) with independent samples t-test. P<0.05 was considered significant.

## Results

### LEF1 is upregulated in CRC cell lines

qRT-PCR showed LEF1 mRNA in HCT116/SW480 was 4.35±0.41/5.22±0.49 folds of NCM460 (P<0.01). Western blot revealed total LEF1 protein in HCT116 (3.18±0.29) and SW480 (4.05±0.37) was significantly higher than NCM460 (1.00±0.10, P<0.01); nuclear LEF1 and β-catenin levels were further elevated in SW480 (2.25±0.21 and 2.18±0.20 folds of HCT116, P<0.05).

### LEF1 promotes CRC cell proliferation

LEF1 overexpression increased HCT116 OD450 at 48h (1.22±0.11 vs. 0.79±0.08, P<0.05) and 72h (1.45±0.14 vs. 0.96±0.10, P<0.05). LEF1 knockdown reduced OD450 at 48h (0.65±0.07 vs. 0.93±0.09, P<0.05) and 72h (0.78±0.08 vs. 1.40±0.13, P<0.05). Wnt3a stimulation enhanced proliferation in LEF1-overexpressing cells (OD450 at 72h: 1.72±0.16 vs. 1.45±0.14, P<0.05).

### LEF1 enhances CRC cell migration and invasion

LEF1 overexpression increased HCT116 migration rate to 74.5±6.2% (vs. 46.8±4.7% in control, P<0.01) and invasive cells to 138±12 (vs. 61±7 in control, P<0.01). LEF1 knockdown reduced migration rate to 37.8±4.5% (vs. 72.6±5.9% in si-NC, P<0.01) and invasive cells to 53±6 (vs. 125±10 in si-NC, P<0.01).

### LEF1 maintains CRC cell stemness

LEF1 overexpression increased HCT116 sphere formation efficiency to 2.8±0.3 folds of control (P<0.01) and upregulated CD44 (1.95±0.18 vs. 1.00±0.08, P<0.05). LEF1 knockdown reduced sphere formation efficiency to 0.4±0.1 folds of si-NC (P<0.01) and downregulated CD44 (0.42±0.04 vs. 1.00±0.08, P<0.05).

### LEF1 activates Wnt/β-catenin signaling

LEF1 overexpression increased nuclear LEF1 (2.20±0.21 vs. 1.00±0.09, P<0.05), LEF1-β-catenin complex (2.05±0.19 vs. 1.00±0.09, P<0.05) and c-Myc (1.98±0.18 vs. 1.00±0.08, P<0.05). LEF1 knockdown showed opposite effects: nuclear LEF1, LEF1-β-catenin complex and c-Myc decreased (P<0.05), while cytoplasmic β-catenin accumulated (P<0.05).

## Discussion

This study confirms LEF1 is upregulated in CRC cells and its overexpression promotes proliferation, migration, invasion and stemness by activating Wnt/β-catenin signaling-consistent with its oncogenic role in gastric and pancreatic cancer<sup>7,8</sup>. Mechanistically, LEF1 translocates to the nucleus, forms a complex with β-catenin and drives transcription of stemness-associated genes (e.g., CD44) and pro-oncogenic genes (e.g., c-Myc)<sup>4</sup>, which enhances CRC's malignant potential. Limitations include lack of in vivo validation; future studies should explore LEF1's crosstalk with the NF-κB pathway in CRC<sup>9</sup>. Targeting LEF1 (e.g., via small-molecule inhibitors of LEF1-β-catenin interaction) may be a promising strategy for CRC treatment<sup>10</sup>.

## Conclusion

LEF1 is upregulated in colorectal cancer cell lines and promotes CRC progression by activating Wnt/ $\beta$ -catenin signaling and regulating stemness-associated genes, highlighting its potential as a therapeutic target for CRC.

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