World Journal of
Clinical Cases

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ABOUT COVER
Editorial Board Member of World Journal of Clinical Cases, Dr. Romano is Professor of Medicine-Gastroenterology at the University of Campania “Luigi Vanvitelli” in Naples, Italy. Dr. Romano received his MD degree cum Laude at the University Federico II in Naples, Italy in 1980 and, after 4 years of Post-Graduate course, he became Specialist in Gastroenterology and Gastrointestinal Endoscopy. Dr. Romano’s research interest was on the cross-talk between H. pylori and gastric epithelial cells, and presently is mainly focused on H. pylori eradication therapy and on the role of nutraceuticals in gastrointestinal diseases. Dr. Romano is presently the Chief of the Endoscopy and Chronic Inflammatory Gastrointestinal Disorders Unit, and Teacher at the University of Campania “Luigi Vanvitelli” in Naples, Italy.

AIMS AND SCOPE
The primary aim of World Journal of Clinical Cases (WJCC, World J Clin Cases) is to provide scholars and readers from various fields of clinical medicine with a platform to publish high-quality clinical research articles and communicate their research findings online.

WJCC mainly publishes articles reporting research results and findings obtained in the field of clinical medicine and covering a wide range of topics, including case control studies, retrospective cohort studies, retrospective studies, clinical trials studies, observational studies, prospective studies, randomized controlled trials, randomized clinical trials, systematic reviews, meta-analysis, and case reports.

INDEXING/ABSTRACTING
The WJCC is now indexed in Science Citation Index Expanded (also known as SciSearch®), Journal Citation Reports/Science Edition, PubMed, and PubMed Central. The 2020 Edition of Journal Citation Reports® cites the 2019 impact factor (IF) for WJCC as 1.013; IF without journal self cites: 0.991; Ranking: 120 among 165 journals in medicine, general and internal; and Quartile category: Q3.

RESPONSIBLE EDITORS FOR THIS ISSUE
Electronic Editor: Yan-Xia Xing; Production Department Director: Yun-Xiaoqian Wu; Editorial Office Director: Jin-Lei Wang.
Overexpression of AMPD2 indicates poor prognosis in colorectal cancer patients via the Notch3 signaling pathway

Qi-Zhong Gao, Yan Qin, Wei-Jia Wang, Bo-Jian Fei, Wei-Feng Han, Jian-Qiang Jin, Xiang Gao

ORCID number: Qi-Zhong Gao 0000-0001-6038-8742; Yan Qin 0000-0002-8578-1103; Wei-Jia Wang 0000-0001-4399-2724; Bo-Jian Fei 0000-0001-2138-3742; Wei-Feng Han 0000-0001-6038-8743; Jian-Qiang Jin 0000-0001-6038-9327; Xiang Gao 0000-0001-6038-8746.

Author contributions: Gao QZ and Qin Y designed the research; Gao QZ performed the research. Qin Y and Jin JQ reviewed the surgical pathology; Fei BJ and Han WF analyzed the data; Gao QZ and Gao X wrote the paper; all authors read and approved the final manuscript.

Supported by the Wuxi Young Medical Talents, Jiangsu Province, China, No. QNRC063.

Institutional review board statement: This study was approved by the Ethics Committee of Affiliated Hospital of Jiangnan University and was performed in accordance with the ethical standards of the Declaration of Helsinki and its later amendments.

Clinical trial registration statement: This registration policy applies to prospective, randomized, controlled trials only.

Informed consent statement: All study participants, or their legal

Abstract

BACKGROUND

AMPD2 is a critical enzyme catalyzing smooth muscle energy supply and metabolism; however, its cellular biological function and clinical implication in colorectal cancer (CRC) are largely unknown.

AIM

To clarify the role of AMPD2 in CRC and study the pathway and prognostic value of its role.

METHODS

AMPD2 expression was analyzed by integrated bioinformatics analysis based on TCGA data sets and immunohistochemistry in tissue microarrays, and the correlation between AMPD2 expression and clinicopathological parameters, Notch3 expression, and prognostic features was assessed. Gene Ontology and Kyoto Encyclopedia of Genes and Genomes analysis were then performed to investigate the regulatory pathway involved. The effects of AMPD2 expression on CRC cells and Notch3 protein expression were investigated by downregulation and overexpression of AMPD2.

RESULTS

AMPD2 mRNA was significantly overexpressed in tumor tissue when compared with normal tissue in a cohort of the TCGA-COAD data set. Biological function enrichment analysis indicated that the Notch pathway strongly correlated with AMPD2 expression, and that the expression of Notch3 and JAG2 mRNA was
INTRODUCTION

Colorectal cancer (CRC) is the third most common cancer and the fourth leading cause of cancer-related deaths worldwide, and remains a major health threat in China\(^\text{[3]}\). CRC patients at an advanced stage often have a poor prognosis due to abnormal tumor metabolism and recurrence. Therefore, it is of clinical significance to identify novel biomarkers that control the severity of CRC as well as biomarkers for the prediction of prognosis\(^\text{[1]}\).

Recently, there has been increased interest in studying the metabolic reprogramming in cancer in the hope of developing metabolism-based anticancer therapy\(^\text{[4]}\). Accordingly, various studies aimed at identifying the metabolic index in blood, body fluids, carcinoma tissue, and gut microbiota have been performed to establish a complete metabolic atlas and explain the possible mechanisms by which these abnormalities are present in gastrocolorectal tumors\(^\text{[5]}\). In several studies, it has been shown that in addition to primary metabolism, many specific secondary metabolites have an important impact on the development and progression of CRC, thereby suggesting that specific metabolic markers can be used as biomarkers for metabolic abnormalities\(^\text{[6]}\). These findings suggested that AMPD2 may act as a metabolic tissue enzyme, which is closely related to the type of CRC, and may play an important role in CRC.

AMPD2 is an important enzyme involved in adenosine monophosphate metabolism and plays an important biological function in adenylyl metabolism in smooth muscle tissue\(^\text{[7]}\). In previous studies, it was shown that AMPD2 affected the nephrotic syndrome and hypercholesterolemia\(^\text{[8]}\). In addition, it has been demonstrated that AMPD2 dramatically affected physiological and pathological processes\(^\text{[9]}\). Despite recent efforts to understand the activities of AMPD2 in the biological mechanism of...
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cancer, little is known about the role of AMPD2 in CRC and it remains to be elucidated whether AMPD2 expression correlates with any of the clinicopathological features of CRC\(^\text{10}\).

In this study, we combined TCGA-COAD data set analyses of both tumor and normal samples to investigate the significance of AMPD2 in CRC. Therefore, in vitro studies were performed to investigate how AMPD2 may affect the CRC-associated regulatory pathway. A total of 201 samples were collected using tissue microarray validation cohort studies to investigate whether AMPD2 could be used as a biomarker for poor CRC prognosis.

### MATERIALS AND METHODS

#### Data collection and preprocessing analysis

In this study, the TCGA dataset was used for analysis of gene expression in CRC tissues and normal tissues. TCGA-COAD RNA-seq data and related clinical data of cancer tissues (478), and normal tissues (41) were downloaded from [https://xenabrowser.net/\(^\text{11}\)](https://xenabrowser.net/). We continued to match and screen the organization label, and obtained 40 pairs of cancer tissues and paired adjacent normal tissues. The data were updated to November 2018. To assess the prospective functions of the genes influenced by AMPD2, we selected a total of 50 TCGA-COAD specimens with the highest expression of AMPD2 and 50 TCGA-COAD specimens with the lowest expression of AMPD2, and follow-up biologic function prediction analysis was performed in the abnormally high expression and low expression groups. Gene Ontology (GO)\(^\text{12}\) and Kyoto Encyclopedia of Genes and Genomes (KEGG)\(^\text{13}\) analyses were employed using R software (version 3.6) Bioconductor module. The datasets GSE97023 were downloaded from the Gene Expression Omnibus (GEO) (https://www.ncbi.nlm.nih.gov/geo/\(^\text{14}\)), to analyze RNA-seq baseline data for CRC cell lines.

#### Cell lines and cell culture, and AMPD2 overexpression and knockdown

Human CRC cell lines SW480 and Co115 were purchased from the Cell Bank of the Chinese Academy of Sciences (Shanghai, China). The cells were cultured in Dulbecco’s Modified Eagle’s Medium (Biowest, France) with 10% fetal bovine serum (Gibco, United States) and 1% penicillin-streptomycin antibiotics (Gibco, United States). Cells were cultured in an incubator at 37°C with 5% CO\(_2\). For AMPD2 overexpression, cells were transfected with AMPD2 overexpression plasmid or blank plasmid purchased from Gene Pharma (Shanghai, China). For AMPD2 knockdown, an AMPD2 specific siRNA (siAMPD2) and a negative control siRNA (siNEG) were chemically synthesized by Gene Pharma (Shanghai, China). Transfection of cells with siRNA was performed using Lipofectamine 2000 (Invitrogen, ThermoFisher Scientific, United States) according to the manufacturer’s guidelines.

#### Western blot analysis

Cells were harvested and lysed in RIPA buffer, containing proteinase and phosphatase inhibitors. The concentration of proteins in cell lysates was determined by a BCA kit (Applygen Technologies, China) following the manufacturer’s instructions. Equal amounts of cell lysates (20 μg protein/lane) were electrophoresed on SDS-polyacrylamide gels and transferred to nitrocellulose membranes. Membranes were blocked, and then probed overnight with appropriate primary antibodies (AMPD2, 1:1000; Notch3, 1:500; GAPDH, 1:8000) in blocking buffer at 4°C. Bound antibodies were detected with Beyotime horseradish (HRP)-conjugated goat anti-rabbit IgG or anti-mouse IgG (at 1:10000 dilution; Genetech, China) and visualized using a Bio-Rad ChemiDoc XRS imaging system.

#### Tissue microarray

A total of 201 CRC patients who underwent CRC surgery between January and August 2014 in the Oncology Department, Affiliated Hospital of Jiangnan University, Wuxi, China, were enrolled in the present study. The patients were followed-up until December 2018. Based on the patient’s medical records, formalin-fixed paraffin-embedded (FFPE) tissue specimens from these patients were collected. Clinical and pathological parameters, including patient age, gender, tumor size, histological grade, primary tumor (pT), lymph node (pN) metastasis, pathological staging, neurological invasion, lymphatic invasion, and vascular invasion were analyzed. Patient data and
tissue samples collected during our study were approved by the Ethics Committee of Affiliated Hospital of the Jiangnan University (Jiangnan, China). After collecting the paraffin blocks, we fabricated tissue microarrays (TMA) using a Tissue microarray sampler (Quick-Ray; UNITMA, Korea). From each colorectal adenocarcinoma tissue, two representative tumor cores with a diameter of 1.5 mm were obtained. Hematoxylin and eosin (H&E) staining was performed on each tissue to confirm tumor tissue integrity and cell morphology. Cases with insufficient cancer tissue or cases with no adenocarcinoma in the core were not included in the study. To ensure the stability of subsequent TMA studies, two areas were sampled in each tumor tissue and normal epithelial tissue.

**Immunohistochemical staining**

Immunohistochemistry was performed using 4 µm sections from FFPE tissue specimens of CRC patients. After incubation in xylene three times for five minutes each time, and subsequent passages in gradient alcohol, the sections were immersed in distilled water for 5 min. Next, an antigen retrieval procedure was performed using a sodium citrate solution for 20 min in boiling water. Sections were incubated with 3% hydrogen peroxide for 5 min to block endogenous peroxidase. Subsequently, the sections were incubated overnight at 4°C with a primary polyclonal antibody directed against AMPD2 (1:200, ProteinTech, China) and Notch3 (1:200, ProteinTech, China). The sections were washed, incubated with the amplification agent and polymerase (reagent A, GTVisionTM III Kit supply, China), then stained with 3,3’-diaminobenzidine (reagent B and C, GTVisionTM III Kit supply, Shanghai, China). Sections were counterstained using hematoxylin. In each section, the staining was scored according to the percentage of positively-stained cells in the entire section (no positive staining or ≤ 5% = 0; 6%-25% positive = 1; 26%-50% positive = 2; 51%-75% positive = 3; and 76%-100% positive = 4). The scoring intensity was determined as previously described: no staining = 0, weak staining = 1, moderate staining = 2, strong staining = 3.[15]

**Statistical analysis**

Cut-off values for AMPD2 and Notch3 were obtained from the receiver operating characteristic curve (ROC) and the area under curve (AUC). Pearson’s Chi-square tests or Fisher’s exact tests were employed to analyze the association between AMPD2 expression, clinicopathological parameters, and Notch3. Moreover, Kaplan-Meier survival analysis was used to determine the probability of overall survival (OS). Data were analyzed using log-rank tests. Univariate and multivariate survival analyses were performed using the Cox proportional hazard model and OS. Statistical analyses were performed using SPSS for Windows 22.0 software (IBM). *P* < 0.05 was considered statistically significant.

**RESULTS**

**AMPD2 is commonly overexpressed in TCGA CRC tissues**

In this study, we evaluated AMPD2 expression in CRC and normal colorectal tissues, and changes in transcriptional levels of AMPD2 were first validated using microarray values in all tumor tissue and normal tissue from the TCGA-COAD data sets. The results showed that AMPD2 mRNA was significantly increased in CRC tissues in the TCGA-COAD data set (*P* = 0.0238; Figure 1A). Moreover, we demonstrated that an increase in AMPD2 mRNA abundance was observed in paired cancerous tissue when compared with paired adjacent normal tissue from the TCGA data set (Figure 1B). In addition, we used the TCGA-COAD data set to correlate mRNA expression with AMPD2. A total of 50 specimens with abnormally-high expression of AMPD2 and 50 specimens of abnormally-low expression of AMPD2 were selected, and differential gene expression was analyzed. According to the high and low expression of AMPD2, a heat map was drawn as shown in Figure 1C.

**Functional implication of AMPD2 associated with the Notch pathway in CRC in vitro**

To further investigate the biological function of the differential expression of transcription levels caused by high expression of AMPD2, we performed GO and KEGG enrichment analysis of the genes that were up-regulated in the AMPD2 overexpression group (Figure 2A and B). When compared to the AMPD2 low expression group, the AMPD2 overexpression group showed a positive regulation of
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Figure 1 The expression level of AMPD2 in the TCGA-COAD data set. A: The expression level of AMPD2 in cancer tissues and paracancerous tissues was determined by two independent samples t test, \( P < 0.05 \) was considered significant; B: In paired samples of cancer tissue and adjacent normal tissues, the AMPD2 expression level was determined by paired t-test, and \( P < 0.05 \) was considered significant; C: AMPD2-based high expression subgroup (50 cases) and low expression subgroup (50 cases) in cancer tissues. A heat map of the difference in gene expression was produced.

Correlation between AMPD2 expression and clinicopathological features in CRC

We analyzed the correlation between high expression of AMPD2 and Notch3 and clinicopathological parameters in CRC patients. Clinicopathological and demographic characteristics are presented in Table 1. Immunohistochemical analysis of AMPD2 and Notch3 expression in 201 CRC patients revealed that AMPD2 and Notch3 were predominantly expressed in the cytoplasm of carcinoma cells (Figure 3A). To assess the classification of AMPD2 and Notch3 protein expression, we used the immunohistochemical semi-quantitative score and predicted the ROC curve for survival by AMPD2 and Notch3 expression levels, and calculated the cut-off value in conjunction with the results of the Youden index. Thus, patients were categorized as high expression of AMPD2 if their immunohistochemical scores were > 0.50. As shown in Table 1, overexpression of AMPD2 significantly correlated with advanced depth of the tumor \( (P = 0.022) \) and poor differentiation \( (P = 0.037) \). As shown in Table 2, univariate Cox analysis for OS indicated a correlation with higher TNM stage \( (HR = 3.198, 95\% CI: 1.915-5.343, P < 0.001) \) and increased expression of AMPD2 \( (HR = 1.769, 95\% CI: 1.094-2.862, P = 0.020) \). Furthermore, multivariate regression analysis indicated...
that a higher TNM stage was associated with a relative risk of death of 3.727 (95% CI: 2.206-6.296, \( P < 0.001 \)) when compared with that of Stage I-II. In addition, overexpression of AMPD2 was associated with a relative risk of death of 2.133 (95% CI: 1.295-3.513, \( P = 0.003 \)). Patients with colorectal adenocarcinomas who belonged to the AMPD2 high expression group (\( n = 61 \)) had a significantly lower cumulative survival rate when compared to patients in the AMPD2 low expression group (\( n = 140 \)) (log-rank \( P = 0.0181 \)). Patients with CRC who had high expression of Notch3 (\( n = 70 \)) had a significantly lower cumulative survival rate when compared to those with low expression of Notch3 (\( n = 131 \)) (log-rank \( P = 0.465 \)). Subgroup survival analysis revealed that patients who showed high expression of both AMPD2 and Notch3 had the worst prognosis when compared with the other three subgroups. Patients with low

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**Table 1** Correlations between clinicopathological characteristics and both AMPD2 and Notch3 expression in 201 colorectal cancer patients

<table>
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<th>Parameters</th>
<th>Total (( n = 201 ))</th>
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<th>( P ) value</th>
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<td></td>
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<td>( \geq 60 )</td>
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<td>Notch3</td>
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*\( P < 0.05 \) was considered statistically significant.
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<td><em>P</em> value</td>
<td>HR (95%CI)</td>
<td><em>P</em> value</td>
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<tr>
<td>Gender (female/male)</td>
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<td>0.986</td>
<td>0.973 (0.630-1.552)</td>
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<td>Age (≥ 60/&lt; 60)</td>
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<td>0.806</td>
<td>1.066 (0.661-1.721)</td>
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<td>Location (rectum/colon)</td>
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<td>0.616</td>
<td>0.888 (0.553-1.428)</td>
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<td>Differentiation (poor, moderate/well)</td>
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<td>0.041</td>
<td>0.727 (0.450-1.173)</td>
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<td><em>&lt; 0.001</em></td>
<td>3.727 (2.206-6.296)</td>
<td><em>&lt; 0.001</em></td>
</tr>
<tr>
<td>AMPD2 (high/low)</td>
<td>1.769 (1.094-2.862)</td>
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<td>2.133 (1.295-3.513)</td>
<td>0.003</td>
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<tr>
<td>Notch3 (high/low)</td>
<td>1.237 (0.747-2.048)</td>
<td>0.408</td>
<td>1.119 (0.668-1.874)</td>
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</tr>
</tbody>
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*p < 0.05* was considered statistically significant. HR: Hazard ratio; CI: Confidence interval.

expression of AMPD2 and low expression of Notch3 showed the highest survival when compared to the other subgroups (*P < 0.001, Figure 3B*).

**DISCUSSION**

Metabolic intermediate and related metabolites are widely present in cells of myometrial and glandular tissues\(^\text{[16]}\). Their associated metabolic pathways have been reported to be central to cancer growth and metastasis\(^\text{[17]}\). Thus, upregulation of AMPD2 in the tumor may explain the metabolic shift in adenosine phosphate synthesis in cancer. This evidence from different studies robustly supports that AMPD2 might be the fundamental gene in tumor transformation, resulting in metabolic adaptation in cancer cells\(^\text{[18]}\). Based on these findings, we suggested that AMPD2 may be a tumor metabolic marker that can be used for the analysis of tumor progression and the prediction of patient prognosis.

In this study, we summarized and analyzed the mRNA expression data of TCGA-COAD, and obtained the expression characteristics of AMPD2 in cancer tissues and adjacent tissues in patients with CRC. A gene function prediction analysis of the differences between high and low AMPD2 expression groups was performed, and the results were enriched in the Notch signaling pathway. Based on these findings, cytological mechanism validation and clinical prognosis-related survival analysis were employed. Our data showed that AMPD2 resulted in CRC progression and poor prognosis in colorectal and CRC tissues. However, our analysis based on gene function enrichment was based on TCGA public database analysis. We constructed cell samples that were not subjected to high-throughput sequencing of RNA-seq. The results were closer to clinical reality; however, when verifying the data, the probability of false negatives was increased. In addition, our cytology validation experiments needed to be carried out in detail, and our CRC cohort sample only included 201 cases. We expect to add cytological evidence and increase the sample size of prospective prognostic cohorts in subsequent studies.

In the present work, we revealed for the first time that overexpression of AMPD2 can promote CRC progression by augmenting tumor proliferation and halting apoptosis, and may serve as a poor prognostic marker for CRC patients. In addition, our data provided evidence that the Notch signaling pathway can affect proline metabolism via AMPD2 in CRC. Taken together, these findings, and our previous report, highlight the potential therapeutic value of targeting AMPD2 as a modulator of proline metabolism in CRC.
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A

- Semaphorin-plexin signaling pathway involved in neuron projection guide etc.
- Semaphorin-plexin signaling pathway involved in axon guidance
- Semaphorin receptor complex
- Semaphorin receptor binding
- Semaphorin receptor activity
- RNA-dependent atpase activity
- Response to atp
- Regulation of axon guidance
- Regulation of axon extension involved in axon guidance
- Receptor signaling complex scaffold activity
- Protein kinase C signaling
- Positive regulation of neural precursor cell proliferation
- Peptide biosynthetic process
- Negative regulation of osteoblast differentiation
- Negative regulation of erbB signaling pathway
- Negative regulation of epidermal growth factor receptor signaling path etc.
- Negative regulation of axon extension involved in axon guidance
- Negative regulation of axon extension
- Negative regulation of angiogenesis
- Kinesin binding
- Histone-lysine n-methyltransferase activity
- Gastrulation with mouth forming second
- Decaydylase activity
- Cofactor transport
- Coated pit
- Cellular response to vascular endothelial growth factor stimulus
- Axon extension involved in axon guidance
- ATP-dependent RNA helicase activity

B

- Vitamin digestion and absorption
- Vascular smooth muscle contraction
- Type II diabetes mellitus
- Taurine and hypotaurine metabolism
- Progestosterone-mediated oocyte maturation
- Phosphatidylinositol signaling system
- Pancreatic secretion
- Notch signaling pathway
- Maturity onset diabetes of the young
- Lysine degradation
- Long-term depression
- Linoleic acid metabolism
- GnRH signaling pathway
- Glycosphingolipid(GPL)- anchor biosynthesis
- Glycine, serine and threonine metabolism
- Gluconophospholipid metabolism
- Gluconolipid metabolism
- Glutathione metabolism
- Gastric acid secretion
- Fructose and mannose metabolism
- Endocytosis
- ECM-receptor interaction
- Dorsal-ventral axis formation
- Cyanocamino acid metabolism
- Base excision repair
- Axon guidance
- Arachidonic acid metabolism
- Alpha-Linolenic acid metabolism
- African trypanosomiasis

Enrich factor

P value

Diff_gene_count

- Biological_process
- Cellular_component
- Molecular_function
Figure 2 Functional enrichment analysis and western blot. A and B: Based on AMPD2, a high expression subgroup (50 cases) and a low expression subgroup (50 cases) in cancer tissues were identified, and functional enrichment analysis of gene expression differences was performed using GO and KEGG maps; C: The expression of AMPD2 in various colorectal cancer cell lines was analyzed according to the GEO-GSE97023 data set; D and E: The Western blot results of up-regulation and down-regulation of AMPD2 in SW480 and Co115 cell lines, immunoblotting (D) and histogram (E).
Figure 3 Immunohistochemical and Kaplan-Meier curves. A: Tissue microarrays of hematoxylin and eosin stained sections. Representative immunohistochemical analysis of AMPD2 levels in colorectal tumor tissue specimens from cancer patients and in adjacent cancer-associated fibroblasts. Immunohistochemical results of Notch3 levels in the same tissues/cells. Photomicrographs of the sections (50 × and 200 × magnification); B: Kaplan-Meier curves showing the impact of AMPD2 expression on overall survival (OS) of 201 colorectal cancer patients (P = 0.0181). Kaplan-Meier curves showing the impact of Notch3 expression on the OS of 201 colorectal cancer patients (P = 0.465). Kaplan-Meier curves showing the impact of AMPD2 and Notch3 subgroup expression on the OS of 201 colorectal cancer patients (P < 0.001).

ARTICLE HIGHLIGHTS

Research background
As an important gastrointestinal tumor, colorectal cancer (CRC) is often accompanied by abnormal energy metabolism in the case of malignant progression and poor prognosis.

Research motivation
As the abnormal energy metabolism in tumor cells has received considerable attention, we have combined the tissue type and biological characteristics of CRC. With AMPD2 as the entry point for research, a variety of scientific methods can be integrated for research.

Research objectives
Clarify the role of AMPD2 in CRC and study the pathway and prognostic value of its role.

Research methods
RNAseq data analysis of the TCGA-COAD data set, GO and KEGG analysis. Western blot was used to detect the expression of Notch3-related pathway proteins, as well as clinical pathological samples combined with patient prognosis analysis.

Research results
AMPD2 is commonly overexpressed in TCGA CRC tissues, and the function of AMPD2 is associated with the Notch signaling pathway in CRC in vitro. In the CRC cohort, as indicated by tissue microarray analysis, high expression of AMPD2 protein was correlated with advanced depth of tumor and poor differentiation.
**Research conclusions**

The mRNA and protein levels of AMPD2 are significantly highly expressed in CRC tissues. The high expression of AMPD2 has a positive relationship with activation of the Notch3 signaling pathway. In patients with CRC, those with high expression of AMPD2 have a poor prognosis.

**Research perspectives**

In the future, we plan to further study the biological mechanism of AMPD2 stimulation of abnormal lipid metabolism in CRC cells.

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**REFERENCES**


