Research Article

High Expression and Clinical Significance of Elafin in Colorectal Cancer

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Objective. The decrease of Elafin is associated with several inflammatory diseases. Exogenous Elafin may be a treatment for IBD. Little data has shown the expression of Elafin in patients of colorectal cancer. Here, we tried to explore Elafin expression in human tissues of colorectal cancer. Methods. We examined the protein expression of Elafin in human tissues of adjacent nontumor and colorectal tumor by immunohistochemistry (IHC) or quantitative real-time polymerase chain reaction (qRT-PCR), then analyzed the clinical and RNA-seq data presented in The Cancer Genome Atlas (TCGA) database to confirm the relationship between Elafin levels and colorectal tumor. Results. Of the 88 paired samples, 68 colorectal cancer tissues indicated a high expression of Elafin compared with 52 matched adjacent noncancerous tissues. And the mRNA levels of Elafin in 35 paired tissues showed a similar trend. The RNA-seq and clinical data were available in 438 colorectal cancer tissues and 41 normal tissues in TCGA database. The RNA-seq data showed that Elafin mRNA was upregulated about twofold in colorectal cancer samples as compared to adjacent noncancerous samples (176.42 ± 402.13 vs. 96.75 ± 150.07; \( P = 0.208 \)). No statistically significant correlation was found between the Elafin expression and the age, gender, tumor invasive stage, lymph node metastasis, and distant metastasis both at the protein and mRNA levels. However, the Elafin expression was correlated with clinical stage based on the AJCC guidelines at protein levels but not mRNA levels. Conclusions. Elafin was upregulated in patients of colorectal cancer, resulting to potential limitations for exogenous Elafin treatment.

1. Introduction

Inflammatory bowel disease (IBD) is a chronic nonspecific inflammatory disease, including ulcerative colitis (UC) and Crohn’s disease (CD). Recently, an increasing morbidity of IBD has shown in Asian populations, which was the low-incidence area previously [1]. The main treatment of IBD was anti-TNF-α therapy, but 40% of patients did not respond [2]. Based above, it is crucial to seek a protective and effective therapeutic method.

The key point of pathogenesis mechanism in IBD was still unclear, but combined effect of genetic, immune, environmental, and microbial factors was widely accepted [3]. Previous studies have confirmed that proteases and protease inhibitors play an important role in chronic inflammation [4–5]. Elafin is a low molecular weight antiprotease, which antagonizes human neutrophil elastase (NE), pancreatic elastase, proteinase 3, and endogenous vascular elastase and also has several functions, such as anti-inflammation, immune regulation, antimicrobe, antiproliferation, vascular remodeling, and wound healing [6]. The decrease of Elafin is associated with several inflammatory diseases [7]. Recently, we also found that Elafin reduced in active IBD patients and was correlated with disease activity negatively [8]. Furthermore, several studies confirmed that probiotic-expressed Elafin protected against inflammation and restored homeostasis in animal models of colitis [9–11], suggesting that exogenous Elafin may be a treatment for IBD. However, differential expressions of Elafin have been reported in several tumors. Elafin was overexpressed and secreted by basal-like breast cancer and ovarian cancer, leading a proliferative effect through the MAP kinase pathway [12]. Elafin was increased and correlated with the differentiation of esophageal cancer [13]. In contrast, Elafin is downregulated in ductal carcinoma in situ, invasive breast tumor, ovarian cystadenoma, borderline ovarian tumor, and invasive
ovarian cancer [14]. Therefore, the safety of engineered probiotic-expressed Elafin needed to be estimated, but little data have showed the Elafin expression in colorectal carcinoma, which could illuminate its role in colorectal tumors.

In this study, we tried to explore the Elafin expression in human tissues of colorectal cancer, which was never investigated previously. We examined the protein expression of Elafin in human mucous tissues of adjacent nontumor and colorectal tumor by immunohistochemistry (IHC). Then, we analyzed the clinical and RNA-seq data presented in The Cancer Genome Atlas (TCGA) database to confirm the mRNA levels of Elafin and relationship between Elafin and colorectal tumor.

2. Materials and Methods

2.1. Clinical Samples. Ninety patients with colon cancers were enrolled, who were diagnosed with histopathology after the resection of colon cancer at Peking University First Hospital from 2017 to 2018. A pair of biopsy samples of the colon cancer tissues and adjacent nontumor tissues was collected from every patient, stored at -80°C after frozen in liquid nitrogen. And the clinical information in these patients was gathered, including age, gender, clinical stage, tumor invasive stage, lymph node metastasis, and distant metastasis. All of the tumor samples (N = 90) and adjacent nontumor tissues (N = 90) were used for tissue microarray analysis to investigate the expression of Elafin protein, but only eighty-eight pairs of patients were used for statistics, due to missing clinical information. Of all colon samples, 35 paired tissues were used for quantitative real-time polymerase chain reaction (qRT-PCR). The patients included 50 males and 38 females, ranging in age from 32 to 91 years. This study was approved by the ethical committee of First Hospital of Peking University, and every patient has provided written informed consent (No. 20171376).

2.2. Immunohistochemical Analysis. Tissue specimens were fixed by 10% neutral formalin and embedded by paraffin. The sections inhibited endogenous peroxidase activity by 3% hydrogen peroxide, after deparaffinization. The sections were incubated with 3,3′-diaminobenzidine (DAB) was used for visualization of the Elafin expression. Following counterstain with hematoxylin, the sections were observed in an optical microscope.

Immunostaining scores of Elafin were accomplished by two experienced investigators independently. The score of staining intensity was as follows: 1 (negative brown), 2 (weak brown), 3 (moderate brown), and 4 (strong brown). The staining extent was based on the rate of positive cells: 0 (0-5%), 1 (6-25%), 2 (26-50%), 3 (51-75%), and 4 (76-100%). The final score was defined as the sum of the intensity and extent of the scores. When discrepancy in the final score was encountered, it was resolved by discussion between two investigators. The specimens were separated into two groups based on the final score: high (>4) and low (≤4).

2.3. RNA Extraction and qRT-PCR. Total RNA from frozen colon tissues was isolated using TRIzol reagent (Invitrogen, Carlsbad, CA, USA). The quality and concentration of RNA were determined using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific, MA, USA). Then, a Reverse Transcriptase Kit (TaKaRa Biotechnology Group, Dalian, China) was used to generate cDNA. qRT-PCR was conducted on the Applied Biosystems 7500 Real-Time PCR System with SYBR Green Master Mix (Thermo Fisher Scientific, Grand Island, NY, USA). The sequences of primers were as follows: Elafin forward: 5′-CTCTTGA- TCGTTGGG TGTTG-3′ and reverse: 5′-AACGGGATCCTGTCATTG AAT-3′; and glyceraldehyde-3-phosphate dehydrogenase forward: 5′-GCCTGGTCAACA- GGGCT-3′ and reverse: 5′-AATTGCCCAGGTGGTAATC-3′.

2.4. Analysis of Colorectal Cancer Data from TCGA. The clinical and RNA-seq data of the 459 colorectal cancer patients and 41 normal tissues were obtained from TCGA database (https://cancergenome.nih.gov/). The clinical data was an abstract from TCGA database, including age, gender, clinical stage, tumor invasive stage, lymph node metastasis, and distant metastasis. The patients with integrated clinical information and mRNA levels of Elafin were enrolled, including 438 colorectal cancer samples and 41 normal tissues finally. The data used in this paper are presented to the public without limitation and restriction. The mRNA expression level of Elafin was analyzed in subjects with different clinicopathological features. The differential expression genes in the cancer samples compared with normal tissues were conducted.

2.5. Statistical Methods

2.5.1. Immunostaining Score. The proportion of a high-score group was calculated. And the paired Chi-square test was applied to analyze the proportions between tumor and nontumor tissues in all and in different clinicopathological characteristics. The relationship between the percentage of a high-score group and the clinicopathological variables was calculated by the Chi-square test or Fisher’s exact test. The survival analysis was compared between different protein levels of Elafin groups by Kaplan-Meier curves and a log-rank test.

2.5.2. RNA Data from qRT-PCR or TCGA Database. Continuous variables were displayed as mean and standard deviation. The relationship between RNA-seq levels of Elafin and clinicopathological features was conducted by an independent two sample t-test. A two-tailed P value of less than 0.05 was defined as statistically significant difference. The SPSS 20.0 software was used for statistical analyses. And the analysis of differential expression genes was through EBSeq.
3. Result

3.1. Expression of Elafin in Colorectal Cancer Tissues and Nontumor Normal Tissues. Eighty-eight paired human cancer tissues and nontumor tissues were selected for immunohistochemical analysis. The subjects were 50 males and 38 females, with an average age of 66.8 ± 10.8 years, ranging in age from 32 to 91 years. Of the 88 paired samples, 68 (77.3%) colorectal cancer tissues indicated a high expression of Elafin compared with 52 (59.1%) matched adjacent noncancerous tissues (Table 1, \( P = 0.010 \); Figures 1(a) and 1(b)). And 35 pairs of tumor and nontumor samples from the same cohort were measured by qRT-PCR. Colorectal cancer tissues showed higher mRNA levels of Elafin than nontumor tissues (Table 1, \( P = 0.039 \)). In addition, the RNA-seq data of 438 colorectal cancer tissues and 41 normal tissues were analyzed. Results showed that Elafin was upregulated about twofold in colorectal cancer samples as compared with nontumor tissues (Table 1, \( P = 0.0208 \)). The result suggested that the Elafin expression in colorectal cancer patients was increased at the protein and mRNA levels, compared with nontumor colon tissues by immunohistochemical scoring and analysis of TCGA database.

3.2. Expression of Elafin in Colorectal Cancer Patients in Different Clinicopathological Features Compared with Nontumor Tissues. Based on a high expression of Elafin in tumor tissues compared with nontumor tissues, eighty-eight paired human tissues were divided by different clinicopathological parameters, including clinical stage, tumor invasive stage, lymph node metastasis, and distant metastasis. A high expression of Elafin evaluated by immunostaining scoring was observed in all subgroups. However, the expression of Elafin between cancer samples and matched adjacent nontumor tissues in some subgroups showed no significant differences, including stage III-IV of clinical stage (\( P = 0.076 \)), stage T4 of tumor invasive (\( P = 0.18 \)), stage N1-N2 of lymph node metastasis (\( P = 0.078 \)), and stage M1 of distant metastasis (Table 2). Systemic bioinformatics analysis of RNA-seq data of colorectal cancer samples from The Cancer Genome Atlas (TCGA) was performed. Differential expression analysis between 438 colorectal cancer tissues and nontumor tissues was performed. Results showed that Elafin expression was increased in colorectal cancer tissues compared with nontumor tissues.

![Figure 1](image-url)  
**Figure 1**: The expression of Elafin in colorectal cancer and nontumor tissues. (a) Elafin expression in normal colonic mucosa epithelium by IHC. (b) Elafin expression in colon cancer tissues by IHC.

### Table 1: Expression of Elafin in colorectal cancer patients and nontumor tissues.

| Methods       | Tumors | Nontumors | Chi-square/t | \( P \) value |
|---------------|--------|-----------|--------------|---------------|
| IHC Total (N) | 88     | 88        | 6.705        | 0.010         |
| High n (%)    | 68 (77.3%) | 52 (59.1%) |              |               |
| Low n (%)     | 20 (22.7%) | 36 (40.9%) |              |               |
| qRT-PCR Total (N) | 35     | 35        | 2.103        | 0.039         |
| Elafin levels | \( 2.30 \pm 0.80 \) | \( 0.61 \pm 0.12 \) |              |               |
| TCGA Total (N) | 438    | 41        | 1.260        | 0.208         |
| Elafin levels | \( 176.42 \pm 402.13 \) | \( 96.75 \pm 150.07 \) |              |               |

Continuous variables are presented as the mean ± SD. IHC: immunohistochemistry; TCGA: The Cancer Genome Atlas.
and 41 nontumor tissues showed high Elafin mRNA levels in cancer samples and matched adjacent nontumor samples in all cases, except some subgroups without statistically significant differences, i.e., stage III of clinical stage, stage T4 of tumor invasive, and stage N1 of lymph node metastasis (Table 3).

### 3.3. The Relationship between Elafin Expression and Clinicopathological Features in Colorectal Cancer Patients.

The relationship between Elafin expression and clinicopathological features was analyzed by immunostaining scores and mRNA data of colorectal cancer patients. The 77.27% (68/88) cancer tissues revealed high scores of immunohistochemical method. As shown in Table 4, no statistically significant correlation was found, both at protein and mRNA level, between the Elafin expression and the age, gender, tumor invasive stage, lymph node metastasis, and distant metastasis. However, Elafin expression was correlated with clinical stage based on the American Joint Committee on Cancer (AJCC) guidelines at a protein level ($P = 0.028$) but not mRNA level ($P = 0.537$).

### 3.4. Survival Analysis of Elafin Expression in Colorectal Carcinoma Patients.

The overall survival (OS) was compared between high and low protein levels of Elafin in 88 colorectal cancer patients. The mean overall survival time was 1530.95 ± 170.05 days in the low-expression group compared with 1636.74 ± 112.44 days in the high-expression group (Figure 2). Nonsignificant differences in the OS between two groups were found ($P = 0.504$).

### 4. Discussion

Elafin, a low molecular weight antiproteinase, was detected in some human epithelial tissues, including bronchial epithelium, intestine epithelium, female genital epithelium, and breast epithelium, and some immunocytes, such as monocytes, alveolar macrophagocytes, neutrophilic granulocytes, and T cells. Elafin have several functions, such as anti-inflammatory, immune regulation, antimicrobial, antiproliferation, vascular remodeling, and wound healing [6]. The expression of Elafin is associated with several inflammatory diseases. For example, the increased expression of Elafin was displayed in patients with psoriasis [15]; however, Elafin levels were decreased in subjects suffering from periodontitis [16], bacterial vaginosis [17], asthma [18], and acute respiratory distress syndrome [19]. Recently, we also found that Elafin was decreased in patients of active IBD and correlated with disease activity negatively [8]. The previous results suggested that intestinal protease and antiprotease imbalance might play an important role in IBD patients, which could...
influence the intestinal inflammation. But another possibility is that the downregulation of Elafin was a consequence in the progression of IBD instead of the cause. Moreover, several studies revealed that exogenous administration of human recombinant Elafin protects against inflammation in animal models. For instance, Vachon et al. [20] found that lung cell lines with high Elafin expression showed reduced inflammatory responses compared to those with low expression.

Table 4: Correlation of Elafin expression with clinicopathological characteristics of colorectal cancer patients.

| Clinical feature                | Total (N) | IHC High n (%) | IHC Low n (%) | χ² | P value | Total (N) | PI3 levels | t | P value |
|--------------------------------|-----------|----------------|---------------|----|---------|-----------|------------|----|---------|
| Age <65                        | 36        | 26 (72.2)      | 10 (27.8)     | 0.885 | 0.347   | 167       | 178.54 ± 374.87 | 0.086 | 0.931   |
| Age ≥65                        | 52        | 42 (80.8)      | 10 (19.2)     | 0.018 | 0.892   | 271       | 175.12 ± 418.71 | -0.799 | 0.425   |
| Gender Male                    | 50        | 39 (77.6)      | 11 (22.4)     | 0.018 | 0.892   | 230       | 161.82 ± 415.29 | 0.617 | 0.537   |
| Gender Female                  | 38        | 29 (76.3)      | 9 (23.7)      | 4.849 | 0.028   | 208       | 192.57 ± 387.41 | 0.617 | 0.537   |
| Clinical stage I-II            | 41        | 36 (87.8)      | 5 (12.2)      | 0.097 | 0.755   | 248       | 186.81 ± 424.74 | -0.183 | 0.855   |
| Clinical stage III-IV          | 47        | 32 (68.1)      | 15 (31.9)     | 3.26  | 0.071   | 190       | 162.87 ± 371.21 | 0.390 | 0.697   |
| Tumor invasive T1-T3           | 64        | 50 (78.1)      | 14 (21.9)     | 3.26  | 0.071   | 384       | 175.11 ± 375.95 | 0.390 | 0.697   |
| Tumor invasive T4              | 24        | 18 (75.0)      | 6 (25.0)      | 0.901 | 0.343   | 54        | 185.79 ± 558.44 | 0.150 | 0.881   |
| Lymph node metastasis N0       | 42        | 36 (85.7)      | 6 (14.3)      | 0.097 | 0.755   | 257       | 182.72 ± 417.92 | 0.390 | 0.697   |
| Lymph node metastasis N1-N2    | 46        | 32 (69.6)      | 14 (30.4)     | 0.901 | 0.343   | 281       | 167.48 ± 379.54 | 0.150 | 0.881   |
| Distant metastasis M0          | 83        | 65 (78.3)      | 18 (21.7)     | 5.23  | 0.022   | 327       | 176.37 ± 514.35 | 0.150 | 0.881   |
| Distant metastasis M1          | 5         | 3 (60.0)       | 2 (40.0)      | 0.901 | 0.343   | 64        | 184.85 ± 392.55 | 0.150 | 0.881   |

Continuous variables are presented as the mean ± SD. IHC: immunohistochemistry; TCGA: The Cancer Genome Atlas.

Figure 2: Survival analysis in 88 colorectal cancer patients between high and low expression of Elafin. The mean overall survival time was 1530.95 ± 170.05 days in the low-expression group compared with 1636.74 ± 112.44 days in the high-expression group.
alveolar spaces of mice treated with recombinant human Ela-
fin intranasally reduced LPS-induced neutrophil infiltration
and inflammation biomarkers of MIP-2 and KC significantly.
Motta et al. [9] engineered lactic acid bacteria-expressed
recombinant Elafin and administrated them to mouse
models of acute and chronic colitis, which showed the remis-
sion of inflammation and the restoration of intestinal
homeostasis. Bermúdez-Humarán et al. [21] compared the
efficacy of lactobacillus secreting Elafin, IL-10, and TGF-β1
in the mouse models of colitis, suggesting that lactic acid
bacteria producing IL-10 or TGF-β1 only worked on some
inflammatory parameters, but administration of Elafin led
to a significant reduction of all inflammatory indicators.
Based on these results, Elafin delivered by lactic acid bacteria
can be an efficient treatment for IBD patients in the future.
However, the differential expressions of Elafin have been
reported in several tumors, which were even associated with
poor outcome, including ovarian cancers [12], breast tumors
[14], and esophageal cancers [13]. A question was raised
based on these findings; delivery of Elafin by lactic acid
bacteria to treat IBD patients is safe or carcinogenic. But
little data have showed the expression of Elafin in patients
doctoral cancer, which cannot illuminate its role in
colorectal tumors.

Based on what we know, this is the first study to explore
the Elafin expression in colorectal cancer. In this study, 77.3%
colorectal cancer tissues indicated an increased expression of Elafin compared with 59.1% matched adjacent
noncancerous tissues. And the Elafin mRNA was upregu-
lated about twofold in colorectal cancer samples as compared
to adjacent noncancerous samples without significance.
Several previous studies reported a similar trend in other
tumors. Labidi-Galy et al. [12] showed that the Elafin expres-
sion of high-grade ovarian carcinoma was upregulated.
Yamamoto et al. [13] indicated 73.5% of esophageal cancer
patients observed immunoreactivity with Elafin antibody
and Elafin expression was associated with differentiation
degree. However, Caruso et al. [14] pointed out that the
expression of Elafin was decreased in 24% of ductal carci-
noma in situ and 83% of invasive breast tumor as compared
to normal breast tissues. These results suggested that the
pleiotropic expression of Elafin was observed on tumors,
which need to be confirmed in different cancers.

Furthermore, our result suggested the Elafin expression
was associated with clinical stage based on the AJCC guide-
lines at protein levels but not mRNA levels. And nonsignifi-
cant differences in the overall survival (OS) between high
and low groups of Elafin levels were found in this study. This
similar trend was also observed in esophageal cancers [13],
by the contrast the levels of Elafin drove poor outcome in
ovarian carcinoma, glioblastoma, and breast tumor and was
related with cell proliferation [12, 14]. Therefore, the Elafin
expression changed and the relationship between Elafin
levels and clinicopathological factors was also different over
various cancers.

Although our data showed that Elafin levels might not
affect the progress of colorectal cancer obviously, upregula-
tion of Elafin was observed in cancer tissues, especially in
an early stage. Several clinical studies have reflected chronic
inflammation status that showed an increasing risk of devel-
opning colorectal cancer; the pattern was widely known as
inflammation-dysplasia-carcinoma [22]. Elafin expression
was increased in an early stage of colorectal cancer, which
might be an adaptive elevation with the inflammatory status.
But downregulation of Elafin in malignant tumor might be
due to the changed inflammatory microenvironment or the
exhaustion of Elafin. And we found that Elafin expressed
both in epithelium and immune cells in normal colonic
mucosa while it was mainly stained in epithelium. In addition
to increased secretion of epithelial cells, we need to pay atten-
tion to the role of immune cell-related Elafin expression in
the progression of colon cancer. But there are some limita-
tions to observe potential sources of Elafin expression.
Tumorigenesis impaired the normal structure of colonic
mucosa, and pathological sections can only evaluate sever-
sites in colorectal cancer. The role of Elafin expression in
the development of colorectal carcinoma needed more
fundamental research in the future.

5. Conclusion
Elafin was upregulated in patients of colorectal cancer, result-
ing to potential limitations for exogenous Elafin treatment.

Data Availability
The clinical data used to support the findings of this study are
included within the article.

Conflicts of Interest
The authors have no conflict of interest.

Authors’ Contributions
Yun Liu and Yu Tian contributed equally to this work.

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