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Research Paper

Effects of Tumor-associated *E. coli* Metabolites on Migration of Colorectal Cancer Cells

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ABSTRACT

Introduction: Colorectal tumors have a close connection with the gut microbiome. A correlation between rearrangement in microbiome composition and disease progression has already been shown. However, the mechanisms underlying interactions between microorganisms and cancer cells, as well as the immediate effects of tumor-associated microbiomes on cancer cells, remain unclear.

Materials & Methods: In this work, we investigated the effects of metabolites produced by tumor-associated *Escherichia coli* strains on the migration of human colorectal cancer cell lines (HCT116, SW480 and HT29).

Results: We identified differences in some biochemical enzyme activity of *E. coli* strains and in the spectrum of synthesized organic acids between tumor-associated strains and the probiotic *E. coli* M-17 strains. Most strains associated with colorectal cancer were unable to utilize sucrose. Specifically, tumor-associated *E. coli* produced more fumaric, malic and maleic acids, whereas the *E. coli* M-17 produced more short-chain fatty acids such as propionic, 2-oxobutyric, and α-ketoglutaric acids (AKGs). Upon exposure to metabolites from tumor-associated *E. coli* strains, HCT116 and SW480 cells showed an increased migration activity, whereas HT29 cells showed decreased migration activity in both 2D and 3D culture models. Immunocytochemistry assay revealed a decrease in E-cadherin in HCT116 and SW480 cells and focal adhesion kinase (FAK)- in HT29, which explains the different effects of *E. coli* metabolites on migratory capacity of colorectal cancer cells.

Conclusion: Therefore, these results suggest that the effect of tumor-associated *E. coli* strains on cancer cells migration depends on their innate type of migration and enhances FAK-dependent single-cell migration accompanied by the loss of E-cadherin in cancer cells with initially low FAK expression. In contrast, this effect was not observed in cancer cells exhibiting a collective migration phenotype.

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1. Introduction

Colorectal cancer is one of the most common malignancies remains a lethal disease worldwide [1]. In the case of colorectal cancer, the microbiota and its metabolites are considered an essential player in the disease progression [2]. It is generally accepted that there are close associations between gut microbiota composition and its metabolites [3] as well as the progression of colorectal cancer [4]. Crosstalk between the host cancer cells and the gut microbiota, mediated by metabolites, can promote cancer progression, and enhanced invasiveness and cancer cell survivability. However, the direct effects of microorganisms and their metabolites on cancer cells have been poorly described.

Escherichia coli is one of the most common representative of the colon microbiota. Commensal *E. coli* is known to promote the regeneration of damaged colon epithelial cells [5]. However, increased colonization of the colonic mucosa by mucosa-associated *E. coli* has been found in patients with colorectal cancer [6].

Our study was designed to understand the role of *E. coli* metabolites isolated from patients' tumor samples in regulating the migratory capacity of colorectal cancer cells. The effects of these metabolites on the migration of three colorectal cancer cell lines were examined on cell monolayers and 3D tumor spheroids.

2. Materials and Methods

2.1. Bacterial strains and cultivation

E. coli strains (Col-93, Col-101, Col-102, Col-103) were isolated from colorectal cancer biopsy samples. Human colon samples were collected at Nizhny Novgorod Regional Oncologic Hospital (Russia). The study involving patients' samples was approved by the Ethics Committee of the Privolzhsky Research Medical University. All methods were carried out in accordance with relevant guidelines and regulations.

Bacterial species identity was determined using matrix- assisted laser desorption/ ionization-time of flight mass spectrometry (MALDI ToF Autoflex speed, Bruker Daltonik GmbH, Germany). Biochemical properties were studied using bacterial biochemical identification kits (RPC Diagnostic Systems, Russia). Routine cultivation was carried out using nutrient agar (24 h, 37 ˚C). Probiotic strain of *E. coli* M17, which is widely used as a component of probiotic drugs to correct dysbiotic conditions, served as a positive control in all the experiments.

2.2. Metabolite preparation

Bacterial strains were seeded in modified eagle medium (DMEM) containing 4.5 mg/L glucose (PanEco, Russia) at a concentration of 1×10^6 CFU/mL and cultured for 24 hours at 37 ˚C. Metabolites were obtained by filtration of the growth media through bacterial filter 0.2 µm (Corning, USA). The resulting solution was diluted 1:1.5 with DMEM with 5% fetal bovine serum (FBS). The final medium was checked for pH, which was in neutral range (7.0-7.2).

2.3. Target liquid chromatography – mass spectrometry analysis

Cell-free metabolites were prepared by centrifuging cultures at 20,000 rcf for 20 minutes. Finally, they were filtered through 0.2 µm filters (Corning, USA). High-performance liquid chromatography coupled with electrospray ionization triple quadrupole tandem mass spectrometry was used for detection of short-chain fatty acids (SCFAs) and organic acids in supernatant liquid. Samples of metabolites were prepared according to the manufacturer's instructions (Shimadzu Corporation) and analyzed using a mass spectrometer liquid chromatography-MS (LC-MS)-8050 coupled with the Nexera XR liquid chromatography system (Shimadzu, Japan).

2.4. Antibiotic susceptibility testing

The disk diffusion susceptibility test was used to determine the susceptibility of isolates of *E. coli* to 9 antibiotics: Ampicillin, trimethoprim, amoxicillin, norfloxacin, ciprofloxacin, ofloxacin, cefotaxime, ceftriaxone, and ceftazidime. The test was performed according to standard protocol. A bacterial inoculum $1–2\times10^8$ CFU/mL was applied to the surface of a 60 mm nutrient agar plate. A commercially prepared, fixed-concentration paper antibiotic disk was placed on the inoculated agar surface. The results were assessed after 18–24 h incubation of the plates at 37 ˚C. The zones of growth inhibition surrounding the antibiotic disk were measured to the nearest millimeter. Zone diameters of each drug were interpreted according to the manufacturer's instruction (NICF, Russia).

2.5. Matrix production assay

To analyze matrix production, the biofilms were grown for 48 hours in DMEM with 4.5 mg/L glucose (PanEco, Russia) in 96-well plates at a bacterial concentration of

1×10^6 CFU/mL. Then the bacterial biofilms were washed three times with phosphate buffered saline (PBS) and stained by Congo red for 15 minutes. The staining solution containing 1% Congo red and 10% Twin 80 was prepared in PBS. After staining, plates were washed three times with PBS, and ethyl alcohol was used for extraction of Congo red from the cells. Optical density (OD) was measured at 500 nm using BioTek Synergy Mx multichannel spectrophotometer (BioTek, USA).

2.6. Bacterial biomass growth

Biofilms were washed three times with PBS, fixed with 96% ethyl alcohol for 15 minutes, and stained with 0.1% gentian violet solution (3 minutes). The dye was then eluted by 96% ethyl alcohol under constant shaking (10 minutes) and the optical density was measured using a multichannel spectrophotometer at a wavelength of 570 nm.

2.7. Colon cancer cell lines

Human colon adenocarcinoma cell lines HCT116, SW480 and HT29 were routinely cultured in DMEM (PanEco, Russia) with 5% fetal bovine serum (HyClone, USA) and passaged twice a week. The cells were cultured in a CO_2-incubator, 37 ˚C, RH 80%, CO_2 5%. All cell lines were obtained from the cell collection of the Ivanovskiy Institute of Virology (Moscow, Russia).

2.8. Spheroids formation and cell migration assay

To obtain tumor spheroids, HCT116 and HT29 cancer cells were seeded in low -attachment 96-well plates (Corning, USA) at 200 cells per 200 µL /well and cultured in the presence of bacterial metabolites. The bacterial metabolites were obtained after overnight culturing of bacterial strains in DMEM with 4.5 mg/L glucose (PanEco, Russia) at a concentration of 1×10^6 CFU/mL at 37 ˚C, filtered (0.2 µm, Corning, USA) and diluted 1:1.5. Spheroids grown in a pure DMEM medium (200 µL per well) were used as a negative control. The size of spheroids was measured in days 3, 5 and 7 for HCT116, and on 4 and 7 days for HT29, because the latter have lower cell division rate.

For the migration assay the spheroids after 5 days of culturing were used. They were gently transferred to a small Petri dish (3.5 mm) and incubated for either 2 (HCT116) or 5 days (HT29). Light microscopy images of the spheroids were acquired after their attachment using DMIL microscope (Leica, Germany) at magnification 100x, and the zones of cell migration were measured using ImageJ software, version 1.4.3.67.

2.9. Wound healing assay

The study of migration activity was carried using the wound healing model with cultural inserts 2 Well (Ibidi, USA). A cell suspension (70 µL) with a concentration of 1×10^5 cells/mL was placed into the wells, incubated for 24 hours (37˚ C, 5% CO_2), and silicone liners were removed after the formation of the monolayer. Then, we added medium contained bacterial metabolites (1:1.5) and cultured until "healing" the monolaer "wound". We changed medium every 2 days. Light microscopy images (Leica, Germany) of the "wounds" were obtained in 1-5 days after removal of the liners at 100x magnification. Migration zones were measured using ImageJ software, version 1.4.3.67.

2.10. Immunostaining assay

For immunocytochemical staining, cells were cultured in 96-well plates for 24 hours after seeding and fixed in 4% formaldehyde for 15 minutes. The following primary antibodies were used: rabbit antibodies against E-cadherin (ab15148, Abcam, USA), rabbit antibodies against focal adhesion kinase (FAK) (ab131435, Abcam, USA). Subsequently, cells were stained with Alexa555-labeled goat anti-rabbit IgG secondary antibody (ab6825, Abcam, USA). Staining was performed in accordance with the manufacturer's protocol. In addition, the cells were stained using DAPI (1:1000) to visualize the cell nuclei and detect cancer cells. Fluorescence images were observed using DMIL fluorescence microscope (Leica, Germany) equipped with the following filters: A4 UV BP 360/40 400 BP 470/40 for DAPI and TX2 green BP 560/40 595 BP 645/75 for Alexa. Intensity values in Figure 4 were obtained while processing photos in the ImageJ software, version 1.4.3.67. Zones with a non-zero signal were selected for processing, and average fluorescence intensity normalized per area was calculated.

2.11. Statistical analysis

Statistical analysis was performed using Statistica software, version 10 (StatSoft. Inc., Tusla, OK, USA). The nonparametric Mann-Whitney U-test was used to compare the data. $P\leq0.05$ were considered statistically significant.

3. Results

Four bacteria species were isolated from patients' tumor and identified as *E. coli* using a combination of biochemical assay and MALDI ToF spectroscopy. Antibiotic sensitivity and biochemical enzyme activity for the tumor-associated *E. coli* strains were obtained and compared with those of standard probiotic *E. coli* M17 strain. Unlike M17, all tumor-associated *E. coli* strains were resistant to at least one of the tested antibiotics. Three out of four strains (Col-101, Col-102, Col-103) were resistant to ampicillin, and one (Col-93) was resistant to amoxicillin (Figure 1A).

Analysis of biofilm activity showed that three tumor-associated strains (Col-93, Col-101, Col-103) increased biomass and synthesized a matrix less actively compared to M17 strain (Figure 1B). One strain (Col-102) demonstrated statistically higher reproduction rate and produced the same volume of matrix as M17. Biochemical activity of the strains varied in some aminoacids and especially in sucrose. Most strains associated with colorectal cancer were unable to utilize sucrose, which is typically observed in only a few *E. coli* that are typically slow- growing or pathogenic strains [7]. Differences in both the proportion and composition of the synthesized metabolites were found between tumor-associated and the probiotic strains. However, the proportion of dominant metabolites (mg/mL) was similar accross all strains (Figure 1C), tumor-associated and M17 control.

While the balance of minor components (µg/mL) was different for the tumor-associated *E. coli* strains compared to M17 control (Figure 1D).

We found higher levels (P≤0.05) of butyric, fumaric, maleic, and glycolic acids in the metabolites of tumor-associated strains compared to probiotic strain M17 (Table 1). The amount of malic acid was increased in Col-101 metabolites was more than 5 times higher than in the other strains and M17. Pyruvic acid and valeric acid level was higher in tumor-associated strains, especially for Col-101, Col-102 and Col-103 (P≤0.05). Daily production of SCFAs such as 2-oxybutyrate, propionate, malonic acid, 2-hydroxyglutaric, 2-oxobutyric, isobutyric acid, α-ketoglutaric acid (AKG) and isobutyric acid by tumor-associated strains was lower (2-5 times) compared to probiotic strain M17 (Table 1). Succinic acid was decreased in all patients' strain metabolites. No changes were observed for isovaleric acid and glyoxylic acid.

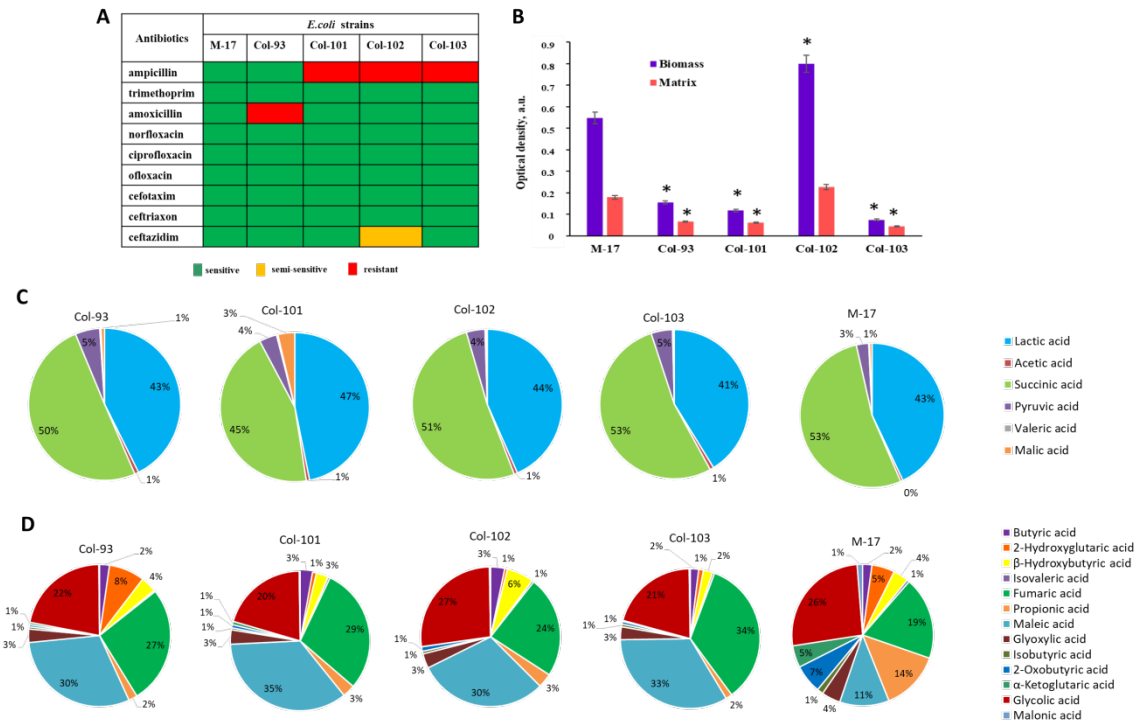

Figure 1. Characterization of patients' derived *E. coli* strains: Antibiotic susceptibility (A), biomass and matrix production of different *E. coli* strains (B), proportion of selected major (C) and minor (D) metabolites produced by *E. coli* strains (C)

Note: Data are presented as Mean±SD, n=10, *P≤0.05 with M17.

Pyruvic acid and valeric acid levels were also elevated in tumor-associated strains, particularly in Col101, Col102, and Col103 (P≤0.05). Daily production of SCFAs—including 2oxybutyrate, propionate, malonic acid, 2hydroxyglutaric acid, 2oxobutyric acid, isobutyric acid, AKG, and isobutyric acid—was 2–5 times lower in tumor-associated strains compared to the probiotic strain M17 (Table 1). Succinic acid levels were reduced in all patient derived strain metabolites. No significant changes were observed for isovaleric acid or glyoxylic acid.Metabolites of the probiotic strain M17 did not affect the migration of HCT116 cells from spheroids and slightly inhibited the migration of HT29 cells (P=0.035) compared to the control without metabolites (Figure 2).

Metabolites of the probiotic strain M17 did not affect migration of HCT116 cells from the spheroids and slightly (P=0.035) inhibited migration of HT29 cells compared to control without any metabolites (Figure 2).

Tumor-associated *E. coli* strains metabolites had different effects on migration of HCT116 and HT29 cells. HCT116 cell line showed higher migration activity in the presence of metabolites from all tumor-associated strains compared to control without any metabolites and M17 strain (Figure 2A). The largest migration area was observed upon exposure to the Col-101 metabolites.

Table 1. Daily production of the selected metabolites by *E. coli* strains

Analyte	Mean±SD				
	M17	Col-093	Col-101	Col-102	Col-103
Lactic acid (mg/L)	138.6±13.3	102.2±39.4*	123.8±23.9	124.6±8.1	112.5±3.7*
Acetic acid (mg/L)	1.7±0.1	2±0.8	1.9±0.2	2.1±0.1*	2.3±0*
Succinic acid (mg/L)	170.8±18.5	120.5±40.7*	118.2±11.4*	147.4±2.1*	144.6±4.1*
Pyruvic acid (mg/L)	8.9±0.9	12.6±4.4	10.1±1.2	11.6±0.6*	12.7±0.2*
Malic acid (mg/L)	1.8±0.3	1.8±0.6	9.7±1.3*	0.5±0.03*	0.3±0.02*
Valeric acid (mg/L)	0.6±0.09	0.6±0.2	0.8±0.09*	0.8±0.01*	0.8±0.04*
β-Hydroxybutyric acid (µg/L)	31.4±2.9	43.6±19	35.8±6.1	70±8.3*	30.2±5.3
ropionic acid (µg/L)	122.7±23	24.2±8.5*	37.3±4.3*	37±2.9*	21±2.6*
Isobutyric acid (µg/L)	12.7±2.4	6.1±0.1*	6.1±0.6*	6.9±2*	8.5±1.6*
Butyric acid (µg/L)	19.1±3.8	27.3±10.3	36.1±4.1*	36.4±4*	27.3±1.4*
2-hydroxyglutaric acid (µg/L)	47±6.1	98.7±43*	11.9±0.8*	6.9±2.8*	15.2±1.8*
Isovaleric acid (µg/L)	5.2±1	4.2±1.9	5.9±1.8	5.1±1.3	6.5±0.5
Fumaric acid (µg/L)	170.1±16.1	325.6±114.8*	372.3±53.2*	263.2±27.2*	476.8±15.5*
Maleic acid (µg/L)	101.8±6.1	366.3±229.3*	446.1±59.6*	337.4±15.9*	465.1±63.5*
Glyoxylic acid (µg/L)	38.9±3.3	36.9±11.9	42.1±5.2	37.8±8.4	41.6±7.4
2-oxobutyric acid (µg/L)	59±5.3	6±2.1*	9.1±3.6*	11.5±0.6*	8.8±0.7*
AKG (µg/L)	45.2±16.5	6.3±5.7*	9.9±1.9*	0.5±0.2*	3.4±1*
Glycolic acid (µg/L)	235.8±35.3	264.7±72.9	257.9±34*	301.5±2.5*	286.4±10.1*
Malonic acid (µg/L)	11.2±2.8	2±1.3*	2.9±0.4*	3±1*	3.3±1.5*

*P≤0.05 vs M17.

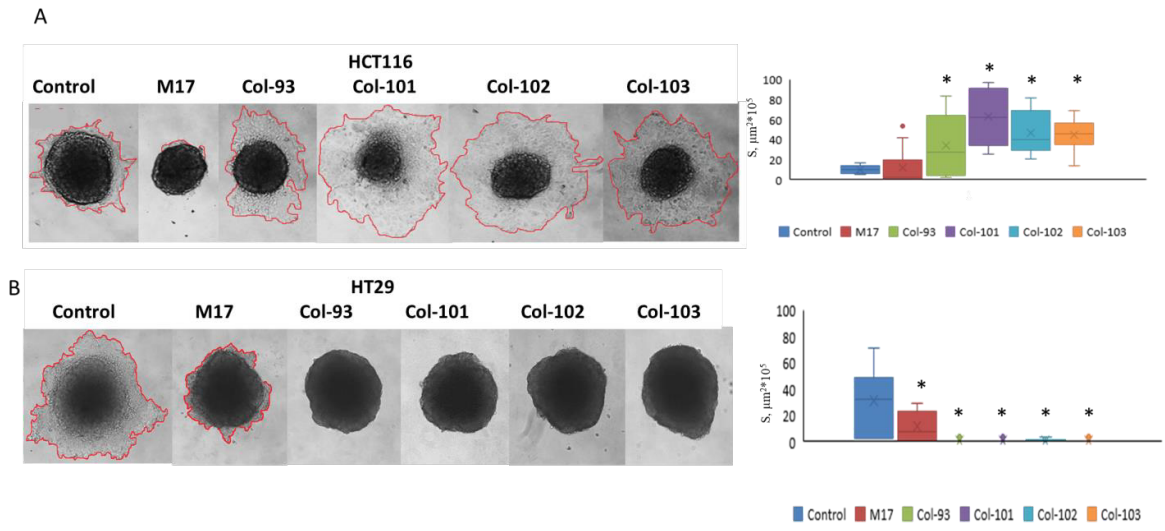

Figure 2. Migration of colorectal cancer cells from the spheroids in the presence of bacterial metabolites: Light microscopy images and the migration area (square) of HCT116 (A) and HT29 (B) spheroids

Note: Data are presented as Mean±SD, n=7, *P≤0.05 with control without metabolites.

The opposite effects were observed for HT29 cells, which actively migrated in control without metabolites but inhibited migration in the presence of *E. coli* metabolites (Figure 2B).

Analysis of cell migration in the model of monolayer "wound healing" was performed for the three cell lines HCT116, SW480 and HT29. Two *E. coli* strains, Col-101 and Col-102, were selected for this test as they demonstrated the most notable effects among other strains obtained from the patients.

Similar to migration from the spheroids, patient-derived *E. coli* metabolites stimulated migration of HCT116 and SW480 cells and inhibited migration of HT29 cells in the "wound healing" model (Figure 3).

Tumor-associated *E. coli* metabolites had distinct effects on the migration of HCT116 and HT29 cells. The HCT116 cell line exhibited increased migratory activity in the presence of metabolites from all tumor-associated strains compared to both the control without metabolites and the M17 strain (Figure 2A). The greatest migration area was observed following exposure to Col101 metabolites.

In contrast, HT29 cells showed the opposite response: They migrated actively in the control condition without metabolites but demonstrated inhibited migration when exposed to *E. coli* metabolites (Figure 2B).

Cell migration was further analyzed using the monolayer "wound healing" model in three colorectal cancer cell lines—HCT116, SW480, and HT29. Two *E. coli* strains, Col101 and Col102, were selected for this assay because they exhibited the most pronounced effects among the patient derived isolates.

Consistent with the spheroid migration results, metabolites from patient derived *E. coli* strains stimulated migration of HCT116 and SW480 cells while inhibiting migration of HT29 cells in the wound healing model (Figure 3).

The M17 metabolites did not change migration of HCT116 and SW480 cells and inhibited migration of HT29 cells. Therefore, the experiments on the cell monolayers and tumor spheroids revealed that tumor-associated *E. coli* metabolites affected migratory capacity of colorectal cancer cells and could either increase or decrease it depending on the specifics of cancer cells.

To identify the molecular mechanisms through which *E. coli* metabolites had different effects on colorectal cancer cell lines, the expression levels of E-cadherin and the FAK were analyzed using immunofluorescence.

E-cadherin expression decreased (P≤0.05) in HCT116 and SW480 cell lines upon exposure to metabolites of the Col-101 strain (Figure 4).

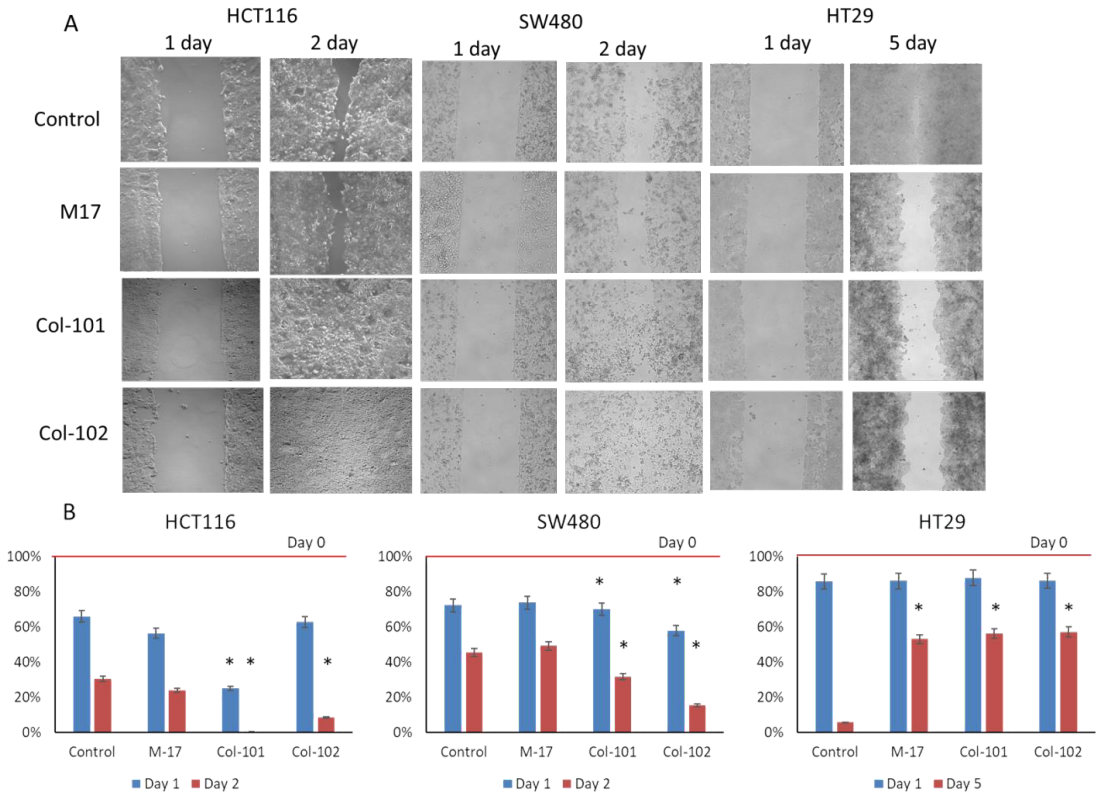

Figure 3. The "wound healing" assay in the presence of *E. coli* metabolites

A) Light microscopy images of HCT116, SW480 and HT29 cells; B) The relative square of the "wound" in the cell monolayer

Note: Data are presented as Mean±SD, n=7, *P≤0.05 with control without metabolites at the same day.

Metabolites of the M17 strain did not alter the migration of HCT116 and SW480 cells but inhibited the migration of HT29 cells. Overall, experiments using both cell monolayers and tumor spheroids demonstrated that tumor-associated *E. coli* metabolites modulate the migratory capacity of colorectal cancer cells and can either enhance or suppress migration depending on the intrinsic properties of the cancer cell line.

To identify the molecular mechanisms underlying these differential effects, the expression levels of Ecadherin and FAK were examined using immunofluorescence analysis. Ecadherin expression significantly decreased (P≤0.05) in HCT116 and SW480 cells following exposure to metabolites from the Col101 strain (Figure 4).

The probiotic M17 strain induced a marked increase (P≤0.05) in E-cadherin level only in HT29 cells, and had no effect on two other cell lines. Since down-regulation of E-cadherin, a major component of adherens junctions, facilitates cell motility and migration, its lower level in HCT116 and SW480 cells correlated with their highest migratory activity upon incubation with Col-101 metabolites.

FAK expression decreasing (P≤0.05) was noted in HT29 cells under the bacterial metabolites of all tested strains, which explains a decrease of migratory capacity of this cell line. Inhibition of FAK activity is known to decrease cell motility due to suppression of cell-matrix attachment. Of note, the initial FAK activity in HT29 cells was higher compared with other cell lines, suggesting their higher migratory potential. In HCT116 and SW480 cell lines FAK level did not change after incubation with bacterial metabolites (Figure 4B). These results suggest that changes in migratory capacity of colorectal cancer cells under the exposure to tumor-associated *E. coli* metabolites can be mediated by both the loss of cadherin-based cell–cell adhesions and attenuation of the FAK signaling.

4. Discussion

It is known that tumor-associated microorganisms play a critical role in the progression of colorectal cancer [8]. However, the mechanisms underlying the impact of microbiome on tumor progression remain poorly elucidated. Here, we analyzed the effect of probiotic and tumor-associated *E. coli* strains on migratory capacity of colorectal cancer cells in vitro.

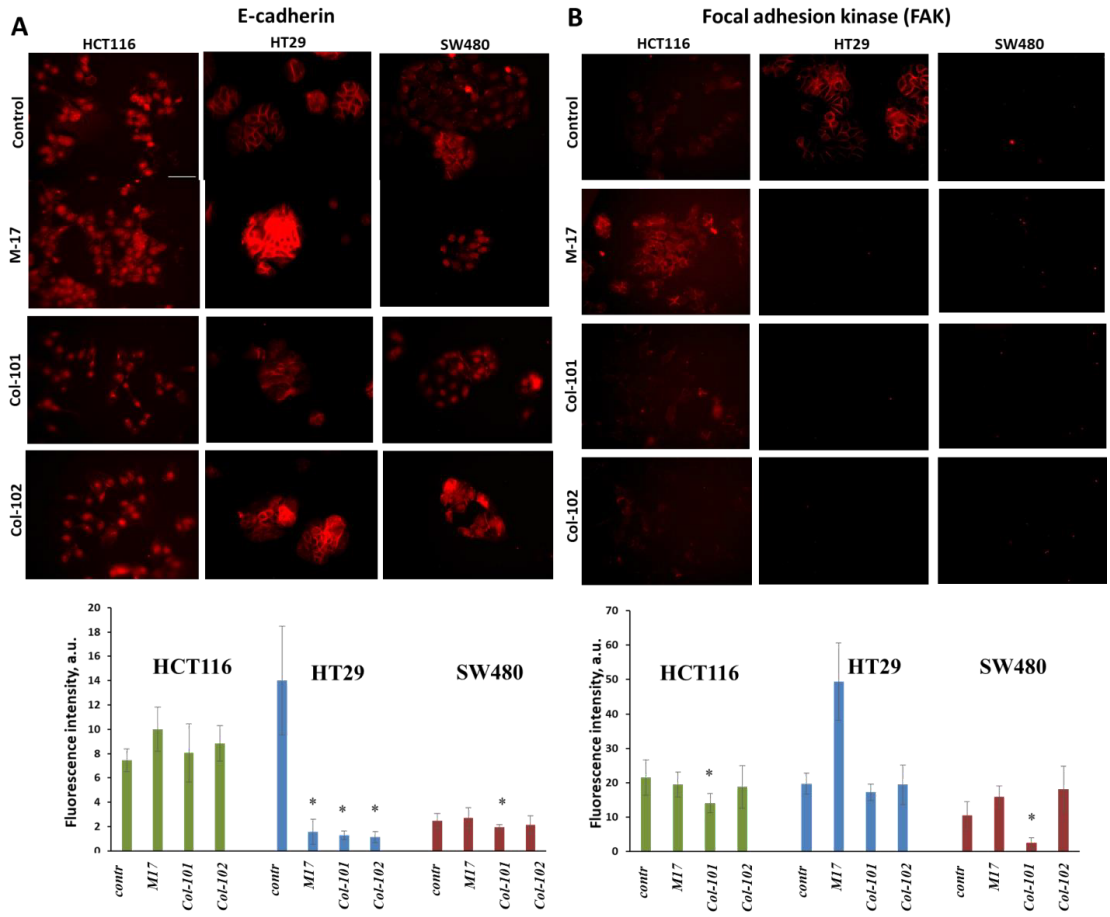

Figure 4. E-cadherin and FAK expression under exposure of cancer cells to *E. coli* metabolites

A) Fluorescence microscopy images of E-cadherin expression and quantification of fluorescence intensity; B) Fluorescence microscopy images of FAK expression and quantification of fluorescence intensity

Note: Scale bar 50 µm for all images. Data are presented as Mean±SD, n=25. *P≤0.05 with control without metabolites.

First, we compared general characteristics of *E. coli* strains obtained from colorectal cancer patients with the standard probiotic strain M17 and found numerous differences between them. Specifically, the tumor-associated strains showed resistance to at least one antibiotic tested, primarily β-lactam antibiotics (ampicillin, amoxicillin), which can be associated with their ability to intracellularly survive during antibiotic treatment [9]. In addition, their biomass growth and biofilm matrix synthesis were reduced compared to M17, indicating that growth on the enterocytes surface is not a dominant type of growth for tumor-associated strains. Also, it was noticed that tumor-associated strains were adapted to utilize glucose, rather than complex disaccharides due to decreased sucrose-related saccharolytic activity, which can be explained by the competition for the intracellular glucose with cancer cells. Previously, it has been shown that intracellular localization provides numerous advantages to the invading microbes, including the immune escape and a favorable nutritional environment. A low microbial biomass is consistently present in colorectal tumors, and they play an important role in cancer development [9].

Characterization of the spectrum of organic acids synthesized by different *E. coli* strains during their metabolism showed that the proportion and the level of synthesized substances were different for the probiotic and tumor-associated strains. The positive impact of microbiota is mostly connected with the production of SCFAs as a result of fermentation of dietary fibers, which are commonly indigestible by the human enzymes. SCFAs are thought to serve as anti-inflammatory substances in the gut, improving the intestinal epithelium barrier and can induce apoptosis of colorectal cancer cells [10, 11].

An excess of malonic acid and AKG was produced by the probiotic strain. Malonic acid inhibites succinate dehydrogenase. The succinate and succinate dehydrogenase complex are the central link of the Krebs cycle and regulates the mitochondrial respiratory chain and provides antioxidant defense by binding excess iron ions [12]. Antitumor effect of AKG was demonstrated on human lung carcinoma H460 and colon adenocarcinoma cell lines HCT116 [13]. Multiple studies have shown that metabolites such as butyrate, propionate, acetate, and niacin contribute to protection of the host against malignation and represent an energy source for the colon epithelial cells [14]. However, the oncometabolites like the lactate, glutamate, fumarate, and succinate are involved in tumor survival and progression [15, 16]. Oncometabolites make the tumor microenvironment more favorable for cell migration [17]. In the study by Ternes et al. it was shown that gut microbial metabolite formate, produced by *F. nucleatum*, enhanced migration potential of HCT116 cells through the formation of focal adhesion points [18]. Sciacovelli et al. showed on renal cancer patients that fumaric acid inhibits tet-mediated demethylation of a regulatory region of the antimetastatic miRNA cluster miR-200ba429, leading to the expression of EMT (epithelial-mesenchymal transition)-related transcription factors, which, in its turn, results in enhanced migratory properties and poor clinical outcome [19]. Malic acid was increased in malignant prostatic hyperplasia, suggesting that this metabolite can be used as a biomarker of prostate cancer [20].

The results of our study showed that metabolites of tumor-associated *E. coli* strains had different effects of migration capacity of colorectal cancer cells depending on their original properties.

Here, we observed more active migration of HCT116 and SW480 cells and inhibition of migration of HT29 cells in the monolayer "healing" model under *E. coli* metabolites. Similar results were obtained using the model of 3D tumor spheroids. We assume that these differences could be associated with different expressions of proteins involved in the processes of intercellular adhesion and adhesion to the substrate, such as E-cadherin and FAK. According to "the human protein atlas" HT29 cell line initially has high expression of genes, associated with collective migration, such as CDH1 (E-cadherin) and PDK2 (FAK) and low expression of single-cell migration-associated markers (ROCK1, EZR and TALIN). While HCT116 and SW480 have higher single-cell migration markers, indicating different types of cell migration specific to these cells. In HCT116 and SW480 cells, for which a single-cell migration is typical, the loss of E-cadherin was the main effect of *E. coli* metabolites. Also, it is worth noting that the most pronounced effect was shown for *E. coli* strain Col-101. It was isolated from the tumor with the most invasive phenotype with the presence of the distant metastases to the liver. Loss of E-cadherin expression results in loss of contact inhibition, increase of cell motility and subsequent single-cell migration [21]. In the work by Tarashi et al. similar effect of *Bacteroides fragilis* toxin that is associated with colorectal cancer on cleavage of E-cadherin and formation of invasive phenotype was demonstrated [22]. Thirunavukkarasan et al. showed that SCFAs increased the level of expression of E-cadherin, and therefore, prevented the formation of the invasive phenotype of cancer cells [23].

In collective cell migration, E-cadherin mediates epithelial cell–cell adhesion and its expression is required to maintain intercellular junctions [21]. In HT29 cells, characterized by collective migration, the main effect of bacterial metabolites was the loss of FAK, while the expression of E-cadherin did not change. It is known that FAK, when it becomes constitutively active due to mutations or elevated activity of alternative signaling pathways, exerts oncogenic properties and allows cancer cells growth and survival without anchorage to the ECM, which is an important step during metastatic process.

5. Conclusion

Our research showed that metabolites from tumor-associated *E. coli* strains enhanced FAK-dependent single-cell migration accompanied by the loss of E-cadherin in cancer cells with initially low FAK expression. At the same time, this effect was not observed in cancer cells with collective migration phenotype. Further studies of the effects of tumor-associated strains on migratory potential of different cancer types are important for development of microbiome correction strategies to improve cancer prognosis.

Ethical Considerations

Compliance with ethical guidelines

The study involving patients' samples was approved by the Ethics Committee of the Privolzhsky Research Medical University, Nizhny Novgorod, Russia (No.: 09 from 30.06.2023). All methods were carried out in accordance with relevant guidelines and regulations.

Data availability

The data that support the findings of this study are available on request from the corresponding author.

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Author's contribution

Conceptualization and supervision: Nadezhda Ignatova and Irina Druzhkova; Methodology and investigation: Maria Pryazhnikova, Alina Abidullina, Andrey Seliverstov, Irina Druzhkova and Nadezhda Ignatova; Writing the original draft: Nadezhda Ignatova, Maria Pryazhnikova, and Irina Druzhkova; Review and editing: Andrey Seliverstov, Sergey Gamayunov; Final approval: All authors.

Conflict of interest

The authors declared no conflict of interest.

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References

[1] Falih Soliman N, Jasim Mohamad B. Clinical and histopathological characteristics of colorectal cancer in Iraq between 2015-2021. Arch Razi Inst. 2022; 77(6):2407-13. [DOI:10.22092/ARI.2022.358613.2263] [PMID]

[2] Kim J, Lee HK. Potential role of the gut microbiome in colorectal cancer progression. Front Immunol. 2022; 12:807648. [DOI:10.3389/fimmu.2021.807648] [PMID]

[3] Leylabadlo HE, Ghotaslou R, Feizabadi MM, Farajnia S, Moaddab SY, Ganbarov K, et al. The critical role of Faecalibacterium prausnitzii in human health: An overview. Microb Pathog. 2020; 149:104344. [DOI:10.1016/j.micpath.2020.104344] [PMID]

[4] Ahmad Kendong SM, Raja Ali RA, Nawawi KNM, Ahmad HF, Mokhtar NM. Gut dysbiosis and intestinal barrier dysfunction: Potential explanation for early-onset colorectal cancer. Front Cell Infect Microbiol. 2021; 11:744606. [DOI:10.3389/fcimb.2021.744606] [PMID]

[5] Chen K, McCulloch J, Das Neves R, Rodrigues G, Hsieh WT, Gong W, et al. The beneficial effects of commensal E. coli for colon epithelial cell recovery are related with Formyl peptide receptor 2 (Fpr2) in epithelial cells. Gut Pathog. 2023; 15(1):28. [DOI:10.1186/s13099-023-00557-w] [PMID]

[6] Lichtenstern CR, Lamichhane-Khadka R. A tale of two bacteria - Bacteroides fragilis, Escherichia coli, and colorectal cancer. Front Bacteriol. 2023; 2:1229077. [DOI:10.3389/fbrio.2023.1229077]

[7] Mohamed ET, Mundhada H, Landberg J, Cann I, Mackie RI, Nielsen AT, et al. Generation of an E. coli platform strain for improved sucrose utilization using adaptive laboratory evolution. Microb Cell Fact. 2019; 18(1):116. [DOI:10.1186/s12934-019-1165-2] [PMID]

[8] Goubet AG. Could the tumor-associated microbiota be the new multi-faceted player in the tumor microenvironment? Front Oncol. 2023; 13:1185163. [DOI:10.3389/fonc.2023.1185163] [PMID]

[9] Schorr L, Mathies M, Elinav E, Puschhof J. Intracellular bacteria in cancer-prospects and debates. NPJ Biofilms Microbiomes. 2023; 9(1):76. [DOI:10.1038/s41522-023-00446-9] [PMID]

[10] Kaźmierczak-Siedlecka K, Marano L, Merola E, Roviello F, Połom K. Sodium butyrate in both prevention and supportive treatment of colorectal cancer. Front Cell Infect Microbiol. 2022; 12:1023806. [DOI:10.3389/fcimb.2022.1023806] [PMID]

[11] Bordonaro M. Further analysis of p300 in mediating effects of Butyrate in Colorectal Cancer Cells. J Cancer. 2020; 11(20):5861-6. [DOI:10.7150/jca.47160] [PMID]

[12] Orlov YP, Butrov AV, Sviridov SV, Afanasyev VV, Kondratiev AN, Tsentsiper LM, et al. Succinate and succinate dehydrogenase as a "fulcrum" in the Krebs cycle in critical conditions. Antibiot Chemother. 2023; 68(1-2):57-68. [DOI:10.37489/0235-2990-2023-68-1-2-57-68]

[13] Sica V, Bravo-San Pedro JM, Izzo V, Pol J, Pierredon S, Enot D, et al. Lethal poisoning of cancer cells by respiratory chain inhibition plus dimethyl α-Ketoglutarate. Cell Rep. 2019; 27(3):820-34.e9. [DOI:10.1016/j.celrep.2019.03.058] [PMID]

[14] Xi Y, Jing Z, Wei W, Chun Z, Quan Q, Qing Z, et al. Inhibitory effect of sodium butyrate on colorectal cancer cells and construction of the related molecular network. BMC Cancer. 2021; 21(1):127. [DOI:10.1186/s12885-021-07845-1] [PMID]

[15] Zheng L, Zhu ZR, Sneh T, Zhang WT, Wang ZY, Wu GY, et al. Circulating succinate-modifying metabolites accurately classify and reflect the status of fumarate hydratase-deficient renal cell carcinoma. J Clin Invest. 2023; 133(11):e165028. [DOI:10.1172/JCI165028] [PMID]

[16] Roupar D, González A, Martins JT, Gonçalves DA, Teixeira JA, Botelho C, et al. Modulation of Designed Gut Bacterial Communities by Prebiotics and the Impact of Their Metabolites on Intestinal Cells. Foods. 2023; 12(23):4216. [DOI:10.3390/foods12234216] [PMID]

[17] Baryła M, Semeniuk-Wojtaś A, Róg L, Kraj L, Małyszko M, Stec R. Oncometabolites-A link between cancer cells and tumor microenvironment. biology (Basel). 2022; 11(2):270. [DOI:10.3390/biology11020270] [PMID]

[18] Ternes D, Tsenkova M, Pozdeev VI, Meyers M, Koncina E, Atatri S, et al. The gut microbial metabolite formate exacerbates colorectal cancer progression. Nat Metab. 2022; 4(4):458-75. [DOI:10.1038/s42255-022-00558-0] [PMID]

[19] Sciacovelli M, Gonçalves E, Johnson TI, Zecchini VR, da Costa AS, Gaude E, et al. Fumarate is an epigenetic modifier that elicits epithelial-to-mesenchymal transition. Nature. 2016; 537(7621):544-7. [DOI:10.1038/nature19353] [PMID]

[20] He J, Han Z, Luo W, Shen J, Xie F, Liao L, et al. Serum organic acid metabolites can be used as potential biomarkers to identify prostatitis, benign prostatic hyperplasia, and prostate cancer. Front Immunol. 2023; 13:998447. [DOI:10.3389/fimmu.2022.998447] [PMID]

[21] Lu YW, Hou XL, Koo HM, Chao WT. Dasatinib suppresses collective cell migration through the coordination of focal adhesion and E-cadherin in colon cancer cells. Heliyon. 2023; 10(1):e23501 [DOI:10.1016/j.heliyon.2023.e23501] [PMID]

[22] Tarashi S, Siadat SD, Ahmadi Badi S, Zali M, Biassoni R, Ponzoni M, et al. Gut bacteria and their metabolites: Which one is the defendant for colorectal cancer? Microorganisms. 2019; 7(11):561 [DOI:10.3390/microorganisms7110561] [PMID]

[23] Thirunavukkarasan M, Wang C, Rao A, Hind T, Teo YR, Siddiquee AA, et al. Short-chain fatty acid receptors inhibit invasive phenotypes in breast cancer cells. Plos One. 2017; 12(10):e0186334. [DOI:10.1371/journal.pone.0186334] [PMID]

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