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Identification of correlation between GIT bacteria and cancer in patients suffer from gastroenteritis in south of Iraq

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Abstract---The study was investigated and diagnosis the bacteria that associated with GIT cancer and GIT diseases a total of 200 blood and biopsy samples were collected during the period from September 2020 to June 2021 and samples were included 100 sample for gastrointestinal cancer patients, 50 for healthy people, and 50 for gastrointestinal patients. Gastrointestinal tract diseases patients were diagnosed clinically and the disease was evaluated by specialist physicians, presented with dyspepsia referred to the Esophago Gastroduodeno Scope Unit for endoscopy at AL-Hussein teaching hospital (Consulting digestive tract). In our current study, three types of bacteria were diagnosed that are related to diseases of the digestive system, including: Streptococcus bovis spp gallolyticus, Fusobacterium nucleatum, Porphyromonas gingivalisbutby by usig PCR technique and found the highest percentage was patients with cancer as following F.nucleatum gene (96%) in patients with cancer, while in patients with GIT diseases (96%) but in the healthy was 36 (72%), whereas the percentage of S.bovis gene (58%) in while patients with cancer but (52%)in patients with GIT diseases while the healthy (40%), the presence of *P.gingivalis* gene (31%) in patients with cancer, while in patients with GIT diseases (28%) in the healthy (22%). Depending on the obtained results the hypothesis these bacteria be has a place in etiology of gastrointestinal cancer was supported with our findings.

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Keywords---Fusobacterium nucleatum, Streptococcus bovis, Porphyromonas gingivalis, GIT cancer, gastric cancer, colon cancer, PCR.

Introduction

Virchow, a German pathologist, discovered a relationship between inflammation and cancer more than 150 years ago. A number of observations clearly suggest that persistent inflammation in the stomach is a prevalent cause of cancer. Cancers of the gastrointestinal tract are more common in diseases that cause a chronically irritated epithelium. The appearance of multifocal tumors in inflamed mucosae contributes to the theory that inflammation is involved in carcinogenesis mechanistically (Virchow, 1863). Cancers of the gastrointestinal tract are a major health problem and represent almost 20% of all cancer related deaths in both men and women (Ferlay et al., 2007). Gastrointestinal Cancer is an important problem in public health worldwide (Rawla and Barsouk, 2019). Colorectal carcinoma is the third most frequent cancer after breast cancer in women and bronchus cancer in men (Thélin and Sikka, 2015). Colorectal carcinoma is the largest cause of death from GIT tumors, in Iraq, colorectal cancer was the seventh top cancers. whereas in Kurdistan, it was the fourth most common cancer for both males and females (Khalil et al., 2018).

Colorectal cancer is a multistep process in which several gene mutations (Nguyen and Duong, 2018). Chronic infection or toxins production, immune evasion, and immunological suppression are all important mechanisms that can lead to carcinogenesis Chronic infection can disrupt the cell cycle, resulting in abnormal cell growth; additionally, toxin production can induce DNA damage from carcinogenic chemicals, which leads to damage to genes, culminating in abnormal cell division and apoptosis (Liardo et al., 2021). Gastric cancer is the quart most common malignancy and the second major cause of cancer-associated deaths, accounting for 10% of total cancer deaths worldwide (Sitarz et al., 2018). The spaciously majority of gastric cancers are adenocarcinomas, gastric cancer is also characterized by large geographical variations in its incidence and indeed more than half of the total gastric cancer are in East Asian countries such as Japan, South Korea and China (Rawla and Barsouk, 2019), scientists divide this cancer of stomach into two main classes: -Gastric cardia cancer (cancer of the top inch of the stomach) and non -cardia gastric cancer (cancer in all other areas of stomach).(Ferlay et al., 2010). Colon cancer is a neoplastic illness of the large intestine that can be caused by both inherited and somatic genetic changes that occur throughout a lifetime (Monson et al., 2013). It has been connected to a variety of factors, including socioeconomic level, a drastic shift in eating patterns, refrigeration, chemical preservatives, and environmental changes (Sawicki et al., 2021). Increased harmful bacterial products, decreased helpful bacterial metabolites, and disturbed tissue barriers are the general processes for bacteriaassociated (or driven) GI cancer. Cancer progression is further aided by abnormal immunology, persistent inflammation, and hyperpreliferation. Microbial infections and intestinal inflammation can affect the integrity of the intestinal barrier, resulting in increased gut permeability, microbial translocation, and immunological activation (Keku et al., 2015). Some bacteria, such as

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Fusobacterium nucleatum, Porphyromonas gingivalis, Helicobacter pylori, and Streptococcus bovis, have been linked to human cancer (Mallika *et al.*, 2020). Oral squamous cell carcinoma (OSCC) can be caused by *P. gingivalis* and *F. nucleatum* (Gholizadeh *et al.*, 2016). Colorectal cancer and pancreatic cancer are more common in F. nucleatum (K Mitsuhashi *et al.*, 2015). S. bovis has been linked to colorectal and colon cancer (Meseeha and Attia, 2018). *S. gallolyticus* (SB biotypes II/2 and I) and *S.infantarius* (biotype II/1). *S. gallolyticus* has a stronger link to colorectal cancers (Kumar *et al.*, 2018) than *S. infantarius*, which has a stronger link to non-colonic cancers (Kaindi *et al.*, 2018). *Porphyromonas gingivalis*, an oral pathogen more closely connected with periodontal disease was linked to digestive tract cancer in addition to *F. nucleatum*. The study was, however, too small to distinguish colorectal cancer from other malignancies (Wang *et al.*, 2021; Abed *et al.*, 2020).

Material and method Study collection:

The study includes 200 samples, 100 samples are patients with cancer, comprising 41 females and 59 males with various histologically proven preoperative GIT carcinomas. The types of cancer in patients with GIT were colon cancer, gastric cancer, and small intestine cancer. The age of patients was between 20-80 years .Two control groups of patients were studied. These included 50 healthy controls and 50 patients suffering from other GIT disease, other than cancer. The non-malignancy conditions were gastric ulcer, and ulcerative colitis. All patients with non-malignant GIT conditions as well as the preoperative GIT cancer patients were initially attending to the Gastroenterology and Hematology Teaching Hospital, during the period between September 2020 to June 2021. Negative control whom are selected after a careful questioning about the general health of each individual especially medical problems related to gastrointestinal diseases.

Gastrointestinal tract diseases in patients were diagnosed clinically and evaluated by specialist physicians, presented at the Esophago Gastroduodeno Scope Unit for endoscopy at AL-Hussein teaching hospital (Consulting digestive tract) in AL-Muthana, Thi-Qar, Basra and Omara provinces. Every participant signed a written agreement after his/her understanding of the project aim and specialist physicians using sterile endoscopy obtained tests that would be performed, tissue biopsies from each person. Biopsy specimens washed and placed in 1 ml of normal saline and /or phosphate buffer saline (PBS) and was preserved at -20°C for molecular analysis.

Bacteria	Type of Primer	Sequence	PCR product (bp)	Reference
Fusobacterium sp	FUSO1-F	GAGAGAGCTTTGCGT CC	610 bp	Nagano et
	FUSO2-R	TGGGCGCTGAGGTTC GAC		al., 2007
Streptococcus	23S rRNA-F	CCCGGCATGTAATGCATGTC		Kawata, et

Table (1) Primers were used in PCR

bovis	23S rRNA-R	TACAACCCCGATGTGTAAACACA	169 bp	al., 2004
P. gingivalis	16S rRNA-F	AGGCAGCTTGCCATACTGCG		Slots et al.,
	16S rRNA-R	ACTGTTAGCAACTACCGATGT	404 bp	1995

Bacterial DNA was extracted from Biopsy samples by using PrestoTM Mini gDNA Bacteria Kit (Geneaid. USA) and done according to company instruction.

Molecular detection of *Fusobacterium nucleatum* by polymerase chain reaction

The gene of FUSO are used to detection of **Fusobacterium nucleatum**, amplification and melting conditions were optimized for the PCR using specific primer, this condition produce the most specific and sufficient PCR product, as shown in table (2).

Table (2)

Optimized thermo-cycling condition for FUSO gene of Fusobacterium nucleatum

NO.	Stage	Temperature	Time	Number of cycle
1	Initial denaturation	95 ∘C	5 min	1
2	Denaturation	95∘C	45 sec	35
3	Annealing	60 ∘C	45 sec	
4	Elongation	72∘C	45 sec	
5	Final elongation	72∘C	10 min	1

Molecular detection of S. bovis by polymerase chain reaction.

The gene of 23SrRNA are used to detection of **S.** *bovis*, amplification and melting conditions were optimized for the PCR using specific primer, this condition produce the most specific and sufficient PCR product, as shown in table (3).

Table (3)
Optimized thermo-cycling condition for 23SrRNA gene of S. bovis

NO.	Stage	Temperature	Time	Number of cycle
1	Initial denaturation	95 ∘C	5 min	1
2	Denaturation	95∘C	45 sec	35
3	Annealing	57 ∘C	45 sec	
4	Elongation	72∘C	45 sec	
5	Final elongation	72∘C	10 min	1

Molecular detection of P. gingivalis by polymerase chain reaction

The gene of 16SrRNA are used to detection of **P. gingivalis**, amplification and melting conditions were optimized for the PCR using specific primer, this

condition produce the most specific and sufficient PCR product, as shown in table (4).

NO.	Stage	Temperature	Time	Number of cycle
1	Initial denaturation	95 ∘C	5 min	1
2	Denaturation	95∘C	45 sec	35
3	Annealing	56.5 ∘C	45 sec	
4	Elongation	72∘C	45 sec	
5	Final elongation	72∘C	10 min	1

Table (4)Optimized thermo-cycling condition for 16SrRNA gene of *P. gingivalis*

Result & Discussion

D

etection of F. nucleatum gene (FUSO gene) by using PCR Technique

The results of detection of *F. nucleatum* among three studied groups (Healthy, patients with GIT and patients with Cancer) by using PCR, revealed as the following *F. nucleatum* was detected in 36 (72%) out 50 of healthy people also *F. nucleatum* was detected in 43 (86%) out 50 in patients with GIT. Finally, the highest percentage recorded in patient with cancer which *F. nucleatum* was detected in 96 (96%) out 100 sample with significant differences between the samples that gave positive and negative to bacteria detection in three groups at p<0.0001 as in table (5) and figure (1):

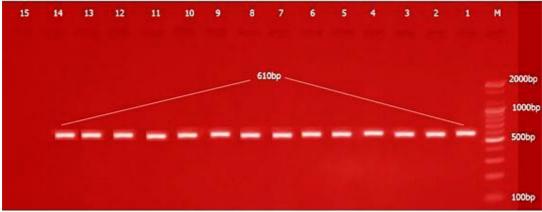


Fig. (1): Agarose gel electrophoresis of PCR product obtained with *Fusobacterium nucleatum* strains -specific primers that generated 610bp amplicon. Lanes (1-14); positive, Lanes (15); negative, Lane M represent 100bp DNA ladder.

Table (5)
Identification of Fusobacterium nucleatum among three studied groups (Healthy,
patients with GIT and patients with Cancer)

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Results	Healthy	GIT	Cancer	P value ^a
	N=50	N=50	N=100	
Positive	36 (72)	43 (86)	96 (96)	<0.0001*

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Negative	14 (28)	7 (14)	4 (4)		
P value ^b	< 0.0001*	< 0.0001*	< 0.0001*		

* represent a significant difference at p<0.05.

A, among all three studied groups. B, between positive and negative results. These findings corroborated the findings of (Cuellar-Gómez et al., 2021). The researchers collected tissue from 30 patients (18 men and 12 women) who had colorectal cancer (CRC) and 30 normal people to delicate the relationship between F. nucleatum and CRC. The results showed that the accumulation of F. nucleatum determined in CRC was significantly greater than in the normal control, which was also found in the current study. Furthermore, the findings agreed with those of (Suehiro et al., 2017), who conducted a study to detect F. nucleatum in stool and investigate its association with colorectal tumors, feces sample were obtained from 60 healthy individuals, 11 patients with colorectal advanced colorectal non adenomas, 19 patients with advanced adenoma/carcinoma, and 158 patients with colorectal cancer.

PCR results recorded more than 260 copies of F. nucleatum were discovered in only 10% of the healthy persons in the control group, but F. nucleatum was found in 55% of the non-advanced adenoma group, 32% of the advanced adenoma/CIS group, and 54% of the colorectal cancer group. The current investigation, on the other hand, discovered F. nucleatum in GIT patients. Lee et al., (2016) found that F. nucleatum was less prevalent in GIT. In a study of 54 patients with inflammatory bowel disease (IBD), including 26 with Crohn's disease (CD), 25 with ulcerative colitis (UC), and 3 with Behcet's disease (BD), 10 Fusobacterium spp were identified: six with F. mortiferum, two with F. varium, and one with F. nucleatum and F. mort. Su et al. (2020), on the other hand, discovered that when they investigated the mechanism by which F. nucleatum promotes intestinal epithelial cell (IEC) mortality, they analyzed F. nucleatum abundance in 44 (ulcerative colitis) UC tissues from patients and 9 normal tissues. F. nucleatum was found in a larger proportion of UC tissues than in normal tissues. Huh et al., (2020) found F. nucleatum played a role in Inflammatory bowel diseases in 1526 fecal samples, the results reported the F. nucleatum was commonly discovered in inflammatory bowel disease (IBD) participants with low microbial diversity; these variations were linked to the patient's health state, sample type, and geographical location.

Furthermore, *F. nucleatum* was found in patients with cancer in numerous studies, including (Kashani *et al.*, 2020), which found that 35 (43 percent) of 80 patients with colorectal cancer (33 male and 47 female) had positive *F.nucleatum* biopsies. According to (Boehm *et al.*, 2020), *Fusobacterium spp.* and *F. nucleatum* were more commonly detected in tumorous tissue of colorectal cancer (CRC) and gastric cancer (GC) compared to non-tumorous tissues. In CRC patients, the frequency and bacterial load were greater than in GC patients. Abed *et al.*, (2020) the circulatory system appears to be the most efficient pathway for *F. nucleatum* to reach colon cancers, as demonstrated in a pre-clinical model.

This most likely affects humans during transitory physiologic bacteremias coming from the mouth. *F.nucleatum*, a gram-negative bacteria, is a widespread part of the oral microbiota (Zhou *et al.*, 2014) *F. nucleatum* bacteria interact with one

another by expressing several virulence factors, and they may attach to a wide range of mammalian cell types, including epithelial and endothelial cells, polymorph nuclear neutrophil, monocyte, erythrocytes, fibroblast, and natural killer (NK) cells (Y. Liu *et al.*, 2019). The cell surface protein FadA is a crucial virulence factor in *F. nucleatum*, regulating the bacterium's adherence and invasion. FadA gene expression was substantially greater in human CRC specimens than in neighboring normal tissues (Rubinstein *et al.*, 2013).

This protein allows *F. nucleatum* to bind to E-cadherin in CRC and epithelial cells, activate the -catenin pathway, and trigger the production of transcription factors lymphoid enhancer factor (LEF)/T cell factor (TCF), all of which promote tumor cell proliferation (Chen *et al.*, 2017). The presence of *F. nucleatum* in the gut has been linked to the development of cancer, namely colorectal cancer (CRC), *F.nucleatum* promotes tumor formation in the CRC microenvironment by causing inflammation and a host immunological response. The cell surface proteins FadA, Fap2, and RadD produced by *F. nucleatum* can drive the host to create inflammatory factors and attract inflammatory cells, providing an environment favorable to tumor formation. Furthermore, *F. nucleatum* can cause immunological suppression of the gut mucosa by reducing the activity of immune cells such as macrophages, T cells, and natural killer cells, which contributes to cancer progression.

Detection of *Streptococcus bovis* gene (23S rRNA gene) by using PCR Technique

The results of detection of *S. bovis* among three studied groups (Healthy, patients with GIT and patients with Cancer) by using PCR, revealed as the following *S. bovis* was detected in 20 (40%) out 50 of healthy people also *S. bovis* was detected in 26 (52%) out 50 in patients with GIT. While, the highest percentage recorded in patient with cancer which *S. bovis* was detected in 58 (58%) out 100 sample with significant differences between the samples that gave positive and negative to bacteria detection in three groups at p<0.05 and significant differences between those groups as in table (6) and figure (2).

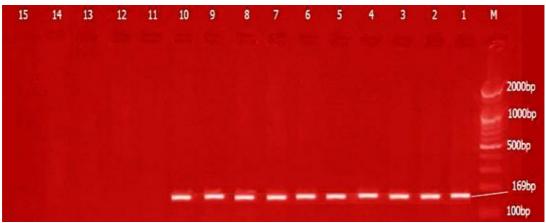


Figure (2): Agarose gel electrophoresis of PCR product obtained with Streptococcus

bovis strains -specific primers that generated 169bp amplicon. Lanes (1-10); positive, Lanes (11-15); negative, Lane M represent 100bp DNA ladder.

Table (6)Identification of Streptococcus bovis among three studied groups (Healthy,
patients with GIT and patients with Cancer)

Results	Healthy N=50	GIT N=50	Cancer N=100	P value ^a
Positive	20 (40)	26 (52)	58 (58)	0.035*
Negative	30 (60)	24 (48)	42 (42)	
P value ^b	0.046*	0.689	0.110	

* represent a significant difference at p<0.05.

A, among all three studied groups. B, between positive and negative results. The current study's findings were consistent with those of (Al-Jashamy *et al.*, 2010), who analyzed a total of 166 stool specimens taken from ill and healthy patients. Out of 166 cases investigated, the overall prevalence of *S. bovis* was determined to be 41 (24.7 percent). 41 (48.6 percent) of these *S. bovis* isolates were discovered in individuals with colonic polyps, adenocarcinomas, inflammatory bowel disease (IBD), and chronic gastrointestinal tract illness (GIT). In the same study, it was discovered that the incidence of colorectal cancer was 24.7 percent, with adenocarcinomas accounting for 51 percent and having the highest incidence in the sigmoid region of the colon. In the majority of IBD and chronic GIT patients, ulcerative colitis was present (41.4 percent).

Our findings were consistent with those of (Heidarian *et al.*, 2017), who collected 29 fecal samples from IBD patients (22 with UC and 7 with CD) and 29 healthy volunteers, and reported on the relative abundance of *streptococcus spp* and its association with disease activity in the inflammatory bowel. As the relative abundance of *Streptococcus spp*. is greater in IBD patients compared to controls, Streptococcus spp. overgrowth was found in 27% of UC (6/22) patients and 42% of CD (3/7).

Streptococcus spp overgrowth was seen in 5% (5/29) of the control groups. On the other hand, the proportion of cancer patients infected with *S. bovis* was 58 (58 percent) out of 100 samples, which is lower than the percentage of cancer patients infected with *F. nucleatum*, which was 96 (96 percent) out of 100 samples. This proportion was agreed upon (Eshaghi *et al.*, 2020) during the identification of *S. bovis* in 55 individuals with colon illnesses the findings found In terms of DNA of *S. bovis*, 3 biopsy samples (5.5 percent) with a 95 percent confidence interval were declared positive and 52 (94.5 percent) were reported negative in 55 biopsy samples from patients with colon illnesses.

Little and colleagues (2019) found in a quality assurance study that 70% of patients were referred for colonoscopy following an episode of *S. bovis* bacteremia, suggesting the need for greater identification of the link of S. bovis bacteremia and malignancy as CRC. *S. bovis* is a Gram-positive group D streptococcus detected in 11% of asymptomatic people' gastrointestinal tract (Krishnan, and Eslick, 2014). McCoy and Mason discovered a link between colorectal cancer

(CRC) and group D streptococci in individuals with endocarditis in 1951. Streptococci are the most common bacteria in the oral cavity and one of the most common bacteria in the human GIT; yet, little is known about their prevalence and functions in the GIT of IBD patients.

Streptococcal interactions with a variety of host cells frequently result in proinflammatory responses. S. suis subtilisin-like protease (SspA) can generate a pro-inflammatory response in macrophages via Toll-like receptor 2 (TLR2) (Frolova et al., 2008). TLR2 expression was shown to be greater in the intestines of IBD patients compared to healthy persons, according to Sybille Landwehr-Kenzel et al. (2014). This observation might explain our patients' higher activity index score indirectly by interacting TLRs with high levels of Streptococci in their gut. Streptococcus protein, rhamnose group А Μ glucose polymers, glucosyltransferase, and S. mutans AgI/II polypeptides are further Streptococci components that can trigger inflammatory responses in human tissue (Landwehr-Kenzel et al., 2014). This bacterium's lipoproteins and other components can cause a pro-inflammatory reaction in the colon. Streptococcus metabolites and structural components interact with several cellular equivalents implicated in the inflammatory response in IBD patients, either directly or indirectly (Heidarian et al., 2017).

Detection of *Porphyromonas gingivalis* gene (16SrRNA gene) by using PCR Technique

The results of detection of *P. gingivalis* among three studied groups (Healthy, patients with GIT and patients with Cancer) by using PCR, revealed as the following *P. gingivalis* was detected in 11 (22%)out 50 of healthy people also *P. gingivalis* was detected in 14 (28%)out 50 in patients with GIT. While, in patient with cancer which *P. gingivalis* was detected in 31 (31%)out 100 sample which recorded the highest value between groups, however there was significant difference between the samples that gave positive and negative to bacteria detection in three groups at p<0.05 and non significant differences between those groups as in table (7) and figure (3).

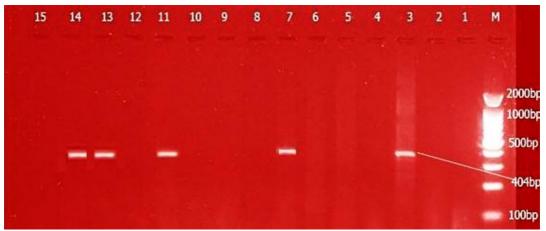


Figure (3): Agarose gel electrophoresis of PCR product obtained with *Porphyromonas gingivalis* strains -specific primers that generated 404bp

amplicon. Lanes (3, 7, 11, 13, 14); positive, other Lanes are negative, Lane M represent 100bp DNA ladder.

Table (7)
Identification of Porphyromonas gingivalis among three studied groups (Healthy,
patients with GIT and patients with Cancer)

Results	Healthy N=50	GIT N=50	Cancer N=100	P value ^a
Positive	11 (22)	14 (28)	31 (31)	0.345
Negative	39 (78)	36 (72)	69 (69)	
P value ^b	<0.0001*	<0.0001*	<0.0001*	

* represent a significant difference at p<0.05.

A, among all three studied groups. B, between positive and negative results. The associated the *P. gingivalis* with GIT and with cancer agreed with (Wang *et al.*, 2021) in their results to detect *P. gingivalis* in feces 77 subjects divided into 22 control individuals and 23 subjects with colorectal cancer once they compared the levels of *P. gingivalis* in the feces from the individuals in each group, observed an increased abundance of *P. gingivalis* in the colorectal cancer group compared with the adenoma and healthy donor groups which indicate that the increased abundance of *P. gingivalis* in the gut microbiota may be a general feature of colorectal cancer.

Kong *et al.*, (2021) used different methods to detect P. gingivalis in different digestive system cancers. The specimens (tissues)from patients diagnosed with histologically confirmed primary tumors were included 50 cases of oral squamous cell carcinoma cancer (OSCC), 50 cases of esophageal squamous cell carcinoma cancer (ESCC), 30 cases of gastric cardia adenocarcinoma (GCA), 30 cases of gastric cancer, the positive samples were identified by PCR as oral squamous 28 (56.00 percent), esophageal squamous cell carcinoma (ESCC) 21 (42.00 percent), gastric cardia adenocarcinoma (GCA) 5 (16.675 percent), gastric cancer (GC) 1 (3.33 percent), and colorectal cancer (CRC) 1 (2.86 percent).

Moreover in our study , *P. gingivalis* was detected in 14 (28%)out 50 in patients with GTI such as inflammatory bow disease , there many studies in model mice provide the relationship between ulcerative colitis and *P. gingivalis* ,Tsuzuno and colleagues, (2021), discovered that oral treatment of P. gingivalis to mice dramatically exacerbated the severity of colitis, and that ingested P. gingivalis damaged the colonic epithelial barrier by lowering the expression of tight junction proteins in vivo. *P. gingivalis*-specific epithelial barrier breakdown was suggested by in vitro permeability experiments utilizing the intestinal epithelial cell line, the disruption of the epithelial barrier by *P. gingivalis* was proposed. *P.gingivalis* aggravates gastrointestinal inflammation in vulnerable hosts by interacting directly with the intestinal epithelial barrier. The same findings were achieved by (Zhao *et al.*, 2021), who discovered that *P. gingivalis* enhanced the severity of UC in part via peptidylarginine deiminase (PPAD) in a mouse model. This aggravation was due to PPAD, which caused an aberrant immunological response and increased the Th17/Treg ratio. *P. gingivalis* has the ability to adhere to and invade

host cells, and oral mucosal epithelial cells are thought to be the most significant intracellular environment for P. gingivalis (Lee *et al.*, 2018).

Bacterial invasion occurs in four stages: (a) entrance, (b) survival, (c) replication, and (d) departure from the host cell (Casadevall, 2008). *P. gingivalis* is linked to a bad prognosis in human colorectal cancer because it colonizes and gets enriched in tumor tissue, activating the NLRP3 inflammasome in the immune microenvironment and eventually promoting colorectal carcinoma growth (Wang *et al.*, 2021). *P. gingivalis* increases distant metastasis and chemoresistance to anti-cancer therapies, as well as the proliferation of oral tumor cells, via altering defensin gene expression, peptidyl-arginine deiminase, and noncanonical -catenin activation. Furthermore, *P. gingivalis* has been linked to precancerous stomach and colon lesions, esophageal squamous cell carcinoma, head and neck carcinoma (larynx, throat, lip, mouth, and salivary glands), and pancreatic cancer (Olsen *et al.*, 2019).

Conclusion

The study found that *S. bovis spp gallolyticus, F. nucleatum, P. gingivalis* participated in causing cancer in the digestive system were found in the samples of people who do not have cancer and people who have problems in the digestive system by using the PCR technique, but the presence of the genes of these bacteria in people who have cancer was higher than it is in patients with Gastrointestinal system problems, and these results supported the theory and previous studies about the role of these bacteria in causing ulcers in the digestive tract.

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