

Microflora of Pericancerous Zone in Patients with Gastric Cancer

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Abstract

This article shows the prevalence of H.pylori strains in microflora of patients with gastric cancer (72,85±5,31 cases) on example of National Cancer Center of Georgia. The 10 species of microorganisms (H.pylori, Staphylococcus spp., Streptococcus spp., E.coli, Proteus spp., Clostridium spp., Lactobacillus spp., Bacteroides spp., Trichomonas spp., Candida spp.) were obtained (all - 113 strains). More of them was H.pylori both in monocultures and in associations.

Keywords: *gastric cancer, Helicobacter pylori, microflora*

Introduction

Despite a dramatic reduction in incidence and mortality rates, gastric cancer (GC) is still one of the most common malignant neoplasias worldwide [7]. The most recent data from the International Agency for Research on Cancer show, that it remains the second most common cancer. Gastric carcinogenesis is a multistep and multifactorial process beginning with H.pylori-associated gastritis in most cases. H.pylori infection, together with other environmental factors and individual susceptibility, determine the final risk for the development of GC [4]. H.pylori is considered as a first grade carcinogen in etiology of GC [1].

The incidence of GC varies widely by country and population, with higher rates among the lower socioeconomic group [6]. Rates appear to be higher in developing than in developed countries. In spite of this, there is more information about H.pylori infection from developed countries, to compare with developing ones [2]

Aim of Study

Because of no studies have shown the incidence of H.pylori and other microorganisms in patients with GC in Georgia, we studied the microflora of these patients on example of Georgian Cancer Center.

Materials and Methods

We have examined 70 patients with GC (III stage). The biopsy spacimens and resection materials were taken during the operations or endoscopy procedures. Transportation, cultivation, incubation of materials and identification of strains were performed by recently applied methods [3, 5]. The data were processed by Student's variation system.

Results

There were 51 patients with H.pylori infection (72,85±5,31%). Microflora of patients with GC is given in the *Tab.1*. According of stains quantity, the microorganisms are spread by this range: H.pylori

(45,13±4,69%), *Candida* spp. (21,23±3,84%), *Staphylococcus* spp (12,38±3,09%), *Escherichia coli* (7,07±2,41%), *Streptococcus* spp (6,19±2,26%), *Lactobacillus* spp. (2,65±1,51%), *Clostridium* spp., *Proteus* spp. (both - 1,76±1,23), *Bacteroides* spp., *Trichomonas* spp. (both - 0,88±0,87%).

Microorganisms were obtained in monocultures (48,5±5,97%) and in associations (51,42±7,47%) (Tab.2).

In monocultures were *H.pylori* and *Candida* spp (85,29(6,08% and 14,70 (6,07% respectively). In association was *H.pylori* in 22 cases (61,11±8,12%). More of them were *H.pylori*+*Candida* spp (50,00±8,33%). Other microorganisms (bacteria, fungi and protozoa) were in associations in 38,88(8,12% cases.

Discussion

The above-stated data, obtained by us, the *H.pylori* infection in patients with GC was in 72,85±5,31%.

The microflora of patients was diversy enough. It was represented by facultative and obligative anaerobes (bacteria, fungi, protozoa) and microaeropiles also. Thus, microflora of pericancerous zone is consist of following species: *H.pylori*, *Staphylococcus* spp., *Streptococcus* spp., *E.coli*, *Proteus* spp., *Clostridium* spp., *Lactobacillus* spp., *Bacteroides* spp., *Trichomonas* spp., *Candida* spp. Most of them was *H.pylori* both in monocultures and in associations.

According to our data, there were a high prevalence of *H.pylori* strains in patients with GC on example of National Cancer Center of Georgia.

N	Microorganisms	Quantity of strains	
		Abs.	%
1	<i>Helicobacter pylori</i>	51	45,13±4,69
2	<i>Staphylococcus</i> spp	14	12,38±3,09
3	<i>Streptococcus</i> spp	7	6,19±2,26
4	<i>Escherichia coli</i>	8	7,07±2,41
5	<i>proteus</i> spp	2	1,76±1,23
6	<i>Clostridium</i> spp	2	1,76±1,23
7	<i>Lactobacillus</i> spp	3	2,65±1,51
8	<i>Bacteroides</i> spp	1	0,88±0,87
9	<i>Trichomonas</i> spp	1	0,88±0,87
10	<i>Candida</i> spp	24	21,23±3,84

Tab.1 Microflora of patients with GC. (n=113)

Monocultures n=34 (48,5±5,97%)				Associations n=36 (51,42±7,47%) H.pylori and others n=22 (61,11±8,12%)											
H.pylori		Candida spp		H.pylori+ gram-positive cocci		H.pylori+ gram-negative rods		H.pylori+ gram-negative rods+gram-positive cocci		H.pylori+ Candida spp.		H.pylori+ gram-negative rods+ Candida spp.		Others	
abs.	%	abs.	%	abs.	%	abs.	%	abs.	%	abs.	%	abs.	%	abs.	%
29	85,29 ±6,08	5	14,70 ±6,07	7	31,81 ±7,76	2	9,09 ±4,76	1	4,54 ±3,45	11	50,00 ±8,33	1	4,54 ±3,45	14	38,88 ±8,12

Tab.2 Microorganisms in monocultures and associations. (n=70)

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Микрофлора периканцерозной зоны у больных раком желудка

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Р Е З Ю М Е

Изучена микрофлора периканцерозной зоны у больных раком желудка. В 72,85±5,31% случаев у пациентов выделены штаммы *H.pylori*. Микрофлора представлена как факультативными и облигатными анаэробами (бактерии, грибы, простейшие), так и микроаэрофильными бактериями. Выделены следующие микроорганизмы: *H.pylori*, *Staphylococcus spp.*, *Streptococcus spp.*, *E.coli*, *Proteus spp.*, *Clostridium spp.*, *Lactobacillus spp.*, *Bacteroides spp.*, *Trichomonas spp.*, *Candida spp.*). С наибольшей частотой встречается *H.pylori* как в виде монокультур, так и в ассоциациях.

Ключевые слова: *рак желудка, Helicobacter pylori, микрофлора*