Microbiota dysbiosis is associated with HPV-induced cervical carcinogenesis

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Abstract. Cervical microbial communities serve a crucial role in the persistence and development of oncogenic human papilloma virus (HPV) infections. In the present study, the authors hypothesised that disturbed heterogeneity of microbial flora was associated with HPV-induced carcinogenesis. Swabs of the cervical microbiota were collected from 250 women and the 16S ribosomal DNA was sequenced using a high throughput assay. The swabs of cervical microbiota were grouped according to the community state types (CSTs) as follows: Healthy cervical swabs; swabs taken from low-grade squamous intra-epithelial lesions (LSIL) and swabs taken from high-grade squamous intra-epithelial lesions (HSIL). Analysis of the bacterial classes revealed that the CST cervical swabs of the volunteers were characterised by Lactobacillus crispatus, Lactobacillus iners and Lactobacillus taiwanensis, however, Gardnerella vaginalis and Lactobacillus acidophilus were absent. In the CST of patients with LSIL the predominant type of bacteria was Lactobacillus acidophilus and Lactobacillus iners, however Lactobacillus crispatus was not detected. Swabs from CST women diagnosed with HSIL exhibited abundant Gardnerella vaginalis and Lactobacillus acidophilus, however, lacked Lactobacillus taiwanensis, Lactobacillus iners and Lactobacillus crispatus. The abundance of

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Lactobacillus acidophilus in swabs from the healthy women was compared with the swabs from the women with LSIL. The results of the present study indicated that the development of HPV-induced cancer is associated with a high diversity of vaginal microbiota, which is involved in the control of viral persistence, and is therefore indicative of disease prognosis.

Introduction

It has been reported that the female cervix maintains communities of microbial species, which have a symbiotic relationship with the host (1). It has been demonstrated that the female cervix is colonized by diverse microbiota, which serve a crucial role in cervicovaginal health (1). However, it has been indicated that the type of organisms present is dependent on the prevailing environmental conditions and host factors (1,2). Over the last decade, it has been indicated that the development and introduction of molecular-based technology has provided novel information regarding the composition of the vaginal-cervical flora, as well as the abnormal colonization of the genital tract by pathogens (2). The aforementioned findings may help to elucidate the microbiome of the genital tract in healthy women and in human papilloma virus (HPV)-dependent carcinogenesis.

The majority of previous studies have indicated that the cervical/vaginal microbial flora has a prevalence of *Lactobacillus* species, which produce lactic acids that maintain an acidic environment and may inhibit pathogenic growth (2-8). Specifically, lactic acid and other related acidic compounds have been reported to inhibit bacterial growth associated with bacterial vaginosis (BV), as well as viral infections (3). In addition, lactic acid has been recognized as a component of the immune defence system, as it has been demonstrated to potentiate the production of protective proinflammatory cytokines by vaginal epithelial cells, to promote the activation of T helper 17 lymphocytes, to stimulate dendritic cell maturation and induce interferon production (1). Over 120 *Lactobacillus* species have been identified and over 20 species have been identified in the vagina (2).

The dominant microorganisms in the vagina of a healthy woman during puberty have been reported to be from the Lactobacillus genus, including L. acidophilus, L. fermentum, L. plantarum, L. brevis, L. jenseni, L. casei, L. catenaforme, L. delbrueckii and L. salivarius (1,2). It is considered that in the majority of cases, vaginal inflammation is not caused by novel microorganisms introduced from the outside, but instead by a disturbance to the proportion and number of microorganisms already existing in the vagina (4). Each bacterium has been reported as a potential etiological factor of inflammation, including Lactobacillus (4). It has been reported that anaerobic bacteria have a significantly increased pathogenic potential compared with aerobic bacteria (5,6). Factors, which have been reported to potentially disturb vaginal biocenosis include the following hormonal changes: Pregnancy, puberty, menopause and hormonal contraception, particularly using low doses of estrogen; vaginal sterilization following chemo- or antibiotic therapy; surgical conditions such as vaginoplasty, erosions, poor genitalia hygiene, including the vulva and the vagina, and lack of a regimented sex life, i.e. frequent, unprotected, lack of a regular sex life (4-6). Large variation in the number and composition of bacteria has been reported among women, and among time intervals for one woman (5,6). Therefore, attempting to evaluate the vaginal microbiome is extremely difficult.

A healthy cervicovaginal microenvironment has been reported to be characterised by high levels of different species of Lactobacillus, including the predominant L. crispatus, L. iners, L. jensenii and L. gasseri. Other species may occur occasionally (2,6). In rare cases, it has been reported that the cervix can be colonized by the same two or four Lactobacillus species (4). The aforementioned cases have been demonstrated to be dependent on a number of genetic and environmental factors, including nationality, diet and age (2,6). A number of previous studies have indicated that, in a significant proportion of healthy women, the Lactobacillus in the vagina may be replaced by other lactic acid-producing bacteria, including Atopobium vaginae, Megaspharea and Leptotrichia species (3). It has been indicated that an abnormal vaginal microenvironment may be caused by sexually transmitted infection (3). It has been reported that trichomoniasis may be caused by colonization with a microorganism not commonly identified within vaginal colonies, including Streptococcus pneumoniae, Haemophilus influenzae and Listeria monocytogenes (6,7). In addition, it has been reported that an abnormal microenvironment may be caused by an invasion of an alternative organism, which is a component of the normal vaginal flora, including Escherichia coli (3). Bacterial vaginosis has been reported as a disorder characterised by a decrease in the quality or quantity of Lactobacillus and the growth of Mycoplasma hominis, Gardnerella vaginalis, Mobiluncus species, Neisseria gonorrhea, Trichomonas vaginalis, Chlamydia trachomatis and Prevotella species (4,5). A previous meta-analysis reported a positive association between cervical HPV infection and BV (6,7). The reverse phenomenon of HPV as a risk factor for BV invasion has also been described (8).

It has been demonstrated that HPV is considered a principal factor responsible for the development of cervical cancer (8). However, it has been suggested that HPV infection alone does not cause cervical carcinogenesis and that other factors, such as prolonged oral contraceptive or smoking, may be involved in

the disease progression (8). To determine whether the vaginal microflora is affected by one of these factors, the present study investigated the association between cervical and vaginal infections, and pre-cancerous lesions of the cervix.

Materials and methods

Patient samples. Women included in the present study were recruited from cervical cancer screening in the Department of Gynaecological Oncology and Gynaecology, Medical University of Lublin in Poland between February 2003 and August 2015. The study group consisted of 250 women. Patients whose molecular analysis indicated that they were HPV-positive [HPV(+)] were included within the analysed group (n=180), whereas the healthy women [HPV(-)] were included within the control group (n=70).

Cytology and HPV status were used to classify the patients into the following 3 groups: Control group [n=70); HPV(-)]; women with low-grade squamous intraepithelial lesions [LSIL; n=95; HPV(-)], and women with high-grade squamous intraepithelial lesions [HSIL; n=85; HPV(+)]. The mean ages of patients with LSIL and HSIL, and the control group, did not significantly differ: 35 years (range, 25-48) and 37 years (range, 29-48) compared with 37 years (range 21-48), respectively (P>0.05). The present study was approved by the Ethics Committee of the Medical University of Lublin (Lublin, Poland). Written informed consent was obtained from all participants in the present study and the research was performed in accordance with the Declaration of Helsinki.

The patient inclusion criteria for the present study for the research and control groups were as follows: i) Cytological diagnosis of LSIL or HSIL or patients with a normal cytological swab; ii) HPV (+) or (-) status; iii) no use of oral and/or vaginal probiotics for 30 days prior to the start of the present study; iv) absence of genital tract infection during the 30 days prior to the classification of patients in the study, and v) a maximum of one sexual partner for 30 days prior to qualification testing.

The exclusion criteria for participating in the present study included the following: i) Vaginal bleeding of unknown etiology; ii) pregnancy; iii) oral contraceptive use or hormone replacement therapy; iv) cigarette smoking; v) history of other types of cancer; vi) systemic diseases; vii) diabetes, and viii) thyroid or other endocrine diseases.

Cervical swabs were collected from patients and to rule out experimental bias or random error. pooling was performed in 3 subgroups as follows: in the control group 23, 23, 24 swabs were pooled; in the LSIL group 31, 32, 32 were pooled, and in the HSIL group 28, 28, 29 swabs were pooled. The pooled cervical swabs were stored immediately at -80°C for a maximum 12 months. The cervical cytological findings were classified according to the Bethesda system (9).

DNA isolation from the swabs. Total DNA was extracted from cells using a DNA isolation kit (QIAamp DNA kit; cat. no. 51306; Qiagen GmbH, Hilden, Germany), according to the manufacturer's protocols.

Identification of HPV DNA. Identification of HPV-derived DNA was performed by polymerase chain reaction (PCR)

Table I. The frequency of bacteria classes in vaginal/cervical swabs.

Class	Healthy (%)	LSIL HPV(+) (%)	HSIL HPV(+) (%)
Actinobacteria	0.21	1.0	8.10
Alphaproteobacteria	0.20	0.03	0.41
Bacilli	96.27	84.00	27.69
Bacterioidia	0.01	0.01	0.00
Betaproteobacteria	0.01	0.01	0.01
Clostridia	0.09	0.16	0.20
Deltaproteobacteria	0.00	0.00	0.01
Flavobacteriia	0.01	0.00	0.03
Gammproteobacteria	0.19	8.20	61.48
Ktedonobactetria	0.01	0.00	0.00
Methanomicrobiota	0.00	0.01	0.00
Mollicutes	0.25	0.03	0.00
Nostocophycideae	0.41	0.02	0.15
Sphingobacteria	0.00	0.01	0.01
Unclassified	2.34-2.63		

LSIL, low-grade squamous intraepithelial lesion; HSIL, high-grade squamous intraepithelial lesion.

amplification of HPV gene sequences. The MY09, MY11, LC1 and LC2 primers (Institute of Biochemistry and Biophysics Polish Academy of Sciences, Warsaw, Poland) that were complementary to the genomic sequence of the predominantly diagnosed HPV types were used, as previously described (10).

Typing of 16S ribosomal DNA (16S rRNA) by PCR-amplification and next generation sequencing. The V4 hypervariable regions of 16S rRNA in bacterial genes were detected by PCR, as previously described (11). Sequencing and sequence analysis was performed at Genomed S.A, Warszawa (Poland).

Statistical analysis. The difference in the mean age of the female patients was tested using the Kruskal-Wallis test and was statistically significant if the calculated P>0.05. Using the 16S rRNA gene sequencing data, the frequency of bacteria occurrences were calculated by multiplying the total number of present bacteria with the percentage of bacterial concentration in the cervical swabs. The statistical analysis was performed using k-means cluster analysis (k-means clustering algorithm) and Statistica 12.0 software (StatSoft Inc., Cracow, Poland).

Results

Identification and cluster analysis of bacteria in the control, LSIL HPV(+) and HSIL HPV(+) groups. 16S rRNA sequence-based methods were used to identify healthy cervical microbial colonies, as well as those associated with HPV-dependent carcinogenesis. The identified microflora were grouped into CSTs as follows: Control, HPV(-); LSIL, HPV(+), and HSIL HPV(+). A total of 6,466 bacteria species, belonging to 74 classes, were identified from the vaginal/cervical swabs of the patients. The major classes observed are presented in Table I.

Identification and cluster analysis of bacterial classes in the control, LSIL HPV(+) and HSIL HPV(+) groups. Frequency analysis of bacterial classes in the CST healthy women, as well as in patients with a diagnosis of LSIL HPV(+) or HSIL HPV(+) revealed the presence of three major clusters. The results of the bacterial classes cluster analysis are presented in Table II. The bacterial classes, which were distinct from the other classes regardless of the type of diagnosis, included Bacilli, Actinobacteria and Gammaproteobacteria (Table II). Analysis of the frequencies of the individual classes demonstrated that the CST composition in the healthy women, as well as the women diagnosed with LSIL was formed predominantly of the Bacilli bacteria. In CST patients with cancer, the Gammaproteobacteria class was additionally detectable. Further cluster analysis, from classes to species, was performed to determine the bacterial species making up the three selected bacteria classes.

Identification and cluster analysis of bacterial species in the control, LSIL HPV(+) and HSIL HPV(+) groups. Analysis of the bacteria species in each of the three classes of bacteria revealed no cluster formation within the Gammaproteobacteria class. The further analysis subsequently focussed only on the Actinobacterium and Bacilli classes of bacterial species. Regardless of the type of diagnosis, the bacterial species within the analysed classes formed two clusters. The results are presented in Tables III and IV (data repository).

The Actinobacterium class included Gardnerella vaginalis and Propionibacterium acnes identified in the CST healthy women; Gardnerella vaginalis and Actinomyces turicensis in the CST women diagnosed with LSIL, and Gardnerella vaginalis, Corynebacterium glaucum, Corynebacterium matruchotii, Propionibacterium acnes and Propionibacterium humerusii in women diagnosed with

Table II. Three major clusters of bacteria classes in volunteers and patients with LSIL and HSIL diagnosis.

Control			LSIL HPV(+	-)		HSIL HPV	(+)	
Class	Gr.	Dist.	Class	Gr.	Dist.	Class	Gr.	Dist.
Bacilli	1	0.00	Bacilli	1	0.00	Bacilli	1	1255.09
Actinobacteria	2	3.01	Gammaproteobacteria	1	0.00	Gammaproteobacteria	1	1255.09
Alphaproteobacteria	2	4.44	Actinobacteria	2	25.94	Actinobacteria	2	0.00
Gammaproteobacteria	2	5.32	Bacteroidia	2	33.90	Alphaproteobacteria	3	23.48
Mollicutes	2	0.38	Clostridia	2	30.74	Bacteroidia	3	2.23
Nostocophycideae	2	13.16	Alphaproteobacteria	3	20.47	Betaproteobacteria	3	1.69
Bacteroidia	3	0.14	Betaproteobacteria	3	2.14	Chrysiogenetes	3	2.48
Betaproteobacteria	3	0.14	Chrysiogenetes	3	2.82	Clostridia	3	11.07
Chrysiogenetes	3	0.50	Deferribacteres	3	2.78	Deferribacteres	3	2.53
Clostridia	3	7.07	Deinococci	3	2.82	Deinococci	3	2.48
Deferribacteres	3	0.50	Deltaproteobacteria	3	2.75	Deltaproteobacteria	3	2.06
Deinococci	3	0.50	Epsilonproteobacteria	3	3.25	Epsilonproteobacteria	3	2.37
Deltaproteobacteria	3	0.50	Erysipelotrichi	3	2.83	Erysipelotrichi	3	2.53
Epsilonproteobacteria	3	0.42	Flavobacteriia	3	2.26	Flavobacteriia	3	1.58
Erysipelotrichi	3	0.50	Fusobacteria	3	2.68	Fusobacteria	3	2.53
Fusobacteria	3	0.34	Ktedonobacteria	3	2.08	Ktedonobacteria	3	2.37
Ktedonobacteria	3	0.30	Methanomicrobia	3	2.56	Methanomicrobia	3	2.48
Methanomicrobia	3	0.42	Mollicutes	3	2.80	Mollicutes	3	7.58
Opitutae	3	0.50	Nostocophycideae	3	33.15	Nostocophycideae	3	11.59
Oscillatoriophycideae	3	0.26	Opitutae	3	2.82	Opitutae	3	2.37
Planctomycetia	3	0.50	Oscillatoriophycideae	3	2.42	Oscillatoriophycideae	3	2.32
Rubrobacteria	3	0.50	Planctomycetia	3	2.80	Planctomycetia	3	2.53
Sphingobacteriia	3	0.26	Rubrobacteria	3	2.82	Rubrobacteria	3	2.53
Synechococcophycideae	3	0,50	Sphingobacteriia	3	2.96	Sphingobacteriia	3	1.43
Synergistia	3	0,50	Synechococcophycideae	3	2.82	Synechococcophycideae	3	2.48
Thermotogae	3	0,50	Synergistia	3	2.82	Synergistia	3	2.53
Flavobacteriia	3	0,06	Thermotogae	3	2.80	Thermotogae	3	2.53

LSIL, low-grade squamous intraepithelial lesion; HSIL, high-grade squamous intraepithelial lesion; Gr., cluster number; Dist., Euclidean.

HSIL, which formed clusters separate from the other bacterial species (Table III, data repository).

The cluster analysis of the *Bacilli* bacterial species revealed the presence of a CST subpopulation, which in the healthy women consisted of *Lactobacillus crispatus*, *Lactobacillus iners* and *Lactobacillus taiwanensis*. In women diagnosed with LSIL it included *Lactobacillus iners* and *Lactobacillus acidophilus*, and in women diagnosed with HSIL it included *Lactobacillus iners*, *Lactobacillus acidophilus* and *Lactobacillus crispatus* (Table IV, data repository). For further analysis, the levels of bacterial characteristics were determined in each of the analysed patient groups (Table V).

The analysis of the bacterial classes indicated that CST cervical swabs of the female patients were colonised by Lactobacillus crispatus, Lactobacillus iners and Lactobacillus taiwanensis, however, Gardnerella vaginalis and Lactobacillus acidophilus were almost not identified. In the CST patients diagnosed with LSIL, the predominant types of bacteria were Lactobacillus acidophilus and Lactobacillus iners, while Lactobacillus crispatus frequency was lower than

in the control group. In CST patients diagnosed with HSIL, high abundance of *Gardnerella vaginalis*, *Lactobacillus acidophilus* was identified, however, *Lactobacillus taiwanensis*, *Lactobacillus iners* and *Lactobacillus crispatus* frequencies were lower than in the control group. The level of *Lactobacillus acidophilus* in the CST patients diagnosed with LSIL swabs were compared with swabs taken from women with HSIL.

Discussion

It has been indicated that the introduction of Next-Generation Sequencing (NGS) into research allowed for the identification of specific ecological niches for microorganisms within living organisms. This was possible due to the amplification and parallel sequencing of gene fragments, which were highly conserved among microorganisms, the most common being the 16S rRNA subunit, as well as RAD51 recombinase and inhibin subunit a (12). Highly conserved regions of the 16S rRNA gene (V1-V9) have been reported to allow for

Table III. The bacteria species of the class Actinobacterium forming clusters in volunteers and patients with L-SIL or H-SIL histopathological diagnosis. Gr.- cluster number, Dist.- Euclidean distance.

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nucosum 0,02 2 Corynebacterium aurimucosum 0,08 2 Actinomyces neuii nucosum 0,02 2 Corynebacterium oyleue 0,06 2 Actinomyces odontolyticus eaee 0,09 2 Corynebacterium diputheriaee 0,04 2 Actinomyces odontolyticus cum 0,02 2 Corynebacterium glaucum 0,05 2 Corynebacterium glaucum 0,06 2 Corynebacterium jarkeium 0,06 2 Corynebacterium jarkeium 0,06 2 Corynebacterium ipophitollavum 0,05 2 Corynebacterium in prophitollavum 0,05 2 Corynebacterium in mucifaciens 0,05 2 Corynebacterium mucchotii 0,06 2 Corynebacterium mucchotii 0,07 2 Corynebacterium mucchotii 0,07 2 Corynebacterium mucchotii 0,08 2 Corynebacterium mucchotii 0,09 2 Propionibacterium mucchotii 0,09 2 Corynebacterium mucchotii 0	Actinomyces turicensis	90,0	2	Corynebacterium amycolatum	0,04	2	Actinomyces georgiae	0,02	2
nucosum 0,02 2 Corynebacterium diphtheriae 0,04 2 Actinomyces turicensis theriae 0,09 2 Corynebacterium diphtheriae 0,04 2 Actinomyces turicensis theriae 0,09 2 Corynebacterium glaucum 0,05 2 Corynebacterium anycolatum cum 0,02 2 Corynebacterium glaucum 0,04 2 Corynebacterium aurinacosum unonolyticum 0,06 2 Corynebacterium jelkelium 0,04 2 Corynebacterium diphtheriae ium 0,06 2 Corynebacterium kuscheri 0,05 2 Corynebacterium diphtheriae penstediii 0,09 2 Corynebacterium lipophiloflavum 0,05 2 Corynebacterium diphtheriae corynebacterium matruchotii 0,05 2 Corynebacterium pseudogenitalium 0,05 2 Corynebacterium ipophiloflavum olo 2 Corynebacterium pseudogenitalium 0,05 2 Corynebacterium pseudogenitalium olo 2 Corynebacterium pseudogenitalium 0,05 2 Corynebacterium pseudogenitalium olo 2 Corynebacterium matruchotii 0,05 2 Corynebacterium pseudogenitalium olo 2 Corynebacterium nucifaciens olo 3 Corynebacterium nucifaciens olo 4 Corynebacterium nucifaciens olo 5 Corynebacterium nucifaciens olo 6 2 Corynebacterium nucifaciens olo 7 Propionibacterium nucifaciens olo 7 Propionibacterium nucifaciens olo 8 2 Corynebacterium nucifaciens olo 9 2 Corynebacterium nucifaciens olo 9 2 Corynebacterium nucifaciens olo 0 2 Corynebacterium nucifaci	Corynebacterium amycolatum	0,02	7	Corynebacterium aurimucosum	80,0	7	Actinomyces neuii	0,02	2
eae 0,09 2 Corynebacterium diphtheriae 0,04 2 Actinomyces turicensis theriae 0,02 2 Corynebacterium glaucum 0,05 2 Corynebacterium aurmucosum cum 0,02 2 Corynebacterium glaucumolyticum 0,04 2 Corynebacterium aurmucosum ium 0,06 2 Corynebacterium kroppenstedii 0,04 2 Corynebacterium diphtheriae ium 0,06 2 Corynebacterium kroppenstedii 0,04 2 Corynebacterium diphtheriae obis inclusium 0,02 2 Corynebacterium matruchotii 0,03 2 Corynebacterium glumpheria dogenitalium 0,02 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium plation dogenitalium 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens dogenitalium 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens elii 0,02 2 Corynebacterium mu	Corynebacterium aurimucosum	0,02	2	Corynebacterium coyleae	90,0	7	Actinomyces odontolyticus	90,0	7
theriae 0,02 2 Corynebacterium glaucum 0,04 2 Corynebacterium anycolatum cum 0,02 2 Corynebacterium glaucumolyticum 0,04 2 Corynebacterium aurimucosum 0,05 2 Corynebacterium glacuronolyticum 0,06 2 Corynebacterium jeikeium 0,04 2 Corynebacterium diphtheriae 0,05 2 Corynebacterium ipophiloffavum 0,05 2 Corynebacterium ipophiloffavum 0,05 2 Corynebacterium ipophiloffavum 0,05 2 Corynebacterium ipophiloffavum 0,05 2 Corynebacterium martuchotti 0,05 2 Corynebacterium ipophiloffavum 0,05 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium kuscheri 0,05 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium ipophiloffavum 0,06 2 Corynebacterium ipophiloffavum 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium ipophiloffavum 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens 0,06 2 Corynebacterium mucifacien 0,06 2 Corynebacterium mucifacienium mucifacienium mucifacienium mucifacienium mucifacienium mucifacienium mucifacienium mucifacienium microaerophilum 0,07 2 Propionibacterium mucifacienium microaerophilum 0,02 2 Propionibacterium microaerophilum 0,02 2 Propionibacterium microaerophilum 0,02 2 Propionibacterium microaerophilum 0,02 2 Propionibacterium microaerophilum 0,03 2 P	Corynebacterium coyleae	60,0	7	Corynebacterium diphtheriae	0,04	7	Actinomyces turicensis	0,02	2
turn 0,02 2 Corynebacterium glucuronolyticum 0,04 2 Corynebacterium aurimucosum uronolyticum 0,06 2 Corynebacterium jetkeium 0,04 2 Corynebacterium coyleae ium 0,06 2 Corynebacterium jetkeium 0,04 2 Corynebacterium diphtheriae penstedtii 0,09 2 Corynebacterium lipophiloflavum 0,05 2 Corynebacterium introphiloflavum 0,05 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium kutscheri faciens 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucicalerivorans 0,05 2 Corynebacterium mucicalerivorans 0,06 2 Corynebacterium ureicelerivorans 0,06 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,08 2 Propionibacterium microaerophilum 0,08 2 Propionibacterium nucroaerophilum 0,08 2 Propionibacterium nucroaerophilum 0,08 2 Propionibacterium microaerophilum 0,08 2 Propionibacterium nucroaerophilum 0,09 2 Propionibacterium nucroaerophilum 0,09 2 Propionibacterium nucroaerophilum 0,09 2 Propionibacterium nucroaerophilum 0,09 2 Pro	Corynebacterium diphtheriae	0,02	2	Corynebacterium glaucum	0,05	7	Corynebacterium amycolatum	0,02	2
uronolyticum 0,06 2 Corynebacterium jeikeium 0,04 2 Corynebacterium diphtheriae ium 0,06 2 Corynebacterium kutscheri 0,05 2 Corynebacterium diphtheriae penstedtii 0,09 2 Corynebacterium kutscheri 0,05 2 Corynebacterium glucuronolyticum cheri 0,25 2 Corynebacterium lipophiloflavum 0,05 2 Corynebacterium piekeium shiloflavum 0,02 2 Corynebacterium matruchotii 0,13 2 Corynebacterium piekeium obdenitalium 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium kutscheri dagenitalium 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens elii 0,02 2 Corynebacterium mucifacerium mucifa	Corynebacterium glaucum	0,02	2	Corynebacterium glucuronolyticum	0,04	7	Corynebacterium aurimucosum	0,02	2
ium 0,06 2 Corynebacterium kroppenstedtii 0,04 2 Corynebacterium diphtheriae penstedtii 0,09 2 Corynebacterium katscheri 0,05 2 Corynebacterium glucuronolyticum cheri 0,25 2 Corynebacterium lipophiloflavum 0,05 2 Corynebacterium jeikeium choliglavum 0,02 2 Corynebacterium matruchotii 0,13 2 Corynebacterium kroppenstedtii uchotii 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium kutscheri fiaciens 0,02 2 Corynebacterium pseudogenitalium 0,06 2 Corynebacterium lipophiloflavum dogenitalium 0,06 2 Corynebacterium sundsvallense 0,05 2 Corynebacterium mucifaciens elii 0,02 2 Corynebacterium triegelii 0,05 2 Corynebacterium mucifaciens elii 0,02 2 Corynebacterium tuberculostearicum 0,12 2 Corynebacterium riegelii rculostearicum 0,06 2 Corynebacterium ureicelerivorans 0,06 2 Corynebacterium ureicelerivorans eleivorans 0,06 2 Corynebacterium acnes 0,06 2 Corynebacterium ureicelerivorans dum 0,09 2 Corynebacterium acnes 0,06 2 Corynebacterium ureicelerivorans dum 0,00 2 Propionibacterium avidum 0,15 2 Corynebacterium ureicelerivorans nuulosum 0,02 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium humerusii 0,09 2 Propionibacterium h	Corynebacterium glucuronolyticum	90,0	7	Corynebacterium jeikeium	0,04	7	Corynebacteriun coyleae	70,0	2
penstedtii 0,09 2 Corynebacterium kutscheri 0,05 2 Corynebacterium glucuronolyticum cheri 0,25 2 Corynebacterium lipophiloflavum 0,05 2 Corynebacterium jeikeium chiloflavum 0,02 2 Corynebacterium matruchotii 0,13 2 Corynebacterium kutscheri uchotii 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium kutscheri dogenitalium 0,02 2 Corynebacterium pseudogenitalium 0,05 2 Corynebacterium lipophiloflavum culostearicum 0,06 2 Corynebacterium sundsvallense 0,05 2 Corynebacterium mucifaciens lii 0,02 2 Corynebacterium uberculostearicum 0,12 2 Corynebacterium riegelii color Corynebacterium uveicelerivorans 0,06 2 Corynebacterium sundsvallense celerivorans 0,06 2 Corynebacterium areicelerivorans 0,06 2 Corynebacterium uveicelerivorans dum 0,06 2 Propionibacterium avidum 0,05 2 Corynebacterium variabile nulosum 0,02 2 Propionibacterium granulosum 0,05 2 Corynebacterium variabile nunlosum 0,02 2 Propionibacterium granulosum 0,03 2 Propionibacterium nicroaerophilum nerusii 0,09 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum nerusii 0,09 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium nicroaerophilum nerusii 0,09 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium nicroaerophilum nerusii 0,09 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium nicroaerophilum nerusii 0,09 2 Propionibacterium nicroaerophilum 0,05 2 Propionibacterium nicroaerophilum	Corynebacterium jeikeium	90,0	7	Corynebacterium kroppenstedtii	0,04	7	Corynebacterium diphtheriae	0,02	7
corynebacterium lipophiloflavum 0,05 2 Corynebacterium jeikeium 0,05 2 Corynebacterium lipophiloflavum 0,03 2 Corynebacterium matruchotii 0,13 2 Corynebacterium kroppenstedtii 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium kroppenstedtii 0,06 2 Corynebacterium kuscheri 0,06 2 Corynebacterium lipophiloflavum 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium mucifaciens 0,06 2 Corynebacterium mucicalerivorans 0,06 2 Corynebacterium riegelii 0,06 2 Corynebacterium mucicalerivorans 0,06 2 Corynebacterium mucicalerivorans 0,06 2 Corynebacterium mucicalerivorans 0,06 2 Corynebacterium mucicalerivorans 0,06 2 Corynebacterium mucicalerium acres 0,05 2 Corynebacterium mucicalerium acres 0,05 2 Corynebacterium mucicalerium mucicalerium mucicalerium mucicalerium granulosum 0,05 2 Propionibacterium granulosum 0,05 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Repropresse Icarrens 0,06 2 Streptomyces Icarrens	Corynebacterium kroppenstedtii	60,0	7	Corynebacterium kutscheri	0,05	7	Corynebacterium glucuronolyticum	0,02	2
ruchotii 0,02 2 Corynebacterium matruchotii 0,13 2 Corynebacterium kroppenstedtii u.chotii 0,06 2 Corynebacterium mucifaciens 0,05 2 Corynebacterium kutscheri 0,06 2 Corynebacterium lipophiloflavum dogenitalium 0,02 2 Corynebacterium riegelii 0,05 2 Corynebacterium lipophiloflavum 0,06 2 Corynebacterium sundsvallense 0,05 2 Corynebacterium mucifaciens 0,06 2 Corynebacterium nucicelerivorans 0,06 2 Corynebacterium uneicelerivorans 0,06 2 Corynebacterium nucicelerivorans 0,06 2 Corynebacterium uneicelerivorans 0,06 2 Corynebacterium uneicelerivorans 0,06 2 Corynebacterium uneicelerivorans 0,06 2 Corynebacterium acnes 0,06 2 Corynebacterium uneicelerivorans 0,06 2 Corynebacterium acnes 0,06 2 Corynebacterium uneicelerivorans 0,06 2 Corynebacterium avidum 0,05 2 Propionibacterium avidum 0,05 2 Propionibacterium avidum 0,05 2 Propionibacterium microaerophilum 0,05 2 Strentomyces lazurens	Corynebacterium kutscheri	0,25	7	Corynebacterium lipophiloflavum	0,05	7	Corynebacterium jeikeium	0,020883	7
uchotii0,062Corynebacterium mucifaciens0,052Corynebacterium kutscheridogenitalium0,022Corynebacterium pseudogenitalium0,062Corynebacterium lipophiloflavumdogenitalium0,062Corynebacterium riegelii2Corynebacterium mucifacienselii0,052Corynebacterium sundsvallense0,052Corynebacterium riegeliisvallense0,062Corynebacterium variabile0,062Corynebacterium sundsvallensecelerivorans0,062Corynebacterium variabile0,062Corynebacterium nuberculostearicumabile0,062Propionibacterium avidum0,052Corynebacterium variabilenuulosum0,062Propionibacterium granulosum0,152Corynebacterium variabilenuulosum0,022Propionibacterium propionibacterium nicroaerophilum0,052Propionibacterium nicroaerophilumnerusii0,092Propionibacterium microaerophilum0,052Propionibacterium nicroaerophilum0,062Propionibacterium nicroaerophilum0,052Propionibacterium nicroaerophilum	Corynebacterium lipophiloflavum	0,02	7	Corynebacterium matruchotii	0.13	7	Corynebacterium kroppenstedtii	0,02	7
figaciens 0,02 2 Corynebacterium pseudogenitalium 0,06 2 Corynebacterium lipophiloflavum dogenitalium 0,06 2 Corynebacterium riegelii 0,05 2 Corynebacterium mucifaciens elii 0,02 2 Corynebacterium sundsvallense 0,05 2 Corynebacterium pseudogenitalium lsvallense 0,06 2 Corynebacterium tuberculostearicum 0,12 2 Corynebacterium isundsvallense celerivorans 0,06 2 Corynebacterium variabile 0,06 2 Corynebacterium sundsvallense celerivorans 0,06 2 Corynebacterium acnes 0,62 2 Corynebacterium neicelerivorans dum 0,06 2 Propionibacterium avidum 0,15 2 Corynebacterium variabile mulosum 0,02 2 Propionibacterium granulosum 0,05 2 Propionibacterium granulosum nerusii 0,09 2 Propionibacterium nicroaerophilum 0,05 2 Propionibacterium granulosum 0,05 2 Propionibacterium microaerophilum	Corynebacterium matruchotii	90'0	7	Corynebacterium mucifaciens	0,05	7	Corynebacterium kutscheri	0,07	7
dogenitalium0,062Corynebacterium riegelii0,052Corynebacterium mucifacienselii0,022Corynebacterium sundsvallense0,052Corynebacterium pseudogenitaliumsvallense0,062Corynebacterium ureicelerivorans0,062Corynebacterium sundsvallensecelerivorans0,062Corynebacterium ureicelerivorans0,062Corynebacterium ureicelerivoransabile0,062Propionibacterium avidum0,152Corynebacterium variabilemulosum0,022Propionibacterium granulosum0,052Propionibacterium numerusiinerusii0,092Propionibacterium nuicroaerophilum0,052Propionibacterium microaerophilumno02Propionibacterium nuicroaerophilum0,052Propionibacterium microaerophilum	Corynebacterium mucifaciens	0,02	2	Corynebacterium pseudogenitalium	90'0	7	Corynebacterium lipophiloflavum	0,16	7
lelii 0,02 2 Corynebacterium sundsvallense 0,05 2 Corynebacterium pseudogenitalium (2) 2 Corynebacterium tuberculostearicum 0,12 2 Corynebacterium riegelii (2) 2 Corynebacterium sundsvallense (3) 2 Corynebacterium sundsvallense (4) 3 2 Corynebacterium sundsvallense (5) 4 2 Corynebacterium sundsvallense (5) 5 2 Corynebacterium tuberculostearicum abile (5) 6 2 Propionibacterium acries (5) 6 2 Corynebacterium ureicelerivorans (5) 6 2 Corynebacterium ureicelerivorans (5) 6 2 Propionibacterium avidum (5) 6 2 Propionibacterium granulosum (5) 6 2 Propionibacterium granulosum (5) 6 2 Propionibacterium humerusii (5) 6 6 2 Propionibacterium nicroaerophilum (5) 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Corynebacterium pseudogenitalium	90,0	7	Corynebacterium riegelii	0,05	7	Corynebacterium mucifaciens	0,02	7
Isvallense0,062Corynebacterium tuberculostearicum0,122Corynebacterium riegeliirculostearicum0,092Corynebacterium sundsvallensecelerivorans0,062Corynebacterium tuberculostearicumabile0,062Propionibacterium acnes0,622Corynebacterium ureicelerivoransdum0,062Propionibacterium avidum0,152Corynebacterium variabileunulosum0,022Propionibacterium granulosum0,052Propionibacterium avidumnerusii0,092Propionibacterium humerusii0,082Propionibacterium microaerophilum0,052Propionibacterium microaerophilum0,052Propionibacterium microaerophilum0,062Strentomyces lazurens0,022Strentomyces lazurens	Corynebacterium riegelii	0,02	7	Corynebacterium sundsvallense	0,05	7	Corynebacterium pseudogenitalium	0,02	7
rculostearicum 0,09 2 Corynebacterium ureicelerivorans 0,06 2 Corynebacterium sundsvallense celerivorans 0,06 2 Corynebacterium tuberculostearicum abile 0,06 2 Corynebacterium ureicelerivorans 0,06 2 Propionibacterium avidum 0,15 2 Corynebacterium variabile dum 0,02 2 Propionibacterium granulosum 0,05 2 Propionibacterium granulosum 0,08 2 Propionibacterium numerusii 0,08 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium 0,05 2 Propionibacterium 0,05 2 Propionibacterium 0,05 2 Propionibacterium 0,05 2 Propionibact	Corynebacterium sundsvallense	90'0	2	Corynebacterium tuberculostearicum	0,12	7	Corynebacterium riegelii	0,02	7
relerivorans 0,06 2 Corynebacterium variabile 0,06 2 Corynebacterium tuberculostearicum abile 0,06 2 Propionibacterium acnes 0,62 2 Corynebacterium ureicelerivorans dum 0,06 2 Propionibacterium avidum 0,15 2 Corynebacterium variabile mulosum 0,02 2 Propionibacterium granulosum 0,08 2 Propionibacterium mumerusii 0,08 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,06 2 Strentomyces lazureus	Corynebacterium tuberculostearicum	0,00	7	Corynebacterium ureicelerivorans	90'0	7	Corynebacterium sundsvallense	90,0	2
abile 0,06 2 Propionibacterium acnes 0,62 2 Corynebacterium ureicelerivorans dum 0,06 2 Propionibacterium avidum 0,15 2 Corynebacterium variabile mulosum 0,02 2 Propionibacterium granulosum 0,08 2 Propionibacterium granulosum nerusii 0,09 2 Propionibacterium humerusii 0,08 2 Propionibacterium granulosum roaerophilum 0,02 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,06 2 Strentomyces lazureus	Corynebacterium ureicelerivorans	90,0	2	Corynebacterium variabile	90'0	7	Corynebacterium tuberculostearicum	0,02	2
dum 0,06 2 Propionibacterium avidum 0,15 2 Corynebacterium variabile nuulosum 0,02 2 Propionibacterium granulosum 0,05 2 Propionibacterium avidum nerusii 0,09 2 Propionibacterium humerusii 0,08 2 Propionibacterium granulosum roaerophilum 0,02 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum	Corynebacterium variabile	90'0	2	Propionibacterium acnes	0,62	7	Corynebacterium ureicelerivorans	0,02	7
mulosum 0,02 2 Propionibacterium granulosum 0,05 2 Propionibacterium avidum nerusii 0,09 2 Propionibacterium humerusii 0,08 2 Propionibacterium granulosum roaerophilum 0,02 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,06 2 Strentomyces Jazureus	Propionibacterium avidum	90,0	7	Propionibacterium avidum	0,15	7	Corynebacterium variabile	0,02	7
nerusii 0,09 2 Propionibacterium humerusii 0,08 2 Propionibacterium granulosum roaerophilum 0,02 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0,05 2 Streptomyces lazureus 0.06 2 Streptomyces lazureus	Propionibacterium granulosum	0,02	2	Propionibacterium granulosum	0,05	7	Propionibacterium avidum	0,02	7
roaerophilum 0,02 2 Propionibacterium microaerophilum 0,05 2 Propionibacterium microaerophilum 0.05 2 Strentomyces lazureus 0.06 2 Strentomyces lazureus	Propionibacterium humerusii	60'0	7	Propionibacterium humerusii	0,08	2	Propionibacterium granulosum	0,02	7
0.06 2 Strentomyces latureus 0.02 2 Strentomyces latureus	Propionibacterium microaerophilum	0,02	7	Propionibacterium microaerophilum	0,05	7	Propionibacterium microaerophilum	60,0	7
o, o	Streptomyces lazureus	90'0	7	Streptomyces lazureus	0,02	7	Streptomyces lazureus	0,02	7

Table IV. The bacteria species of the class Bacilli forming clusters in volunteers and patients with L-SIL or H-SIL histopathological diagnosis. Gr.- cluster number, Dist.- Euclidean distance.

Control			T-SIT			H-SIL		
Bacteria species	Dist.	Ğ.	Bacteria species	Dist.	Ğr.	Bacteria species	Dist.	Ğ.
	633,17	1	Lactobacillus iners	0,00	1	Lactobacillus iners	0,00	
Lactobacillus iners	633,17	_	Lactobacillus acidophilus	0,00	_	Lactobacillus acidophilus	0,00	_
Lactobacillus taiwanensis	0,00	1	Actinobacillus parahaemolyticus	8,19	2	Lactobacillus crispatus	0,00	_
Actinobacillus parahaemolyticus	1,43	2	Actinobacillus porcinus	8,17	2	Actinobacillus parahaemolyticus	3,84	2
Actinobacillus porcinus	1,35	2	Actinobacillus rossii	8,17	2	Actinobacillus porcinus	3,88	7
Actinobacillus rossii	1,43	2	Alkalibacillus haloalkaliphilus	8,07	2	Actinobacillus rossii	3,88	2
Alkalibacillus haloalkaliphilus	1,19	2	Alkalibacillus salilacus	7,30	2	Alkalibacillus haloalkaliphilus	3,86	2
Alkalibacillus salilacus	0,47	2	Bacillus alcaliinulinus	8,06	2	Alkalibacillus salilacus	3,01	2
Bacillus alcaliinulinus	1,11	2	Bacillus anthracis	8,19	2	Bacillus alcaliinulinus	3,88	2
Bacillus anthracis	1,43	2	Bacillus arbutinivorans	8,20	2	Bacillus anthracis	3,88	2
Bacillus arbutinivorans	1,43	2	Bacillus aryabhattai	8,19	2	Bacillus arbutinivorans	3,80	2
Bacillus aryabhattai	1,35	2	Bacillus axarquiensis	8,20	2	Bacillus aryabhattai	3,78	7
Bacillus axarquiensis	1,35	2	Bacillus azotoformans	8,16	2	Bacillus axarquiensis	3,88	7
Bacillus azotoformans	1,43	2	Bacillus benzoevorans	8,14	2	Bacillus azotoformans	3,88	7
Bacillus benzoevorans	1,43	2	Bacillus cereus	8,15	2	Bacillus benzoevorans	3,88	2
Bacillus cereus	1,433	2	Bacillus flexus	8,18	2	Bacillus cereus	3,84	7
Bacillus flexus	1,43	2	Bacillus foraminis	8,20	2	Bacillus flexus	3,88	7
Bacillus foraminis	1,43	2	Bacillus fordii	8,19	2	Bacillus foraminis	3,86	7
Bacillus fordii	1,43	2	Bacillus fortis	8,19	2	Bacillus fordii	3,88	2
Bacillus fortis	1,43	2	Bacillus ginsenggisoli	8,16	2	Bacillus fortis	3,88	7
Bacillus ginsenggisoli	1,35	2	Bacillus hackensackii	8,20	2	Bacillus ginsenggisoli	3,88	7
Bacillus hackensackii	1,43	2	Bacillus herbersteinensis	8,19	2	Bacillus hackensackii	3,86	7
Bacillus herbersteinensis	1,35	2	Bacillus horneckiae	8,07	2	Bacillus herbersteinensis	3,88	7
Bacillus horneckiae	1,43	2	Bacillus isabeliae	8,13	2	Bacillus horneckiae	3,86	7
Bacillus isabeliae	1,43	2	Bacillus koreensis	8,19	2	Bacillus isabeliae	3,88	7
Bacillus koreensis	1,43	2	Bacillus litoralis	8,17	2	Bacillus koreensis	3,88	7
Bacillus litoralis	1,43	2	Bacillus mucilaginosus	8,17	2	Bacillus litoralis	3,88	7
Bacillus mucilaginosus	1,27	2	Bacillus oleronius	8,17	2	Bacillus mucilaginosus	3,78	7
Bacillus oleronius	1,43	2	Bacillus olivae	8,20	2	Bacillus oleronius	3,88	7
Bacillus olivae	1,27	2	Bacillus oryzae	8,15	2	Bacillus olivae	3,86	7
Bacillus oryzae	1,43	2	Bacillus pseudomegaterium	8,19	2	Bacillus oryzae	3,88	7
Bacillus pseudomegaterium	1,35	2	Bacillus sonorensis	8,15	2	Bacillus pseudomegaterium	3,86	7

Table IV. Continued.

ms s	Gr. 2			5		i	
ms s	2 2	Bacteria species	Dist.	5	Bacteria species	Dist.	Gr.
s s	2	Bacillus thermoamylovorans	8,20	2	Bacillus sonorensis	3,88	2
5 5		Brevibacillus brevis	8,20	2	Bacillus thermoamylovorans	3,84	7
S 5	2	Brevibacillus centrosporus	8,14	2	Brevibacillus brevis	3,80	7
6	2	Brevibacillus choshinensis	8,02	2	Brevibacillus centrosporus	3,86	7
	2	Brevibacillus formosus	7,81	2	Brevibacillus choshinensis	3,78	7
	2	Brevibacillus ginsengisoli	7,78	2	Brevibacillus formosus	3,50	7
	2	Brevibacillus invocatus	8,18	2	Brevibacillus ginsengisoli	3,67	7
	2	Brevibacillus limnophilus	8,12	2	Brevibacillus invocatus	3,86	7
Drevied cutus unmopratus	2	Brevibacillus panacihumi	8,07	2	Brevibacillus limnophilus	3,78	7
Brevibacillus panacihumi 0,71		Brevibacillus reuszeri	8,17	2	Brevibacillus panacihumi	3,68	7
Brevibacillus reuszeri 1,43		Geobacillus thermoglucosidans	8,18	2	Brevibacillus reuszeri	3,88	7
Geobacillus thermoglucosidans 1,35		Lactobacillus acidifarinae	8,17	2	Geobacillus thermoglucosidans	3,56	7
Lactobacillus acidifarinae 1,43		Lactobacillus amylolyticus	8,20	2	Lactobacillus acidifarinae	3,88	7
Lactobacillus acidophilus 19,47		Lactobacillus antri	19,75	2	Lactobacillus amylolyticus	3,86	7
Lactobacillus amylolyticus 1,35	2	Lactobacillus apis	7,11	2	Lactobacillus antri	3,54	7
Lactobacillus antri 1,43		Lactobacillus brantae	8,17	2	Lactobacillus apis	2,78	7
Lactobacillus apis 118,51	1 2	Lactobacillus camelliae	8,12	2	Lactobacillus brantae	3,69	7
Lactobacillus brantae 0,71	2	Lactobacillus casei	8,18	2	Lactobacillus camelliae	3,74	7
Lactobacillus camelliae 0,47	2	Lactobacillus coleohominis	8,20	2	Lactobacillus casei	3,88	7
Lactobacillus casei 1,43	2	Lactobacillus crispatus	721,14	2	Lactobacillus coleohominis	1,50	7
Lactobacillus coleohominis 1,43	2	Lactobacillus diolivorans	8,20	2	Lactobacillus diolivorans	3,86	2
Lactobacillus diolivorans 1,43	2	Lactobacillus equi	8,18	2	Lactobacillus equi	3,71	7
Lactobacillus equi 1,43	2	Lactobacillus equicursoris	8,13	2	Lactobacillus equicursoris	3,84	7
Lactobacillus equicursoris 1,43	2	Lactobacillus fabifermentans	7,99	2	Lactobacillus fabifermentans	3,88	7
Lactobacillus fabifermentans 1,43	2	Lactobacillus faeni	7,06	7	Lactobacillus faeni	3,27	7
Lactobacillus faeni 0,23	2	Lactobacillus farraginis	8,20	2	Lactobacillus farraginis	3,86	7
Lactobacillus farraginis 1,43	2	Lactobacillus fermentum	8,17	2	Lactobacillus fermentum	3,49	2
Lactobacillus fermentum 1,35	2	Lactobacillus frumenti	5,83	7	Lactobacillus frumenti	3,80	7
Lactobacillus frumenti 1,43	2	Lactobacillus gallinarum	22,36	2	Lactobacillus gallinarum	16,20	7
Lactobacillus gallinarum 2,23	2	Lactobacillus gasseri	5,54	2	Lactobacillus gasseri	3,57	7
Lactobacillus gasseri 1,43	2	Lactobacillus gastricus	8,20	7	Lactobacillus gastricus	3,88	7
Lactobacillus gastricus 1,35	2	Lactobacillus gigeriorum	6,92	7	Lactobacillus gigeriorum	2,30	7
Lactobacillus gigeriorum 0,55	2	Lactobacillus guizhouensis	8,20	2	Lactobacillus guizhouensis	3,88	7

Table IV. Continued.

Control			TIS-TI			TIS-H		
Bacteria species	Dist.	Ğr.	Bacteria species	Dist.	Ğ.	Bacteria species	Dist.	Ğr.
Lactobacillus guizhouensis	1,27	2	Lactobacillus hamsteri	7,78	2	Lactobacillus hamsteri	3,72	2
Lactobacillus hamsteri	0,07	2	Lactobacillus helveticus	12,5	2	Lactobacillus helveticus	8,65	2
Lactobacillus helveticus	2,38	2	Lactobacillus hilgardii	8,20	2	Lactobacillus hilgardii	3,70	2
Lactobacillus hilgardii	1,43	2	Lactobacillus ingluviei	8,06	2	Lactobacillus ingluviei	3,88	2
Lactobacillus ingluviei	1,43	2	Lactobacillus intermedius	22,70	2	Lactobacillus intermedius	1,78	2
Lactobacillus intermedius	7,40	2	Lactobacillus intestinalis	8,02	2	Lactobacillus intestinalis	3,73	2
Lactobacillus intestinalis	1,27	2	Lactobacillus japonicus	6,42	2	Lactobacillus japonicus	3,82	2
Lactobacillus japonicus	1,59	2	Lactobacillus jensenii	268,38	2	Lactobacillus jensenii	39,95	2
Lactobacillus jensenii	1,43	2	Lactobacillus johnsonii	113,22	2	Lactobacillus johnsonii	10,03	2
Lactobacillus johnsonii	0,87	2	Lactobacillus kalixensis	8,16	2	Lactobacillus kalixensis	3,88	2
Lactobacillus kalixensis	1,43	2	Lactobacillus kisonensis	8,20	2	Lactobacillus kisonensis	3,86	2
Lactobacillus kisonensis	1,43	2	Lactobacillus kitasatonis	5,94	2	Lactobacillus kitasatonis	0,56	2
Lactobacillus kitasatonis	00,00	2	Lactobacillus letivazi	7,74	2	Lactobacillus letivazi	3,65	2
Lactobacillus letivazi	1,11	2	Lactobacillus manihotivorans	8,20	2	Lactobacillus manihotivorans	3,84	2
Lactobacillus manihotivorans	1,43	2	Lactobacillus mucosae	8,19	2	Lactobacillus mucosae	3,81	2
Lactobacillus mucosae	1,43	2	Lactobacillus oris	80,9	2	Lactobacillus oris	3,73	2
Lactobacillus oris	1,43	2	Lactobacillus paracasei	8,19	2	Lactobacillus paracasei	3,88	2
Lactobacillus paracasei	1,35	2	Lactobacillus parafarraginis	8,20	2	Lactobacillus parafarraginis	3,86	2
Lactobacillus parafarraginis	1,43	2	Lactobacillus parakefiri	8,19	2	Lactobacillus parakefiri	3,76	2
Lactobacillus parakefiri	1,43	7	Lactobacillus paraplantarum	7,97	2	Lactobacillus paraplantarum	3,88	2
Lactobacillus paraplantarum	1,43	2	Lactobacillus pentosus	8,89	2	Lactobacillus pentosus	3,66	2
Lactobacillus pentosus	1,03	2	Lactobacillus plantarum	7,78	2	Lactobacillus plantarum	3,69	2
Lactobacillus plantarum	1,03	2	Lactobacillus reuteri	7,26	2	Lactobacillus reuteri	3,88	2
Lactobacillus reuteri	1,43	2	Lactobacillus rhamnosus	8,04	2	Lactobacillus rhamnosus	3,63	2
Lactobacillus rhamnosus	0,00	2	Lactobacillus ruminis	8,20	2	Lactobacillus ruminis	3,86	2
Lactobacillus ruminis	1,43	7	Lactobacillus salivarius	8,20	2	Lactobacillus salivarius	3,77	2
Lactobacillus salivarius	1,43	2	Lactobacillus senmaizukei	7,43	2	Lactobacillus senmaizukei	3,27	2
Lactobacillus senmaizukei	0,79	2	Lactobacillus siliginis	8,11	2	Lactobacillus siliginis	3,86	2
Lactobacillus siliginis	1,35	2	Lactobacillus similis	8,20	2	Lactobacillus similis	3,76	2
Lactobacillus similis	1,43	2	Lactobacillus suebicus	8,18	2	Lactobacillus suebicus	3,84	2
Lactobacillus suebicus	1,43	2	Lactobacillus taiwanensis	477,97	2	Lactobacillus taiwanensis	156,77	2
Lactobacillus thailandensis	1,35	2	Lactobacillus thailandensis	8,15	2	Lactobacillus thailandensis	3,80	7
Lactobacillus tucceti	0,87	7	Lactobacillus tucceti	7,80	7	Lactobacillus tucceti	3,30	7
Lactobacillus ultunensis	48,75	7	Lactobacillus ultunensis	48,09	7	Lactobacillus ultunensis	45,05	7

Table IV. Continued.

list. Gr. Bacteria species I list. 1,43 2 Lactobacillus vaginalis I soldensis 1,35 2 Lactobacillus versmoldensis I soldensis 1,35 2 Lactobacillus scalinarum in I tone 1,43 2 Lentibacillus salinarum in I tone 1,43 2 Lysinibacillus salinarum in I tovorans 0,87 2 Lysinibacillus salinarum in I toronicapiens 1,43 2 Lysinibacillus parviboronicapiens in I toronicapiens 1,43 2 Lysinibacillus parviboronicapiens in I toronicapiens 1,43 2 Lysinibacillus castaneae I toronicapiens 1,43 2 Paenibacillus castaneae I toronicapiens 1,43 2 Paenibacillus calluosirophicus I toronicapiens 1,43 2 Paenibacillus elgii I toronicapiens 1,43 2 Paenibacillus phicus in I toronicapiens 1,43 2 Paenibacillus penensis I toronicapiens 1,43 2 Paenibacillus ginsengagri I toronicapiens 1,43 2 Paenibacillus sinengari I toronicapiens 1,43 2 Paenibacillus sinengari I toronicapiens I	T-SIT		TIS-H	
1,43Lactobacillus vaginalis1,35Lactobacillus versmoldensis0,79Lentibacillus versmoldensis0,47Lentibacillus salinarum1,43Lentibacillus salinarum1,43Lysinibacillus parviborans1,43Lysinibacillus parviboronicapiens1,43Lysinibacillus parviboronicapiens1,43Lysinibacillus caespits1,43Lysinibacillus caespits1,43Paenibacillus caespits1,43Paenibacillus caespits1,43Paenibacillus colulositynicus1,43Paenibacillus colulositynicus1,43Paenibacillus elgii1,43Paenibacillus gansuensis1,43Paenibacillus ginsengagri1,43Paenibacillus ginsengagri1,43Paenibacillus macerans1,43Paenibacillus macerans1,43Paenibacillus motobuensis1,43Paenibacillus panila1,43Paenibacillus panila1,43Paenibacillus punila1,43Paenibacillus ponymyca1,43Paenibacillus ponymyca1,43Paenibacillus ponymyca1,43Paenibacillus polymyca1,43Paenibacillus polymyca1,43Paenibacillus polymyca1,43Paenibacillus polymyca1,43Paenibacillus polymyca1,43Paenibacillus polymyca1,43Paenibacillus polymyca1,43Paenibacillus polymyca	Bacteria species	Ğ.	Bacteria species	Dist.
1,35 Lactobacillus versmoldensis 0,79 Lentibacillus kapialis 1,43 Lentibacillus salinarum 1,43 Lentibacillus salinarum 1,43 Lentibacillus provintolerans 0,87 Lysinibacillus parviboronicapiens 1,19 Lysinibacillus parviboronicapiens 1,19 Lysinibacillus parviboronicapiens 1,43 Lysinibacillus caespitis 1,43 Leenibacillus celtulosityticus 1,43 Paenibacillus celtulosityticus 1,43 Paenibacillus elgii 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus macerans 1,43 Paenibacillus motobuensis 1,43 Paenibacillus poini		2	Lactobacillus vaginalis	3,73
0,79 Lactobacillus kapialis 1,43 Lentibacillus kapialis 1,43 Lentibacillus salinarum 1,43 Lysinibacillus poronitolerans 0,87 Lysinibacillus parviboronicapiens 1,19 Lysinibacillus parviboronicapiens 1,19 Lysinibacillus parviboronicapiens 1,43 Lysinibacillus caespitis 1,43 Lysinibacillus caespitis 1,43 Lysinibacillus cellulosityticus 1,43 Lysinibacillus elgii 1,43 Lysinibacillus amacerans 1,43 Lysinibacillus panacillus panacillus panacillus paenibacillus panacillus paenibacillus polymyxa 1,43 Lysinibacillus polymyxa 1,43 Lysinibacillus polymyxa 1,43 Lysinibacillus polymyxa 1,43 Lysinibacillus paenibacillus polymyxa 1,43 Lysinibacillus paenibacillus polymyxa 1,43 Lysinibacillus paenibacillus polymyxa 1,43 Lysinibacillus paenipacillus polymyxa 1,43 Lysinipacillus paenibacillus polymyxa 1,43 Lysinipacillus paenibacillus polymyxa 1,43 Lysinipacillus paenibacillus paenibacillus polymyxa 1,43 Lysinipacillus paenibacillus paenibacillus polymyxa	Lactobacillus versmoldensis	2	Lactobacillus versmoldensis	3,88
0,47 Lentibacillus kapialis 1,43 Lentibacillus salinarum 1,43 Lysinibacillus boronitolerans 0,87 Lysinibacillus parviboronicapiens 1,19 Lysinibacillus parviboronicapiens 1,19 Lysinibacillus avylanityticus 1,43 Lysinibacillus caespitis 1,43 Lysinibacillus cellulositoros 1,43 Lysinibacillus cellulositrophicus 1,43 Lysinibacillus elgii 1,43 Lysinibacillus iamilae 1,43 Lysinibacillus jamilae 1,43 Lysinibacillus jamilae 1,43 Lysinibacillus mendelii 1,43 Lysinibacillus panacisoli 1,43 Lysinibacillus panacisoli 1,43 Lysinibacillus panacisoli 1,43 Lysinibacillus polymyxa 1,43 Lysinibacillus polymyxa 1,43 Lysinibacillus polymyxa 1,43 Lysinibacillus polymyxa 1,43 Lysinibacillus painibacillus polymyxa 1,43 Lysinibacillus painibacilus polymyxa 1,43 Lysinibacilus painibacilus polymyxa 1,43 Lysinibacilus painibacilus painibacilus polymyxa 1,43 Lysinibacilus painibacilus painibacilus polymyxa	Lactobacillus zeae	2	Lactobacillus zeae	3,86
1,43 Lentibacillus salinarum 1,43 Lysinibacillus boronitolerans 0,87 Lysinibacillus persolivorans 1,43 Lysinibacillus sylanifyticus 1,43 Lysinibacillus sylanifyticus 1,43 Lysinibacillus castaneae 1,43 Lysinibacillus cellulosityrophicus 1,43 Laenibacillus eliulosityricus 1,43 Laenibacillus eliicis 1,43 Laenibacillus eliicis 1,43 Laenibacillus gansuensis 1,43 Laenibacillus motobuensis 1,43 Laenibacillus motobuensis 1,43 Laenibacillus motobuensis 1,43 Laenibacillus panacisoli 1,43 Laenibacillus polymyxa 1,43 Laenibacillus polymyxa 1,43 Laenibacillus polymyxa 1,43 Laenibacillus polymyxa 1,43 Laenibacillus residui	Lentibacillus kapialis	2	Lentibacillus kapialis	3,48
1,43 2 Lysinibacillus boronitolerans 0,87 2 Lysinibacillus fusiformis 1,43 2 Lysinibacillus sylanilyticus 1,19 2 Lysinibacillus sylanilyticus 1,43 2 Paenibacillus caespitis 1,43 2 Paenibacillus cellulositrophicus 1,43 2 Paenibacillus elini 1,43 2 Paenibacillus elini 1,43 2 Paenibacillus elini 1,43 2 Paenibacillus filicis 1,43 2 Paenibacillus filicis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus jamilae 1,43 2 Paenibacillus gensuensis 1,43 2 Paenibacillus motobuensis 1,43 2 Paenibacillus mendelii 1,43 2 Paenibacillus motobuensis 1,43 2 Paenibacillus motobuensis 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus pini	Lentibacillus salinarum	2	Lentibacillus salinarum	3,81
0,87 Lysinibacillus cresolivorans 1,35 Lysinibacillus fusiformis 1,43 Lysinibacillus sylanifyticus 1,43 Lysinibacillus caspaneae 1,43 Paenibacillus cellulosityricus 1,43 Paenibacillus cellulosityricus 1,43 Paenibacillus elgii 1,35 Paenibacillus elgii 1,35 Paenibacillus filicis 1,43 Paenibacillus filicis 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus macerans 1,43 Paenibacillus macerans 1,43 Paenibacillus macerans 1,43 Paenibacillus macerans 1,43 Paenibacillus motobuensis 1,43 Paenibacillus panacisoli 1,43 Paenibacillus poin 1,43 Paenibacillus pii 1,43 Paenibacillus poin 1,43 Paenibacillus poin 1,43 Paenibacillus poin 1,43 Paenibacillus residui	Lysinibacillus boronitolerans	2	Lysinibacillus boronitolerans	3,88
1,35 Lysinibacillus fusiformis 1,43 Lysinibacillus parviboronicapiens 1,19 Lysinibacillus parviboronicapiens 1,43 Paenibacillus cellulosilyticus 1,43 Paenibacillus cellulosilyticus 1,43 Paenibacillus elgii 1,43 Paenibacillus elgii 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus macerans 1,43 Paenibacillus motobuensis 1,43 Paenibacillus motobuensis 1,43 Paenibacillus motobuensis 1,43 Paenibacillus panacisoli 1,43 Paenibacillus panacisoli 1,43 Paenibacillus polymyxa	Lysinibacillus cresolivorans	2	Lysinibacillus cresolivorans	3,66
1,43 2 Lysinibacillus parviboronicapiens 1,19 2 Paenibacillus sylamilyticus 1,43 2 Paenibacillus castaneae 1,43 2 Paenibacillus cellulositrophicus 1,43 2 Paenibacillus cellulositrophicus 1,43 2 Paenibacillus elgii 1,43 2 Paenibacillus elgii 1,43 2 Paenibacillus ginsensis 1,43 2 Paenibacillus ginsensis 1,43 2 Paenibacillus ginsensis 1,43 2 Paenibacillus mandelii 1,43 2 Paenibacillus mandelii 1,43 2 Paenibacillus mandelii 1,43 2 Paenibacillus mandelii 1,43 2 Paenibacillus monobuensis 1,43 2 Paenibacillus ponthalenovorans 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus polymysa	Lysinibacillus fusiformis	2	Lysinibacillus fusiformis	3,88
1,19 2 Lysinibacillus xylanilyticus 1,43 2 Paenibacillus caespitis 1,43 2 Paenibacillus castaneae 1,43 2 Paenibacillus cellulosityticus 1,43 2 Paenibacillus elgii 1,43 2 Paenibacillus elgii 1,43 2 Paenibacillus filicis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus mendelii 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus penensis 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus residui	Lysinibacillus parviboronicapiens	2	Lysinibacillus parviboronicapiens	3,78
1,43 2 Paenibacillus caespitis 1,43 2 Paenibacillus castaneae 1,43 2 Paenibacillus cellulosityticus 1,43 2 Paenibacillus cellulosityticus 1,43 2 Paenibacillus elgii 1,43 2 Paenibacillus ginsensis 1,43 2 Paenibacillus fiticis 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus motobuensis 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus puni 1,43 2 Paenibacillus poin 1,43 2 Paenibacillus pini 1,43 2 Paenibacillus pini 1,43 2 Paenibacillus pini 1,43 2 Paenibacillus polymyxa	Lysinibacillus xylanilyticus	2	Lysinibacillus xylanilyticus	3,68
1,43 2 Paenibacillus castaneae 1,43 2 Paenibacillus cellulosityticus 1,43 2 Paenibacillus cellulositrophicus 1,43 2 Paenibacillus elgii 1,43 2 Paenibacillus elgii 1,43 2 Paenibacillus filicis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus mendelii 1,43 2 Paenibacillus polymensis 1,03 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa	Paenibacillus caespitis	2	Paenibacillus caespitis	3,84
icus 1,43 2 Paenibacillus cellulosityicus 1,43 2 Paenibacillus cellulositrophicus 1,43 2 Paenibacillus ehimensis 1,43 2 Paenibacillus ehimensis 1,43 2 Paenibacillus filicis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus motobuensis Paenibacillus motobuensis 1,43 2 Paenibacillus motobuensis Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus pocheonensis 1,43 2 Paenibacillus posymyxa Paenibacillus residui	Paenibacillus castaneae	2	Paenibacillus castaneae	3,84
icus 1,35 2 Paenibacillus cellulositrophicus 1,43 2 Paenibacillus ehimensis 1,43 2 Paenibacillus elimensis 1,43 2 Paenibacillus filicis 1,43 2 Paenibacillus forsythiae 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus mendelii 1,43 2 Paenibacillus motobuensis Paenibacillus panacisoli 1,43 2 Paenibacillus pocheonensis 1,43 2 Paenibacillus residui	Paenibacillus cellulosilyticus	2	Paenibacillus cellulosilyticus	3,88
1,43 2 Paenibacillus ehimensis 1,43 2 Paenibacillus ehimensis 1,43 2 Paenibacillus ginis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus jamilae 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus motobuensis 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus ponorimensis 1,43 2 Paenibacillus poin 1,43 2 Paenibacillus poin 1,43 2 Paenibacillus poin 1,43 2 Paenibacillus poin 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa	Paenibacillus cellulositrophicus	2	Paenibacillus cellulositrophicus	3,86
1,35 Paenibacillus ehimensis 1,43 Paenibacillus elgii 1,43 Paenibacillus filicis 1,43 Paenibacillus gansuensis 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus macerans 1,43 Paenibacillus mendelii 1,43 Paenibacillus motobuensis 1,43 Paenibacillus motobuensis 1,03 Paenibacillus panacisoli 1,43 Paenibacillus ponacisoli 1,43 Paenibacillus poini 1,43 Paenibacillus polymyxa	Paenibacillus cookii	2	Paenibacillus cookii	3,88
1,43 Paenibacillus filicis 1,35 Paenibacillus filicis 1,43 Paenibacillus gansuensis 1,43 Paenibacillus gansuensis 1,43 Paenibacillus gansuensis 1,43 Paenibacillus jamilae 1,43 Paenibacillus macerans 1,43 Paenibacillus mendelii 1,43 Paenibacillus motobuensis 1,03 Paenibacillus panacisoli 1,43 Paenibacillus panacisoli 1,43 Paenibacillus pini 1,43 Paenibacillus pocheonensis 1,43 Paenibacillus poin 1,43 Paenibacillus polymyxa 1,43 Paenibacillus polymyxa 1,43 Paenibacillus residui	Paenibacillus ehimensis	2	Paenibacillus ehimensis	3,86
1,35 Paenibacillus filicis 1,43 Paenibacillus gansuensis 1,43 Paenibacillus gansuensis 1,43 Paenibacillus ginsengagri 1,43 Paenibacillus jamilae 1,43 Paenibacillus macerans 1,43 Paenibacillus motobuensis 1,43 Paenibacillus motobuensis 1,43 Paenibacillus panacisoli 1,43 Paenibacillus panacisoli 1,43 Paenibacillus pini 1,43 Paenibacillus residui	Paenibacillus elgii	2	Paenibacillus elgii	3,86
1,43 2 Paenibacillus forsythiae 1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus materii 1,43 2 Paenibacillus motobuensis 1,43 2 Paenibacillus naphthalenovorans 1,03 2 Paenibacillus panacisoli 1,43 2 Paenibacillus poncheonensis 1,43 2 Paenibacillus poin 1,43 2 Paenibacillus poilus peribacillus poilus poilus poilus peribacillus poilus peribacillus poilus peribacillus poilus peribacillus peribacillu	Paenibacillus filicis	2	Paenibacillus filicis	3,88
1,43 2 Paenibacillus gansuensis 1,43 2 Paenibacillus ginsengagri 1,43 2 Paenibacillus jamilae 1,43 2 Paenibacillus macerans 1,43 2 Paenibacillus mendelii 1,43 2 Paenibacillus motobuensis 1,03 2 Paenibacillus panacisoli 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus pocheonensis 1,43 2 Paenibacillus poin 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus residui	Paenibacillus forsythiae	2	Paenibacillus forsythiae	3,86
1,432Paenibacillus ginsengagri1,432Paenibacillus jamilae1,432Paenibacillus macerans1,432Paenibacillus mendelii1,432Paenibacillus motobuensis1,032Paenibacillus ourofinensis1,032Paenibacillus panacisoli1,432Paenibacillus pini1,432Paenibacillus pocheonensis1,432Paenibacillus polymyxa1,432Paenibacillus residui1,432Paenibacillus residui	Paenibacillus gansuensis	2	Paenibacillus gansuensis	3,86
1,432Paenibacillus jamilae1,432Paenibacillus macerans1,432Paenibacillus mendelii1,432Paenibacillus motobuensis0rans1,432Paenibacillus naphthalenovorans1,032Paenibacillus panacisoli1,432Paenibacillus pini1,432Paenibacillus pini1,432Paenibacillus pocheonensis1,432Paenibacillus polymyxa1,432Paenibacillus residui	Paenibacillus ginsengagri	2	Paenibacillus ginsengagri	3,81
1,432Paenibacillus macerans1,432Paenibacillus macerans1,432Paenibacillus motobuensis1,032Paenibacillus ourofinensis1,432Paenibacillus panacisoli1,432Paenibacillus pini1,432Paenibacillus pocheonensis1,432Paenibacillus polymyxa1,432Paenibacillus residui1,432Paenibacillus residui	Paenibacillus jamilae	2	Paenibacillus jamilae	3,80
1,432Paenibacillus macerans1,432Paenibacillus mendelii1,432Paenibacillus motobuensis1,032Paenibacillus panacisoli1,432Paenibacillus panacisoli1,432Paenibacillus pini1,432Paenibacillus pocheonensis1,432Paenibacillus polymyxa1,432Paenibacillus residui1,432Paenibacillus residui	Paenibacillus lactis	2	Paenibacillus lactis	3,86
1,43 2 Paenibacillus mendelii 1,43 2 Paenibacillus motobuensis 1,03 2 Paenibacillus naphthalenovorans 1,03 2 Paenibacillus panacisoli 1,43 2 Paenibacillus pini 1,43 2 Paenibacillus pior 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus residui	Paenibacillus macerans	2	Paenibacillus macerans	3,88
1,432Paenibacillus motobuensis1,032Paenibacillus naphthalenovorans1,032Paenibacillus ourofinensis1,432Paenibacillus pini1,432Paenibacillus pocheonensis1,432Paenibacillus polymyxa1,432Paenibacillus residui	Paenibacillus mendelii	2	Paenibacillus mendelii	3,86
orans 1,43 2 Paenibacillus naphthalenovorans 1,03 2 Paenibacillus ourofinensis 1,43 2 Paenibacillus panacisoli 1,43 2 Paenibacillus pini 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus residui	Paenibacillus motobuensis	2	Paenibacillus motobuensis	3,88
 1,03 2 Paenibacillus panacisoli 1,43 2 Paenibacillus pini 1,43 2 Paenibacillus poorheonensis 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus residui 	Paenibacillus naphthalenovorans		Paenibacillus naphthalenovorans	3,88
1,432Paenibacillus panacisoli1,352Paenibacillus pini1,432Paenibacillus pocheonensis1,432Paenibacillus polymyxa1,432Paenibacillus residui	Paenibacillus ourofinensis	2	Paenibacillus ourofinensis	3,84
1,35 2 Paenibacillus pini 1,43 2 Paenibacillus pocheonensis 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus residui	Paenibacillus panacisoli	2	Paenibacillus panacisoli	3,81
1,43 2 Paenibacillus pocheonensis 1,43 2 Paenibacillus polymyxa 1,43 2 Paenibacillus residui	Paenibacillus pini		Paenibacillus pini	3,88
yxa 1,43 2 Paenibacillus polymyxa i 1,43 2 Paenibacillus residui	Paenibacillus pocheonensis	2	Paenibacillus pocheonensis	3,86
i 1,43 2 Paenibacillus residui	Paenibacillus polymyxa	2	Paenibacillus polymyxa	3,80
	Paenibacillus residui	2	Paenibacillus residui	3,88
Paenibacillus vortex	Paenibacillus vortex 8,17	2	Paenibacillus vortex	3,88

Table IV. Continued.

Bacteria species Dist. Gr. Pentibacillus vorosnigansis 1.11 2 Pentibacillus vorosnigansis 8.19 2 Pentibacillus vorosnigansis 3.88 2 Pontibacillus natrius 1.23 2 Pentibacillus halophilas 3.88 2 Pontibacillus natrius 1.13 2 Strephococcus adulacibilities halophilas 3.88 2 Strephococcus adulacibilities 1.13 2 Strephococcus adulacibilities 3.88 2 Strephococcus adulacibilities 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2 3.88 2	Control			T-SIT			H-SIL		
1,11 2 Paenibacillus wooxongensis 8,07 2 Paenibacillus wooxongensis 3,11 1,43 2 Paenibacillus vinjungensis 8,19 2 Paenibacillus vinjungensis 3,68 1,52 2 Pontibacillus marinus 8,19 2 Pontibacillus marinus 3,68 1,53 2 Pontibacillus marinus 8,19 2 Pontibacillus marinus 3,65 1,43 2 Streptococcus agalacchitats 8,18 2 Streptococcus agalacchitats 3,88 1,43 2 Streptococcus agalacchitats 1,85 2 Streptococcus agalacchitats 3,18 2 Streptococcus agalacchitats 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,18 3,	Bacteria species	Dist.	Ğr.	Bacteria species	Dist.	Ğ.	Bacteria species	Dist.	Ğr.
143 2 Paenthacillus xinjiungensis 8,19 2 Panitabacillus shinjiungensis 3,80 127 2 Ponitabacillus halophilus 8,02 2 Ponitabacillus halophilus 3,68 1,31 2 Ponitabacillus halophilus 8,19 2 Ponitabacillus halophilus 3,68 1,11 2 Sreptococcus agalactiae 97,05 2 Sreptococcus agalactiae 3,65 1,27 3 Sreptococcus agalactiae 8,18 2 Sreptococcus agalactiae 3,18 1,27 2 Sreptococcus agaratis 8,16 2 Sreptococcus agricus 3,88 1,43 2 Sreptococcus agaratis 8,17 2 Sreptococcus aguitume 3,88 1,43 2 Sreptococcus aguitume 8,17 2 Sreptococcus aguitume 3,88 1,43 2 Sreptococcus aguitume 8,19 2 Sreptococcus aguitume 3,88 1,43 2 Sreptococcus aguitume 8,13 2 Sreptococcus aguitume 8,13	Paenibacillus woosongensis	1,11	2	Paenibacillus woosongensis	8,07	2	Paenibacillus woosongensis	3,71	2
1.27 2 Pontibacillus halophilus 8,02 2 Pontibacillus halophilus 3,68 1.13 2 Sreptoroccus quantum 8,19 2 Pontibacillus marinus 3,88 1.11 2 Sreptoroccus agalactius 3,88 2 Sreptoroccus agalactius 3,88 1.27 2 Streptoroccus augunous 10,85 2 Sreptoroccus agalactius 3,88 1.27 2 Streptoroccus augunous 10,85 2 Streptoroccus augunous 3,88 1.27 2 Streptoroccus augunous 1,46 2 Streptoroccus augunous 3,88 1.43 2 Streptoroccus augunous 8,17 2 Streptoroccus augunous 3,88 1.43 2 Streptoroccus augunits 8,19 2 Streptoroccus augunits 3,88 1.43 2 Streptoroccus augunits 3,88 3,89 3,80 1.43 2 Streptoroccus augunits 3,88 3,80 3,80 1.43 2 Streptoroccus auguni	Paenibacillus xinjiangensis	1,43	2	Paenibacillus xinjiangensis	8,19	2	Paenibacillus xinjiangensis	3,80	2
1.35 2 Pontibacillus marinus 8,19 2 Prontibacillus marinus 3,88 1,43 2 Srephococcus agalactiae 9,755 2 Srephococcus agalactiae 3,65 1,43 2 Srephococcus agalactiae 8,18 2 Srephococcus agalactiae 3,88 1,27 2 Strephococcus agalactiae 8,16 2 Srephococcus agalactiae 3,88 1,43 2 Strephococcus points 8,16 2 Strephococcus agalactiae 3,88 1,43 2 Strephococcus specifications 8,17 2 Strephococcus specifications 3,80 1,43 2 Strephococcus specifications 8,19 2 Strephococcus specifications 3,88 1,43 2 Strephococcus macrations 8,19 2 Strephococcus specifications 3,88 1,43 2 Strephococcus macrations 8,19 2 Strephococcus macrations 3,88 1,43 2 Strephococcus macrations 8,19 2 Strephococcus macrations	Pontibacillus halophilus	1,27	2	Pontibacillus halophilus	8,02	2	Pontibacillus halophilus	3,68	2
1,11 2 Streptococcus agalactiae 97,05 2 Streptococcus agalactiae 3.65 1,43 2 Streptococcus agalactiae 8,18 2 Streptococcus agalactiae 3.88 1,43 2 Streptococcus agarantis 3.81 3.88 1,43 2 Streptococcus agarantis 8,16 2 Streptococcus agarantis 3.88 1,27 2 Streptococcus portions 8,17 2 Streptococcus cristans 3,81 1,43 2 Streptococcus gallinaceus 8,20 2 Streptococcus gallinaceus 3,80 1,43 2 Streptococcus gallinaceus 8,20 2 Streptococcus gallinaceus 3,80 1,43 2 Streptococcus gallinaceus 8,19 2 Streptococcus gallinaceus 3,80 1,43 2 Streptococcus gallinaceus 8,19 2 Streptococcus gallinaceus 3,88 1,43 2 Streptococcus gallinaceus 8,13 2 Streptococcus gallinaceus 3,88 1,43	Pontibacillus marinus	1,35	2	Pontibacillus marinus	8,19	2	Pontibacillus marinus	3,88	2
143 2 Streptococcus alactolyticus 8,18 2 Streptococcus alactolyticus 3,88 127 2 Streptococcus anginosus 10,85 2 Streptococcus anginosus 3,84 127 2 Streptococcus australis 3,8 3,84 127 2 Streptococcus australis 3,8 3,8 143 2 Streptococcus point 3,8 3,8 143 2 Streptococcus galinaceus 8,17 2 Streptococcus galinaceus 3,8 143 2 Streptococcus galinaceus 8,19 2 Streptococcus galinaceus 3,8 143 2 Streptococcus galinaceus 8,19 2 Streptococcus galinaceus 3,8 143 2 Streptococcus galinaceus 8,19 2 Streptococcus galinaceus 3,8 143 2 Streptococcus galinaceus 8,19 2 Streptococcus galinaceus 3,8 143 2 Streptococcus multeri 8,08 2 Streptococcus multeri <td< td=""><td>Streptococcus agalactiae</td><td>1,11</td><td>2</td><td>Streptococcus agalactiae</td><td>97,05</td><td>2</td><td>Streptococcus agalactiae</td><td>3,65</td><td>2</td></td<>	Streptococcus agalactiae	1,11	2	Streptococcus agalactiae	97,05	2	Streptococcus agalactiae	3,65	2
127 2 Streptococcus anginosus 10,85 2 Streptococcus anginosus 25.55 14.3 2 Streptococcus anstratis 8,16 2 Streptococcus sustratis 3,88 1.27 2 Streptococcus and stratus 8,17 2 Streptococcus stratus 3,88 1.43 2 Streptococcus stratus 8,07 2 Streptococcus stratus 3,88 1.43 2 Streptococcus stratus 8,19 2 Streptococcus stratus 3,88 1.43 2 Streptococcus stratus 8,19 2 Streptococcus stratus 3,88 1.43 2 Streptococcus stratus 7,97 2 Streptococcus stratus 3,88 1.43 2 Streptococcus madenicus 7,97 2 Streptococcus stratus 3,88 1.43 2 Streptococcus mutans 8,18 2 Streptococcus stratus 3,88 1.43 2 Streptococcus stratus 8,18 2 Streptococcus stratus 3,88 <td< td=""><td>Streptococcus alactolyticus</td><td>1,43</td><td>2</td><td>Streptococcus alactolyticus</td><td>8,18</td><td>2</td><td>Streptococcus alactolyticus</td><td>3,88</td><td>2</td></td<>	Streptococcus alactolyticus	1,43	2	Streptococcus alactolyticus	8,18	2	Streptococcus alactolyticus	3,88	2
143 2 Streptococcus australis 8.16 2 Streptococcus australis 3.84 127 2 Streptococcus australis 8.17 2 Streptococcus ristatus 3.88 143 2 Streptococcus gallinaceus 8.20 2 Streptococcus gallinaceus 3.80 143 2 Streptococcus gallinaceus 8.20 2 Streptococcus gallinaceus 3.80 143 2 Streptococcus gallinaceus 8.19 2 Streptococcus gallinaceus 3.88 143 2 Streptococcus gallinaceus 8.19 2 Streptococcus gallinaceus 3.88 143 2 Streptococcus gallinaceus 8.15 2 Streptococcus gallinaceus 3.88 143 2 Streptococcus gallieri 8.18 2 Streptococcus gallierius 3.88 143 2 Streptococcus macedonicus 8.18 2 Streptococcus gallierius 3.88 143 2 Streptococcus macedonicus 8.18 2 Streptococcus gallierius <td< td=""><td>Streptococcus anginosus</td><td>1,27</td><td>2</td><td>Streptococcus anginosus</td><td>10,85</td><td>2</td><td>Streptococcus anginosus</td><td>25,55</td><td>2</td></td<>	Streptococcus anginosus	1,27	2	Streptococcus anginosus	10,85	2	Streptococcus anginosus	25,55	2
1,27 2 Streptococcus bovis 7,46 2 Streptococcus bovis 3,84 1,43 2 Streptococcus cristatus 8,17 2 Streptococcus fyri 3,88 1,43 2 Streptococcus galitaceus 8,19 2 Streptococcus galitaceus 3,88 1,43 2 Streptococcus infantis 8,19 2 Streptococcus infantis 3,88 1,43 2 Streptococcus infantis 7,96 2 Streptococcus infantis 3,88 1,43 2 Streptococcus infantis 7,97 2 Streptococcus infantis 3,88 1,43 2 Streptococcus infantis 8,13 2 Streptococcus infantis 3,88 1,43 2 Streptococcus matans 8,13 2 Streptococcus origin 3,88 1,43 2 Streptococcus origin 3,88 3,89 3,84 1,43 2 Streptococcus origin 3,84 3,84 3,84 1,43 2 Streptococcus origin 8	Streptococcus australis	1,43	2	Streptococcus australis	8,16	2	Streptococcus australis	3,88	2
1,43 2 Streptococcus cristatus 8,17 2 Streptococcus fyit 3,818 1,43 2 Streptococcus fyit 8,07 2 Streptococcus fyit 3,80 1,43 2 Streptococcus gallinaceus 8,20 2 Streptococcus gallinaceus 3,80 1,43 2 Streptococcus intermedius 8,15 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus intermedius 8,15 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus intermedius 8,15 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus mutans 7,97 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus mutans 8,18 2 Streptococcus mutans 3,88 1,43 2 Streptococcus mutans 8,18 2 Streptococcus mutans 3,88 1,43 2 Streptococcus mutans 8,18 2 Streptococcus mutans 3,88	Streptococcus bovis	1,27	2	Streptococcus bovis	7,46	2	Streptococcus bovis	3,84	2
1,35 2 Streptococcus fyyi 8,07 2 Streptococcus fyyi 3,80 1,43 2 Streptococcus galdinaceus 8,20 2 Streptococcus galdinaceus 3,80 1,43 2 Streptococcus galdinaceus 8,19 2 Streptococcus galdinaceus 3,88 1,43 2 Streptococcus intermedius 8,19 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus intermedius 8,08 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus milleri 8,08 2 Streptococcus milleri 19,66 1,43 2 Streptococcus milleri 8,08 2 Streptococcus milleri 3,88 1,43 2 Streptococcus milleri 8,13 2 Streptococcus milleri 3,88 1,43 2 Streptococcus ordits 8,18 2 Streptococcus ordits 3,88 1,43 2 Streptococcus ordits 8,18 2 Streptococcus ordits 3,88	Streptococcus cristatus	1,43	2	Streptococcus cristatus	8,17	2	Streptococcus cristatus	3,8186	2
1,43 2 Streptococcus gallinaceus 8.20 2 Streptococcus gallinaceus 3,80 1,43 2 Streptococcus gallinaceus 8,19 2 Streptococcus gordonii 3,88 1,43 2 Streptococcus intermedius 8,15 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus macedonicus 7,97 2 Streptococcus macedonicus 3,88 1,43 2 Streptococcus materi 8,08 2 Streptococcus materi 3,88 1,43 2 Streptococcus materi 8,13 2 Streptococcus materi 3,88 1,43 2 Streptococcus materi 8,13 2 Streptococcus materi 3,88 1,43 2 Streptococcus ordis 8,19 2 Streptococcus materi 3,88 1,43 2 Streptococcus parasanguinis 8,18 2 Streptococcus parasanguinis 3,88 1,43 2 Streptococcus parasanguinis 8,18 2 Streptococcus parasanguinis 3,88	Streptococcus fryi	1,35	2	Streptococcus fryi	8,07	2	Streptococcus fryi	3,80	2
1,43 2 Streptococcus gordonii 8,19 2 Streptococcus infantis 3,88 1,43 2 Streptococcus intermedius 3,80 3,88 1,43 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus macedonicus 3,88 1,43 2 Streptococcus macedonicus 19,66 1,43 2 Streptococcus macedonicus 19,66 1,43 2 Streptococcus materi 19,66 1,43 2 Streptococcus materi 8,13 2 Streptococcus materi 3,88 1,43 2 Streptococcus ordis 3,89 2 Streptococcus ordis 3,88 1,43 2 Streptococcus ordis 3,89 2 Streptococcus ordis 3,88 1,43 2 Streptococcus ordis 1,73 2 Streptococcus ordis 3,88 1,43 2 Streptococcus pasteuri 8,18 2 Streptococcus pasteuri 3,88 1,43 2 Streptococcus su	Streptococcus gallinaceus	1,43	2	Streptococcus gallinaceus	8,20	2	Streptococcus gallinaceus	3,80	2
1,43 2 Streptococcus infantis 7,96 2 Streptococcus infantis 3,80 1,43 2 Streptococcus intermedius 8,15 2 Streptococcus intermedius 3,88 1,43 2 Streptococcus mutens 3,88 3,88 1,43 2 Streptococcus mutens 3,88 1,43 2 Streptococcus mutens 3,88 1,43 2 Streptococcus mutens 3,88 1,43 2 Streptococcus oligefermentans 3,88 1,43 2 Streptococcus origatitis 3,88 1,43 2 Streptococcus streamginits 8,19	Streptococcus gordonii	1,43	2	Streptococcus gordonii	8,19	2	Streptococcus gordonii	3,88	2
1,432Streptococcus intermedius8,152Streptococcus intermedius3,881,432Streptococcus macedonicus7,972Streptococcus malleri3,881,432Streptococcus milleri19,661,432Streptococcus mutans3,881,432Streptococcus ordis3,881,432Streptococcus ordis3,811,432Streptococcus parsamginis8,182Streptococcus parsamginis3,881,432Streptococcus parsamginis8,182Streptococcus parsamginis3,881,432Streptococcus parsamginis8,182Streptococcus parsamginis3,881,432Streptococcus parsamginis8,192Streptococcus parsamginis3,881,432Streptococcus maniferi3,883,881,432Streptococcus maniferi3,881,432Streptococcus maniferi3,881,552Streptococcus maniferi3,881,572Streptococcus maniferi3,881,582Streptococcus maniferi3,881,592Streptococcus maniferi3,881,432Streptococcus maniferi3,881,502Streptococcus maniferi3,881,432Streptococcus maniferi3,881,432Streptococcus maniferi3,881,432Streptococcus maniferi3,88<	Streptococcus infantis	1,43	2	Streptococcus infantis	7,96	2	Streptococcus infantis	3,80	2
1,432Streptococcus macedonicus7,972Streptococcus macedonicus3,881,352Streptococcus milleri8,082Streptococcus milleri19,661,432Streptococcus mutans8,132Streptococcus oligofermentans3,881,432Streptococcus oralis8,092Streptococcus oralis3,881,432Streptococcus oralis8,182Streptococcus oralis3,881,432Streptococcus paraxanguinis8,182Streptococcus paraxanguinis3,881,432Streptococcus paraxanguinis8,182Streptococcus paraxanguinis3,881,432Streptococcus paraxanguinis8,192Streptococcus sanguinis3,881,432Streptococcus sanguinis8,192Streptococcus thermophilus3,861,432Streptococcus vestibularis8,202Streptococcus vestibularis3,861,432Virgibacillus hermophilus8,202Virgibacillus byunsanensis3,861,432Viridibacillus arvi8,182Viridibacillus arvi3,811,552Viridibacillus arvi8,182Viridibacillus arvi3,881,552Viridibacillus arvi8,182Viridibacillus arvi3,881,552Viridibacillus arvi8,182Viridibacillus arvi3,88	Streptococcus intermedius	1,43	2	Streptococcus intermedius	8,15	2	Streptococcus intermedius	3,88	2
1,35 2 Streptococcus milleri 8,08 2 Streptococcus milleri 19,66 1,43 2 Streptococcus milleri 3,88 3,88 1,43 2 Streptococcus ordis 3,89 1,43 2 Streptococcus ordis 3,89 1,43 2 Streptococcus ordis 3,89 1,43 2 Streptococcus praction 3,81 1,43 2 Streptococcus praction 3,81 1,43 2 Streptococcus praction 3,88 1,43 2 Streptococcus sanguinis 3,86 1,43 2 Streptococcus sanguinis 3,87 <	Streptococcus macedonicus	1,43	2	Streptococcus macedonicus	7,97	2	Streptococcus macedonicus	3,88	2
1,43 2 Streptococcus mutans 7,98 2 Streptococcus mutans 3,88 1,43 2 Streptococcus oligofermentans 8,13 2 Streptococcus oligofermentans 3,88 1,43 2 Streptococcus oralis 8,09 2 Streptococcus oralis 3,84 1,43 2 Streptococcus parasanguinis 8,18 2 Streptococcus parasanguinis 3,88 1,43 2 Streptococcus parasanguinis 8,18 2 Streptococcus parasanguinis 3,88 1,43 2 Streptococcus parasanguinis 8,19 2 Streptococcus parasanguinis 3,86 1,43 2 Streptococcus sanguinis 8,19 2 Streptococcus sanguinis 3,86 1,43 2 Streptococcus thermophilus 8,20 2 Streptococcus thermophilus 3,78 1,55 2 Streptococcus tigurinus 3,86 3 3,47 1,43 2 Streptococcus tegrinus thermophilus 8,19 2 Streptococcus vestibularis 3,47	Streptococcus milleri	1,35	2	Streptococcus milleri	80'8	2	Streptococcus milleri	19,66	2
1,43 2 Streptococcus oligofermentans 8,13 2 Streptococcus ordis 3,80 1,43 2 Streptococcus ordis 8,09 2 Streptococcus ordis 3,84 1,43 2 Streptococcus parasanguinis 8,18 2 Streptococcus parasanguinis 3,88 1,43 2 Streptococcus pasteuri 8,18 2 Streptococcus pasteuri 3,88 1,27 2 Streptococcus pasteuri 8,19 2 Streptococcus pasteuri 3,88 1,43 2 Streptococcus pasteuri 8,19 2 Streptococcus pasteuri 3,88 1,43 2 Streptococcus sanguinis 8,20 2 Streptococcus sanguinis 3,86 1,55 2 Streptococcus tigurinus 8,20 2 Streptococcus tigurinus 3,78 1,57 2 Streptococcus vestibularis 8,03 2 Streptococcus vestibularis 3,86 1,43 2 Virgibacillus thermophilus 8,20 2 Virgibacillus byunsanensis 3,84 </td <td>Streptococcus mutans</td> <td>1,43</td> <td>2</td> <td>Streptococcus mutans</td> <td>7,98</td> <td>2</td> <td>Streptococcus mutans</td> <td>3,88</td> <td>2</td>	Streptococcus mutans	1,43	2	Streptococcus mutans	7,98	2	Streptococcus mutans	3,88	2
1,43 2 Streptococcus oralis 8,09 2 Streptococcus oralis 3,80 1,43 2 Streptococcus parasanguinis 8,18 2 Streptococcus parasanguinis 3,88 1,43 2 Streptococcus pasteuri 3,88 3,88 1,43 2 Streptococcus pasteuri 3,88 1,57 2 Streptococcus pasteuri 3,88 1,43 2 Streptococcus pasteuri 3,88 1,55 2 Streptococcus sanguinis 3,8 1,55 2 Streptococcus teamorphilus 3,8 1,55 2 Streptococcus teamorphilus 3,78 1,57 2 Streptococcus teamorphilus 3,78 1,57 2 Streptococcus vestibularis 3,78 1,43 2 Streptococcus vestibularis 3,8 1,43 2 Streptococcus vestibularis 3,8 1,43 2 Virgibacillus byunsamensis 3,8 1,43 2 Virgibacillus salexigens 3,6	Streptococcus oligofermentans	1,43	2	Streptococcus oligofermentans	8,13	2	Streptococcus oligofermentans	3,88	2
1,43 2 Streptococcus orisratti 10,78 2 Streptococcus parasanguinis 3,84 1,43 2 Streptococcus parasanguinis 8,18 2 Streptococcus parasuni 3,88 1,43 2 Streptococcus pasteuri 3,8 3,8 1,57 2 Streptococcus pasteuri 3,8 1,57 2 Streptococcus sanguinis 3,8 1,55 2 Streptococcus sanguinis 3,8 1,55 2 Streptococcus sanguinis 3,8 1,55 2 Streptococcus suguinis 3,8 1,57 2 Streptococcus suguinis 3,8 1,57 2 Streptococcus suguinis 3,78 1,57 2 Streptococcus suguinis 3,78 1,57 2 Streptococcus suguinis 3,8 1,43 2 Streptococcus stigurinus 3,8 1,43 2 Virgibacillus sulainis 3,8 1,43 2 Virgibacillus sulainis 3,8 1,43	Streptococcus oralis	1,43	2	Streptococcus oralis	8,09	2	Streptococcus oralis	3,80	2
1,432Streptococcus parasanguinis8,182Streptococcus parasanguinis3,881,432Streptococcus pasteuri3,881,272Streptococcus sanguinis8,192Streptococcus sanguinis3,861,432Streptococcus thermophilus8,202Streptococcus thermophilus3,781,552Streptococcus tigurinus7,822Streptococcus tigurinus3,781,272Streptococcus vestibularis8,032Streptococcus vestibularis3,471,432Ureibacillus thermophilus8,192Ureibacillus thermophilus3,861,432Virgibacillus byunsanensis8,202Virgibacillus salexigens3,861,432Viridibacillus salexigens8,202Viridibacillus arvi3,810,872Viridibacillus neidei8,182Viridibacillus neidei3,88	Streptococcus orisratti	1,43	2	Streptococcus orisratti	10,78	2	Streptococcus orisratti	3,84	2
1,432Streptococcus pasteuri8,182Streptococcus pasteuri3,881,272Streptococcus sanguinis8,192Streptococcus sanguinis3,861,432Streptococcus thermophilus8,202Streptococcus thermophilus3,781,552Streptococcus tigurinus7,822Streptococcus tigurinus3,781,272Streptococcus vestibularis8,032Streptococcus vestibularis3,471,432Ureibacillus thermophilus8,192Ureibacillus thermophilus3,861,432Virgibacillus salexigens8,202Virgibacillus byunsanensis3,861,432Virgibacillus salexigens8,202Virgibacillus salexigens3,840,872Viridibacillus arvi8,182Viridibacillus arvi3,671,352Viridibacillus neidei8,182Viridibacillus neidei3,88	Streptococcus parasanguinis	1,43	2	Streptococcus parasanguinis	8,18	2	Streptococcus parasanguinis	3,88	2
1,272Streptococcus pseudopneumoniae7,732Streptococcus sanguinis3,861,432Streptococcus thermophilus8,202Streptococcus thermophilus3,881,352Streptococcus tigurinus7,822Streptococcus tigurinus3,781,272Streptococcus tigurinus8,032Streptococcus vestibularis3,471,432Ureibacillus thermophilus8,192Ureibacillus thermophilus3,861,432Virgibacillus salexigens8,202Virgibacillus salexigens3,840,872Viridibacillus arvi8,182Viridibacillus arvi3,671,352Viridibacillus neidei8,182Viridibacillus neidei3,88	Streptococcus pasteuri	1,43	2	Streptococcus pasteuri	8,18	2	Streptococcus pasteuri	3,88	2
1,432Streptococcus sanguinis8,192Streptococcus sanguinis3,861,352Streptococcus tigurinus7,822Streptococcus tigurinus3,781,272Streptococcus vestibularis8,032Streptococcus vestibularis3,471,432Ureibacillus thermophilus8,192Ureibacillus thermophilus3,861,432Virgibacillus byunsanensis8,202Virgibacillus byunsanensis3,861,432Virgibacillus salexigens8,202Virgibacillus salexigens3,840,872Viridibacillus arvi8,182Viridibacillus neidei3,671,352Viridibacillus neidei8,182Viridibacillus neidei3,88	Streptococcus pseudopneumoniae	1,27	2	Streptococcus pseudopneumoniae	7,73	2	Streptococcus pseudopneumoniae	3,88	2
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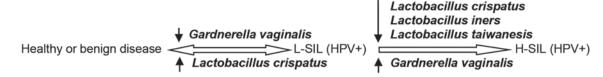


Figure 1. Proposed model for the analysis of the association between occurrence of the bacterial species and histopathological diagnosis.

Table V. Analysis of the selected bacteria species frequency in control, LSIL and HSIL diagnosed patients. Frequencies >10 have been highlighted.

Species	Control	LSIL	HSIL
Actinomyces turicensis	0	0.63	0
Corynebacterium glaucum	80.0	0	0.19
Corynebacterium matruchotti	0	0.07	0.19
Gardnerella vaginalis	11.47	46.93	304.49
Lactobacillus acidophilus	20.87	1273.62	1193.89
Lactobacillus crispatus	2506.01	405.03	245.87
Lactobacillus iners	3772.35	3183.67	1217.21
Lactobacillus taiwanensis	320.69	410.57	116.49
Propionibacterium acnes	0.88	0.42	0.48
Propionibacterium humerusii	0.16	0.13	0.14

phylogenetic and taxonomic characterisation of the analysed microbial communities (12). In the present study, the V4 hypervariable regions of 16S rRNA were used, which allowed for the identification of 3 CSTs of HSIL HPV(+), LSIL HPV(+) and the healthy group HPV(-).

In addition, >70 classes of bacteria were identified and the analysis of their frequencies demonstrated that cervical swabs of flora obtained from the volunteers and women diagnosed with LSIL HPV(+) were predominantly composed of the *Bacilli* class. The presence of *Gammaproteobacteria* and *Actinobacterium* classes in patients with HSIL HPV(+) were also detected. Further analysis revealed no cluster formation within the *Gammaproteobacteria* class and, therefore, this class was excluded from the present study.

Further analysis focussed only on the Actinobacterium and Bacilli classes of bacterial species. Regardless of the type of diagnosis, the bacterial species within the analysed classes only formed two clusters. It was observed that swabs from healthy women were characterised by an increased level of Lactobacillus crispatus, Lactobacillus iners and Lactobacillus taiwanensis. However, Gardnerella vaginalis and Lactobacillus acidophilus were absent. In the CST patients diagnosed with LSIL HPV(+) the predominant types of bacteria were Lactobacillus acidophilus and Lactobacillus iners, and there was no presence of Lactobacillus crispatus detected. The CST cervical swabs obtained from women with HSIL HPV(+) were rich in Gardnerella vaginalis and Lactobacillus acidophilus, while Lactobacillus taiwanensis, Lactobacillus iners and Lactobacillus crispatus were not detected. However, similar levels of Lactobacillus acidophilus were identified in the control and LSIL HPV(+) groups.

In the majority of healthy women in the present study, Lactobacillus crispatus, Lactobacillus iners and Lactobacillus taiwanensis were the dominant cervical microbiota. According to previous studies, these species were also reported to be dominant in the vaginal microbiota of Asian women (6,13). The women with the highest risk of HSIL HPV(+) indicated low levels of *Lactobacillus crispatus*, Lactobacillus iners and Lactobacillus taiwanensis. It has been reported that hydrogen peroxide-producing Lactobacilli are present in 96% of women with a normal vaginal bacterial community (4). In addition, species in the Lactobacillus genus have been reported to maintain a low pH by producing lactic acid (4). It has been reported that Lactobacillus crispatus was associated with a low vaginal pH compared with Lactobacillus iners, suggesting that these two species differ in ecological function (14). The cervical swabs obtained from healthy women consisted mainly of Lactobacillus bacteria. Due to their presence, the physiological pH value (3.6-4.5) was achieved by fermentation of epithelial glycogen. In addition, it has been reported that Lactobacillus bacteria have a high adherence potential, which allows them to adhere tightly to the vaginal epithelium and cover its surface, protecting the vagina from colonisation by pathogenic microorganisms (15-17). A number of Lactobacillus species can form biofilms and produce bacteriocins and hydrogen peroxide, which together have been reported to inhibit the development of undesirable anaerobes in the vagina (15,16). Lactobacillus iners has been previously reported to become a predominant part of the microbial community in the vaginal microbiota transition between abnormal and normal states (17). HPV infection can alter the mucosal metabolism and host immunity, and can induce changes in the vaginal microbiota (18).

It has been reported that microbe-induced inflammation can contribute to cervical cancer by stimulating the production of specific cytokines and chemokines, which promote proliferation and/or inhibit apoptosis (18,19). Microbiota have been demonstrated to increase, as well as decrease susceptibility to HPV infection (18,19). An association between vaginal microbiota and HPV infection was previously described by Gao et al (19). They observed a significant presence of Lactobacillus species, including Lactobacillus gallinarum, Lactobacillus iners and Lactobacillus gasseri in all women as well as Lactobacillus gasseri and Gardnerella vaginalis in HPV(+) women. The reduced population of the Lactobacillus species and the presence of Fusobacteria species in HPV(+) patients was also observed by Lee et al (6). The present study demonstrated that bacterial communities in the cervix are more complex than previously thought. The analyses suggest an association between HPV infection and decreased abundance of Lactobacillus species and increased abundance of Gammaproteobacteria anaerobes.

The aforementioned results are similar to those reported by Lee *et al* (6) and Dareng *et al* (8). The changes to the 'core microbiome' may be associated with changes in human health and risk of exposure to HPV infection and cervical cancer development.

In summary, analysis of the association between the occurrence of bacterial species and the histopathological diagnosis in the analysed population revealed that the vaginal microbiota may be clustered into two groups. Cluster 1 was predominantly affected by *Lactobacillus crispatus*, *Lactobacillus iners* and *Lactobacillus taiwanensis* and Cluster 2 predominated by *Gardnerella vaginalis*. The frequency of *Lactobacillus acidophilus* was identical in the clustered groups. The proposed mechanism of a cervical cancer formation may start with a sexually transmitted carcinogenic HPV infection (Fig. 1).

The fastest rate of HPV clearance may occur in women with Cluster 1 bacteria as the dominant microbiota as >50% of all infections were cleared within a year. The lowest clearance rate may occur in women classified with Cluster 2 dominant microbiota. In the aforementioned patients the chance of HSIL(+) development gradually increases, representing the growth of a clonal high-grade lesion up to a number of years following HPV infection. It was recently demonstrated that *Gardnerella vaginalis*, a dominant Cluster 2 bacterium, was able to adhere to and displace precoated protective *Lactobacilli* from vaginal epithelial cells, while other BV-associated anaerobes, including *Atopobium vaginae*, were less virulent (20).

The findings of the present study demonstrated a possible interaction between bacterial flora and HPV infection, as well as an association between this interaction and clinical cervical neoplasia. It was observed that bacterial dysbiosis, characterized by a predominance of *Gardnerella vaginalis* and a concomitant paucity of *Lactobacillus crispatus*, *Lactobacillus iners* and *Lactobacillus taiwanensis*, may be an HPV-dependent cofactor for cervical neoplasia development. However, without continuous observation it is difficult to confirm that microbiota dysbiosis contributes to HPV infection and carcinogenesis. Future researches are required to confirm the results of 16S rRNA sequencing and determine that microflora dysbiosis may be associated with HPV-induced cervical carcinogenicity.

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Availability of data and materials

The datasets used and/or analyzed during the present study are available from the corresponding author on reasonable request. The datasets presented in Tables III and IV can be found online at the following webpages: http://www.katbiolkom.ump.edu.pl/wp-content/uploads/2018/07/table_III.docx and http://www.

katbiolkom.ump.edu.pl/wp-content/uploads/2018/07/table_ IV.doc x (The repository of the University of Medical Sciences, Poznan, Poland).

Authors' contributions

WK conceived the study, collected samples, wrote the materials and methods and edited the manuscript. MWC analyzed the data and wrote the results and discussion sections. JK conceived the study, collected samples and contributed resources. DK performed laboratory assays. WW conceived the study, prepared figures and wrote background information. AK conceived the study, collected samples, contributed resources and approved the final draft. AGJ conceived the study, contributed resources, collected samples and approved the final draft.

Ethics approval and consent to participate

The investigations were approved by the Ethics Committee of the Medical University of Lublin (Lublin, Poland; Resolution of the Bioethics Committee; approval no: 0254/30/2002. Written informed consent was obtained from all individuals, and the research was performed by the principles of the Helsinki Declaration.

Patient consent for publication

Study participants provided written informed consent for the publication of any data and associated images.

Competing interests

The authors declare that they have no competing interests.

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