

Original Research Article

Intra- And inter-Individual Variation in Population of *Lactobacilli* and *Bifidobacteria* in Faeces of Some Healthy Individuals.

ABSTRACT

Aims: To evaluate the variation of *lactobacilli* and *bifidobacteria* population within and between healthy individuals.

Methodology: Five healthy participants were recruited, and advised not to consume yoghurt, antibiotics, alcohol and steroid during the study. Three (3) fecal samples from each participant obtained at two weeks interval were examined for each subject bacteria. The samples were collected in sterile specimen jars and immediately taken to the laboratory for analysis. MRS and BIM-25, a selective medium were used for the enumeration of *lactobacillus spp* and *Bifidobacteria* respectively using plate count method. Target bacteria were confirmed by PCR technique and biochemical tests.

Results: All isolates picked from their respective selective media were confirmed to be *lactobacillus* and *bifidobacteria*. The confirmation was carried out using both biochemical tests and PCR. The results of the statistical analysis of the data obtained using SPSS version 16 showed that intra-individual variation of the population of *Lactobacillus* and *Bifidobacteria* was significantly lower than inter-individual variation at $P = .05$.

Conclusion: This study establishes the fact that the composition level of *lactobacilli* and *bifidobacteria* varies within and between healthy human gut at different points in time.

1. INTRODUCTION

Lactobacilli and *bifidobacteria* constitute two extremely important groups of probiotic bacteria of the gastrointestinal microbiota of man and animals. There is a substantial and growing body of evidence that these microbes provide benefits to the host in which they reside (Walter, 2008, Reuter, 2001). Understanding the roles of these two groups of bacteria in the intestine continues to be a significant challenge. Human gastrointestinal tract (GIT) has over the time been identified as the organ richly endowed with ample numbers of microorganisms (Prosser, 2007). This in effect constitutes a high level of the complexity of the gut microbial communities. Available literature has shown that the bacteria residing in the human gut is estimated to be over 400 species (Wall 2006, Sheil *et al.* 2007, Prosser, 2007) and ranges between 10^{11} - 10^{12} cells per gram of faeces. Among these numbers of species are those that are able to influence significant commercial and clinical interests (Abubakar *et al.*, 2009). Research has shown that the varying population distribution of microbial cells across various region of the gut is influenced by a number of factors such as biochemical and physiological requirements which are peculiar to certain region of the gut, thus provides an environment that could either be suitable or unsuitable for individual groups of bacteria (Freter R *et al.*, 1995). Available literature has also demonstrated that human stomach is colonized by very few microbes majority of which are transient, of those that resides in such a hostile environment noted for its low pH of 3 or 1 are characterized by their exceptional capability to survive acidic pH environment (Hammes and Hertel *et al.*, 2006). Non-pathogenic microbial cells usually referred to as "indigenous microbiota", constitute complex microbial community (CMC). The CMC also constitute non-indigenous microbes that are able to confer

pathogenic activities, and are hence considered as opportunistic pathogens (Freter *et al*, 1995). *Lactobacilli* and *Bifidobacteria* species which are among the indigenous microbiota constitute the two extremely important groups of probiotic bacteria. Probiotics have been generally considered to play significant role in immune modulation, digestive and respiratory functions and are also able to alleviate infectious disease in children (Lebeer *et al*, 2008; FAO/WHO, 2001).

The gastrointestinal microbiota is a very complex community with different habitats constituting the mouth, stomach, small intestine, large intestine and rectum. Literature reports have shown that near stability exist within these habitats. However, stability of the gut microbiota is influenced by Host's individuality. This means that considerable interpersonal or individual variation exists. Thus, individual will have fixed microbiota as far as quantities and qualitative structure of both lactobacilli and bifidobacteria are concerned (Reuter, 1963). There are emerging evidences that shows significant variation of the composition level of lactobacillus and bifidobacteria in human gut, and that the population level of these subject probiotics are peculiar to individuals.

This present study is aimed at evaluating the inter- and intra- individual variation of *lactobacilli* and *bifidobacteria* among healthy individuals.

2. MATERIALS AND METHOD

Prior to collection of samples, participants were advised not to consume yoghurt, antibiotics, alcohol and steroid three weeks before and during the time of collection of sample in order not alter the microbial population level in their gut. Fecal samples were collected into a sterile screw-capped plastic container from five (5) healthy volunteers who are within the age bracket of 25 - 35 years old. Written consents were obtained from individual participants. The participants were advised not to consume yoghurt, antibiotics, alcohol and steroid 3 weeks prior to and during the time of collection of samples and to also maintain their usual diet. Three sets of the faecal sample were obtained from individual volunteers over the space of 3weeks, which make up to a total of 15 samples per week.

The reference bacteria cells for identification of the target bacteria were generously donated by Middlesex University's Microbiology Laboratory. These strains were also used for the optimization of PCR conditions as positive control for the genus – specific primers.

2.1 Isolation, characterization and Quantification of *Lactobacillus* spp and *Bifidobacteria*

Collected faecal samples were immediately processed upon arrival to the Microbiology Laboratory of Middlesex University Laboratory. 1 gram (wet weight) of the faecal sample obtained from individual volunteers was weighed and collected in a 30ml sterile universal bottle, another 1gram was weighed and stored in the freezer at -20°C for the PCR analysis. For the microbiological analysis, 9ml of buffered solution was added to fecal sample and then thoroughly homogenized using the vortex machine.

2.1.1 Microbiological enumeration of bacteria

2.1.1.1 *Lactobacillus*

Using aseptic technique, the well homogenized samples were serially diluted into tubes containing 9ml of peptone water from 10^{-1} to 10^{-6} . 100µl from each of the diluted suspensions (10^1 to 10^6) were separately inoculated in triplicate on plates of Rogosa agar media (*Lactobacillus* Selecting Agar, pH 5.4 ± 0.2, Oxoid, CM0627). Sterile spreader was used to evenly distribute the inoculums. The inoculated plates were incubated under anaerobic condition using an anaerobic gas jar containing gaspaks (GasPak™ EZ Gas Generating container system, Becton Dickson and Company, USA) at 37°C for 72hrs.

After 72hrs of incubation, plates that contains between 30-300 colony forming unit (cfu) of the isolates were selected and the representative colonies which differ in terms of their morphotype (varying sizes, colours and shapes) were counted. Three to four colonies based on their differences in size and shapes were aseptically picked from both culture plate with an inoculating loop and sub-cultured on MRS agar

75 (de Man Rogosa Sharpe, pH 6.2 ± 0.2, Oxoid, CM0359). After incubation, the isolates were subjected to
76 further characterization.

77 **2.1.1.2 Bifidobacteria**

78 On the other hand, faecal samples were serially diluted in phosphate buffer solution supplemented with
79 L-cysteine up to 10⁻⁶. 100µl aliquots of each of the diluted colony suspensions were inoculated in
80 triplicate onto BIM-25 bifidobacteria selective media. Plates were then incubated anaerobically (85%
81 nitrogen, 10% hydrogen, and 5% carbon dioxide supplied by gas packs in anaerobic jars) at 37°C for 72
82 hours. Representative isolates with different morphology were aseptically picked and sub-cultured on a
83 Reinforced Clostridial Medium (RCM) agar for further characterization.

84 **2.1.2 Identification of the bacterial isolates**

85 Identification of each isolated colony was further carried out in order to ensure precise quantitation of
86 the target bacteria.

87 **2.1.2.1 Lactobacilli**

88 Various biochemical tests which include Grams reaction, Catalase test, Motility test, Bile aesculine test,
89 Phenol red Glucose broth with gas production test, and API 50 CHL system to determine the sugar
90 fermentation pattern were carried with strict adherence to the standard of the Health protection agency
91 (HPA, 2010)

92 **2.1.2.2 Bifidobacteria**

93 Colonies that appeared in different morphologies; pale-pink, red, bright pink, and the very small colonies
94 were picked, Gram-stained and observed by optical microscopy at oil emersion magnification to
95 determine their cell morphology and Gram staining reaction. Identification of the selected colonies were
96 further confirmed by detecting the presence of fructose-6-phosphate phosphoketolase (F6PPK) activity.

97 **2.2 PCR Qualitative analysis**

98 Known colonies of *lactobacillus acidophilus* and *Bifidobacterium adolescent* which were used as
99 reference strains were prepared in a suspension and used directly as a template to test the sensitivity of
100 the primers (**see table 1**).

101 **2.2.1 Lactobacillus spp**

102 PCR reaction was carried out in a total volume of 25µl with reaction mixture that contains 2.5µL of 10x
103 PCR buffer, 2µl of 2.5mM dNTP, 2µl of 25mM MgCl₂, 1µl of 1µM primer each of the forward and
104 reverse, 0.2µl of 5U/µl of Red hot *Taq* DNA, 15.3 sterile water and 1µL of suspension of colony
105 template. Colony of *lactobacillus acidophilus* was used as the DNA template under the following PCR
106 conditions; initial denaturation temperature of 96°C for 5min for disruption of the cell wall and eruption of
107 the cell content, followed by 30cycles of which each cycles consisted of each step of denaturation at
108 95°C for 30sec, annealing at 54.4°C for 30sec and extension for 30secs at 72°C. The final extension
109 was set at 72°C for 7min and final hold at 4°C. Sterile water was used as negative control in all the
110 experiments.

111 **2.2.2 Bifidobacteria spp**

112 Amplification of the target bacterial DNA was performed with primers g-Bifid-F and g-Bifid-R (table 1)
113 in a PCR iCycler apparatus. The PCR mixture was composed of 1X PCR buffer from 10X reaction
114 buffer with 1.5 mM of MgCl₂, 0.2 mM of deoxynucleotide triphosphates (dNTPs) from 20mM, 0.125µl
115 each of forward and reverse primer, and 0.625U of Red hot Thermoscientific *Taq* DNA polymerase
116 from 5U/µl. Colony PCR was performed to identify the different colonies obtained from the BIM-25
117 bifidobacteria selective media. A reaction volume of 24µl was inoculated with 1µl of the tested colony
118 suspension. *B. adolescentis* was used as the positive control, while distilled water was used as the
119 negative control. The set up were placed in the PCR machine under the following conditions; Initial

denaturation of 95°C for 5min, followed by 30cycles of which each cycles consisted of each step of denaturation at 94°C for 30sec, annealing at 55°C for 30sec and extension for 30secs at 72°C. The final extension was set at 72°C for 5min and final hold at 4°C.

Table 1. Primers used in this study.

Bacteria	Primers	Sequence	Product size (bp)	Reference
<i>Lactobacillus</i>	LbLMA1-rev	CTCAAACTAAACAAAGTTTC	250	Dubernet <i>et al</i> , 2002
	R16-1	CTTGTACACACCGCCCGTCA		
<i>Bifidobacterium</i>	g-Bifid-F	CTCCTGGAAACGGGTGG	549-563	Matsuki <i>et al</i> ,2002
	g-Bifid-R	ACATCTATAGCCCTTCTTGTGG		

2.3 Gel Electrophoresis of the PCR products

All the PCR products obtained after amplification were checked for the expected size on 2% (w/v) agarose gel stained with ethidium bromide. Gels were run for 45minutes at 110V in TBE electrophoresis buffer. Size marker of 100bp was used on each gel. Gels were visualized with an UV trans-illuminator.

3.0 RESULTS AND DISCUSSION

3.1 Bacteria counts

Following incubation, colony counts were made from dilution plates of the two selective media that contained discrete colonies that falls within the range of 30 to 300. The total population of each genus of *lactobacilli* and *Bifidobacteria* cultured on Rogosa and BIM-25 agar respectively was calculated as CFU per gram (wet weight) of feces.

Table 2. *Lactobacillus sp.* and *Bifidobacteria sp.* load isolated from faecal samples of different participants.

Probiotics	Participants				
	A	B	C	D	E
<i>Lactobacillus</i>	5.67 ± 1.20 ^a	19.00 ± 1.15 ^b	6.33 ± .88 ^a	0.500 ± .17 ^a	8.23 ± .53 ^a
<i>Bifidobacteria</i>	18.33 ± 1.45 ^b	17.00 ± 1.73 ^a	7.97 ± .43 ^b	18.33 ± 2.60 ^b	7.73 ± .69 ^a

Values are means of triplicate readings ± standard deviation. Values followed by the same superscript letter in a column are not significantly different at $P = .05$.

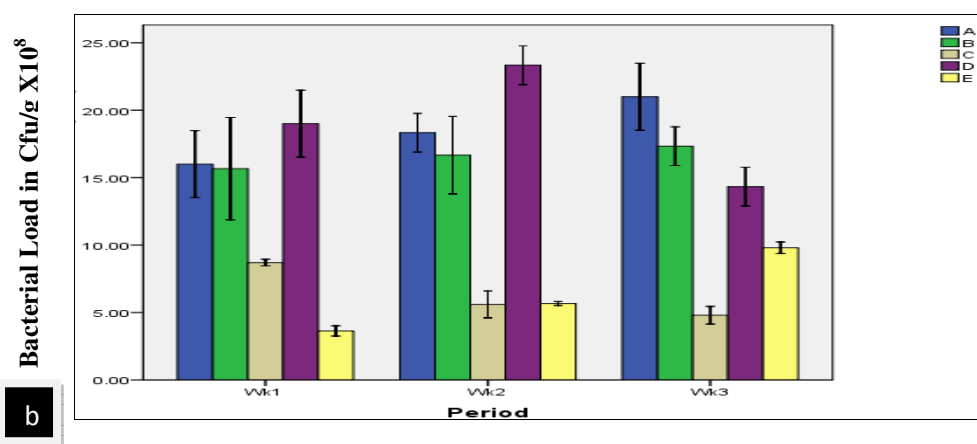
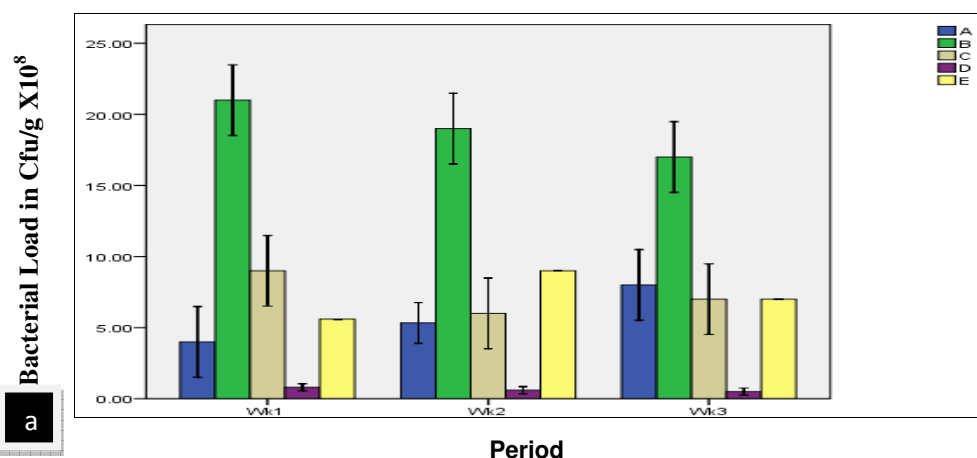


Fig. 1: a). Mean *Lactobacilli* load in CFU/g(x10⁸) from faecal samples of participants. **b).** Mean *Bifidobacteria* load CFU/g(x10⁸) from faecal samples of participants. Each sample from respective participants was obtained once for each week at 2weeks interval.
Key: A-E=Participants

The results of the statistical analysis of the data obtained using SPSS version 16 showed that there was significant difference at $P = .05$ within the participants for both *Lactobacillus* and *Bifidobacteria* respectively. The *Lactobacillus* load for participant **A** increased significantly from 4.5×10^8 cfu/g at week one to $5.33 \pm 0.33 \times 10^8$ cfu/g by week two and $8.00 \pm 0.58 \times 10^8$ cfu/g by the third week as represented in figure one. A different pattern however was observed for participant **B** in which there was decrease in the *Lactobacillus* load from week one through to week three and an increase of *Bifidobacteria* from week one through to the third week. Participant **C** and **E** had an irregular pattern in which there was significant decrease by week two and an increase by week three for participant **C** and a significant increase by week but decreased by week three for participant **E** respectively. There was however no significant increase or decrease for the *Lactobacillus* load in participant **D**.

There was significant difference in the level of *Bifidobacteria* load isolate from participants as seen in figure 2. Participant **A** increased significantly from $16.33 \pm 0.33 \times 10^8$ CFU/g at week one to $22.57 \pm 0.57 \times 10^8$ CFU/g by week three. The same pattern was observed for participant **E**. Participant **B** recorded a constant load without significant difference in their values all through the three weeks of experiment. The result pattern for participants **C** showed a decrease by week two and constant by week three, while participant **D** increased by week two and decreased significantly by week three. Comparatively, there was significant difference at $P = .05$ for the two bacteria (the *Lactobacillus* and *Bifidobacteria*) in their load among participants **A-E** as recorded in **table 1**. Participant **B** however maintained high level of both genera.

The result as obtained in this study shows a significant inter-individual variation of the composition level of both *Lactobacilli* and *Bifidobacteria* (**Figure 1**). The result also shows intra-individual variation of the subject bacteria at different time point as demonstrated in table 2. This supports the findings of (Reuter, 2001, Hammes and Hertel, 2006) which demonstrated inter- and intra-individual variation in the fecal microbiota of different healthy human subjects.

The population level of *Lactobacillus* as obtained in this study ranges between 10^6 and 10^8 cfu/g, although with an exception (**table 2**), is in agreement with Walter, 2008 who explained that, when total anaerobic culturing techniques are used, *Lactobacilli* form a very small proportion of the cultivable human fecal microbiota and can rarely be cultured at population levels exceeding 10^8 CFU/g. Previous studies have also reported averages of 10^6 and 10^8 CFU/g (Dal Bello and Hertel, 2006, Dal Bello *et al.* 2003). This accounts for only about 0.01% of the total cultivable counts (Walter 2008). As evidenced in this study, lower levels of *Lactobacillus* have also been observed in previous study on healthy (Hopkins *et al.* 2001).

Kimura *et al.*, 1997 in their analysis of bifidobacterial and *Lactobacilli* populations present in the feces of 10 human subjects showed that each subject harboured numerically predominant strains that were characteristic of the particular human host. The Human Microbiome Project consortium 2012 showed that intra-individual fluctuations of microbial composition occur at different stages of life due to a number of factors including but not limited to environmental changes, lifestyle and pathological events. (Buddington and Sangild, 2011) also in their findings showed that the type and number of microbial species that persist and colonise the GI is not determined by chance, but by a combination of factors including inflammatory state of the host, diet, host genetics and environmental factors. It is not clear the factors that modulate the composition of the intestinal microbial populations of individual humans are not known, although it has been concluded by some that the genetic characteristics of the host are important.

Table 3. Result showing the Biochemical characteristics of *Lactobacillus spp* isolates.

P	CIM	GR/CM	BA	PRGB	↑	CT	MT
A	Rhizoid	+/Long rod	+	+	—	—	—
	Circular	+/Short rod	+	+	—	—	—
B	Rhizoid	+/Long rod	+	+	—	—	—
	Circular	+/Short rod	—	+	—	—	—
C	Circular	+/Short rod	+	+	—	—	—
	Rhizoid	+/Long rod	+	+	—	—	—
D	Circular	+/Short rod	+	+	—	—	—
	Rhizoid	+/Long rod	+	+	—	—	—
E	Circular	+/Short rod	+	+	—	—	—

P; Participant, CIM; Colony morphology, GR; Gram's reaction, CM; Cell morphology, BA; Bile aesculin test, PRGB; Phenol red glucose broth, ↑; Gas production, CT; Catalase test, MT; Motility test.

Table 4. API result indicating species identified using the apiweb™ computer software

Subject	Colony Morphology	identification comment	Specie/strain identified
A	Rhizoid	Very good	<i>Lactobacillus acidophilus</i> 1
	Circular 2mm	good	<i>Lactobacillus fermentum</i>
B	Rhizoid	Doubtful	<i>Lactobacillus acidophilus</i> 1,2 and 3
	Circular 2mm	Doubtful	<i>Lactobacillus fermentum</i> 1, <i>lactobacillus acidophilus</i> 3
C	Circular 2mm	good	<i>Lactobacillus salivarius</i>
	Rhizoid	Very good	<i>Lactobacillus acidophilus</i> 1
D	Rhizoid	Doubtful	<i>Lactobacillus acidophilus</i> 1 and 3
E	Circular 2mm	Very good	<i>Lactobacillus plantarum</i>

198

199 **Table 5: Gram Staining and F6PPK test for the confirmation of Bifidobacteria isolates**

Colony type	Gram's reaction and cell morphology	Results of F6PPK TEST
Pale pink colonies with dark centres	Gram positive, cocobacilli, club shape, Y and V branching Diplo & strep	Positive
Red colonies	Gram positive, cocobacilli, club shape Y and V branching	Positive
Very small colonies	Gram positive, cocobacilli, club shape Y and V branching	Slight colour change
Bright pink colonies	Gram positive, cocobacilli, club shape Y and V branching	Positive

200

201

202

203

204

205

206

207

208

209

210

All the isolates recovered from selective medium for the respective target bacteria were confirmed to be *Lactobacillus spp* and *bifidobacteria spp* respectively (**table 3, 4 and 5**). Lactobacilli were confirmed using the API CHL kits and identification was done with API-web program. PCR analyses also confirmed the lactobacillus colony. On the other hand, Bifidobacteria were identified by the detection of fructose-6-phosphate phosphoketolase (F6PPK) enzyme in cellular extracts as described by Scardovi 1986, and also confirmed by PCR method, see **Fig. 3**. The primer sets (**table 1**) used in this study was adopted from Dubernet *et al.*, 2002 and Matsuki *et al*, 2002, and these corresponds to the flanking sequence of the 16S rRNA gene which is known to be highly conserved among the *genus lactobacillus* and *Bifidobacteria* respectively.

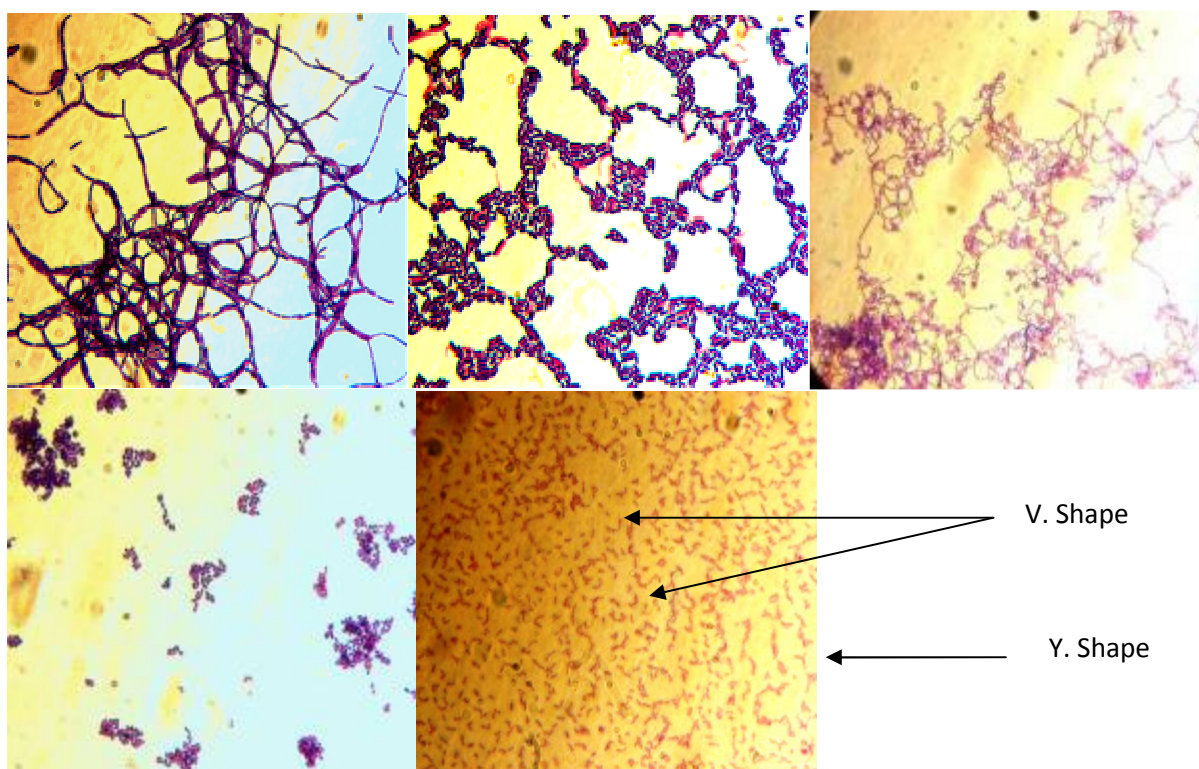


Fig. 2: Cell Morphology of isolates: **a -d**). Representative of different species of *lactobacillus* sp **e**). “V” and “Y” shape *Bifidobacteria* sp. at X1000 magnification.

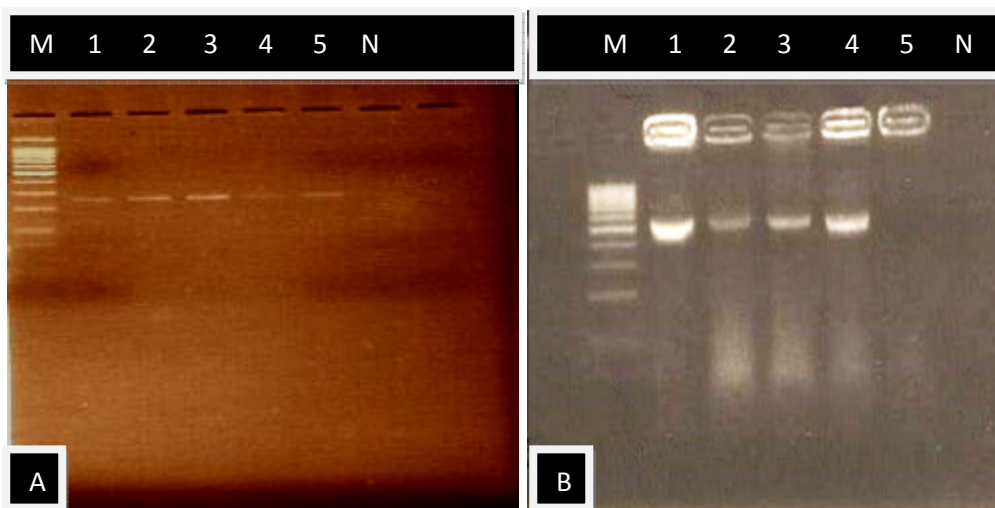


Fig. 3. Electrophoretic detection of amplified DNA of *lactobacillus* spp and *Bifidobacteria* spp. **A).** Lane 1 shows the known *Lactobacillus acidophilus* used as positive control in this experiment. Lane 2 – 5 shows the band of *lactobacillus* spp isolated from the individual volunteer isolates (250bp). **B).** Lane 1- positive control, Lane 2 -4 shows band of *Bifidobacterium* isolated from the individual participants (549 – 563bp), lane 5 shows a failed PCR product. The **N** is negative control and **M** is the DNA size marker of 100bp.

Although the methodology as used in this study did not permit the strict detection of specie of both genera to determine which specie is numerically predominant in the samples, but *L. acidophilus*, *L. fermentum*, *L. salivarius* and *L.plantarum* were the common isolates in this study, where *L.plantarum*

was found repeatedly only in one patient . It is therefore, most likely to have certain species of either genus that is unique to individual subjects. Evidence in this study thus suggests the possibility of isolating only a small number of either specie of both genera which in effect might not represent the true inhabitants of participant's intestinal tract. Genus *Bifidobacterium* has been discovered to contain up to four or five different species that is commonly isolated in adults (Gavini *et al.* 2001), while previous studies have revealed the following species of lactobacilli that are commonly found in human faeces: *L. paracasei*, *L. rhamnosus*, *L. gasseri*, *L. fermentum*, *L. plantarum* (Vaughan, 2005).

It is possible that the isolates in this study might have been transient bacteria as previous studies have shown that most of the probiotic bacteria present in faeces are allochthonous members derived from fermented food, oral cavity, or at the proximal parts of the colon (Reuter, 2001). Literature reports have also shown that human have to some extent a stable autochthonous Lactobacillus and Bifidobacteria microbiota (Reuter, 2001). A clear characteristic of autochthonous intestinal inhabitants is shown by the stable population of strains over several months in the intestinal tract without having significant upstream populations (Reuter, 2001). It is also known that autochthonous strains that naturally persist in human subjects over long periods are tested by nature for their functionality in the gut, and they are thought to likely possess adaptive traits to benefit their human host (Walter, 2008).

Further study is necessary to reveal the molecular differences that exist between the allochthonous and autochthonous species of both genera of lactobacilli and Bifidobacteria found in human feces. This is important in order to ascertain the true indigenous probiotic bacteria and their functional role in bowel health a. Geographical distribution with possibility of specificities in the composition of lactobacillus and bifidobacteria microbiota in human gut is also a desirable factor to look into.

CONCLUSION

Although, the data as obtained necessarily suggests a need to have a sufficient number of baseline samples when comparing the level of bacterial population within and between individual subjects. However, this data concord with previous studies which establish the fact that population level of lactobacilli and Bifidobacteria varies within and between individuals.

CONSENT

All authors declare that 'written informed consent was obtained from the patient for publication of this case report and accompanying images. A copy of the written consent is available for review by the editorial office/chief editor/editorial board members of this journal.

ETHICAL APPROVALS

All authors hereby declare that all experiments have been examined and approved by the appropriate ethics committee and have therefore been performed in accordance with the ethical standards laid down in the 1964 declaration of Helsinki.

REFERENCE

Abu Bakar F, Abdulamir A.S, Nordin S and Yoke T.S. (2010). Methods for Precise Detection of Probiotic Microflora: Using Adjusted Molecular Biology Protocols, Primer Sets and PCR assays. <http://scialert.net/fulltext/?doi=biotech.2010.25.32&org=11>

Buddington R. K. and Sangild P. T (2011). Companion Animals Symposium: development of the mammalian gastrointestinal tract, the resident microbiota, and the role of diet in early life. *Journal of Animal Science*, vol. 89, no. 5, pp. 1506–1519.

Dal Bello, F., and C. Hertel. 2006. Oral cavity as natural reservoir for intestinal lactobacilli. *Syst. Appl. Microbiol.* **29**:69–76.

Dal Bello, F., J. Walter, W. P. Hammes, and C. Hertel. 2003. Increased complexity of the species composition of lactic acid bacteria in human feces revealed by alternative incubation condition. *Microb. Ecol.* **45**:455–463.

- 278 Freter R and De Macias M.N. (1995). *Factors Affecting The Colonization Of the Gut by Lactobacilli and*
279 *Bacteria*. www.old-herborn-university.de/literature/books/OHUni_book_8_article_3.pdf
280 Hammes W.P and Hertel C. (2006). *The Genera Lactobacillus and Carnobacterium* in: The prokaryotes.
281 **4**: 320 – 404.
282
- 283 Hopkins M J, Sharp R, Macfarlane G T (2001). Age and disease related changes in intestinal bacterial
284 populations assessed by cell culture, 16S rRNA abundance, and community cellular fatty acid profiles.
285 *Gut* **48** (2): 198 – 205.
286
- 287 Gavini F, Cayuela C, Antoine J-M, Lecoq C, Lefebvre B, Membreacute J-M, Neut C (2001). Differences
288 in the distribution of bifidobacterial and entrobacterial species in human faecal microflora of three
289 different (children, adults, elderly) age groups. *Microb Ecol Health Dis* **13**(1): 40 – 45.
- 290 Human Microbiome Project Consortium. (2012). Structure, function and diversity of the healthy human
291 microbiome. *Nature* **486**, 207–214. doi: 10.1038/nature11234.
- 292 Joint FAO/WHO (Food and Agriculture Organization/World Health Organization), 2001. Health and
293 nutritional properties of probiotics in food including powder milk with live lactic acid bacteria.
- 294 Kimura, K., Cartney, A. L. M. C., Connell, M. A. M. C., & Tannock, G. W. (1997). Analysis of Fecal
295 Populations of Bifidobacteria and Lactobacilli and Investigation of the Immunological Responses of
296 Their Human Hosts to the Predominant Strains, **63**(9), 3394–3398.
- 297 Labeer S, Vanderleyden J and De Keersmaecker S.C.J. 2008. Genes and Molecules of Lactobacilli
298 Supporting Probiotic Action. *Microbiol. Mol. Biol. Rev.* **72**: 728 – 764.
- 299 Matsuki, T. Watanabe, K. Fujimoto, J. Miyamoto, Y. Takada, T. Matsumkto, K. Oyaizu, H. and
300 Tanaka, R. (2002) Development of 16 S rRNA-Gene-Targeted Group-Specific Primers for the
301 Detection and Identification of Predominant Bacteria in Human Feces. p. 5445-5451. *Appl. Environ.*
302 <http://aem.asm.org/content/68/11/5445.full.pdf+html>
- 303 Million M, Maraninchi M, Henry M, Armougom F, Richet H, Carrieri P, Valero R, Racciah D, Vialettes B
304 and Raoult D. (2011). *Obesity-associated gut microbiota is enriched in Lactobacillus reuteri and*
305 *depleted in Bifidobacterium animalis and Methanobrevibacter smithii*. DOI:10.1038/ijo.2011.153.
306
- 307 Prosser J. (Ed.) 2007. Genomic diversity of cultivable lactobacillus population residing in the neonatal
308 and adult gastrointestinal tract. FEMS. *Microbiol. Ecol.* **59**: 127 – 137.
309
- 310 Reuter, G. 1963. Vergleichende Untersuchungen über die Bifidus-Flora im Säuglings- und
311 Erwachsenenstuhl. *Zbl. Bakt. I Orig.* **191**: 486 - 507
312
- 313 Reuter G. 2001. The Lactobacillus and Bifidobacterium Microflora of the Human Intestine: Composition
314 and Succession. *Curr. Issues Intest. Microbiol.* **2**(2): 43-53.
315
- 316 Scardovi V (1986). the genus Bifidobacterium. Page 1418 in Bergey's manual of systematic
317 bacteriology j.g. holt ed. Wilmliams and Wilkins V co., Baltimore m.d..
318
- 319 Sekirov I, Russel S.L, Antunes C.M and Finlay B.B. (2010). *Gut Microbiota in Health and Disease.*
320 *Physiol Rev* **90**: 859–904.
321
- 322 Sheil B, Shanahan F, and O'Mahony L. (2007). *Probiotic Effects on Inflammatory Bowel Disease. J.*
323 *Nutr.* **137**: 819 – 824.
324
- 325 Vaughan E. E, Heilig H. G, Ben-Amor K, De Vos W. M. (2005). Diversity, vitality and activities of
326 intestinal lactic acid bacteria and bifidobacteria assessed by molecular approaches. *FEMS Microbiol*
327 *Rev.* **29**(3):477-490.
328

329 Wall R, Fitzgerald G, Hussey S, Ryan T, Murphy B, Ross B, and Stanton C (2006). *Genomic diversity of*
 330 *cultivable Lactobacillus populations residing in the neonatal and adult gastrointestinal tract*. Prosses J
 331 (Ed). www.medicinabiointegrata.com/doc/probiotici/Lactobacilli.pdf
 332
 333 Walter J. 2008. Ecological Role of Lactobacilli in the Gastrointestinal Tract: Implications for
 334 Fundamental and Biomedical Research. *Appl. Environ. Microbiol.* Retrieved from:
 335 www.ncbi.nlm.nih.gov/pmc/articles/PMC2519286/pdf
 336
 337 Walter, J., C. Hertel, G. W. Tannock, C. M. Lis, K. Munro, and Hammes W. P. (2001). Detection of
 338 *Lactobacillus*, *Pediococcus*, *Leuconostoc*, and *Weissella* species in human feces by using group-
 339 specific PCR primers and denaturing gradient gel electrophoresis. *Appl. Environ. Microbiol.* 67:2578 –
 340 2585.
 341