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<b>Running Title (within 10 words)</b>	Effect of BIOVITA 3 administration on constipation improvement
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## Abstract

9 BIOVITA 3 bacterial species (BIOVITA 3), a probiotic blend powder containing  
10 *Clostridium butyricum* IDCC 1301, *Weizmannia coagulans* IDCC 1201, and *Bacillus*  
11 *subtilis* IDCC 1101, has been used as a food ingredient for gut health. However, its  
12 efficacy in improving constipation has not been reported. Therefore, we aimed to  
13 investigate the functional effects of oral administration of BIOVITA 3 as well as its  
14 component strains alone (at  $1.0 \times 10^9$  CFU/day) in Sprague-Dawley (SD) rats with  
15 loperamide-induced constipation. The study included fecal analysis, gastrointestinal  
16 transit ratio, histopathological analysis, short chain fatty acids (SCFAs), and metagenome  
17 analysis. As results, the BIOVITA 3 group showed significant improvements in fecal  
18 number, water content, gastrointestinal transit ratio, and thickening of the mucosal layer.  
19 In the SCFAs analysis, all probiotic-treated groups showed an increase in total SCFAs  
20 compared to the loperamide-constipated group. Changes in microbial abundance and the  
21 diversity index of three groups (normal, constipated, and BIOVITA 3) were also defined.  
22 Of these, the BIOVITA 3 showed a significant improvement in loperamide-constipated  
23 SD-rats. This study suggests the possibility that BIOVITA 3 can be applied as an  
24 ingredient in functional foods to relieve constipation.

25

26 Keywords: constipation; probiotics; BIOVITA 3 bacterial species; gut microbiota

27

28     **Introduction**

29     Constipation is one of the most common gastrointestinal disorders and is associated  
30 with bowel obstruction, insufficient bowel movements, and the feeling of incomplete  
31 evacuation (Filipović et al., 2017). It is influenced by changes in diet and psychological  
32 and social factors, often leading to chronic gastrointestinal issues (Crowell et al., 2007).  
33 There is increasing interest in improving gastrointestinal disorders and alleviating fecal  
34 problems with probiotics (Zhao et al., 2015, Yu et al., 2017, Jung et al., 2022), such as  
35 *Bacillus* and *Lactobacillus*, as they have shown beneficial effects in improving intestinal  
36 health, including constipation, bowel movements, and intestinal barrier function (Rhayat  
37 et al. 2019, Zhang et al. 2023).

38     Probiotics are live microorganisms that confer health benefits on the host when  
39 administered in adequate amounts (Hill et al., 2014). Probiotics have been shown to have  
40 potential utility as a treatment for constipation with fewer side effects than chemical drugs.  
41 The existing research results indicate that probiotics can affect intestinal motility by  
42 altering the levels of neurotransmitters and short-chain fatty acids (SCFAs), and by  
43 regulating the gut microbiota and immunity (Dimidi et al., 2017). Numerous trials of  
44 probiotic supplementation have been conducted in animals and humans to test the efficacy  
45 of probiotics against constipation (Chen et al., 2020, Qiu et al., 2022).

46     BIOVITA 3 bacterial species (BIOVITA 3) is a freeze-dried probiotic blend powder  
47 that contains three spore-forming bacteria (*Clostridium butyricum* IDCC 1301,  
48 *Weizmannia coagulans* IDCC 1201, and *Bacillus subtilis* IDCC 1101). It was developed  
49 in 1959 and was the probiotic nutritional supplement in South Korea used to improve the  
50 function of children's intestines. BIOVITA 3 have different oxygen requirements, and  
51 consequently are known to proliferate throughout the gastrointestinal tract, from the small  
52 intestine to the large intestine, and exert positive effects on intestinal function (Kim, 2021).

53 A recent *in vivo* study found that *C. butyricum* IDCC 1301 improved high fat diet-induced  
54 colonic inflammation (Choi et al., 2023). *B. subtilis* IDCC 1101 and *W. coagulans* IDCC  
55 1201 have been evaluated as safe probiotics for human use (Bang et al., 2021, Kim et al.,  
56 2022). Although the gut health benefits of their microbial components are expected, no  
57 studies have reported on the constipation improvement of blend probiotics BIOVITA 3.

58 The purpose of this study therefore was to investigate the effects of BIOVITA 3  
59 bacterial species on loperamide-induced constipation. Body weight, fecal parameters  
60 (fecal number and water content), gastrointestinal transit (GIT) ratio, and  
61 histopathological analyses were conducted, and changes in fecal short-chain fatty acids  
62 (SCFAs) and microbial communities were observed.

63

## 64 **Materials and Methods**

### 65 **Preparation of probiotics**

66 *B. subtilis* IDCC 1101, *W. coagulans* (formerly *B. coagulans*, commercially *L.*  
67 *sporogenes*) IDCC 1201, and *C. butyricum* IDCC 1301 were obtained from Ildong  
68 Bioscience Co., Ltd (Pyeongtaek, South Korea). BIOVITA 3 was manufactured by  
69 mixing the three probiotics powder listed above (*B. subtilis* IDCC 1101, *W. coagulans*  
70 IDCC 1201, and *C. butyricum* IDCC 1301) while according to the in-house manual of  
71 Ildong Bioscience Co., Ltd (Pyeongtaek, South Korea) (Lot. No. ID-R0301).

### 72 **Animals and reagents**

73 Male Sprague-Dawley (SD) rats (6 weeks old) were purchased from Orientbio Inc.,  
74 (Seongnam, South Korea), and housed two per cage. Animals were kept at a  
75 temperature of  $22 \pm 3^\circ\text{C}$  and relative humidity of 30–70% and were given free access to  
76 tap water and a regular rodent diet (Envigo, Indianapolis, IN). Rats were acclimated for  
77 seven days prior to use and *in vivo* experiments were conducted in accordance with the

78 Efficacy Evaluation Center at Dt&CRO Co., Ltd. (220112, 2022.04.28). Loperamide  
79 hydrochloride (L0154) was purchased from Tokyo Chemical Industry Co., Ltd. (Tokyo,  
80 Japan). Phosphate-buffered saline (PBS, 10010023) was purchased from Gibco (Grand  
81 Island, NY). Dried starch was provided by Ildong Bioscience Co., Ltd. (Pyeongtaek,  
82 South Korea).

83

#### 84 **Experimental design**

85 Rats were randomly divided into six groups (n = 10 per group): G1 (non-constipated  
86 group; Normal), G2 (loperamide-induced constipation group; Constipation), G3  
87 (*Bacillus subtilis* IDCC 1101), G4 (*Weizmannia coagulans* IDCC 1201), G5  
88 (*Clostridium butyricum* IDCC 1301), and G6 (BIOVITA 3). During the administration  
89 period, constipation was induced by the oral administration of loperamide (4 mg/kg) for  
90 seven days in rats in all groups except for G1. Starch (probiotic powder excipient) or  
91 probiotic powder was orally administered to the rats in each group for seven days. Rats  
92 in the G1 and G2 groups were orally administered 0.2 g of starch. Rats in the test groups  
93 were orally administered probiotic powder at  $1.0 \times 10^9$  CFU/day. All administered  
94 samples were dissolved in PBS before use. Body weights and food and water intake  
95 were recorded daily. All rats were euthanized at the end of the administration period,  
96 and fecal and colon tissue samples were collected for subsequent analysis.

#### 97 **Fecal number and water content**

98 Fecal pellets in cages were collected on the sixth day of administration. The collected  
99 feces were counted and measured as the fecal pellet weight. After drying in the oven at  
100 60°C for 24 h, the feces were weighed. The water content (%) in fecal samples was  
101 calculated as follows: (initial weight of feces – dried weight of feces)/initial weight of  
102 feces x 100. All feces were stored at -80°C for subsequent analysis.

103 **Intestinal transit ratio**

104 The intestinal transit ratio was measured by a modification of the method of Xu et al.  
105 (2012). Rats were fasted for 18 h on the last day of treatment and administered  
106 loperamide and the test substances. Then, a charcoal meal (10% charcoal powder) and  
107 5% arabic gum were immediately administered. All rats were fasted and denied water  
108 for 30 min, euthanized by CO<sub>2</sub> inhalation, and their intestines were excised. Total  
109 intestinal length and distance traveled by the charcoal meal were measured. The  
110 intestinal transit ratio (%) was calculated as the transit distance of the charcoal  
111 meal/total length of the intestinal tract x 100.

112 **Histological analysis by hematoxylin and eosin staining**

113 Colon tissues were fixed in 10% formaldehyde, dehydrated, and embedded in  
114 paraffin. Then, 5 µm sections were prepared and stained with hematoxylin and eosin  
115 (H&E). Pathological changes were observed using an E600 (Nikon, Japan) research  
116 microscope.

117 **SCFAs analysis**

118 SCFAs were quantitated with a high-performance liquid chromatography-ultraviolet  
119 (HPLC-UV) system according to the method of Leite et al. (2023). Feces (1 g) were  
120 extracted with 8 mL of distilled water by vortexing for 15 min. The extracted samples  
121 were centrifuged for 15 min, 9,000 rpm at 4°C. The supernatant was filtered through a  
122 0.45 µm Millipore filter (Whatman, Kent, UK), and the filtrate was injected by HPLC  
123 (Alliance e2695; Waters Corp.) equipped with a UV detector (2998; Waters Corp.) and  
124 a COREGEL 87H3 C<sub>18</sub> column (7.8 mm x 300 mm x 5 µm; Concise Separations, USA).  
125 The column temperature was set at 35°C, and the sample tray temperature was set at  
126 4°C. The mobile phase was 5 nM H<sub>2</sub>SO<sub>4</sub> in water and the flow rate was 0.6 mL/min.  
127 The injection volume was 10 µL and the detection wavelength was 210 nm. The

128 concentrations of acetic, propionic, and butyric acid were determined by constructing  
129 calibration curves using the respective standard reagents.

130

### 131 **16S rRNA-based metagenomic analysis**

132 16S rRNA gene sequencing was performed to analyze the microbiome in SD rats  
133 with loperamide-induced constipation. DNA was extracted using a PowerSoil® DNA  
134 Isolation Kit (Cat. No. 12888, MO BIO, Carlsbad, CA, USA) according to the  
135 manufacturer's instructions. Each sample was prepared according to Illumina  
136 Sequencing Library protocols. Extracted DNA was amplified with V3–V4 region and  
137 sequenced using MiSeq™ (Illumina, San Diego, CA, USA) by Macrogen (Seoul, South  
138 Korea). The microbiome was investigated using the 16S rRNA gene-based Microbial  
139 Taxonomic Profiling (MTP) platform of EzBioCloud Apps (ChunLab, Seoul, South  
140 Korea). ChunLab's 16S rRNA database (DB ver. PKSSU4.0) was used for the  
141 taxonomic assignment of 16S rRNA amplicon reads (Yoon et al., 2017). Alpha diversity  
142 and beta diversity were subsequently analyzed. Alpha diversity was evaluated by ACE,  
143 Chao1, Shannon, and Simpson indices. Beta diversity was investigated by generalized  
144 UriFrac, using principal coordinates analysis (PCoA) to analyze the differences between  
145 samples. Linear discriminant analysis (LDA) effect size was analyzed using the linear  
146 discriminant analysis effect size (LEfSe) algorithm to identify the bacterial biomarkers  
147 differentially represented between the groups at different taxonomic levels.

148

149 **Statistical analysis**

150 The results were analyzed using the Statistical Package for Social Sciences version  
151 27.0 (SPSS, Chicago, IL) and are presented as the mean  $\pm$  standard deviation (SD). An  
152 analysis of variance (ANOVA) test was used to determine differences among samples at  
153 a significance level of  $p < 0.05$ . Microbial taxonomic abundance and gut microbiota  
154 diversity were compared using the Wilcoxon rank-sum test in the EzBioCloud Apps  
155 platform (ChunLab, Seoul, South Korea).

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157 **Results and Discussion**

158 **Part I: Effect of BIOVITA 3 and its component strains in SD-rats with**  
159 **loperamide-induced constipation**

160 **Body weight and food efficiency ratio (FER)**

161 No significant differences in body weights ( $p > 0.05$ ) were seen among the groups (Fig.  
162 1a). Body weights increased from 247.6 – 250.8 g on day 1 to 282.2 – 289.3 g on day 6  
163 of the administration period. The body weight gain, food intake, and FER of group G1-  
164 G6 are shown in Table.1. There was no significant difference ( $p > 0.05$ ) in body weight  
165 gain among all groups (G1-G6). There was no significant difference ( $p > 0.05$ ) in food  
166 intake among all groups except G6. Following the induction of constipation, the food  
167 intake of the G6 group (21.3 g/day) was significantly lower ( $p < 0.05$ ) than that of the G1  
168 group (24.6 g/day). However, the FER of the G6 was not significantly different from  
169 those of the other groups (G1-G5). The FER for all groups (G1-G6) ranged from 0.29 to  
170 0.33, with no significant difference in FER among groups.

171 **Fecal number and water content**

172 The fecal number and water content of feces were measured to investigate the fecal  
173 parameters of rats with loperamide-induced constipation treated with the three IDCC  
174 strains and BIOVITA 3. The average numbers of fecal pellets per cage were 32.3, 2.6,  
175 4.0, 3.0, 8.8, and 8.2 in G1-G6 groups, respectively (Fig. 1b). A statistically significant  
176 decrease ( $p < 0.01$ ) in fecal number was seen in the G2 with constipation compared to G1.  
177 Statistically significant increases ( $p < 0.01$ ) in the fecal number were seen in the G5 and  
178 G6 groups compared to G2. The water content in each group (G1-G6) was 39.8, 29.7,  
179 36.6, 41.5, 42.7, and 48.2%, respectively (Fig. 1c). A significant reduction was seen in  
180 the G2 group ( $p < 0.01$ ) compared to the G1 group. However, there were statistically

181 significant increases in the G3 ( $p < 0.05$ ), G5 ( $p < 0.05$ ), and G6 ( $p < 0.01$ ) groups  
182 compared to G2. Therefore, the results of the G2 group confirmed that loperamide-  
183 induced constipation in SD rats, and that the IDCC strains and BIOVITA 3 had significant  
184 effects on fecal number and water content in constipated groups.

### 185 **Gastrointestinal transit ratio**

186 Intestinal transit times reflect intestinal motility, which can be assessed by the transit  
187 speed of the digestive tract (Kim et al., 2017, Inatomi and Honma, 2021). The intestinal  
188 charcoal transit ratio is important in the diagnosis of constipation and for the G1-G6  
189 groups were 72.1, 70.4, 78.6, 77.2, 75.4, and 77.3%, respectively, as shown in Fig. 1d.  
190 The transit ratio in G2 decreased by 1.7% compared to G1, but the differences between  
191 the two groups were not significant ( $p > 0.05$ ). There was a statistically significant  
192 increase in probiotic-treated groups G3 ( $p < 0.05$ ), G5 ( $p < 0.01$ ), and G6 ( $p < 0.01$ )  
193 compared to G2.

### 194 **Histological analysis of colon tissue**

195 To confirm that probiotics could alleviate the histopathological alterations in  
196 constipated SD rats, H&E staining was performed to observe the morphology of the colon.  
197 As shown in Fig. 2b, the mucosal layer length of G2 (272.0  $\mu\text{m}$ ) was significantly lower  
198 than that of G1 (322.4  $\mu\text{m}$ ), and all groups treated with probiotic powders showed  
199 increased lengths, compared to G2. In particular, there was a significant difference in the  
200 G6 ( $p < 0.05$ ) compared to the G2. In terms of the muscle layer, the G2 (156.4  $\mu\text{m}$ ) was  
201 significantly shorter than that of the G1 (207.2  $\mu\text{m}$ ) (Fig. 2c). G3 (183.2  $\mu\text{m}$ ), G4 (207.4  
202  $\mu\text{m}$ ), G5 (184.6  $\mu\text{m}$ ), and G6 (162.6  $\mu\text{m}$ ) showed increased lengths compared to G2.  
203 Among them, G4 was significantly different ( $p < 0.01$ ) compared to G2. The results of  
204 this study were consistent with previous studies in which the thickness of the mucosal

205 layer of colonic tissue decreased in the constipation-induced group compared to the  
206 normal group, while it increased in the probiotic-treated group (Kim et al., 2015, Kim et  
207 al., 2017). The mucosal layer and muscle layer of colon tissue play important roles in  
208 both maintaining intestinal functions (intestinal motility, absorption and secretion,  
209 immune function, etc.) and creating a healthy gut environment. These results showed that  
210 G4 and G6 significantly improved the muscle layer and mucosal layer, respectively.  
211 Moreover, when leukocyte infiltration was observed in colon tissue, the number of  
212 animals observed was reduced in both G4 (n=2) and G6 (n=1) compared to G2 (n=4),  
213 while the frequency of inflammation was reduced in BIOVITA 3 (G6), thus indicating an  
214 improvement over G4. Consequently, most of the constipation improvement scores  
215 showed significant improvements with the G6.

216 Several studies have reported improvements in constipation by the oral administration  
217 of probiotics to loperamide-induced SD rats. In this model, the fecal number, water  
218 content, and gastrointestinal transit ratio decreased in the constipation-induced group  
219 compared to the normal group, while these constipation indicators increased in the  
220 probiotic-treated group, thus alleviating constipation symptoms (Kim et al., 2015, Inatomi  
221 and Honma, 2021, Jung et al., 2022). Furthermore, several studies have compared and  
222 analyzed the improvement in constipation by treatment with single and mixed probiotic  
223 strains, and these also demonstrated that mixed strains were more effective in improving  
224 constipation (Kim et al., 2017, Cheng et al., 2023). These previous research findings are  
225 consistent with our results, in which we found that BIOVITA 3 (mixed strains) had a  
226 therapeutic effect in alleviating constipation.

227

228

## 229 **Part II: Effect of BIOVITA 3 on SCFAs production and Gut Microbiome**

### 230 **Fecal SCFAs production**

231 SCFAs are primary metabolites that are produced by gut microbiota or probiotics,  
232 which are mainly composed of acetic acid, propionic acid, and butyric acid. (Shi et al.,  
233 2016). The concentration of SCFAs in the fecal samples were analyzed by HPLC-UV.  
234 Acetic, propionic, butyric acid, and total SCFAs content in the G2 were reduced  
235 compared to the G1, confirming the induction of constipation (Table. 2). The total SCFAs  
236 content in G2 (1638.18 ppm) was significantly lower than that in G1 (2690.05 ppm). The  
237 three IDCC groups (G3 – G5) and the BIOVITA 3 group (G6) all showed increased acetic  
238 acid, propionic acid, and total SCFAs compared to the G2 group. The total SCFAs content  
239 of G4 (3673.67 ppm) and G6 (3893.55 ppm) was significantly increased compared to G2  
240 ( $p < 0.05$ ) and was highest in G6. G5 showed an increase in butyric acid compared to G2,  
241 which is considered to be the effect of *C. butyricum* IDCC 1301, which has the ability to  
242 produce butyric acid. These results are consistent with previous studies that reported  
243 increased SCFAs when probiotics were administered in loperamide-induced constipation  
244 (Kim et al., 2015, Kim et al., 2017, Cheng et al., 2023).

245 The three SCFAs play an important role in human health with physiological activities  
246 ranging from immune system regulation to metabolic pathway modulation (Xiong et al.,  
247 2022). Increased SCFAs in the colon have been correlated with a reduced risk of certain  
248 conditions including constipation and cancer (Hooper et al. 2002), and the content of fecal  
249 SCFAs was reported to be significantly lower in constipated patients than in healthy  
250 individuals (Shi et al., 2016). SCFAs are anions in the colon that promote the absorption  
251 of sodium and water, promote the proliferation of colonic epithelial cells and mucosal  
252 growth, and act as important nutrients (Ruppin et al., 1980, Fukunaga et al., 2003). Acetic

253 acid and butyric acid released in the colon have been shown to increase water content and  
254 gastrointestinal transit rate, and to alleviate the symptoms of constipation in a microbial-  
255 dependent manner (Wang et al., 2020). Therefore, an increase in total SCFAs is associated  
256 with constipation relief. We consider it to be the case that BIOVITA 3 and its component  
257 strain administered in this study increased total SCFAs in loperamide-induced constipated  
258 rats, thereby improving fecal water content and GIT, and ultimately relieving constipation.

259 However, the profile of fecal SCFAs in this study exhibited some differences from  
260 previous studies, with the content of propionate being higher than acetate. Acetate was  
261 predominant on the second day of administration (data not shown), but propionate was  
262 predominant on the sixth day. According to Annison et al. (2003) "SCFAs can be sensitive  
263 to changes in substrate supply," and the ratio of acetate, propionate, and butyrate was  
264 shown to vary depending on the type of starch. We conclude that the proportion of SCFAs  
265 changed because of the effect of the test substances during the administration period.

#### 266 **Alteration of taxonomic composition**

267 At the phylum level, *Firmicutes* and *Bacteroides* were the major gut microbiota in SD  
268 rats (Fig. 3a). At the family level, *Porphyromonadaceae* was only found in rats in the G6  
269 group (Fig. 3b). We primarily found increases in the genus *Parabacteroides*. These  
270 bacteria were recently reported to enhance the physiological properties of carbohydrate  
271 metabolism and the secretion of SFCAs (Wang et al., 2019, Cui et al., 2022).  
272 *Enterobacteriaceae* appear similar in G1 and G6 but not in G2.

#### 273 **Change of microbial diversity**

274 The alpha diversity index was analyzed by species richness (ACE and Chao 1) and  
275 community diversity indices (Shannon and Simpson). There was a significant difference  
276 in the ACE and Chao1 indices between the G1 group and loperamide-induced constipated

277 groups (G2 and G6), but there were no significant differences between the G2 and G6  
278 groups (Fig. 3c). The Shannon index, which is an indicator of microbiota diversity, was  
279 significantly different between the loperamide-induced constipated groups (G2 and G6)  
280 and the G1 group. An increased Shannon index was seen in G6 compared to G2, but the  
281 difference was not significant (Fig. 3d). The Simpson index showed a contrasting trend  
282 with the Shannon index, indicating increased microbial diversity. The PCoA of beta  
283 diversity at the genus level showed that the three groups (n=6) were divided into PC1  
284 (32.61%) and PC2 (21.88%) (Fig. 3e). There was a significant difference between G2 and  
285 G6 ( $p < 0.01$ ).

#### 286 **Core gut microbiota analysis using linear discriminant analysis effect size**

287 This study utilized the LEfSe algorithm to identify core gut microbiota for constipation  
288 responses to probiotic treatment. Fecal samples from the G1, G2, and G6 groups were  
289 analyzed at the genus and species levels (Fig. 4). The results showed that the loperamide-  
290 induced constipation samples (G2) had a higher abundance of *Lactobacillus* and a lower  
291 abundance of *Romboutsia*, *Turicibacter*, and *Pseudoflavonifractor* than the normal  
292 samples in the G1 group. Additionally, *Ruminococcus* and *Fusicatenibacter* were  
293 identified as core gut microbiota for treatment responses in the G6 group, whereas  
294 *Lactobacillus* was identified as core gut microbiota in the G2 group. Furthermore,  
295 EU622720\_s, *Lactobacillus reuteri* group, *Blautia faecis*, and *Fusicatenibacter*  
296 *saccharivorans* were identified as core gut microbiota in the G6 group, whereas  
297 FJ880321\_s and *Lactobacillus intestinalis* were identified as core gut microbiota in the  
298 G2 group.

299 *Ruminococcus* and *Fusicatenibacter* are fiber-degrading bacteria that produce SCFAs  
300 as a byproduct of fiber fermentation (Belenguer et al., 2007). The bacterial-derived SCFAs

301 are known to play a role in promoting healthy bowel movements by stimulating the  
302 growth of beneficial bacteria, reducing inflammation, and improving gut motility (Den  
303 Besten et al., 2013). *Limosilactobacillus reuteri* is a bacterium that produces luterin, an  
304 antibacterial substance that has antibacterial activity against pathogenic microorganisms  
305 (Kim et al., 2015). Recently, *Blautia facis* has been found to be a acetic acid-producing  
306 bacterium belonging to the genus *Blautia* that has attracted substantial attention as a gut  
307 microbiota that brings about potential health benefits such as the prevention of respiratory  
308 infections and anti-inflammatory effects (Liu et al., 2021, Verstraeten et al., 2022)  
309 Therefore, the increase in these beneficial microbes (*Ruminococcus*, *Fusicatenibacter*, *L.*  
310 *reuteri*, *B. facis*) in the BIOVITA 3 group might have indirectly contributed to an  
311 improved gut environment, in addition to increased gut motility due to SCFA production.  
312 This also indicates that an increase in these genera may be a response to increased dietary  
313 fiber intake, which in turn, promotes healthy bowel movements. Further research will be  
314 needed to confirm these hypotheses.

315

316

317 **Conclusion**

318 The effect of BIOVITA 3 on loperamide-induced constipation was investigated in SD  
319 rats by analyzing the fecal characteristics (fecal number, water content), intestinal transit  
320 time, colonic morphology, SCFAs production, and gut microbiota.

321 The primary results of this study were as follows: First, this study confirmed the  
322 loperamide-induced constipation model. Second, single or blend probiotics were  
323 administered orally, and the blend probiotic BIOVITA 3 effectively improved  
324 constipation symptoms, significantly increasing fecal numbers, the fecal water content,  
325 GIT ratio, and the mucosal layer in colon. Third, BIOVITA 3 had a beneficial effect on  
326 alleviating constipation by altering the gut microbiome and increasing total SCFAs,  
327 which play an important role in promoting bowel regularity, maintaining intestinal barrier  
328 integrity, and regulating immune function.

329 In this study, BIOVITA 3 showed better effects in relieving constipation than using  
330 probiotics alone. We believe that the synergistic effects of the three probiotic-specific  
331 strains in BIOVITA 3 led to effects on improving constipation, and one of the key  
332 mechanisms is thought to be the production of SCFAs in the gut. The BIOVITA 3  
333 increased the production of SCFAs in the gut, which led to improved GIT by promoting  
334 intestinal motility, increased fecal water content through enhanced water absorption,  
335 increased bowel movement frequency, and, ultimately, relief of constipation symptoms.  
336 We also suggest that BIOVITA 3 increases useful microorganisms and changes intestinal  
337 microbial diversity, and that it has the potential to maintain, and improve host intestinal  
338 health. The results strongly suggest that BIOVITA 3 supplementation has the potential  
339 to be developed as a therapeutic and preventive strategy for constipation. Further research  
340 is needed to understand the mechanisms of action by which these probiotics improve  
341 constipation.

342



343 **Conflicts of Interest**

344 No potential conflict of interest relevant to this article was reported.

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350 materials for this study.

351 **Author Contributions**

352 Conceptualization: Oh I

353 Data curation: Jang YJ

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357 Investigation: Kim JE

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359 Writing - review & editing: All authors

360

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363 **Ethics Approval**

364 This animal study was conducted with the approval of the Experimental Animal  
365 Ethics Committee at Dt&CRO (Yongin, South Korea) (approval number: 220112, study  
366 number: DTE220027).

367

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476 **Figure legend**

477 Fig. 1 Effect of BIOVITA 3 and its component strains treatment of loperamide-induced  
478 constipated SD rats. (a) Change in body weight, (b) Number of feces per cage, (c) Water  
479 content (%) in fecal, and (d) Gastrointestinal charcoal transit ratio (%). Bars represent  
480 the mean  $\pm$  SD (n = 10).  $\dagger\dagger p < 0.01$  vs. G1,  $*p < 0.05$  and  $**p < 0.01$  vs. G2. G1, normal  
481 group; G2, loperamide-induced constipation group; G3: *B. subtilis* IDCC 1101 and  
482 loperamide-induced constipation group; G4: *W. coagulans* IDCC 1201 and loperamide-  
483 induced constipation group; G5: *C. butyricum* IDCC 1301 and loperamide-induced  
484 constipation group; G6: BIOVITA 3 and loperamide-induced constipation group.

485

486 Fig. 2 Histological analysis of colon tissue stained with H&E. (a) Photographs of colon  
487 sections, (b) Mucosal layer length. (c) Muscle layer length.  $\dagger p < 0.05$  vs. G1,  $*p < 0.05$   
488 and  $**p < 0.01$  vs. G2. G1, normal group; G2, loperamide-induced constipation group;  
489 G3: *B. subtilis* IDCC 1101 and loperamide-induced constipation group; G4: *W.*  
490 *coagulans* IDCC 1201 and loperamide-induced constipation group; G5: *C. butyricum*  
491 IDCC 1301 and loperamide-induced constipation group; G6: BIOVITA 3 and  
492 loperamide-induced constipation group.

493

494 Fig. 3 Comparative analysis of the fecal microbiome in loperamide-induced constipated  
495 SD rats. (a) Taxonomic abundance at the phylum level and (b) family level. (c) Alpha-  
496 diversity index values were statistically analyzed by the Wilcoxon rank-sum test. (d)  
497 Principal coordinate analysis (PCoA) of beta-diversity.  $*p < 0.05$  and  $**p < 0.01$ ,  
498 significantly different by PERMANOVA. G1: normal group; G2: loperamide-induced  
499 constipation group; G6: BIOVITA 3 and loperamide-induced constipation group.

500

501 Fig. 4 Core gut microbial analysis in SD rats with loperamide-induced constipation by  
502 treated probiotics. The biomarkers identified by the linear discriminant analysis (LDA)  
503 effect size algorithm are shown with heat maps of the log-scaled relative abundance.  
504 Each plot represents biomarkers in the fecal samples in the G1, G2, and G6 groups at  
505 the genus level (A) and species level (B) (n = 8 in each group).  
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507 **Tables.**

508 Table. 1 Body weight gain, food intake, and food efficiency ratio in SD rats with  
 509 loperamide-induced constipation.

Parameter	Groups <sup>1</sup>					
	G1	G2	G3	G4	G5	G6
Constipation <sup>2</sup>	-	+	+	+	+	+
Body weight gain (g/day)	8.0±0.9	7.3±1.1	6.9±1.4	7.7±1.6	7.7±0.8	6.6±1.4 <sup>†</sup>
Food intake (g/day)	24.6±0.9	22.9±1.1	23.8±1.1	24.3±1.2	22.8±1.3	21.3±1.4
FER*	0.33±0.04	0.32±0.07	0.29±0.07	0.32±0.08	0.34±0.05	0.31±0.09

510 <sup>1</sup> G1: Normal group; G2: loperamide-induced constipation group; G3: *B. subtilis* IDCC  
 511 1101 and loperamide-induced constipation group; G4: *W. coagulans* IDCC 1201 and  
 512 loperamide-induced constipation group; G5: *C. butyricum* IDCC 1301 and loperamide-  
 513 induced constipation group; G6: BIOVITA 3 and loperamide-induced constipation group.

514 <sup>2</sup> (-): Constipation not induced, (+): Constipation induced. \* Food efficiency ratio (FER)  
 515 = body weight gain (g)/ food intake (g). <sup>†</sup>  $p < 0.05$  vs. G1 by ANOVA test

516

Table. 2 The concentration of short-chain fatty acids (SCFAs) in SD rats with loperamide-induced constipation.

Groups <sup>1</sup>	The concentration of short-chain fatty acids (SCFAs, ppm)			
	Acetic acid	Propionic acid	Butyric acid	Total SCFAs
			77.66 ±	
G1	965.90 ± 117.38	1646.50 ± 488.85	49.61	2690.05 ± 532.05
			50.45 ±	1638.18 ±
G2	673.93 ± 191.19 †	913.80 ± 816.80	87.37	645.56 †
			15.06 ±	2549.37 ±
G3	836.04 ± 345.12	1698.273 ± 960.82	30.11	1271.69
	1219.60 ±		27.64 ±	3673.67 ±
G4	203.51 *	2426.44 ± 721.84	47.87	568.99 *
			62.03 ± 124.0	3209.29 ±
G5	1207.09 ± 318.78	1940.17 ± 1549.11	6	1371.95
	1292.25 ±			3893.55 ± 1031.94
G6	209.91 *	2601.30 ± 921.44	< 5	*

517 <sup>1</sup> G1: Normal group; G2: loperamide-induced constipation group; G3: *B. subtilis* IDCC  
518 1101 and loperamide-induced constipation group; G4: *W. coagulans* IDCC 1201 and  
519 loperamide-induced constipation group; G5: *C. butyricum* IDCC 1301 and loperamide-  
520 induced constipation group; G6: BIOVITA 3 and loperamide-induced constipation group.  
521 Values are means ± SD (n= 10). † *p* < 0.05 vs. G1, \* *p* < 0.05 vs. G2.

## Figures

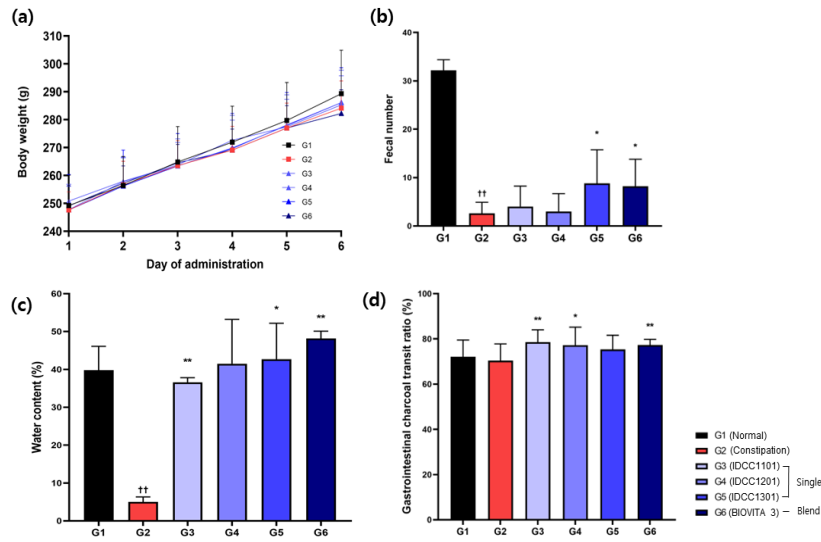


Fig. 1 Effect of BIOVITA 3 and its component strains treatment of loperamide-induced constipated SD rats. (a) Change in body weight, (b) Number of feces per cage, (c) Water content (%) in fecal, and (d) Gastrointestinal charcoal transit ratio (%). Bars represent the mean  $\pm$  SD (n = 10).  $\dagger\dagger p < 0.01$  vs. G1,  $*p < 0.05$  and  $**p < 0.01$  vs. G2. G1, normal group; G2, loperamide-induced constipation group; G3: *B. subtilis* IDCC 1101 and loperamide-induced constipation group; G4: *W. coagulans* IDCC 1201 and loperamide-induced constipation group; G5: *C. butyricum* IDCC 1301 and loperamide-induced constipation group; G6: BIOVITA 3 and loperamide-induced constipation group.

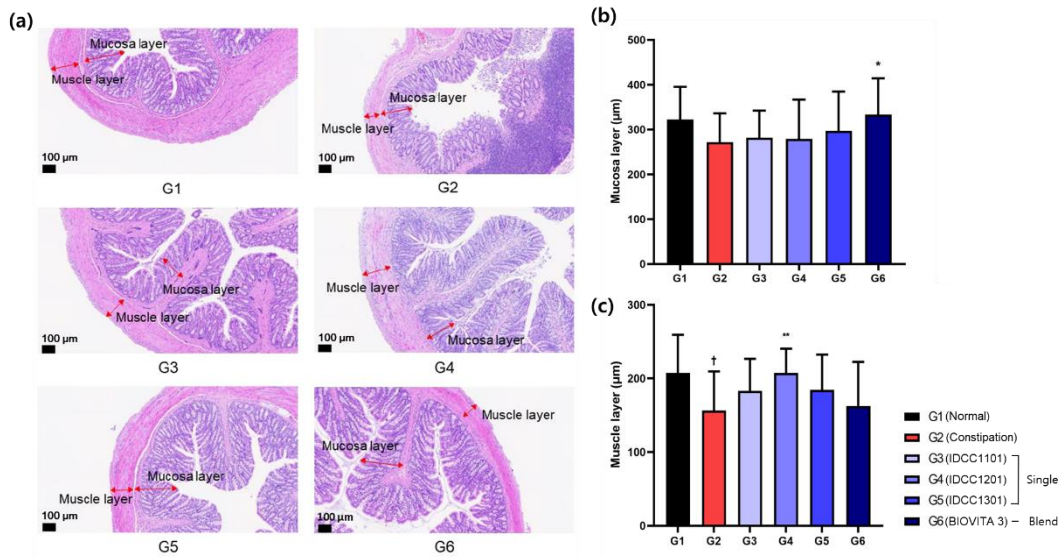


Fig. 2 Histological analysis of colon tissue stained with H&E. (a) Photographs of colon sections, (b) Mucosal layer length. (c) Muscle layer length. † $p < 0.05$  vs. G1, \* $p < 0.05$  and \*\* $p < 0.01$  vs. G2. G1, normal group; G2, loperamide-induced constipation group; G3: *B. subtilis* IDCC 1101 and loperamide-induced constipation group; G4: *W. coagulans* IDCC 1201 and loperamide-induced constipation group; G5: *C. butyricum* IDCC 1301 and loperamide-induced constipation group; G6: BIOVITA 3 and loperamide-induced constipation group.

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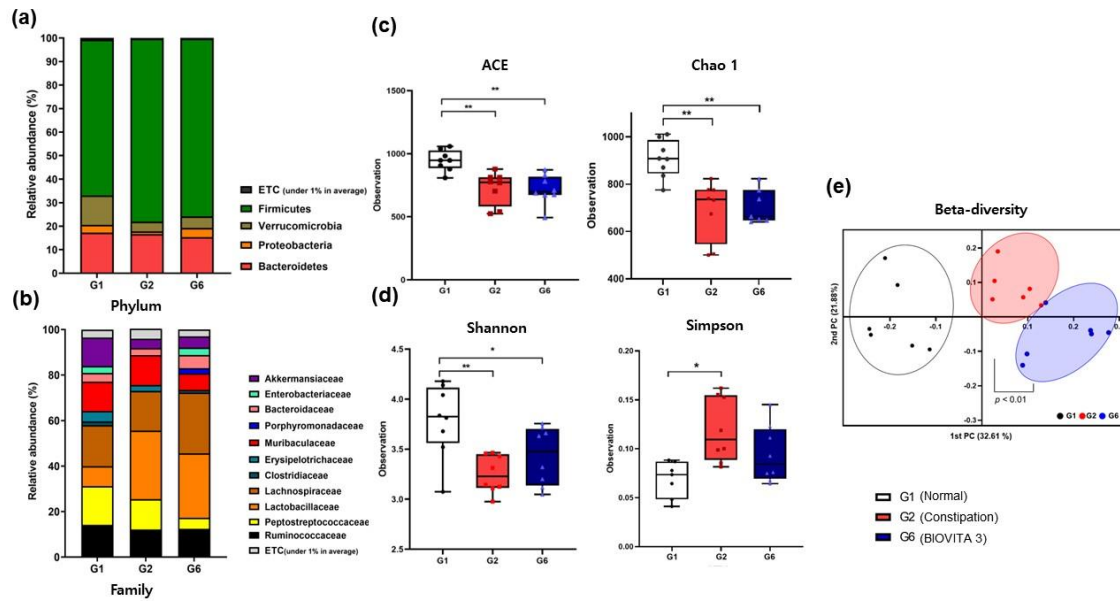


Fig. 3 Comparative analysis of the fecal microbiome in loperamide-induced constipated SD rats. (a) Taxonomic abundance at the phylum level and (b) family level. (c) Alpha-diversity index values were statistically analyzed by the Wilcoxon rank-sum test. (d) Principal coordinate analysis (PCoA) of beta-diversity. \* $p < 0.05$  and \*\* $p < 0.01$ , significantly different by PERMANOVA. G1: normal group; G2: loperamide-induced constipation group; G6: BIOVITA 3 and loperamide-induced constipation group.

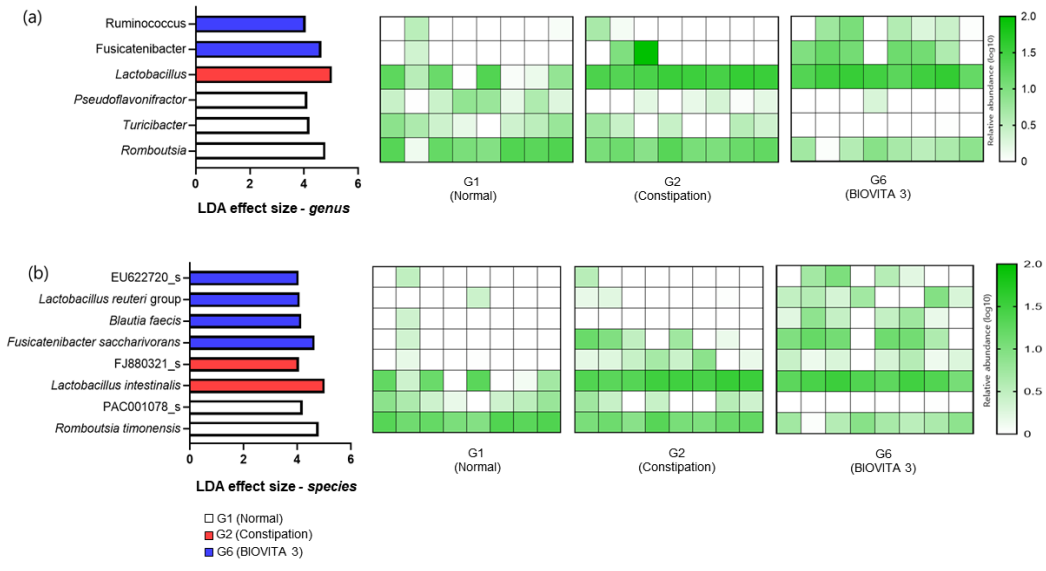


Fig. 4 Core gut microbial analysis in SD rats with loperamide-induced constipation by treated probiotics. The core microbiota identified by the linear discriminant analysis (LDA) effect size algorithm is shown with heat maps of the log-scaled relative abundance. Each plot represents biomarkers in the fecal samples in the G1, G2, and G6 groups at the genus level (a) and species level (b) (n = 8).