1   [Regular article]

2   **Relationship between gastrointestinal environment and physical conditions in elite**

3   **athletes**

4

5   Nobuhiko Akazawa[1.2*], Mariko Nakamura[1], Nobuhiko Eda[1.3], Haruka Murakami[4.5],

6   Takashi Nakagata[4.6], Hinako Nanri[4.6], Jonguk Park[7], Koji Hosomi[8.9], Kenji

7   Mizuguchi[7.10], Jun Kunisawa[8], Motohiko Miyachi[4.11*], Masako Hoshikawa[1]

8

9   [1]Department of Sport Science and Research, Japan Institute of Sports Sciences, 3-15-1

10   Nishigaoka, Kita-ku, Tokyo 115-0056, Japan

11   [2]Faculty of Sports and Life Science, National Institute of Fitness and Sports in Kanoya,

12   1 Shiromizu, Kanoya, Kagoshima 891-2393, Japan

13   [3]Department of Fundamental Education, Dokkyo Medical University, 880

14   Kitakobayashi, Mibu, Shimotsuga, Tochigi 321-0293, Japan

15   [4]Department of Physical Activity Research, National Institutes of Biomedical

16   Innovation, Health and Nutrition, 1-23-1 Toyama, Shinjuku-ku. Tokyo 162-0052, Japan

17   [5]Faculty of Sport and Health Science, Ritsumeikan University, 1-1-1 Nojihigashi,

18   Kusatsu, Shiga 525-0085, Japan

19   [6]Laboratory of Gut Microbiome for Health, Microbial Research Center for Health and

20   Medicine, National Institutes of Biomedical Innovation, Health and Nutrition, 3-17

21   Senrioka Shinmachi, Settsu, Osaka 566-0002, Japan

22   [7]Artificial Intelligence Center for Health and Biomedical Research, National Institutes

23   of Biomedical Innovation, Health and Nutrition, 7-6-8 Saito-Asagi, Ibaraki, Osaka 567-

24   0085, Japan

25   [8]Laboratory of Vaccine Materials and Laboratory of Gut Environmental System,

26   Microbial Research Center for Health and Medicine, National Institutes of Biomedical

27   Innovation, Health and Nutrition, 7-6-8 Saito-Asagi, Ibaraki, Osaka 567-0085, Japan

28   [9]Graduate School of Veterinary Science, Osaka Metropolitan University, 1-58 Rinku

29   Oraikita, Izumisano, Osaka 598-8531, Japan

30   [10]Institute for Protein Research, Osaka University, 3-2 Yamadaoka, Suita, Osaka 565-

31   0871, Japan

32   [11]Faculty of Sport Sciences, Waseda University, 2-579-15 Mikajima, Tokorozawa,

33   Saitama 359-1192, Japan

34

35

37

42   *** Corresponding authors:**

43   Nobuhiko Akazawa, Ph.D

44   E-mail: akazawa@nifs-k.ac.jp

45

46   Motohiko Miyachi, Ph.D

47   E-mail: miyachim@waseda.jp

Abstract

Heavy exercise training may negatively affect the gastrointestinal status of athletes, often leading to poor athletic performance and physical condition. The gut microbiome plays aa important role in the pathogenesis of gastrointestinal disorders. However, the relationship between the gut environment and conditions in athletes remains to be investigated. In this study, we aimed to determine the relationship between the gut microbiome, stool pattern, and the physical condition of elite athletes. A total of 92 elite athletes participated in this study, and their gut microbiomes, stool patterns, and physical conditions were evaluated. The gut microbiome was analyzed using 16S rRNA sequencing. The stool patterns and subjective physical conditions were evaluated using questionnaires. The participants were divided into better and poorer physical condition groups based on the median value of the physical condition score. The prevalence of abnormal stool patterns was significantly higher in the poorer condition group than that in the better condition group. The abundance of *Faecalibacterium* was significantly higher and that of *Bifidobacterium* was significantly lower in the better condition group than those in the poorer condition group. Principal component analysis revealed that the stool pattern could be explained by the *Faecalibacterium* abundance and the physical condition scores. Together, these findings suggest that the gut microbiome, especially the *Faecalibacterium* and *Bifidobacterium* abundance, affects the stool patterns and physical conditions of elite athletes, indicating that the gut microbiome may play a role in controlling the gastrointestinal environment affected by physiological stress such as intense exercise.

73 **タイトル：**

74 エリートアスリートにおける腸内環境とコンディションの関係

75 **著者：**

76 赤澤暢彦 [1,2]、中村真理子 [1]、枝伸彦 [1,3]、村上晴香 [4,5]、中潟崇 [4,6]、南里妃名子 [4,6]、朴

77 鍾旭 [7]、細見晃司 [8,9]、水口賢司 [7,10]、國澤純 [8]、宮地元彦 [4,11]、星川雅子 [1]

78 **所属：**

79 [1] 国立スポーツ科学センタースポーツ研究部、[2] 鹿屋体育大学スポーツ生命科学系、[3]

80 獨協医科大学基本医学基盤教育部門、[4] 国立研究開発法人医薬基盤・健康・栄養研

81 究所身体活動研究部、[5] 立命館大学スポーツ健康学部、[6] 国立研究開発法人医薬基

82 盤・健康・栄養研究所健康マイクロバイオームプロジェクト, [7] 国立研究開発法人医薬

83 基盤・健康・栄養研究所 AI 健康・医薬研究センター, [8] 国立研究開発法人医薬基盤・

84 健康・栄養研究所ワクチンマテリアルプロジェクト, [9] 大阪公立大学獣医学研究科、[10]

85 大阪大学蛋白質研究所、[11] 早稲田大学スポーツ科学学術院

86

87 **抄録：**

88 高強度運動トレーニングは腸内環境を悪化させ、身体コンディションや競技パフォーマ

89 ンスの低下と関連する。腸内細菌は胃腸障害の病因に寄与しているが、アスリート

90 の腸内環境とコンディションの関係性は明らかにされていなかった。そこで本研究で

91 は、日本人エリートアスリートにおける腸内細菌、排便状態、および身体コンディション

92 の関係性を検討することを目的とした。様々な競技のエリートアスリート 92 名を対象

93 に、腸内細菌、排便状態、および身体コンディションを評価した。腸内細菌を 16s

94 rRNA 技術により測定し、排便状態と身体コンディションは質問紙により測定した。さら

95 に、身体コンディションのスコアによりコンディション高値群とコンディション低値群に群

96 分けした。コンディション低値群は高値群に比べて、下痢や便秘などの排便症状の割

97 合が有意に高かった。また、コンディション高値群に比べて、コンディション低値群で

98   は *Faecalibacterium* 属の占有率は有意に低く、*Bifidibacterium* 属の占有率は有意に

99   高かった。さらに、排便症状の頻度の多さは *Facalibacterium* 属の占有率と関連するも

100   のであった。これらのことから、*Faecalibacterium* や *Bifidibacterium* などの腸内細菌は

101   アスリートの排便症状やコンディションと関連することが明らかになり、腸内環境を維持

102   することがコンディショニングに重要であることが示唆された。

Introduction

Athletes require intense exercise training to enhance their athletic performance. Many athletes are under prolonged stress conditions due to training, competition, and/or their lifestyle, which are major factors of decrease in physical condition, overtraining, and underperformance in sports.[1] Deterioration of physical condition under high stress and insufficient recovery is caused by a systemic dysfunction of the cardiovascular and digestive systems through endocrine responses, autonomic nervous activity, and immune function.[2] Athletes in poor physical condition often exhibit decreased heart rate and maximal oxygen uptake during exercise, as well as gastrointestinal symptoms such as nausea, vomiting, or diarrhea.[3] Additionally, 30–50% of endurance athletes suffer from gastrointestinal symptoms during training periods.[4] Intense and prolonged exercise stress are thought to induce mechanical force to abdominal organs and changes in sympathetic and parasympathetic nerve activity leading decrease in splanchnic blood flow, which contributes to damage gastrointestinal mucosal membrane.[5] Further, this gastrointestinal ischemia during exercise and reperfusion after exercise cause deteriorate mucosal function including tight junction dysfunction, thereby increasing intestinal epithelial permeability.[6] Recently, it has been reported that four days of military training not only increases intestinal permeability by 60 % but also alters the gut microbiome composition.[7] Therefore, it is important to assess the possible relationships between physical condition and the gastrointestinal environments in athletes.

The gut microbiome plays a crucial role in gastrointestinal homeostasis. Gut bacteria break down dietary fibers, which cannot be digested by humans, and are involved in the production of short-chain fatty acids (SCFA) and the synthesis of vitamins that are beneficial to the host. Moreover, the gut microbiome plays a role in other biological functions, such as immune functions, enzyme activity, and hormone secretion.[8] The gut

1

128 microbiome forms a complex ecosystem, and its composition, profile, and diversity as an

129 aggregate reflects the health status of the host;[2] loss of the diversity and balance of the

130 gut microbiome may result in immune allergies and metabolic disorders, leading to

131 obesity and lifestyle-related diseases.[9] Moreover, the compositional profile of the gut

132 microbiome is affected by several factors, such as aging, environmental factors, and

133 lifestyle factors.[10] Exercise induces changes in the composition and function of the gut

134 microbiome and promotes increased energy metabolism and improved physical

135 function.[11] The gut microbiomes of elite rugby athletes are highly diverse and are

136 associated with enhanced pathways related to amino acid biosynthesis, carbohydrate

137 metabolism, and SCFA synthesis.[12] In addition, the extent of training in swimmer athletes

138 has been reported to exhibit a positive correlation with the gut microbiome, especially in

139 *Faecalibacterium* and *Coprococcus* genera, which are involved in SCFA synthesis.[13]

140 However, these studies did not evaluate stool conditions such as stool status (e.g.,

141 frequency, volume, form, color, feeling, etc.), stool pattern (e.g., constipation or diarrhea),

142 and physical condition (e.g., body condition and recovery status) of athletes, and the

143 association between these parameters and the gut microbiome remains unclear.

144   In this study, we aimed to investigate the relationship between the

145 gastrointestinal environment and the physical condition of athletes, and then detect the

146 gut microbiome affected by stool pattern and physical condition. In this study, we

147 conducted stool collection and a questionnaire survey on the stool status, stool pattern,

148 and physical condition of elite Japanese athletes in a cross-sectional design. We first

149 analyzed whether gut microbiome compositional profiles were different among groups

150 divided by stool pattern, and then analyzed whether gut microbiome composition and

151 stool pattern were different between groups divided by subjective physical condition.

152

153 **Materials and methods**

154 **Subjects**

155 We recruited elite Japanese athletes who belonged to a national team in their respective

156 sports disciplines and were competing at an international level. A total of 92 athletes (51

157 men and 41 women) aged 24 ± 5 years participated in the present study. All participants

158 were informed of the purpose and methods as well as the risks of the study, and each

159 provided informed consent for participation. This study was performed in accordance

160 with the principles of the Declaration of Helsinki and approved by the ethics committees

161 of the Japan Institute of Sports Sciences (049-01) and the National Institute of Biomedical

162 Innovation, Health, and Nutrition (KENEI 91). The participants belonged to the national

163 team of Olympic reinforcement-designed athletes in one of the following sports events

164 and disciplines and were classified into six categories according to their performance

165 characteristics based on a previous study:[14] Power/sprint (track and field sprinters and

166 jumpers; n=13), endurance (race walkers, short-track ice speed skaters, bicycle track

167 cyclists, and alpine skiers; n=26), martial arts (fencers; n=38), artistic sports (rhythmic

168 gymnastics; n=1), ball games (soccer players; n=1), and others (sailing athletes, alpine

169 and halfpipe snowboarders; n=13). We collected fecal samples from all participants and

170 measured their stool status, stool pattern, and subjective physical condition using a cross-

171 sectional design.

172

173 **Measurements**

174 *Stool condition*

175 We evaluated stool volume, form, color, feeling, and frequency as stool status for one

176 month using the developed assessment tool.[15] The stool volume was estimated by the

177 number of fecal units (response number 1 to 8, from 1, 0.5, to 8, >4 units) referring to the

178   stool model unit (2 cm diameter × 10 cm length, cylindrical in shape). Stool form was

179   measured using the modified Bristol Stool Scale. The seven types range from very hard

180   (type 1) to very loose (type 7). For stool color assessment, the closest of the six colors

181   indicated on the fecal assessment tool compared to the actual color was selected according

182   to the color standard Z8721: 1, 5Y8/12 (yellow); 2, 2.5Y7/12 (light yellowish-brown); 3,

183   10YR5/8 (yellowish-brown); 4, 7.5YR7/12 (brown); 5, 5Y4/4 (greenish-dark brown);

184   and 6, 2.5GY4/3 (dark brown). In addition, the questionnaire included questions on the

185   comfort of defecation (1, comfortable; 2, uncomfortable). The frequency of defecation

186   was evaluated as the number of times excretion occurred per week, using six responses

187   ranging from less than two to more than seven times per week. The stool pattern of

188   habitual gastrointestinal complaints was chosen within 1-4 patterns (1, normal; 2, tend to

189   constipation; 3, tend to diarrhea; and 4, repeated to constipation and diarrhea).

190

191   *Gut microbiome*

192   Fecal sampling and DNA extraction were performed as previously described.[16]

193   Briefly, fecal samples were collected using commercial vials containing guanidine

194   thiocyanate (GuSCN) solution (TechnoSuruga Laboratory Co., Ltd., Shizuoka, Japan)

195   and stored at room temperature. DNA was extracted from the fecal samples by the bead

196   beating method using a Cell Destroyer PS1000 (Bio Medical Sciences, Tokyo, Japan) and

197   a Gene Prep Star PI-80X device (Kurabo Industries Ltd., Osaka, Japan). The DNA

198   samples were stored at –30 °C until further use.

199   16S rRNA sequencing and analyses were performed as described in previous

200   studies.[16,17] Briefly, the V3-V4 region of the 16S rRNA gene was amplified from fecal

201   DNA samples using KOD-plus-v2 (Toyobo, Osaka, Japan) and the following primers:

202   forward,   5′-

203 TCGTCGGCAGCGTCAGATGTGTATAAGCGACAGCCTACGGGNGGCWGCAG-

204 3′ ; reverse, 5′-

205 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTACHVGGGTATCTA

206 ATCC-3′. Sequencing was performed by paired-end methods using the Illumina MiSeq

207 instrument and the MiSeq v3 Reagand Kit (Illumina, San Diego, CA, United States)

208 according to the manufacturer's instructions. Sequence reads from Illumina MiSeq were

209 analyzed using the Quantitative Insights Into Microbial Ecology (QIIME) and Analysis

210 Automating Script (Auto-q) (https://github.com/attayeb/auto-q). The paired-end reads

211 obtained were selected, and chimeric sequences were removed using USEARCH v6.1.

212 Open-reference operational taxonomic unit (OTU) picking and taxonomy classification

213 were performed based on sequence similarity (>97%) using the UCLUST software with

214 the SILVA v128 reference sequence. The top 15 most abundant microbiomes at the genus

215 level are represented in this study.

216

217 *Physical condition*

218 We used two self-reported surveys to gauge their level of physical condition as

219 follows: (1) My condition was good physically, in addition to (2) I recovered well

220 physically, with values ranging from 1 (never) to 7 (always), modified from a previous

221 study.[18] Scores were recorded on a 7-point Likert scale, and we evaluated a total of two

222 scores in this study.

223

224 *Dietary habit questionnaire*

225 Habitual diet during the preceding month was assessed using a brief self-

226 administered diet history questionnaire (BDHQ).[19] The daily intake of total volume and

227 energy, protein, fat, carbohydrate, and fiber was calculated from the records.

228

Statistical analysis

All statistical analyses were performed using SPSS version 24 (IBM Inc., Chicago, IL, USA). The participants were divided into normal, constipation, or diarrhea-compliant groups based on their habitual stool pattern, and better or poorer physical condition groups based on their median physical condition score. Two subjects were excluded from the analysis because they answered that both constipation and diarrhea recurred. Continuous, ordinal, and categorical variables were analyzed using analysis of variance (ANOVA), followed by an LSD post-hoc test, Kruskal-Wallis test, and X^2 test for the normal, constitution, and diarrhea groups, respectively. Unpaired t-tests and X^2 tests were used to compare data between the better and poorer physical condition groups. Statistical analyses of the gut microbiome were performed using R software (version 3.4.2, https://www.r-project.org/). Alpha diversity indices, including Chao1 and Observed index, were calculated using the *estimate_richness* function in the "phyloseq" package. Principal coordinate analysis (PCoA) based on the Bray-Curtis distance metric was performed using multivariate techniques of global view using the *dudi.pco* function in the "vegan" and "ade4" packages. Principal component analysis (PCA) was conducted using the fviz_pca_biplot function in the "FactoMineR" package to identify the relationship between stool condition and gut microbiome in the better and poorer condition groups. Figures, including boxplots, PCoA, and PCA plots, were created using the "ggplot" package. The sample size was determined a priori, based on the expected differences in the proportion of participants with abnormal stool patterns. Setting the verification power to 95%, with an effect size of 0.5 (moderate) and a significance level of $\alpha = 0.05$, the analysis determined a minimum total sample size of 62 participants to detect differences between the better and poorer condition groups. Data are presented as mean ± standard

6

253 deviation (SD) or counts with distribution percentage, as appropriate. Statistical

254 significance for all comparison was set *a priori* at $p < 0.05$ for all comparisons.

255

256 **Results**

257   Table 1 shows the participant characteristics and stool status of the three stool

258 pattern groups. The proportion of men and women, sports events, age, height, weight,

259 body mass index, and macronutrients did not significantly differ among the groups. The

260 frequency and form of stool defecation in the constipation group were significantly lower

261 than those in the normal and diarrhea groups ($p < 0.05$). The stool volume, color, and

262 odor did not differ between the groups. The percentage of athletes experiencing

263 comfortable defecation was lower in the diarrhea group than that in the normal and

264 constipation groups. Figure 1A shows the gut microbiome community structure at the

265 genus level obtained using PCoA. Figure 1B shows a comparison of the abundance of the

266 gut microbiome at the phylum level among stool pattern groups. The distribution of

267 *Bacteroidetes* was significantly lower and that of *Firmicutes* was significantly higher in

268 the constipation group than in the diarrhea group ($p < 0.05$). Figure 1C shows the

269 differences in alpha diversity among the groups. The Chao1 and observed indices in the

270 diarrhea group were significantly lower than those in the constipation groups ($p < 0.05$).

271 [Table 1 insert]

272 [Figure 1 insert]

273   Figure 2 shows the ratio of gastrointestinal complaints of stool patterns between

274 the better and poorer condition groups. The poorer condition group exhibited a

275 significantly higher frequency of abnormal stool patterns ($p < 0.05$). Table 2 shows the

276 characteristics of the participants in the better and poorer condition groups. The total

277 intake volume and intake of energy and fiber in the better condition group were higher

7

278   than those in the poorer condition group, whereas the proportion of sex and sports events,

279   height, weight, body mass index, and stool status did not differ significantly. Figure 3A

280   shows the comparison of the most abundant gut microbiome at the genus level in the

281   better and poorer condition groups. The distribution of *Faecalibacterium* was

282   significantly higher and that of *Bifidobacterium* was significantly lower in the better

283   condition group than those in the poorer condition group. Figure 3B shows the PCA of

284   stool status and patterns based on the fviz_pca_biplot function. The abundance of

285   *Faecalibacterium* was consistent with the physical condition score and adverse direction

286   for gastrointestinal complaints of stool patterns such as constipation and diarrhea.

287   [Figure 2 insert]

288   [Figure 3 insert]

289   [Table 2 insert]

290

291   **4. Discussion**

292   The present study investigated the relationship between the gut microbiome,

293   stool status and pattern, and the physical condition of elite Japanese athletes. We found

294   significant differences in the gut microbiome composition (*Bacteroidetes* and *Firmicutes*

295   phyla) and alpha diversity between constipation and diarrhea groups. We revealed that

296   athletes in the better physical condition group exhibited a lower frequency of habitual

297   gastrointestinal complaints of stool pattern, a higher abundance of *Faecalibacterium* and

298   a lower abundance of *Bifidobacterium* genus in the microbiome compared to athletes in

299   the poorer physical condition group. In addition, *Faecalibacterium* genus was associated

300   with stool pattern, physical condition score, and food intake in the PCA biplot analysis.

301   These results suggest that the physical condition of athletes is associated with their

302   gastrointestinal environment.

303   Athletes who perform intense and long-duration exercise suffer from a decrease

304   in functional digestive status and gastrointestinal issues such as irritable bowel syndrome

305   (IBS).[4] Recently, several studies have revealed that the gut microbiome plays a key role

306   in the pathogenesis of gastrointestinal diseases.[20,21] In a systemic review, the abundances

307   of *Faecalibacterium* and *Bifidobacterium* were lower and those of *Bacteroides* and

308   *Lactobacillaceae* and *Enterobacteriaceae* family were higher in patients with IBS than

309   those in healthy control.[21] Vundeputte et al. have reported that species richness was

310   increased in the harder stool consistency, measured by the Bristol Stool Scale,[22] and that

311   the stool moisture content was negatively correlated with microbial cell count.[23] In the

312   present study, we evaluated the stool patterns of the elite athlete and demonstrated that

313   the diarrhea group with relatively soft stool exhibited a lower alpha diversity, a higher

314   abundance of the *Bacteroidetes* phylum and a lower abundance of the *Firmicutes* phylum

315   (Figure 1) compared to the constipation group with relatively hard stool, which is

316   consistent with previous studies.[22,23] These results suggest that gastrointestinal

317   complaints of stool patterns of elite Japanese athletes may be mediated, in part, by the gut

318   microbiome.

319   Athletes generally do not experience health issues when sufficient rest and

320   recovery are maintained, even under significant training stress. However, an imbalance

321   between stress and recovery may negatively affect the physical condition, athletic

322   performance, and skills development of athletes.[24] Intensive training can impair physical

323   conditions and is associated with gastrointestinal disorders, such as diarrhea, cramping,

324   bleeding, and flatulence, in over 50% of endurance athletes.[25] Furthermore, intense

325   exercise also delays gastric-emptying time, reduces vagal tone, elevates adrenergic

326   activity, and induces mechanical movement of intestinal contents, all of which contribute

327   to gastrointestinal symptoms.[4] In terms of nutrition, athletes in the better physical

328   condition group, consumed a higher total volume of food, as well as more energy and

329   fiber, compared to those in the poorer physical condition group (Table 2). Low energy

330   availability has been linked to increased fatigue, injury, and illness, impaired adaptation

331   to training, and delayed recovery.[26] Consistent with this, King et al. demonstrated that

332   high carbohydrate consumption over 14 d reduced gastrointestinal complaints following

333   endurance exercise.[27] Additionally, dietary fiber plays a critical role in the health, as it is

334   metabolized into beneficial SCFAs, which support bowel movement regulation, protect

335   intestinal mucus barrier function, and enhance gut microbiome diversity.[28] In the present

336   study, athletes in the poorer physical condition group exhibited more abnormal stool

337   patterns than those in the better physical condition group (Figure 2). This distinction

338   highlights the relationship between physical condition and stool patterns based on self-

339   reported physical conditions, including recovery status. These findings suggest that

340   increasing food intake, particularly fiber-rich foods—a practice known as "gut

341   training"—could be beneficial in mitigating gastrointestinal disorders.

342   We observed differences in the abundance of *Bifidobacterium* and

343   *Faecalibacterium* in the gut microbiome between the better and poorer physical condition

344   groups (Figure 3A). *Bifidobacterium* is the predominant bacteria in Japanese individuals,

345   contributing to intestinal homeostasis via energy metabolism through the production of

346   SCFAs, which help maintain a luminal acidic environment that protects against harmful

347   bacteria and pathogenic substances colonization.[2,29] Additionally, *Bifidobacterium* exerts

348   anti-inflammatory effects by promoting adiponectin and suppressing interleukin (IL)-6

349   which areinvolved in glucose and fatty acid oxidation metabolism.[30] Previous studies

350   have shown decreased *Bifidobacterium* level in patients with IBS suffering from

351   constipation or diarrhea.[31] On the contrary, a Japanese cohort study did not observed

352   significant differences in *Bifidobacterium* levels among patients with IBS.[32] In our study,

353 *Bifidobacterium* abundance was higher in the poorer physical condition group, which

354 exhibited many abnormal stool patterns, suggesting that the relationship between

355 gastrointestinal symptoms and *Bifidobacterium* abundance may be influenced by

356 confounding factors such as race or geographical location. However, we recently

357 demonstrated that *Bifidobacterium* levels are higher during exercise training season in

358 elite Japanese athletes.[33] These findings suggest that the interaction between the

359 gastrointestinal environment and intense exercise training could influence the levels of

360 *Bifidobacterium* in elite Japanese athletes.

361 *Faecalibacterium*, particularly the species *Faecalibacterium prausnitzii*, is one

362 of the most abundant microbiomes in the gut and plays a crucial role in maintaining gut

363 health.[34] This bacterium contributes to the prebiotic fermentation of non-digestible food

364 to produce butyrate, a primary energy source for colonocytes and involved in intestinal

365 metabolism. Additionally, butyrate exerts anti-inflammatory effects by inhibiting nuclear

366 factor kappa B (NF-kB) transcription and synthesizing pro-inflammatory cytokines like

367 IL-8.[34] *Faecalibacterium prausnitzii* has also been shown to inhibit NF-kB activation and

368 IL-8 secretion in a Crohn's disease model, even without butyrate production.[35] A recent

369 study using machine learning for multi-disease diagnosis demonstrated that

370 *Faecalibacterium prausnitzii* is associated with Crohn's disease in a large cohort

371 design.[36] Furthermore, *Faecalibacterium* abundance is reduced in patients with IBS

372 symptoms.[37] In the present study, we revealed an association between *Faecalibacterium*

373 and physical conditions as well as stool patterns in elite athletes. This suggests that

374 *Faecalibacterium* play a role in regulating gastrointestinal symptoms and influencing

375 physical conditions.

376 The biplot PCA analysis (Figure 3B) revealed that the clusters separated

377 depending on the physical condition; the better condition group tended to be in the upper

11

378 right and the poorer physical condition group tended to be on the left side. Moreover, the

379 constipation group gathered in the upper left, and the diarrhea group gathered in the lower

380 left, which is distributed among many athletes in poorer condition. This stool pattern

381 score showed an adverse direction on the physical condition score, food intake, and the

382 abundance of the genus *Faecalibacterium* abundance. *Faecalibacterium* affects

383 gastrointestinal functions including the maintenance of gut barrier integrity as described

384 above.[34] We revealed an association between *Faecalibacterium*, physical condition, and

385 stool patterns in elite athletes. Therefore, these results support the notion that the

386 relationship between the physical condition of athletes and gastrointestinal disorders is

387 mediated by the gut microbiome, especially the bacterium *Faecalibactarium*, which is

388 related to the amount of food intake, including fiber. However, it remains unclear how

389 the *Faecalibacterium* abundance is related to the physical conditions in this study.

390 *Faecalibacterium*, as a producer of SCFA like butyrate, plays a significant role in skeletal

391 muscle physiology and function via pathways that promote glycogen metabolism,

392 promotion of mitochondrial biogenesis, and the reduction of oxidative stress or

393 inflammation.[38] Moreover, SCFAs such as butyrate can influence serotonin synthesis,

394 which is associated with central higher-order behavior, mood disturbance, fatigue

395 sensation, and cardiovascular functions.[2] These effects suggest that Faecalibacterium

396 could potentially affect subjective physical condition through neurotransmitter and

397 hormonal responses.

398   The present study has several limitations. First, it was conducted using a

399 relatively small sample size. Previous studies have reported that gut microbiome is

400 affected by sex or sports characteristics.[39,40] In this study, we recruited only international-

401 level athletes; therefore, the number of participants in each sport was limited. Although

402 the sample size was sufficient to analyze the differences in physical condition and the

403   proportion of sex and sports events did not differ between the groups, the findings of this

404   study may not be generalized to specific athletic group. Second, the present study relied

405   on a simple self-reported questionnaire based on a previous study[18] to assess the physical

406   condition and gastrointestinal environment. While we aimed to compare the gut

407   microbiome between different subjective physical condition groups or subjective

408   gastrointestinal environments, future studies should incorporate objective parameters of

409   the physical condition and defecation status. Third, we could not control habitual diet. A

410   previous study showed that dietary intervention with high-fat/low-fiber or low-fat/high-

411   fiber for 10 days could affects gut microbiome composition in healthy individual.[41] On

412   the contrary, other studies have shown that varying carbohydrate or protein intake 4 days

413   during intense training did not significantly affect the gut microbiome in military

414   personnel.[7] These findings suggest that the effect of diet on the gut microbiome may vary

415   and interact with exercise training. Further studies are warranted to investigate the effect

416   of dietary "gut training" intervention. Lastly, the present study was used a cross-sectional

417   design, so a causal relationship, such as whether exercise-induced deterioration of

418   physical condition leads to decreased *Faecalibacterium* abundance or exercise-induced

419   decrease in *Faecalibacterium* abundance leads to deterioration of the physical condition,

420   could not be determined. Furthermore, we did not assess the functional or mechanistic

421   insight of gut microbiome, such as specific metabolomic pathways (e.g., organic enzymes,

422   carbohydrate degradation, or SCFA signaling). Further studies with longitudinal design

423   are needed to establish the precise mechanism and relationship between the gut

424   microbiome and the physical conditions of athletes.

425   In conclusion, we investigated the relationship between the gut microbiome,

426   stool status and pattern, and the physical condition of elite athletes. The alpha diversity

427   and compositional gut microbiome at the phylum level differed among the habitual stool

13

428 patterns. Subjective physical condition was associated with stool patterns. Furthermore,

429 the *Faecalibactarium* genus had a lower distribution in the poorer physical condition

430 group and was associated with stool patterns. This study suggests that the gut microbiome

431 profiles, especially those of *Feacalibacterium*, are one of the possible candidates

432 associated with progressing gastrointestinal disorders accompanied by deterioration of

433 physical condition due exercise training.

434

439

440 **Contribution**

441 Experiment conception and design: NA and MM. Experiment implementation: NA, MN,

442 NE, HM, TN, HN, and MH. Data analysis: JP, KH, KM, and JK. Analyzing and advisory:

443 NA and MM. All authors approved the final version of the manuscript.

444

445 **Conflict of Interest**

446 The authors declare no conflict of interests.

References

447   **References**

448   1. MacKinnon LT. 2000. Special feature for the Olympics: effects of exercise on the

449   immune system: overtraining effects on immunity and performance in athletes.

450   *Immunol Cell Biol* 78: 502-509.

451   2. Clark A, Mach N. 2016. Exercise-induced stress behavior, gut-microbiota-brain axis

452   and diet: a systematic review for athletes. *J Int Soc Sports Nutr* 13: 43.

453   3. de Oliveira EP, Burini RC, Jeukendrup A. 2014. Gastrointestinal complaints during

454   exercise: Prevalence, etiology, and nutritional recommendations. *Sports Med* 44

455   Suppl 1:S79-85.

456   4. Diduch BK. 2017. Gastrointestinal conditions in the female athlete. *Clin Sports Med*.

457   36: 655-669.

458   5. Waterman JJ, Kapur R. 2012. Upper gastrointestinal issues in athletes. *Curr Sports*

459   *Med Rep* 11: 99-104.

460   6. Van Houten JM, Wessells RJ, Lujan HL, DiCarlo SE. 2015. My gut feeling says rest:

461   Increased intestinal permeability contributes to chronic diseases in high-intensity

462   exercisers. *Med Hypotheses* 85: 882-886.

463   7. Karl JP, Margolis LM, Madslien EH, Murphy NE, Castellani JW, Gundersen Y, Hoke

464   AV, Levangie MW, Kumar R, Chakraborty N, Gautam A, Hammamieh R,

465   Martini S, Montain SJ, Pasiakos SM. 2017. Changes in intestinal microbiota

466   composition and metabolism coincide with increased intestinal permeability in

467   young adults under prolonged physiological stress. *Am J Physiol Gastrointest*

468   *Liver Physiol* 312: G559-G571.

469   8. Flint HJ, Duncan SH, Scott KP, Louis P. 2015. Links between diet, gut microbiota

470   composition and gut metabolism. *Proc Nutr Soc* 74: 13-22.

471 9. Arumugam M, Raes J, Pelletier E, Le Paslier D, Yamada T, Mende DR, Fernandes GR,

472   Tap J, Bruls T, Batto JM, Bertalan M, Borruel N, Casellas F, Fernandez L, Gautier

473   L, Hansen T, Hattori M, Hayashi T, Kleerebezem M, Kurokawa K, et al. 2011.

474   Enterotypes of the human gut microbiome. *Nature* 473: 174-180.

475 10. O'Toole PW, Jeffery IB. 2018. Microbiome-health interaction in older people. *Cell*

476   *Mol Life Sci* 75(1): 119-28.

477 11. Dalton A, Mermier C, Zuhl M. 2019. Exercise influence on the microbiome-gut-brain

478   axis. *Gut Microbes* 10: 555-568.

479 12. Barton W, Penney NC, Cronin O, Garcia-Perez I, Molloy MG, Holmes E, Shanahan

480   F, Cotter PD, O'Sullivan O. 2018. The microbiome of professional athletes differs

481   from that of more sedentary subjects in composition and particularly at the

482   functional metabolic level. *Gut* 67: 625-633.

483 13. Hampton-Marcell JT, Eshoo TW, Cook MD, Gilbert JA, Horswill CA, Poretsky R.

484   2020. Comparative analysis of gut microbiota following changes in training

485   volume among swimmers. *Int J Sports Med* 41(5): 292-299.

486 14. Akazawa N, Ohiwa N, Shimizu K, Suzuki N, Kumagai H, Fuku N, Suzuki Y. 2022.

487   The association of *ACTN3* R577X polymorphism with sports specificity in

488   Japanese elite athletes. *Biol Sport* 39(4):905-911.

489 15. Ohno H, Murakami H, Tanisawa K, Konishi K, Miyachi M. 2019. Validity of an

490   observational assessment tool for multifaceted evaluation of faecal condition. *Sci*

491   *Rep* 9: 3760.

492 16. Hosomi K, Ohno H, Murakami H, Natsume-Kitatani Y, Tanisawa K, Hirata S, Suzuki

493   H, Nagatake T, Nishino T, Mizuguchi K, Miyachi M, Kunisawa J. 2017. Method

494   for preparing DNA from feces in guanidine thiocyanate solution affects 16S

495   rRNA-based profiling of human microbiota diversity. *Sci Rep* 7: 4339.

496   17. Mohsen A, Park J, Chen YA, Kawashima H, Mizuguchi K. 2019. Impact of quality

497   trimming on the efficiency of reads joining and diversity analysis of illumina

498   paired-end reads in the context of QIIME1 and QIIME2 microbiome analysis

499   frameworks. *BMC Bioinformatics* 20(1):581.

500   18. Eliakim A, Nemet D, Bar-Sela S, Higer Y, Falk B. 2002. Changes in circulating IGF-

501   I and their correlation with self-assessment and fitness among elite athletes. *Int J*

502   *Sports Med* 23(8):600-603.

503   19. Kobayashi S, Murakami K, Sasaki S, Okubo H, Hirota N, Notsu A, Fukui M, Date C.

504   2011. Comparison of relative validity of food group intakes estimated by

505   comprehensive and brief-type self-administered diet history questionnaires

506   against 16 d dietary records in Japanese adults. *Public Health Nutr* 14(7): 1200-

507   1211.

508   20. Wang L, Alammar N, Singh R, Nanavati J, Song Y, Chaudhary R, Mullin GE. 2020.

509   Gut microbial dysbiosis in the irritable bowel syndrome: A systematic review and

510   meta-analysis of case-control studies. *J Acad Nutr Die* 120: 565-586.

511   21. Pittayanon R, Lau JT, Yuan Y, Leontiadis GI, Tse F, Surette M, Moayyedi P. 2019.

512   Gut microbiota in patients with irritable bowel syndrome-a systematic review.

513   *Gastroenterology* 157: 97-108.

514   22. Vandeputte D, Falony G, Vieira-Silva S, Tito RY, Joossens M, Raes J. 2016. Stool

515   consistency is strongly associated with gut microbiota richness and composition,

516   enterotypes and bacterial growth rates. *Gut* 65: 57-62.

517   23. Vandeputte D, Kathagen G, D'hoe K, Vieira-Silva S, Valles-Colomer M, Sabino J,

518   Wang J, Tito RY, De Commer L, Darzi Y, Vermeire S, Falony G, Raes J. 2017.

519   Quantitative microbiome profiling links gut community variation to microbial

520   load. *Nature* 551: 507-511.

17

521   24. Kellmann M. 2010. Preventing overtraining in athletes in high-intensity sports and

522   stress/recovery monitoring. *Scand J Med Sci Sports* 20 Suppl 2: 95-102.

523   25. Peters HP, Bos M, Seebregts L, Akkermans LM, van Berge Henegouwen GP, Bol E,

524   Mosterd WL, de Vries WR. 1999. Gastrointestinal symptoms in long-distance

525   runners, cyclists, and triathletes: prevalence, medication, and etiology. *Am J*

526   *Gastroenterol* 94: 1570-1581.

527   26. Thomas DT, Erdman KA, Burke LM. 2016. American college of sports medicine joint

528   position statement. Nutrition and athletic performance. *Med Sci Sports Exerc*

529   48(3): 543-68.

530   27. King AJ, Etxebarria N, Ross ML, Garvican-Lewis L, Heikura IA, McKay AKA, Tee

531   N, Forbes SF, Beard NA, Saunders PU, Sharma AP, Gaskell SK, Costa RJS, and

532   Burke LM. 2022. Short-term very high carbohydrate diet and gut-training have

533   minor effects on gastrointestinal status and performance in highly trained

534   endurance athletes. *Nutrients* 14(9).

535   28. Desai MS, Seekatz AM, Koropatkin NM, Kamada N, Hickey CA, Wolter M, Pudlo

536   NA, Kitamoto S, Terrapon N, Muller A, Young VB, Henrissat B, Wilmes P,

537   Stappenbeck TS, Núñez G, Martens EC. 2016. A dietary fiber-deprived gut

538   microbiota degrades the colonic mucus barrier and enhances pathogen

539   susceptibility. *Cell* 167(5): 1339-1353.e21.

540   29. Mattarelli P, Holzapfel W, Franz CMAP, Endo A, Felis GE, Hammes W, Pot B, Dicks

541   L, Dellaglio F. 2014. Recommended minimal standards for description of new

542   taxa of the genera Bifidobacterium, Lactobacillus and related genera. *Int J Syst*

543   *Evol Microbiol* 64: 1434–1451.

544   30. Rivière A, Selak M, Lantin D, Leroy F, De Vuyst L. 2016. Bifidobacteria and

545   butyrate-producing colon bacteria: importance and strategies for their stimulation

546   in the human gut. *Front Microbiol* 7: 979.

547   31. Zhong W, Lu X, Shi H, Zhao G, Song Y, Wang Y, Zhang J, Jin Y, Wang S. 2019.

548   Distinct microbial populations exist in the mucosa-associated microbiota of

549   diarrhea predominant irritable bowel syndrome and ulcerative colitis. *J Clin*

550   *Gastroenterol* 53(9):660-672.

551   32. Tana C, Umesaki Y, Imaoka A, Handa T, Kanazawa M, Fukudo S. 2010. Altered

552   profiles of intestinal microbiota and organic acids may be the origin of symptoms

553   in irritable bowel syndrome. *Neurogastroenterol Moti.* 22(5):512-519, e114-515.

554   33. Akazawa N, Nakamura M, Eda N, Murakami H, Nakagata T, Nanri H, Park JG,

555   Hosomi K, Mizuguchi K, Kunisawa J, Miyachi M, Hoshikawa M. 2023. Gut

556   microbiota alternation with training periodization and physical fitness in Japanese

557   elite athletes. *Front Sport Act Living* 5: 1219345.

558   34. Lopez-Siles M, Duncan SH, Garcia-Gil LJ, Martinez-Medina M. 2017.

559   Faecalibacterium prausnitzii: from microbiology to diagnostics and prognostics.

560   *ISME J* 11: 841-852.

561   35. Sokol H, Pigneur B, Watterlot L, Lakhdari O, Bermúdez-Humarán LG, Gratadoux JJ,

562   Blugeon S, Bridonneau C, Furet JP, Corthier G, Grangette C, Vasquez N, Pochart

563   P, Trugnan G, Thomas G, Blottière HM, Doré J, Marteau P, Seksik P, Langella P.

564   2008. Faecalibacterium prausnitzii is an anti-inflammatory commensal bacterium

565   identified by gut microbiota analysis of Crohn disease patients. *Proc Natl Acad*

566   *Sci U S A* 105: 16731-16736.

567   36. Su Q, Liu Q, Lau RI, Zhang J, Xu Z, Yeoh YK, Leung TWH, Tang W, Zhang L,

568   Liang JQY, Yau YK, Zheng J, Liu C, Zhang M, Cheung CP, Ching JYL, Tun HM,

569   Yu J, Chan FKL, Ng SC. 2022. Faecal microbiome-based machine learning for

570   multi-class disease diagnosis. *Nat Commun* 13: 6818.

571   37. Li G, Yang M, Jin Y, Li Y, Qian W, Xiong H, Song J, Hou X. 2018. Involvement of

572   shared mucosal-associated microbiota in the duodenum and rectum in diarrhea-

573   predominant irritable bowel syndrome. *J Gastroenterol Hepatol* 33: 1220-1226.

574   38. Hughes RL. 2019. A review of the role of the gut microbiome in personalized sports

575   nutrition. *Front Nutr* 6:191.

576   39. Takagi T, Naito Y, Inoue R, Kashiwagi S, Uchiyama K, Mizushima K, Tsuchiya S,

577   Dohi O, Yoshida N, Kamada K, Ishikawa T, Handa O, Konishi H, Okuda K,

578   Tsujimoto Y, Ohnogi H, Itoh Y. 2019. Differences in gut microbiota associated

579   with age, sex, and stool consistency in healthy Japanese subjects. *J Gastroenterol*

580   54(1):53-63.

581   40. Jang LG, Choi G, Kim SW, Kim BY, Lee S, Park H. 2019. The combination of sport

582   and sport-specific diet is associated with characteristics of gut microbiota: An

583   observational study. *J Int Soc Sports Nutr* 16(1):21.

584   41. Wu GD, Chen J, Hoffmann C, Bittinger K, Chen YY, Keilbaugh SA, Bewtra M,

585   Knights D, Walters WA, Knight R, Gilroy E, Gupta K, Baldassano R, Nessel L,

586   Li H, Bushman FD, Lewis JD. 2011. Linking long-term dietary patterns with gut

587   microbial enterotypes. *Science* 334(6052):105-108.

588

589 **Figure legends**

590 **Figure 1.** The gut microbiome profiles among the complaints of stool pattern groups. (A)

591 principal coordinate analysis of the gut microbiota profiles at the genus level, (B) alpha

592 diversity of the gut microbiome, and (C) differences in the relative abundance of phyla in

593 the microbiome of constipation, diarrhea, and normal groups. * $p < 0.05$ vs. normal group.

594 [#] $p < 0.05$ constipation vs. diarrhea groups.

595

596 **Figure 2.** The frequency of gastrointestinal complaint of stool patterns between the

597 poorer and better physical condition groups.

598

599 **Figure 3**. The gut microbiome profiles between the better and poorer physical condition

600 groups. (A) Comparison of the relative abundance of the gut microbiota at the genus level

601 between the poorer and better physical condition groups. * $p < 0.05$ better vs. poorer

602 groups. (B) Principal component analysis of gastrointestinal status profiles using

603 fviz_pca_biplot function.

604

605 **Supplemental Figure 1**. The sample of subjective questionnaire.

606

607 **Supplemental Figure 2**. The sample of stool sheet for volume, form, and color.

21

Table 1. The participants' characteristics, stool status, and macronutrients between normal, constipation, and diarrhea group.

	All			Normal			Constipation			Diarrhea		
Number, n	90			61			16			13		
Women, n (%)	39		(43)	24		(39)	11		(69)	4		(31)
Age, years	24	±	4	24	±	5	24	±	4	25	±	4
Height, cm	170	±	9	169	±	8	168	±	8	174	±	11
Weight, kg	64	±	9	63	±	9	62	±	11	67	±	8
Body mass index, kg/m^2	22.1	±	2.1	22.1	±	2.0	21.9	±	2.9	22.3	±	2.1
Sports event, n (%)												
Power/Sprint	13		(21)	8		(13)	1		(6)	4		(31)
Endurance	26		(43)	17		(28)	8		(50)	1		(8)
Martial arts	37		(61)	25		(41)	6		(38)	6		(46)
Artistic	1		(2)	0		(0)	1		(6)	0		(0)
Ball games	1		(2)	1		(2)	0		(0)	0		(0)
Others	12		(20	10		(16)	0		(0)	2		(15)
Stool status												
Frequency, times/wk [#]	6.4	±	1.2	6.5	±	1	5.4	±	1.5 [ab]	6.8	±	0.8
Volume, unit	3.8	±	1.6	4.1	±	1.5	3.5	±	1.7	3.2	±	1.6
Color, unit	3.9	±	1	3.9	±	0.9	3.6	±	1.3	3.8	±	1
Form, unit [#]	3.9	±	0.9	3.9	±	0.7	3.3	±	0.8 [ab]	4.3	±	1.3
Comfortable, n (%) [†]												
Comfortable	75		(83)	55		(90)	12		(75)	8		(62) [a]
Uncomfortable	15		(17)	6		(10)	4		(25)	5		(48) [a]
Macronutrients												
Total intake volume, g	2744	±	1212	2867	±	1293	2407	±	1032	2581	±	970
Total energy, kcal	2340	±	930	2440	±	965	2198	±	977	2041	±	625
Protein, %	16	±	3	16	±	3	18	±	5	16	±	2
Fat, %	26	±	6	27	±	6	26	±	4	26	±	4
Carbohydrate, %	57	±	8	58	±	8	56	±	7	58	±	6
Fiber, g	15	±	7	16	±	8	15	±	7	12	±	3

[#] $p < 0.05$ by Kruskal-Wallis test and [†] $p < 0.05$ by X^2 test among the groups.

[a] $p < 0.05$ vs. Normal group and [b] $p < 0.05$ vs. Diarrhea group

Table 2. The participants' characteristics, stool status, and macronutrients between better and poorer condition group.

	Better			Poorer		
Number, n	39			51		
Women, n(%)	14		(36)	25		(49)
Age, years	24	±	5	24	±	4
Height, cm	171	±	8	169	±	9
Weight, kg	65	±	9	63	±	10
Body mass index, kg/m^2	22.2	±	2.1	22.0	±	2.1
Sports event, n (%)						
Power/Sprint	5		(10)	8		(21)
Endurance	12		(24)	14		(36)
Martial arts	16		(31)	21		(54)
Artistic	0		(0)	1		(3)
Ball games	1		(2)	0		(0)
Others	5		(10)	7		(18)
Stool status						
Frequency, times/wk	6.4	±	1.2	6.3	±	1.2
Volume, unit	4.2	±	1.5	3.6	±	1.6
Color, unit	3.9	±	1.0	3.8	±	1.0
Form, unit	3.9	±	0.8	3.8	±	0.9
Comfortable, n (%)						
Comfortable	35		(90)	40		(78)
Uncomfortable	4		(10)	11		(22)
Macronutrients						
Total intake volume, g	3112	±	1363 [a]	2461	±	1008
Total energy, kcal	2636	±	1054 [a]	2113	±	758
Protein, %	16	±	3	16	±	3
Fat, %	26	±	6	26	±	5
Carbohydrate, %	57	±	8	57	±	7
Fiber, g	17	±	6 [a]	13	±	6

[a] $p < 0.05$ vs. Poorer group.

Fig1

Fig2

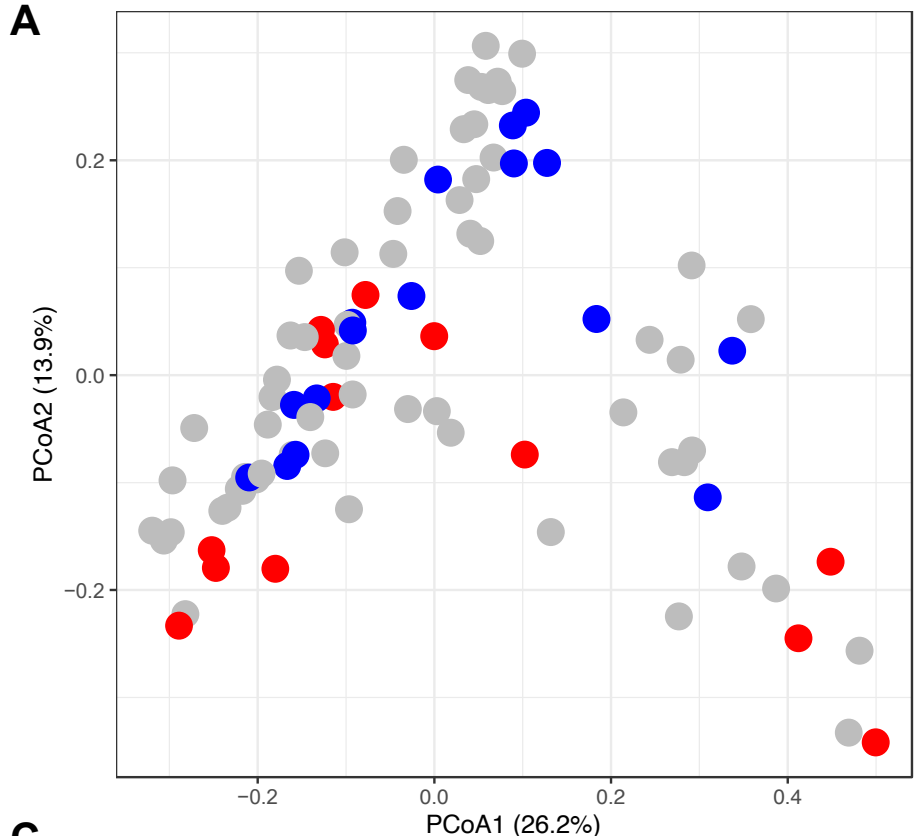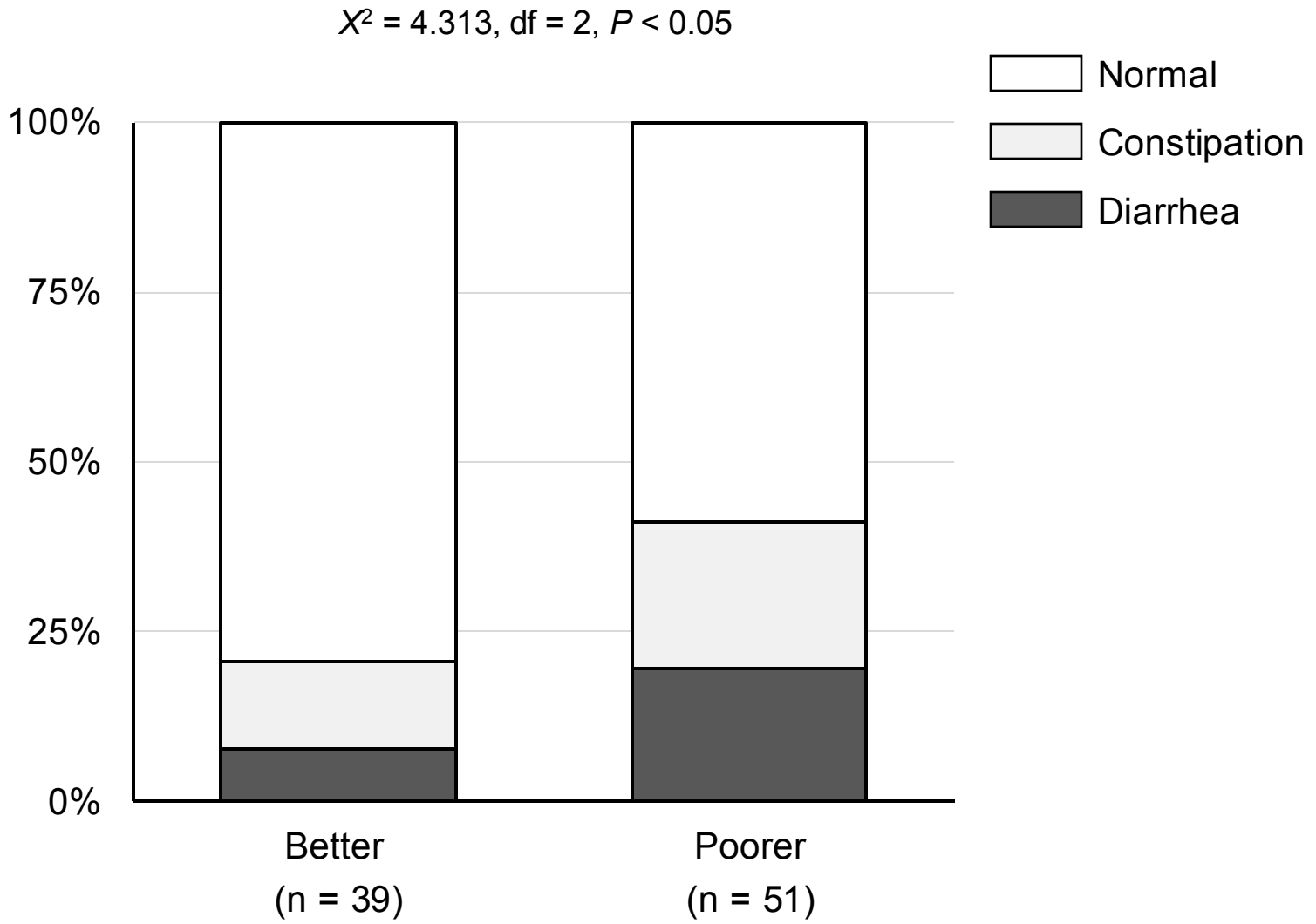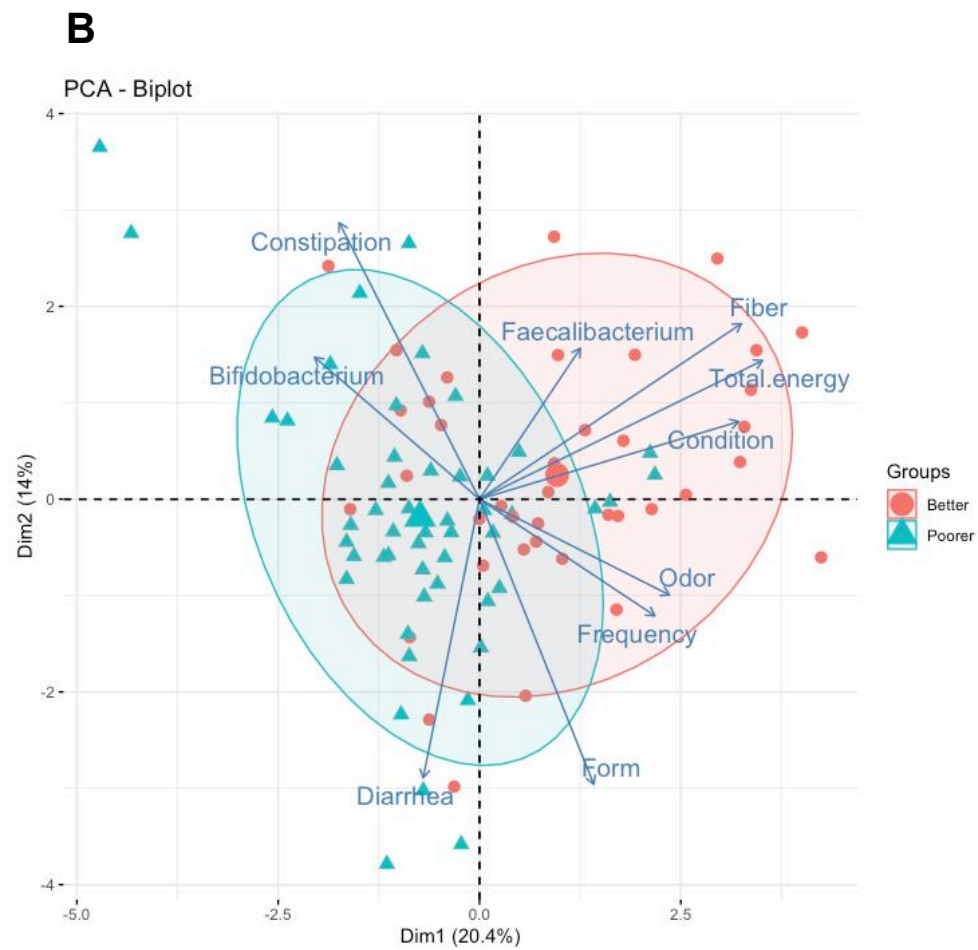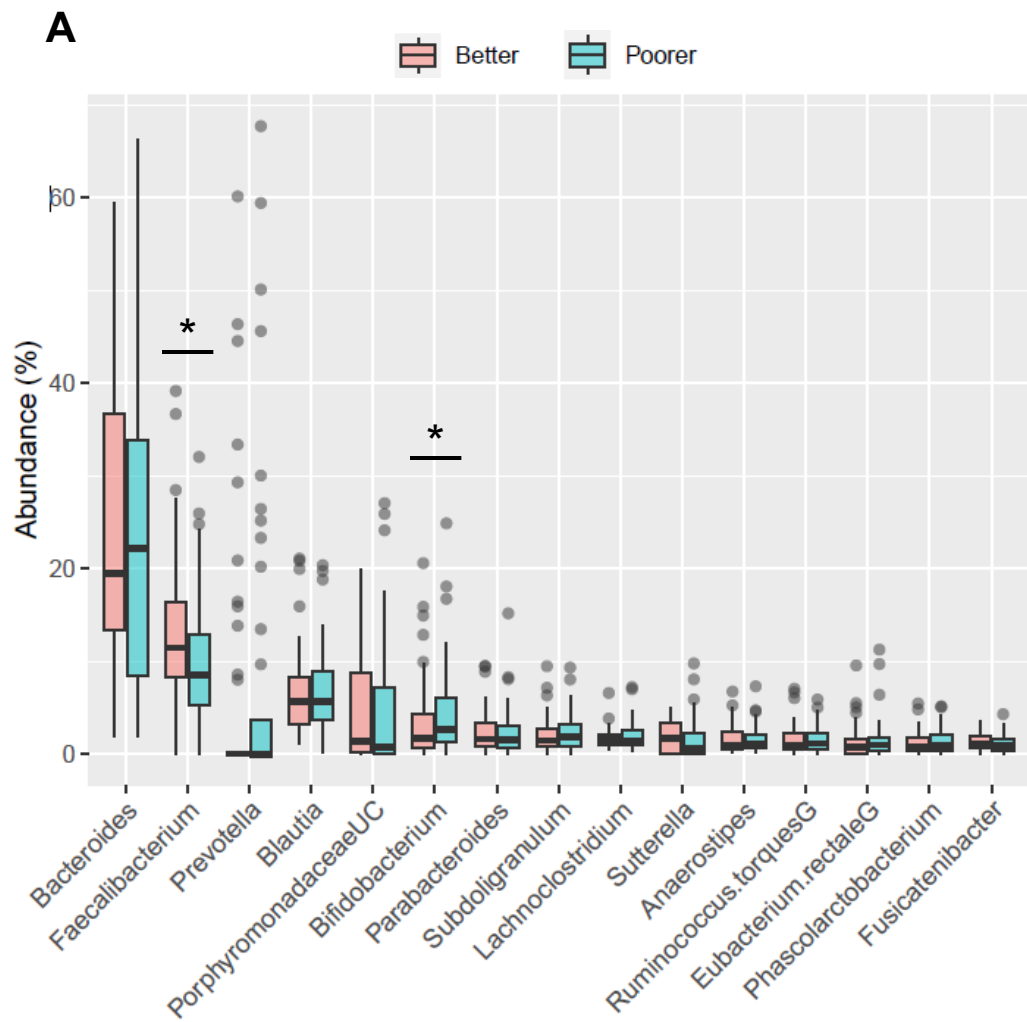$X^2 = 4.313$, df = 2, $P < 0.05$

A

B

PCA - Biplot
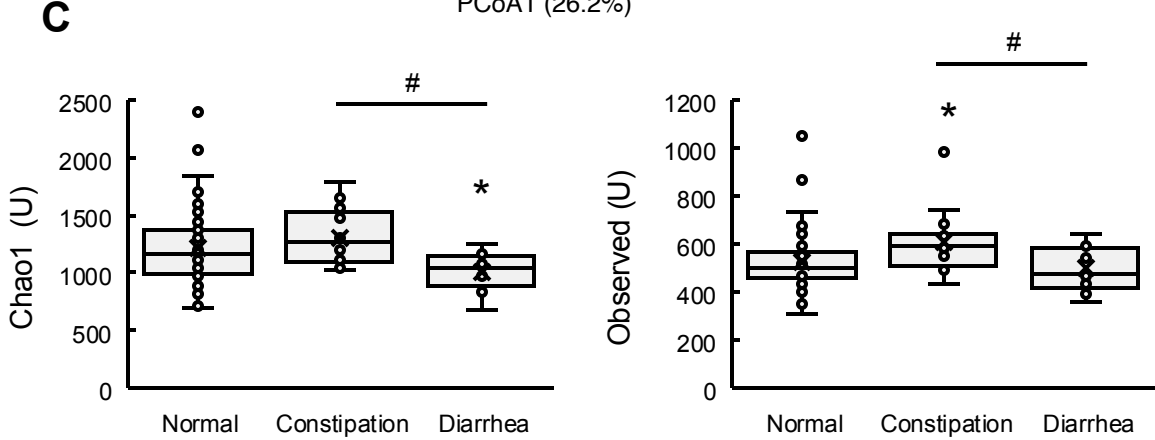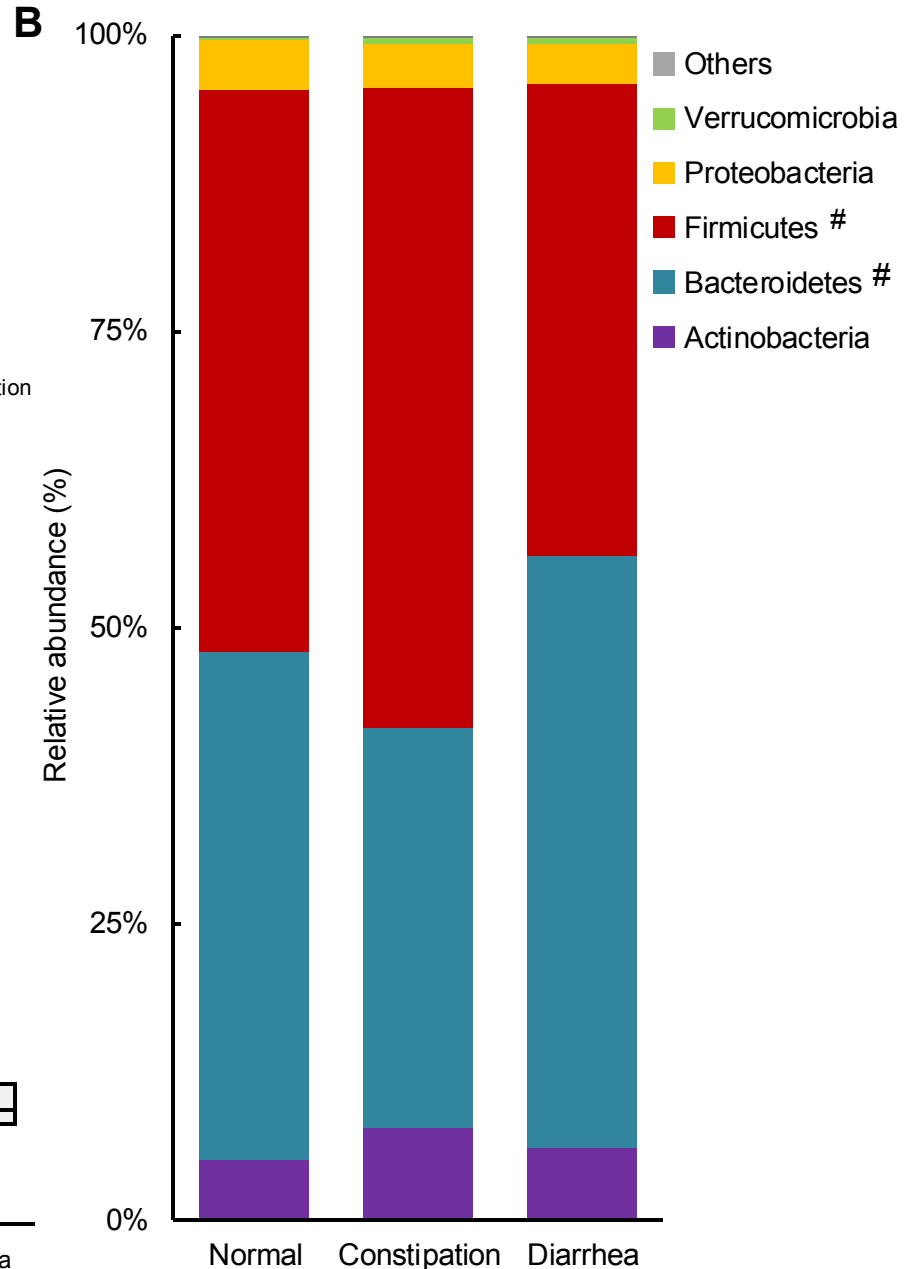
ここ最近の習慣的な排便状況に関する質問
(Question for habitual stool status)

1. 1週間あたりの排便回数 (Frequency of defecation per week)

☐ 1. 週7回以上
(More than 7 times)

☐ 2. 6回
(6 times)

☐ 3. 5回
(5 times)

☐ 4. 4回
(4 times)

☐ 5. 3回
(3 times)

☐ 6. 週2回未満
(Less than 2 times)

2. 排便に関して、「排便量」「色」「形状」をシートから番号を回答ください。
(For stool status, please respond the corresponding number of "Volume" "Form" "Color" from stool sheet.)

1) 1回あたりの排便量
(Stool volume per one time) ☐

2) 最も多い便の色
(Most common stool color) ☐

3) 最も多い便の形状
(Most common stool form) ☐

3. 排便後の爽快感 (Feeling comfort after defecation)

☐ 1. なし
(Uncomfortable)

☐ 2. あり
(Comfortable)

4. 排便パターン (Stoop pattern)

☐ 1. 快便
(Normal)

☐ 2. 便秘がち
(Tend to constipation)

☐ 3. 下痢がち
(Tend to diarrhea)

☐ 4. 便秘と下痢を繰り返す
(Repeated constipation and diarrhea)

ここ最近の身体コンディション関する質問
(Question for physical condition)

1. 身体的なコンディションが良かった (My condition was good physically)

☐ | ☐ | ☐ | ☐ | ☐ | ☐ | ☐

全くない (Never) | ほとんどない (Seldom) | 時々ある (Sometimes) | ある (Often) | よくある (More often) | 非常にある (Very often) | いつもある (Always)

2. 身体的にリカバリーができていた (I recovered well physically)

☐ | ☐ | ☐ | ☐ | ☐ | ☐ | ☐

全くない (Never) | ほとんどない (Seldom) | 時々ある (Sometimes) | ある (Often) | よくある (More often) | 非常にある (Very often) | いつもある (Always)

腸みえるシート®

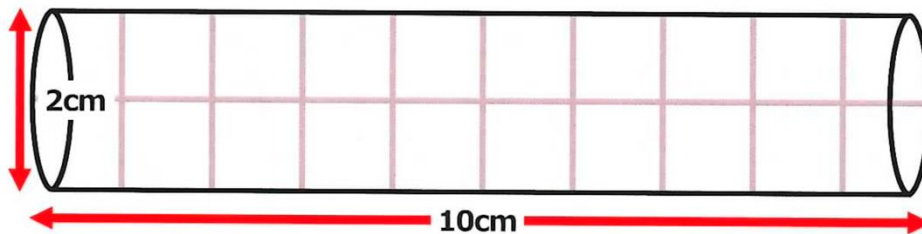(ちょう)

1 **1回の排便量** **あなたの排便量(うんち)は一回あたりどのくらいの量ですか？**

(Stool volume) (How much is your defecation volume each bowel movement?)

▶ **便モデル（2cm×10cm）の円柱に換算してみましょう**

(Please convert to a cylinder stool model unit (2cm×10cm))

1	2	3	4	5	6	7	8
0.5 本	1 本	1.5 本	2 本	2.5 本	3 本	3.5 本	4 本 以上

便モデル (Stool volume model)

2cm — 10cm

2 **便の色** **シートの色とうんちを比べてください。最も近い色の数字は何番ですか？**

(Stool color) (Please compare your defecation to the color of the sheet. What is the number of closest color?)

1	2	3	4	5	6

3 **便の形状** **シートの形状とうんちを比べてください。最も近い形状の数字は何番ですか？**

(Stool form) (Please compare your defecation to the form of the sheet. What is the number of closest form?)

1	2	3	4	5	6	7
分離した硬い木の実のような便（排便困難を伴う）	硬便が集合したソーセージ状の便	表面にひび割れがあるソーセージ状の便	平滑で柔らかいソーセージ状あるいは蛇状の便	柔らかく割面が鋭い小塊状の便（排便が容易）	ふわふわした不定形の小片便、泥状便	固形物を含まない水様便
(Separate hard lumps, like nuts (Hard to pass))	(Sausage-shaped but lumpy)	(Like a sausage but with cracks on its surface)	(Like a sausage or snake, smooth and soft)	(Soft blots with clear-cut edges (passed easily))	(Fluffy pieces with ragged edges, a mushy stool)	(Watery, no solid pieces)