

Supplementary materials for the article:

Ul-Haq A. et al. Characterization of Faecal Microbiomes of Osteoporotic Patients in Korea.  
Pol J Microbiol. 2022, Vol. 71, No 4, 601–613

Table SI  
Characteristics of subjects.

	Healthy control group (n = 60)	Osteoporosis patients group (n = 16)	Total	<i>p</i> -value
<b>Age</b>	59.1 ± 9.8	66.3 ± 8.9		<i>p</i> > 0.05
~59	29	3	32	
60~74	28	7	35	
> 75	6	2	8	
<b>Gender</b>				
Male	33	2	35	
Female	27	14	41	
<b>BMI</b>	24.2 ± 4.2	23.4 ± 2.8		
<b>BMD</b>	-0.75 ± 1.1	-2.85 ± 0.3		<i>p</i> > 0.05
<b>Smoking</b>			76	<i>p</i> > 0.05
Yes	15	0	15	
No	45	16	61	
<b>Alcohol</b>			76	<i>p</i> > 0.05
Yes	16	0	16	
No	44	16	60	
<b>Hypertension</b>				<i>p</i> > 0.05
Yes	19	2	21	
No	41	14	55	
<b>DM</b>				<i>p</i> > 0.05
Yes	2	3	5	
No	58	13	71	
<b>Blood chemistry</b>				
Glucose	103.0 ± 23.99	95.5 ± 11.2		<i>p</i> > 0.05
Cholesterol	211.1 ± 51.8	173.3 ± 67.3		<i>p</i> > 0.05
Triglyceride	168.8 ± 180.7	79.3 ± 26.9		<i>p</i> > 0.05
Protein	7.5 ± 0.3	7.5 ± 0.6		<i>p</i> > 0.05
Albumin	4.5 ± 0.3	4.4 ± 0.3		<i>p</i> > 0.05
BUN	14.5 ± 4.1	14.9 ± 4.2		<i>p</i> > 0.05

Wilcoxon rank-sum test was used to analyze the significance between the two groups (HC vs. OP).  
BMI – body mass index, BMD – bone mineral density, DM – diabetes mellitus, BUN – blood urea nitrogen

Table SII

Averaged taxonomic compositions in osteoporotic (OP) patients and healthy controls (normal).

Taxon rank	Taxon name	Normal (%)	Osteoporosis (%)
Phylum	Proteobacteria	7.73	8.40
	Actinobacteria	6.18	5.53
	Bacteroidetes	35.63	39.04
	Firmicutes	50.19	46.96
	ETC (under 1% on average)	0.26	0.07
Class	Bacteroidia	35.62	39.04
	Bacilli	3.43	1.98
	Actinobacteria	4.49	4.32
	Gammaproteobacteria	6.64	6.29
	Coriobacteriia	1.69	1.20
	Negativicutes	1.54	1.11
	Clostridia	45.05	43.80
	Betaproteobacteria	0	1.77
ETC (under 1% on average)	1.53	0.49	
Order	Veillonellales	1.32	0
	Coriobacteriales	1.69	1.20
	Bacteroidales	35.62	39.04
	Enterobacteriales	6.28	5.77
	Clostridiales	45.05	43.80
	Bifidobacteriales	4.38	4.13
	Lactobacillales	3.39	1.69
	Burkholderiales	0	1.77
	ETC (under 1% on average)	2.26	2.60
Family	<i>Christensenellaceae</i>	1.14	1.23
	<i>Bifidobacteriaceae</i>	4.38	4.13
	<i>Rikenellaceae</i>	3.31	4.14
	<i>Bacteroidaceae</i>	17.05	17.17
	<i>Streptococcaceae</i>	1.25	1.14
	<i>Prevotellaceae</i>	11.44	14.25
	<i>Veillonellaceae</i>	1.32	0
	<i>Porphyromonadaceae</i>	2.37	1.14
	<i>Coriobacteriaceae</i>	1.69	1.20
	<i>Enterobacteriales</i>	1.45	1.34
	<i>Lachnospiraceae</i>	19.63	17.94
	<i>Lactobacillaceae</i>	1.58	0
	<i>Ruminococcaceae</i>	23.28	23.99
	<i>Enterobacteriaceae</i>	4.77	4.41
	<i>Muribaculaceae</i>	0	1.06
	<i>Comamonadaceae</i>	0	1.26
ETC (under 1% on average)	5.33	5.60	

Taxon rank	Taxon name	Normal (%)	Osteoporosis (%)
Genus	<i>Ruminococcus_g2</i>	2.60	2.72
	<i>Subdoligranulum</i>	1.30	1.46
	<i>Ruminococcus_g4</i>	1.10	1.19
	<i>Oscillibacter</i>	3.06	3.01
	<i>Prevotella</i>	9.91	13.07
	<i>Blautia</i>	3.34	2.43
	<i>Clostridium_g24</i>	1.60	0
	<i>Lactobacillus</i>	1.54	0
	<i>Escherichia</i>	4.75	4.41
	<i>Bifidobacterium</i>	4.38	4.12
	<i>Eubacterium_g23</i>	1.30	1.40
	<i>Roseburia</i>	2.79	2.67
	<i>Dialister</i>	1.32	0.00
	<i>Alistipes</i>	3.31	4.14
	<i>Bacteroides</i>	17.05	17.17
	<i>Eubacterium_g5</i>	1.08	0
	<i>Dorea</i>	1.28	1.33
	<i>Streptococcus</i>	1.16	1.13
	<i>Enterobacteriales_g</i>	1.45	1.34
	<i>Parabacteroides</i>	2.34	1.14
	<i>Pseudoflavonifractor</i>	1.06	0
	<i>Fusicatenibacter</i>	1.06	1.26
	<i>Ruminococcus</i>	1.03	1.34
	<i>Anaerostipes</i>	1.38	1.37
	<i>Faecalibacterium</i>	9.09	9.71
	<i>Lachnospira</i>	0	1.13*
	<i>Comamonas</i>	0	1.23
	<i>Sporobacter</i>	0	1.06
ETC (under 1% on average)	19.72	20.16	

Relative abundances less than 1 % were expressed as etc. Wilcoxon rank-sum test was used to analyze the significance between the two groups (HC vs. OP).

\* –  $p < 0.05$

Table SIII

The Kruskal–Wallis  $H$  tests and LEfSe analysis of the associations between osteoporotic (OP) patients and healthy controls (normal).

Taxon name	Taxon rank	LDA score (log10)	$p$ -value	Normal (%)	Osteoporosis (%)
<i>Lachnospira</i>	Genus	3.26565	0.03377	0.745	1.127
<i>Solibacillus</i>	Genus	3.00469	0.00626	0.000	0.203
<i>PAC000195_g</i>	Genus	2.86011	0.03013	0.186	0.300
Micrococcales	Order	2.64011	0.02476	0.019	0.100
<i>Micrococcaceae</i>	Family	2.4495	0.02476	0.019	0.074
<i>PAC000741_g</i>	Genus	2.40379	0.01389	0.012	0.060
<i>Bacillaceae</i>	Family	2.31576	0.03989	0.019	0.056
<i>PAC001435_g</i>	Genus	2.09686	0.03248	0.008	0.039
<i>PAC001231_g</i>	Genus	-2.00047	0.02109	0.020	0.017

Only those with  $p$ -values less than 0.05 and absolute LDA scores greater than 2 were summarized.

% – the averaged taxonomic compositions of each group, LDA – Linear Discriminant Analysis