

Supplementary Material



# Fecal, Milk, Uterine, Airborne Dust, and Water Microbiota in Dairy Farms in Southern Vietnam: A Pilot Study

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Supplementary Table S1: The dominant families (representing > 1%) in fecal microbiota of six cows.

	Farm 1					Farm 2			Farm to farm difference (P value)
	a	b	c	Mean±SD	d	e	f	Mean±SD	
Ruminococcaceae	21.0	29.1	25.9	25.4±4.07	26.7	28.0	22.2	25.6±3.07	0.932
Bacteroidaceae	11.3	13.2	7.37	10.6±2.98	14.3	14.1	13.3	13.9±0.54	0.136
Clostridiaceae	11.5	9.63	11.6	10.9±1.11	9.20	7.72	10.8	9.25±1.56	0.206
Lachnospiraceae	9.46	6.91	17.3	11.2±5.42	9.25	4.51	7.82	7.19±2.43	0.305
Rikenellaceae	3.92	2.69	2.96	3.19±0.65	3.90	4.78	4.89	4.52±0.54	0.052
Paraprevotellaceae	5.66	3.82	2.15	3.88±1.75	2.12	3.03	2.59	2.58±0.46	0.283
Succinivibrionaceae	5.87	0.19	0.32	2.13±3.24	1.88	0.57	0.91	1.12±0.68	0.627
S24-7	2.81	1.42	2.07	2.10±0.69	0.59	0.95	0.98	0.84±0.22	0.040
Spirochaetaceae	1.39	0.21	2.57	2.10±1.18	0.97	1.04	1.16	0.84±0.09	0.040
Erysipelotrichaceae	1.08	1.70	1.47	1.42±0.32	0.97	0.99	1.02	0.99±0.02	0.080
p-2534-18B6	0.00	0.00	0.01	0.00±0.00	1.23	3.46	0.94	1.88±1.38	0.078
RF6	1.08	0.13	0.36	0.52±0.50	0.36	0.86	1.45	0.89±0.54	0.438
Turicibacteraceae	0.79	0.20	0.23	0.41±0.33	0.44	0.32	1.06	0.61±0.39	0.540
Others	24.6	30.7	25.6	26.8±3.46	28.16	29.6	30.9	29.6±1.38	0.275

a-f, individual dairy cows.

Supplementary Table S2: The dominant families (representing > 1%) in milk microbiota of six cows.

	Farm 1				Farm 2				Farm to farm difference (P value)
	a	b	c	Mean±SD	d	e	f	Mean±SD	
Streptococcaceae	31.6	45.1	57.8	44.8±13.1	0.10	0.20	8.85	3.05±5.02	0.007
Dermaocccaceae	17.7	11.1	12.8	13.9±3.45	19.6	29.8	17.1	22.2±6.71	0.129
Methylobacteriaceae	12.5	11.3	12.1	12.0±0.61	21.3	24.6	13.3	19.8±5.84	0.083
Bacillaceae	6.56	5.17	5.91	5.88±0.69	34.9	25.4	14.1	24.8±10.4	0.035
Moraxellaceae	4.76	1.20	1.82	2.59±1.90	2.99	3.48	19.6	8.70±9.47	0.335
Staphylococcaceae	10.3	0.21	0.05	3.54±5.90	0.25	0.04	4.32	1.54±2.42	0.616
Weeksellaceae	3.93	0.89	1.74	2.19±1.57	0.10	0.26	5.35	1.90±2.98	0.891
Lactobacillaceae	0.31	8.53	0.18	3.01±4.78	0.06	0.09	0.03	0.06±0.03	0.346
Planococcaceae	0.05	0.15	0.03	0.08±0.06	0.44	3.57	4.46	2.82±2.11	0.087
Enterobacteriaceae	1.82	0.17	0.60	0.86±0.86	1.46	1.44	2.43	1.78±0.57	0.198
Corynebacteriaceae	0.36	2.99	0.26	1.20±1.55	0.57	0.53	2.80	1.30±1.30	0.938
Enterococcaceae	0.43	5.13	0.24	1.93±2.77	0.01	0.00	0.36	0.12±0.21	0.322
Ruminococcaceae	0.40	0.39	0.44	0.41±0.03	0.76	1.09	0.67	0.84±0.22	0.029
Bifidobacteriaceae	0.25	0.13	2.79	1.06±1.50	0.13	0.09	0.12	0.11±0.02	0.338
Pseudomonadaceae	1.88	0.28	0.25	0.80±0.93	0.06	0.13	0.14	0.11±0.04	0.268
Gordoniaceae	0.22	0.09	0.25	0.19±0.09	1.05	0.56	0.25	0.62±0.41	0.143
Brevibacteriaceae	0.05	0.00	0.03	0.03±0.03	0.96	0.07	0.12	0.38±0.50	0.285
Others	6.85	7.18	2.74	5.59±2.47	15.2	8.59	6.05	9.95±4.73	0.230

a-f, individual dairy cows.

Supplementary Table S3: The dominant families (representing > 1%) in uterine microbiota of six cows.

	Farm 1				Farm 2				Farm to farm difference (P value)
	a	b	c	Mean±SD	d	e	f	Mean±SD	
Dermaocccaeae	0.55	3.90	39.4	14.6±21.5	25.7	3.35	25.9	18.3±13.0	0.811
Bacillaceae	0.35	2.61	21.0	7.99±11.3	11.4	2.99	19.2	11.2±8.11	0.710
Methylobacteriaceae	0.61	2.18	22.2	8.33±12.0	15.2	1.43	10.6	9.08±7.01	0.930
Bacteroidaceae	39.8	1.19	0.01	13.7±22.6	0.00	8.75	1.71	3.49±4.64	0.488
Ruminococcaceae	14.3	4.36	0.10	6.25±7.29	0.42	22.90	4.85	9.39±11.9	0.717
Mycoplasmataceae	0.98	34.5	0.03	11.8±19.6	0.00	0.42	0.00	0.14±0.24	0.360
Clostridiaceae	8.15	1.35	0.03	3.18±4.36	0.00	9.11	3.35	4.15±4.61	0.803
Porphyromonadaceae	0.18	17.4	0.00	5.86±9.99	2.53	1.08	0.41	1.34±1.08	0.480
Lachnospiraceae	6.68	1.11	0.05	2.61±3.56	0.42	4.72	3.31	2.82±2.19	0.937
Fusobacteriaceae	0.00	12.4	0.00	4.13±7.16	2.53	0.00	0.05	0.86±1.45	0.481
Leptotrichiaceae	0.00	0.00	0.00	0.00±0.00	12.7	0.01	0.34	4.35±7.23	0.356
Actinomycetaceae	8.71	2.18	0.00	3.63±4.53	0.00	0.01	0.02	0.01±0.01	0.239
Pseudomonadaceae	0.25	1.73	2.24	1.41±1.03	1.27	0.34	4.97	2.19±2.45	0.635
Acetobacteraceae	0.10	0.44	3.02	1.19±1.60	0.84	0.33	3.02	1.40±1.43	0.873
Tissierellaceae	0.01	5.47	0.04	1.84±3.14	0.84	0.00	0.00	0.28±0.48	0.443
Succinivibrionaceae	0.96	0.06	0.00	0.34±0.54	0.00	4.29	0.60	1.63±2.32	0.402
Paraprevotellaceae	2.42	0.42	0.01	0.95±1.29	0.00	2.29	0.47	0.92±1.21	0.978
Rikenellaceae	1.30	0.23	0.00	0.51±0.69	0.00	3.21	0.73	1.31±1.68	0.487
RF16	1.04	0.31	0.00	0.45±0.53	0.00	2.28	1.09	1.12±1.14	0.407
Moraxellaceae	0.17	0.22	0.76	0.38±0.33	0.84	0.08	1.82	0.91±0.87	0.380
Enterobacteriaceae	0.03	0.17	1.55	0.58±0.84	0.84	0.07	1.05	0.65±0.52	0.908
Pasteurellaceae	0.01	0.00	0.00	0.00±0.01	3.38	0.00	0.32	1.23±1.87	0.317
Micrococcaceae	0.01	0.12	1.32	0.48±0.73	0.84	0.13	1.10	0.69±0.50	0.706
Caulobacteraceae	0.04	0.19	1.29	0.51±0.68	0.42	0.09	1.30	0.60±0.63	0.865
Bradyrhizobiaceae	0.04	0.10	0.79	0.31±0.42	1.69	0.03	0.53	0.75±0.85	0.467
Mogibacteriaceae	0.25	1.82	0.00	0.69±0.99	0.00	0.80	0.13	0.31±0.43	0.574

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	Farm 1				Farm 2				Farm to farm difference (P value)
	a	b	c	Mean±SD	d	e	f	Mean±SD	
Erysipelotrichaceae	0.72	0.16	0.00	0.29±0.38	0.00	1.04	0.50	0.51±0.52	0.585
Peptostreptococcaceae	0.18	0.77	0.03	0.33±0.39	0.00	0.96	0.21	0.39±0.50	0.872
Comamonadaceae	0.02	0.05	0.47	0.18±0.25	1.27	0.01	0.21	0.50±0.68	0.490
Spirochaetaceae	1.23	0.06	0.00	0.43±0.69	0.00	0.50	0.16	0.22±0.26	0.648
p-2534-18B6	0.00	0.00	0.00	0.00±0.00	0.00	1.63	0.15	0.59±0.90	0.318
Alcaligenaceae	0.09	0.04	0.00	0.04±0.05	1.27	0.16	0.09	0.51±0.66	0.293
Hyphomicrobiaceae	0.01	0.02	0.09	0.04±0.04	1.27	0.01	0.10	0.46±0.70	0.360
RFP12	0.03	0.00	0.00	0.01±0.02	0.00	1.14	0.11	0.42±0.63	0.326
Others	10.7	4.42	5.54	6.89±3.35	14.4	25.8	11.7	17.3±7.48	0.093

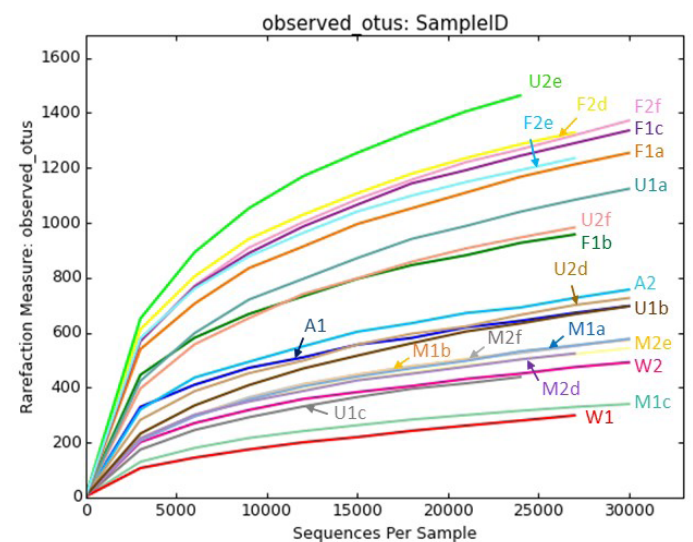
a–f, individual dairy cows.

**Supplementary Table S4:** Family level proportions of water and airborne dust microbiota of farm 1 and 2.

	Farm 1		Farm 2	
	W	A	W	A
Chthoniobacteraceae	2.00	0.00	0.00	0.00
Tissierellaceae	0.00	2.22	0.22	1.62
Weeksellaceae	0.00	1.61	1.28	0.39
Acetobacteraceae	0.00	3.10	0.00	1.20
Bacillaceae	0.10	1.32	0.01	0.08
Bacteroidaceae	0.00	0.00	22.1	19.8
Campylobacteraceae	0.00	0.23	0.00	1.00
Caulobacteraceae	0.00	2.04	0.23	0.89
Chitinophagaceae	0.63	0.20	0.96	2.18
Clostridiaceae	0.36	1.00	0.33	1.69
Comamonadaceae	0.00	0.40	1.30	1.32
Corynebacteriaceae	0.00	1.93	0.98	3.07
Cytophagaceae	1.11	0.15	0.00	0.00
Dermaococcaceae	0.01	2.62	0.01	0.01
Flavobacteriaceae	0.00	1.10	0.00	0.15
Halomonadaceae	0.00	3.32	0.00	0.00
Hyphomicrobiaceae	0.11	5.78	0.14	0.04
Intrasporangiaceae	0.00	3.38	0.00	0.02
Lachnospiraceae	0.95	1.02	0.19	0.06
Lactobacillaceae	18.5	1.62	4.73	2.14
Methylobacteriaceae	1.03	0.15	0.01	0.31
Micrococcaceae	0.00	3.07	0.01	0.69
Moraxellaceae	51.8	19.6	48.3	17.2
Nocardioidaceae	0.00	1.50	0.00	0.03
Oxalobacteraceae	0.01	0.59	1.05	0.89
Paenibacillaceae	1.30	0.37	0.28	0.24
Phyllobacteriaceae	0.00	2.52	0.00	0.00
Planococcaceae	0.72	1.38	0.46	16.5

Promicromonosporaceae	0.17	1.83	0.00	0.00
Pseudanabaenaceae	0.00	0.00	1.07	0.00
Pseudomonadaceae	0.01	3.88	0.03	12.0
Rhodobacteraceae	0.00	2.29	0.00	0.17
Ruminococcaceae	0.40	0.50	0.80	2.15
Saprospiraceae	0.00	1.09	0.00	0.00
Sphingomonadaceae	2.81	1.51	2.09	0.46
Xanthomonadaceae	0.00	1.54	1.10	0.22
Others	18.6	25.2	12.4	13.5

W, water samples; A, airborne dust samples.



**Supplementary Figure 1:** Rarefaction curves of the observed operational taxonomic units (OTUs) for the fecal, milk, uterine, airborne dust, and water microbiota in dairy farms. F, fecal samples; M, milk samples; U, uterine samples; A, airborne dust samples; W, water samples; a–f, individual dairy cows; 1–2, the farm number.