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Supplemental information

Nutritional and ecological perspectives of the interrelationships between diet and the gut microbiome in multiple sclerosis: Insights from marmosets

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SUPPLEMENTARY INFORMATION

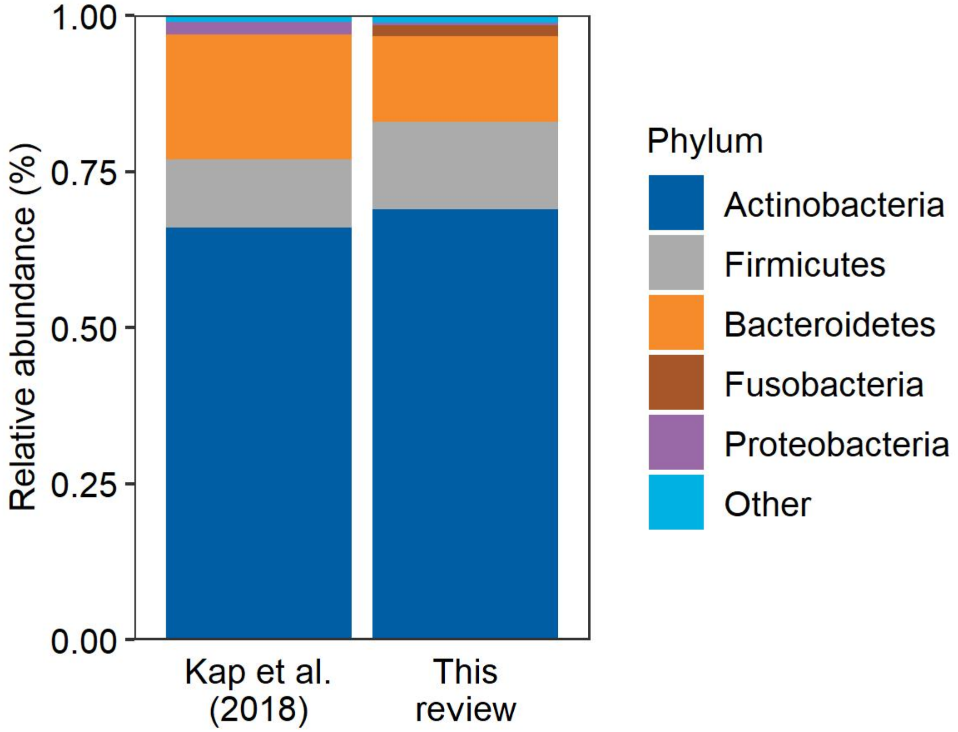

Figure S1. Differences in taxa found between analyses. Diagram compares taxa reported by Kap et al. (2018) with the reanalysis presented in this review. Bar graphs represent phylum abundances.

Table S1. Gut microbiome composition of healthy marmosets (related to Supplementary Figure S1). Table shows mean and standard deviation, minimum, maximum, and median relative abundances for each taxon across all marmoset samples taken at day -56 and day -7, prior to disease induction. Below the phylum level, only taxa with a mean relative abundance >1% are shown. Percentages next to OTU names indicate percentage sequence identity with that species.

Taxonomic Level	Taxon	Mean (%)	Standard deviation	Min (%)	Max (%)	Median (%)
Phylum	Actinobacteria	69.06	17.31	2.30	92.17	72.15
Phylum	Bacteroidetes	13.98	9.81	1.18	35.36	10.56
Phylum	Firmicutes	13.65	5.44	4.67	23.37	13.04
Phylum	Fusobacteria	1.81	10.20	0	57.71	0
Phylum	Proteobacteria	1.09	1.00	0.05	4.33	0.76
Phylum	Tenericutes	0.01	0.01	0	0.04	0
Family	Bifidobacteriaceae	63.20	16.39	1.63	87.15	67.17
Family	Lachnospiraceae	7.67	4.30	1.04	16.42	6.89
Family	Coriobacteriaceae	5.92	3.01	0.65	12.71	5.33
Family	Bacteroidaceae	5.32	6.48	0.04	32.83	3.17
Family	Prevotellaceae	5.30	3.65	0.12	12.40	5.42
Family	Veillonellaceae	4.46	3.64	0.61	19.04	3.41
Family	Uncl. Bacteroidales	2.46	2.88	0.03	13.92	1.55
Family	Fusobacteriaceae	1.83	10.28	0	58.17	0
Family	Acidaminococcaceae	1.04	0.69	0.19	3.27	0.86
Genus	*Bifidobacterium*	63.06	16.36	1.47	86.96	67.09
Genus	*Bacteroides*	5.32	6.49	0.04	32.85	3.18
Genus	*Megamonas*	2.21	1.45	0.26	6.16	2.24
Genus	*Megasphaera*	2.09	2.51	0.20	14.14	1.56
Genus	*Fusobacterium*	1.83	10.29	0	58.21	0
OTU	OTU1 *Bifidobacterium callitrichos* (100%)	42.63	13.97	0.34	68.79	41.96
OTU	OTU2 *Bifidobacterium aesculapii* (100%)	8.18	7.24	0.12	33.99	5.81
OTU	OTU5 *Bacteroides* sp. (93.4%)	4.32	4.14	0.04	13.83	2.69
OTU	OTU3 *Parolsenella catena* (96.59%)	3.87	2.74	0.48	9.44	2.94
OTU	OTU7 *Prevotella* sp. (83.73%)	3.65	3.13	0	11.27	2.89
OTU	OTU4 *Bifidobacterium dentium* (97.34%)	3.12	4.62	0	19.86	0.90
OTU	OTU9 *Lachnospiraceae* sp. (95.79%)	2.84	2.01	0.03	7.86	2.30
OTU	OTU8 *Lachnospiraceae* sp. (96.29%)	2.77	1.74	0.23	6.92	2.68
OTU	OTU6 *Bifidobacterium reuteri* (98.54%)	2.46	1.34	0.03	5.34	2.41
OTU	OTU23 *Bifidobacterium hapali* (96.76%)	2.20	1.97	0.33	8.77	1.66
OTU	OTU12 *Fusobacterium varium* (100%)	1.87	10.53	0	59.56	0
OTU	OTU10 *Bacteroides salanitronis* (91.27%)	1.81	2.67	0	13.19	1.01
OTU	OTU50 *Bifidobacterium callimiconis* (98.04%)	1.65	3.75	0	18.58	0.12

OTU	OTU73 *Bifidobacterium tissierii* (99.27%)	1.37	1.70	0	8.84	0.73
OTU	OTU13 *Lachnospiraceae* sp. (95.3%)	1.17	1.07	0	4.44	0.81
OTU	OTU24 *Megamonas* sp. (97.9%)	1.06	0.99	0.01	4.56	0.79
OTU	OTU20 *Phascolarctobacterium succinatutens* (92.31%)	1.04	0.70	0.19	3.28	0.86

Table S2. Coefficients and 95% confidence intervals for mixed-effects models predicting diversity metrics (related to Figure 1). Coefficients were considered significant (*) if the 95% confidence interval did not overlap zero. Variables with no coefficient shown for a given diversity metric were not present in top-ranked models ($\Delta\text{AIC}_c < 2$) predicting that metric. Positive and negative coefficients indicate YBS and WBS, respectively, for diet; symptomatic and healthy marmosets, respectively, for pathology; and increases and decreases over the course of the experiment, respectively, for time.

Measure	Diet				Pathology			Time			
	Lower CI	Coef	Upper CI		Lower CI	Coef	Upper CI	Lower CI	Coef	Upper CI	
Bray-Curtis dissimilarity	-1.211	-0.808	-0.405	*				0.159	0.340	0.520	*
Simpson diversity	-0.713	-0.095	0.185					0.135	0.326	0.518	*
Pielou evenness	-0.631	-0.042	0.265		-0.469	0.064	1.055	0.105	0.322	0.538	*
Species richness	-0.878	-0.045	0.365		-0.887	-0.049	0.355	-0.301	-0.024	0.088	

Table S3. Gut microbiome composition at different time points of marmosets fed the WBS and YBS diets (related to Figures 2 and 3). Table shows mean and standard deviations of relative abundances for each diet treatment and for each taxon across all marmoset samples taken at each experimental time point. Below the phylum level, only taxa with a mean relative abundance >1% are shown. Percentages next to OTU names indicate percentage sequence identity with that species. WBS, water-based supplement; YBS, yogurt-based supplement; SD, standard deviation

Taxonomic Level	**Taxon**	**WBS (% Mean ± SD)**				**YBS (% Mean ± SD)**			
		-56	**-7**	**21**	**49**	**-56**	**-7**	**21**	**49**
Phylum	Actinobacteria	63.34±13.66	68.22 ± 27.42	59.61 ± 13.35	56.44 ± 18.44	67.56 ± 12.84	76.90 ± 10.50	73.11 ± 7.84	67.91 ± 12.03
	Bacteroidetes	17.59 ± 11.58	13.48 ± 9.34	24.71 ± 14.92	25.72 ± 19.41	13.62 ± 10.03	11.23 ± 8.89	13.61 ± 6.68	15.62 ± 8.53
	Firmicutes	16.89 ± 3.45	10.38 ± 5.76	13.71 ± 5.92	14.73 ± 5.36	16.79 ± 5.12	10.53 ± 3.60	11.48 ± 4.37	14.77 ± 3.55
	Proteobacteria	1.19 ± 0.73	0.57 ± 0.71	1.62 ± 0.88	2.29 ± 3.28	1.33 ± 0.89	1.03 ± 0.61	0.83 ± 0.47	1.26 ± 0.88
	Tenericutes	0.02 ± 0.01	0.01 ± 0.00	0.02 ± 0.03	0.07 ± 0.08	0.01 ± 0.01	0.01 ± 0.00	0.08 ± 0.15	0.19 ± 0.42
Family	Acidaminococcaceae	1.26 ± 0.68	0.54 ± 0.22	0.97 ± 0.39	1.06 ± 0.93	1.33 ± 0.89	1.03 ± 0.61	0.83 ± 0.47	1.26 ± 0.88
	Anaeroplasmataceae	0.02 ± 0.01	0.01 ± 0.00	0.02 ± 0.03	0.06 ± 0.08	0.01 ± 0.01	0.01 ± 0.00	0.08 ± 0.15	0.19 ± 0.42
	Bifidobacteriaceae	58.24 ± 13.29	62.48 ± 25.34	54.89 ± 13.13	49.67 ± 20.68	62.74 ± 12.57	68.03 ± 12.12	66.75 ± 8.61	63.49 ± 12.21
	Coriobacteriaceae	4.85 ± 1.68	5.51 ± 2.90	4.53 ± 1.99	6.56 ± 3.17	4.58 ± 3.41	8.62 ± 2.24	6.14 ± 2.47	4.18 ± 2.16
	Enterobacteriaceae	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00	1.24 ± 3.39	0.02 ± 0.02	0.01 ± 0.00	0.01 ± 0.01	0.02 ± 0.03
	Lachnospiraceae	11.17 ± 3.48	4.46 ± 2.36	3.66 ± 1.65	9.29 ± 3.98	9.99 ± 4.20	4.89 ± 2.17	3.98 ± 2.61	6.99 ± 3.06
	Porphyromonadaceae	1.04 ± 0.91	0.82 ± 0.88	1.68 ± 1.84	4.39 ± 5.76	0.36 ± 0.68	0.93 ± 1.09	0.81 ± 0.92	1.90 ± 2.56
	Prevotellaceae	6.20 ± 3.13	5.07 ± 3.91	9.88 ± 4.88	6.38 ± 6.01	4.32 ± 3.46	5.52 ± 4.37	7.19 ± 5.80	6.77 ± 6.28
	Sutterellaceae	0.76 ± 0.65	0.27 ± 0.30	0.40 ± 0.34	0.32 ± 0.23	0.97 ± 0.73	0.30 ± 0.39	0.31 ± 0.23	0.67 ± 0.79
	Veillonellaceae	3.71 ± 3.37	4.93 ± 5.81	8.54 ± 7.53	3.50 ± 1.98	4.85 ± 2.37	4.29 ± 2.52	6.40 ± 3.87	6.03 ± 3.43
Genus	Asteroleplasma	0.02 ± 0.01	0.01 ± 0.00	0.02 ± 0.03	0.06 ± 0.08	0.01 ± 0.01	0.01 ± 0.00	0.08 ± 0.15	0.19 ± 0.42
	Bifidobacterium	57.88 ± 13.24	61.95 ± 25.19	54.39 ± 13.14	49.19 ± 20.49	62.38 ± 12.51	67.55 ± 12.06	66.21 ± 8.58	62.98 ± 12.13
	Megasphaera	1.53 ± 1.44	3.16 ± 4.44	3.56 ± 3.04	1.91 ± 1.32	1.95 ± 1.22	1.67 ± 1.45	3.69 ± 2.19	3.63 ± 2.35
	Phascolarctobacterium	0.71 ± 0.36	0.33 ± 0.17	0.55 ± 0.23	0.58 ± 0.50	0.68 ± 0.49	0.59 ± 0.34	0.45 ± 0.28	0.67 ± 0.47
	Succinatimonas	0.02 ± 0.02	0.16 ± 0.32	0.24 ± 0.29	0.15 ± 0.24	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00
	Sutterella	0.76 ± 0.64	0.26 ± 0.29	0.40 ± 0.34	0.32 ± 0.23	0.97 ± 0.73	0.30 ± 0.39	0.30 ± 0.23	0.66 ± 0.79
OTU# 2	*Bifidobacterium aesculapii* (100%)	7.72 ± 4.10	11.57 ± 10.58	5.53 ± 3.71	5.98 ± 4.14	3.78 ± 2.70	9.12 ± 7.23	3.05 ± 2.72	8.95 ± 10.33
3	*Parolsenella catena* (96.59%)	2.23 ± 1.02	3.77 ± 2.31	2.92 ± 1.69	2.98 ± 2.32	2.17 ± 2.06	7.09 ± 1.81	4.80 ± 2.35	1.50 ± 1.02
4	*Bifidobacterium dentium* (97.34%)	1.27 ± 1.74	1.95 ± 2.69	6.91 ± 7.91	3.72 ± 6.86	3.46 ± 4.74	5.64 ± 6.80	14.04 ± 8.93	6.30 ± 3.40
7	*Prevotella* (83.73%)	4.01 ± 2.07	3.89 ± 3.74	7.88 ± 5.06	4.68 ± 5.30	2.52 ± 2.62	3.98 ± 3.87	5.08 ± 4.81	4.92 ± 5.75
13	Lachnospiraceae (95.30%)	2.08 ± 0.94	0.54 ± 0.34	0.40 ± 0.28	1.72 ± 1.59	1.52 ± 1.29	0.49 ± 0.43	0.36 ± 0.30	0.45 ± 0.36
14	Lachnospiraceae (96.31%)	0.65 ± 0.29	0.54 ± 0.69	0.47 ± 0.41	1.84 ± 2.31	0.91 ± 0.97	0.57 ± 0.79	0.48 ± 0.51	1.83 ± 1.42

15	*Megasphaera paucivorans* (95.57%)	0.59 ± 0.66	1.12 ± 1.66	1.08 ± 1.13	0.52 ± 0.35	0.72 ± 0.59	0.54 ± 0.43	1.12 ± 0.88	1.06 ± 0.88
20	*Phascolarctobacterium succinatutens* (92.31%)	1.26 ± 0.68	0.53 ± 0.22	0.97 ± 0.38	1.04 ± 0.92	1.31 ± 0.89	1.03 ± 0.60	0.82 ± 0.47	1.25 ± 0.88
24	*Megamonas* (97.90%)	1.24 ± 1.35	0.46 ± 0.50	1.44 ± 0.73	0.38 ± 0.47	1.28 ± 1.02	1.23 ± 0.73	0.85 ± 0.68	0.62 ± 0.45
28	*Parabacteroides* (96.23%)	0.06 ± 0.07	0.44 ± 0.65	0.86 ± 1.13	0.54 ± 1.19	0.04 ± 0.09	0.27 ± 0.34	0.36 ± 0.45	0.52 ± 1.11
32	*Parolsenella* (96.83%)	0.29 ± 0.18	0.13 ± 0.14	0.14 ± 0.09	0.12 ± 0.17	0.20 ± 0.25	0.32 ± 0.19	0.31 ± 0.29	0.08 ± 0.07
35	*Bifidobacterium moukalabense* (96.82%)	0.25 ± 0.23	0.17 ± 0.17	0.11 ± 0.12	0.29 ± 0.29	0.22 ± 0.20	0.21 ± 0.16	0.12 ± 0.12	0.39 ± 0.53
37	Muribaculaceae (87.94%)	0.11 ± 0.11	0.04 ± 0.04	0.05 ± 0.05	0.66 ± 0.82	0.06 ± 0.04	0.01 ± 0.01	0.07 ± 0.04	0.52 ± 1.09
38	*Parolsenella* (97.32%)	0.17 ± 0.23	0.06 ± 0.09	0.04 ± 0.07	0.13 ± 0.33	0.46 ± 0.32	0.08 ± 0.15	0.06 ± 0.10	0.20 ± 0.24
40	*Bifidobacterium goeldii* (98.29%)	0.38 ± 0.49	0.36 ± 0.38	0.20 ± 0.20	0.34 ± 0.32	0.26 ± 0.21	0.21 ± 0.21	0.24 ± 0.28	0.82 ± 1.21
42	*Enterobacter hormaechei* (100%)	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00	1.21 ± 3.35	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.01	0.02 ± 0.03
45	*Streptococcus* (97.90%)	0.22 ± 0.21	0.17 ± 0.27	0.18 ± 0.24	0.08 ± 0.13	0.10 ± 0.14	0.14 ± 0.10	0.10 ± 0.12	0.04 ± 0.06
47	*Succinatimonas hippei* (96.10%)	0.02 ± 0.02	0.16 ± 0.32	0.24 ± 0.29	0.15 ± 0.24	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00
56	Anaeroplasmataceae (95.31%)	0.02 ± 0.01	0.01 ± 0.00	0.02 ± 0.03	0.06 ± 0.08	0.01 ± 0.01	0.01 ± 0.00	0.08 ± 0.15	0.20 ± 0.44
58	*Bifidobacterium catulorum* (100%)	0.02 ± 0.02	0.09 ± 0.18	0.02 ± 0.02	0.04 ± 0.06	0.01 ± 0.01	0.01 ± 0.01	0.05 ± 0.06	0.15 ± 0.24
59	*Kineothrix* (97.03%)	0.04 ± 0.06	0.03 ± 0.05	0.03 ± 0.04	0.26 ± 0.51	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00
72	*Parolsenella catena* (96.10%)	0.89 ± 0.50	0.60 ± 0.37	0.55 ± 0.44	1.31 ± 1.34	0.97 ± 0.59	0.41 ± 0.40	0.47 ± 0.49	1.44 ± 1.89
73	*Bifidobacterium tissierii* (99.27%)	0.80 ± 0.55	1.90 ± 3.13	1.17 ± 1.12	3.60 ± 2.77	1.55 ± 0.87	1.17 ± 0.80	1.31 ± 0.53	3.35 ± 2.35
129	*Bifidobacterium hapali* (97.32%)	0.55 ± 0.67	0.09 ± 0.11	0.08 ± 0.11	0.31 ± 0.41	0.48 ± 0.44	0.70 ± 0.65	0.18 ± 0.13	0.52 ± 0.45
136	*Megamonas* (96.97%)	0.28 ± 0.21	0.19 ± 0.26	0.53 ± 0.65	0.29 ± 0.42	0.08 ± 0.08	0.68 ± 0.67	0.34 ± 0.32	0.17 ± 0.25
145	*Bifidobacterium avesanii* (97.80%)	0.09 ± 0.11	0.09 ± 0.15	0.29 ± 0.53	0.06 ± 0.08	0.15 ± 0.16	0.19 ± 0.21	0.47 ± 0.49	0.24 ± 0.24