

Randomized Controlled Study to Evaluate Microbial Ecological Effects of CPP-ACP and Cranberry on Dental Plaque

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Appendix

Appendix Table 1. Bacterial prevalence at the baseline visit across the three treatment groups

Bacterial Species	All Samples (n = 71)	CPP-ACP (n = 22)	All-in-One (n = 23)	Control (n = 26)	P-value
<i>Actinomyces gerensceriae</i>	70 (99%)	21 (96)	23 (100%)	26 (100%)	0.32
<i>Corynebacterium durum</i>	70 (99%)	21 (96)	23 (100%)	26 (100%)	0.32
<i>Lactobacillus gasseri</i>	13 (18%)	2 (9%)	4 (17%)	7 (27%)	0.28
<i>Neisseria flavescens</i>	63 (89%)	19 (86%)	22 (96%)	22 (85%)	0.44
<i>Prevotella denticola</i>	56 (79%)	17 (77%)	18 (78%)	21 (81%)	0.95
<i>Rothia aeria/dentocariosa</i>	71 (100%)	22 (100%)	23 (100%)	26 (100%)	δ
<i>Streptococcus mitis/oralis</i>	71 (100%)	22 (100%)	23 (100%)	26 (100%)	δ
<i>Streptococcus mutans</i>	54 (76%)	16 (73%)	18 (78%)	20 (77%)	0.90
<i>Streptococcus parasanguinis</i>	5 (7%)	0 (0%)	1 (4%)	4 (15%)	0.09
<i>Streptococcus salivarius/ thermophilus</i>	71 (100%)	22 (100%)	23 (100%)	26 (100%)	δ
<i>Streptococcus sanguinis</i>	71 (100%)	22 (100%)	23 (100%)	26 (100%)	δ
<i>Streptococcus sobrinus</i>	2 (2.8%)	0 (0%)	0 (0%)	2 (8%)	0.17
<i>Scardovia wiggsiae</i>	42 (59%)	13 (59%)	13 (57%)	16 (62%)	0.94
<i>Veillonella parvula</i>	71 (100%)	22 (100%)	23 (100%)	26 (100%)	δ

Baseline prevalence data showing number of samples in which the bacterial species was detected and values in brackets representing % prevalence. No significant differences between the treatment groups at the baseline visit ($P > 0.05$; chi-square test). δ: no statistics computed because bacterial prevalence was a constant.

Appendix Table 2. Demographic characteristics of the study population

	CPP-ACP Group	All-in-One Group	Control Group	<i>P</i>-values
Mean Age \pm S.D	14.33 \pm 1.64	14.0 \pm 1.55	14.03 \pm 1.79	0.70
Female, n(%)	19(63%)	16(53%)	19(63%)	0.46

Appendix Table 3. Relative abundance of each *caries-associated* bacterial species at the baseline and recall visits, and the subsequent fold change in bacterial load over time

Bacterial Species	ΔCt Baseline Visit			ΔCt Recall Visit			$\Delta\Delta Ct$			Fold change		
	CPP-ACP	All-in-One	Control	CPP-ACP	All-in-One	Control	CPP-ACP	All-in-One	Control	CPP-ACP	All-in-One	Control
<i>Veillonella parvula</i>	-9.75	-9.50	-8.32	-8.06	-6.37	-8.46	1.68	3.13	-0.14	0.31	0.11	1.10
<i>Streptococcus mutans</i>	3.51	1.85	2.55	4.45	3.99	1.23	0.94	2.14	-1.33	0.52	0.23	2.51
<i>Actinomyces gerensceriae</i>	-4.33	-5.56	-4.60	-2.75	-4.46	-4.36	1.58	1.10	0.24	0.33	0.47	0.85
<i>Streptococcus parasanguinis</i>	9.55	9.27	7.97	10.40	10.59	9.42	0.85	1.32	1.45	0.56	0.40	0.37
<i>Streptococcus sobrinus</i>	9.55	9.86	9.44	10.26	10.59	9.92	0.71	0.73	0.48	0.61	0.60	0.72
<i>Scardovia wiggsiae</i>	5.37	4.94	5.09	6.18	4.92	4.49	0.81	-0.01	-0.60	0.57	1.01	1.52
<i>Lactobacillus gasseri</i>	9.01	8.63	9.13	9.10	9.04	9.21	0.09	0.41	0.08	0.94	0.75	0.95
<i>Prevotella denticola</i>	-0.32	0.72	1.28	-1.45	-0.19	-0.96	-1.12	-0.92	-2.25	2.18	1.89	4.74

The Ct value of each bacterial target was normalized to the mean Ct value of all bacterial species ($\Delta Ct = Ct_{\text{bacterial species}} - Ct_{\text{mean of all bacterial species}}$). The $\Delta\Delta Ct$ for each bacterial species was then calculated as follows: $\Delta\Delta Ct = \Delta Ct_{\text{bacterial species (recall visit)}} - \Delta Ct_{\text{bacterial species (baseline visit)}}$. Fold increase, or decrease, in bacterial abundance from the baseline to recall visit for each trial group was calculated based on the formula: $2^{-\Delta\Delta Ct}$. Ratio below 1 indicates lower relative abundance; a ratio above 1 indicates higher relative abundance.

Appendix Table 4. Relative abundance of each *health-associated* bacterial species at the baseline and recall visits, and the subsequent fold change in bacterial load over time

Bacterial Species	ΔCt Baseline Visit			ΔCt Recall Visit			ΔΔCt			Fold change		
	CPP-ACP	All-in-One	Control	CPP-ACP	All-in-One	Control	CPP-ACP	All-in-One	Control	CPP-ACP	All-in-One	Control
<i>Corynebacterium durum</i>	0.77	-0.81	-0.86	-3.09	-3.43	-1.80	-3.85	-2.61	-0.94	14.45	6.11	1.92
<i>Neisseria flavescens</i>	-0.06	1.14	1.58	-1.09	-2.48	2.23	-1.03	-3.62	0.65	2.05	12.27	0.64
<i>Streptococcus sanguinis</i>	-7.92	-7.27	-8.31	-9.47	-9.05	-7.19	-1.55	-1.78	1.12	2.92	3.44	0.46
<i>Streptococcus mitis/oralis</i>	-6.60	-6.13	-6.64	-6.34	-6.11	-6.03	0.26	0.02	0.62	0.84	0.98	0.65
<i>Rothia aeria/dentocariosa</i>	-5.63	-4.39	-6.00	-5.59	-5.12	-5.10	0.04	-0.73	0.89	0.97	1.65	0.54
<i>Streptococcus salivarius/thermophilus</i>	-3.14	-2.74	-2.31	-2.56	-1.93	-2.59	0.59	0.81	-0.27	0.67	0.57	1.21

The Ct value of each bacterial target was normalized to the mean Ct value of all bacterial species ($\Delta Ct = Ct^{\text{bacteria species}} - Ct^{\text{mean of all bacterial species}}$). The $\Delta\Delta Ct$ for each bacterial species was then calculated as follows: $\Delta\Delta Ct = \Delta Ct^{\text{bacterial species (recall visit)}} - \Delta Ct^{\text{bacterial species (baseline visit)}}$. Fold increase, or decrease, in bacterial abundance from the baseline to recall visit for each trial group was calculated based on the formula: $2^{-\Delta\Delta Ct}$. Ratio below 1 indicates lower relative abundance; a ratio above 1 indicates higher relative abundance.