

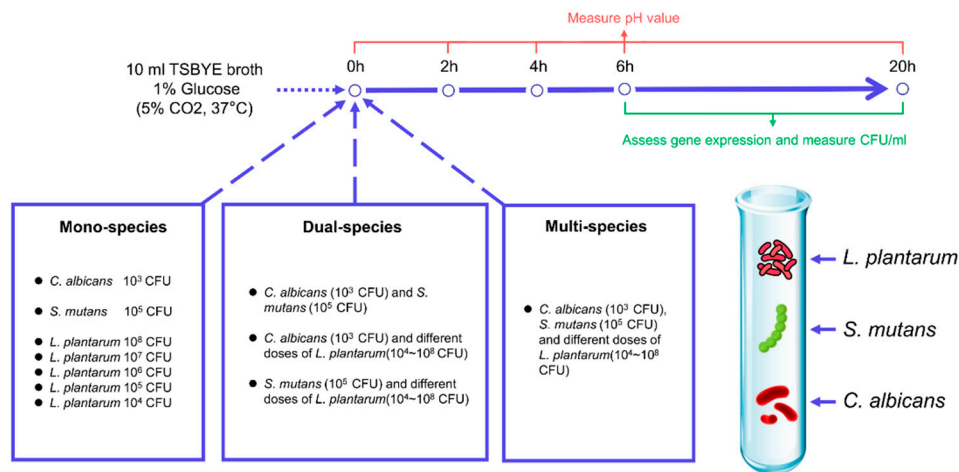
## Supplement

**Table S1. Genes of interest**

Microorganisms	Genes	Function
<i>L. plantarum</i>	<i>plnA</i>	Encode plantaricins
	<i>plnN</i>	Encode plantaricins
	<i>PcrA</i>	ATP-dependent DNA helicase
	<i>atpD</i>	ATPase complex and acid tolerance
<i>S. mutans</i>	<i>eno</i>	Putative enolase
	<i>lacC/G</i>	Galactose metabolism
	<i>HWPI</i>	Hyphal growth and adhesion to host cells
<i>C. albicans</i>	<i>ECE1</i>	Hyphal growth and adhesion to host cells
	<i>CHT2</i>	Fungal cell wall chitin remodeling
	<i>ERG4</i>	Antifungal medication resistance

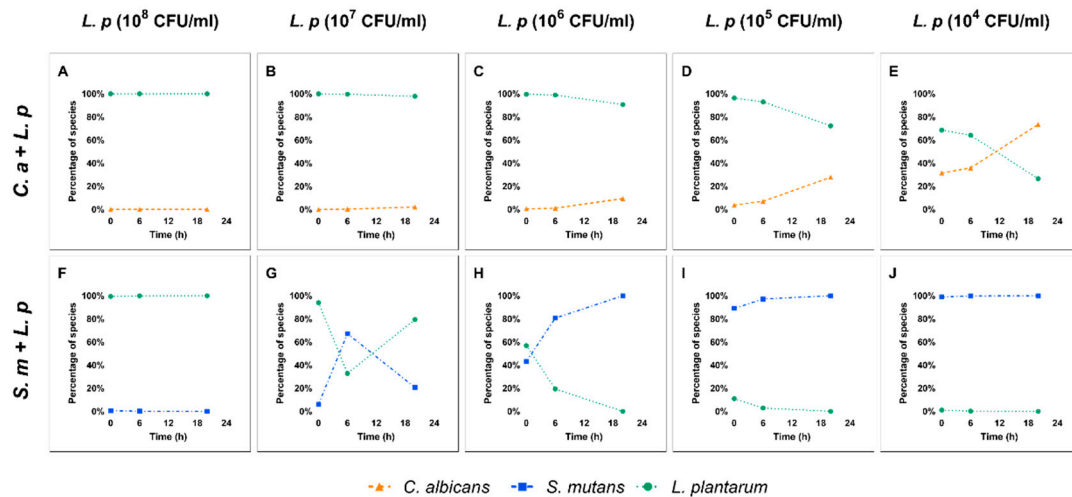
**Table S2. Primers used in RT-qPCR [27]**

Genes	Primers	Sequence	Amplicon size (bp)
<i>atpD</i>	Sm_atpD_F	TGTTGATGGTCTGGGTGAAA	176
	Sm_atpD_R	TTTGACGGTCTCCGATAACC	
<i>eno</i>	Sm_eno_F	CAGCGTCTTCAGTTCCATCA	194
	Sm_eno_R	TCACTCAGATGCTCCAATCG	
<i>lacG</i>	Sm_lacG_F	ATTGGATGCGTGCTTTTGATGG	94
	Sm_lacG_R	CGACCGACACCCTTAATCTGG	
<i>lacC</i>	Sm_lacC_F	GCTGGAATTACATCGGCTCTTGC	157
	Sm_lacC_R	CCTCCGCTACCTCAATTTGTTGG	
<i>ACT1</i>	Ca_ACT1_F	TGCTCCAGAAGAACACCCA	182
	Ca_ACT1_R	CACCTGAATCCAAAACAATACCAGT	
<i>HWP1</i>	Ca_HWP1_F	TGGTGCTATTACTATTCCGG	182
	Ca_HWP1_R	CAATAATAGCAGCACCGAAG	
<i>ECE1</i>	Ca_ECE1_F	GCTGGTATCATTGCTGATAT	168
	Ca_ECE1_R	TTCGATGGATTGTTGAACAC	
<i>CHT2</i>	Ca_CHT2_F	TTGGGATGCTTCTGGGGCTT	111
	Ca_CHT2_R	GCAGAAGAAGATGGGGCAACAC	
<i>ERG4</i>	Ca_ERG4_F	TCAAATGTGCCAATGGTTCT	101
	Ca_ERG4_R	AGCCCAAGTCAATGTTTGAA	
<i>rpoB</i>	Lp14_rpoB_F	CACCGTACCCGTAGAAGTTATGC	106
	Lp14_rpoB_R	GGAGACCTTGATCCAAGAACCA	
<i>pcrA</i>	Lp14_pcrA_F	AGGAGGTCTGGGTCTCAACG	118
	Lp14_pcrA_R	AAGGTCCGTTGCTCGCTAGT	
<i>plnN</i>	Lp14_plnN_F	ATTGCCGGGTTAGGTATCG	146
	Lp14_plnN_R	CCTAAACCATGCCATGCAC	
<i>plnA</i>	Lp14_plnA_F	GTGGAAAGAGTAGTGCGTATTC	135
	Lp14_plnA_R	CGCCATCTATACGAAATATAACTTG	



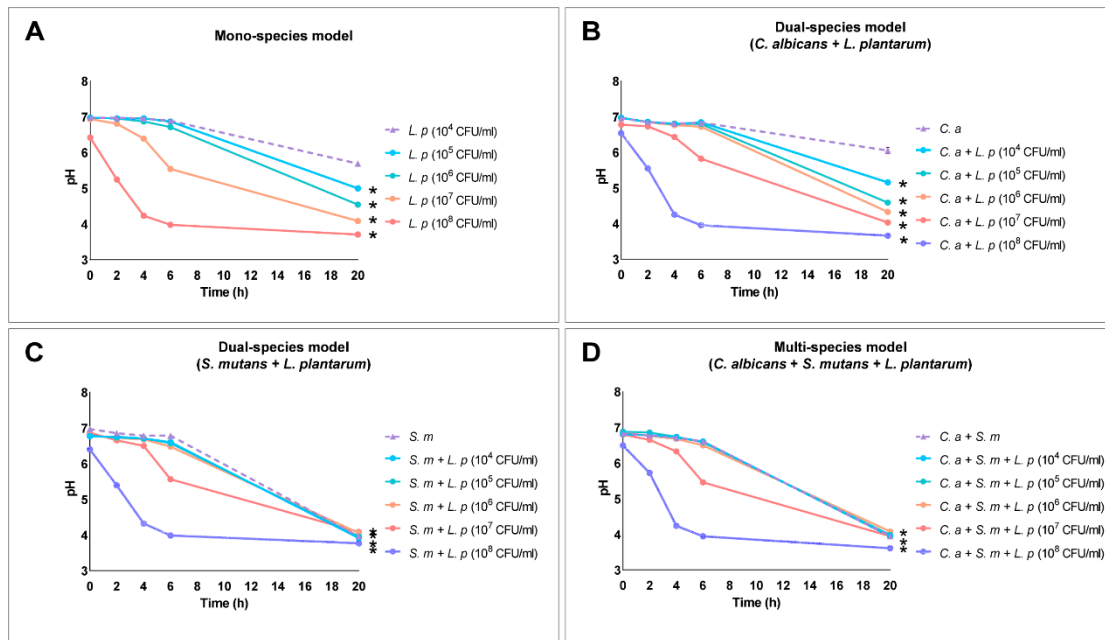
**Figure S1. Schematic study design**

The starting concentration for microorganisms was 10<sup>3</sup> CFU/ml for *C. albicans*, 10<sup>5</sup> CFU/ml for *S. mutans* and 10<sup>4</sup>–10<sup>8</sup> CFU/ml for *L. plantarum*. *C. albicans* (10<sup>3</sup> CFU/ml) and *S. mutans* (10<sup>5</sup> CFU/ml) were used to mimic high caries risk in a clinical condition. The maximum inoculation level of *L. plantarum* (10<sup>8</sup> CFU/ml) is the lower dose of probiotics utilized in commercial probiotic products (10<sup>9</sup>–10<sup>12</sup> CFU/ml as a single dosage). Mono-species, dual-species and multi-species model were used to assess the intervention between *C. albicans*, *S. mutans* and different doses of *L. plantarum* (10<sup>4</sup> – 10<sup>8</sup> CFU/ml).



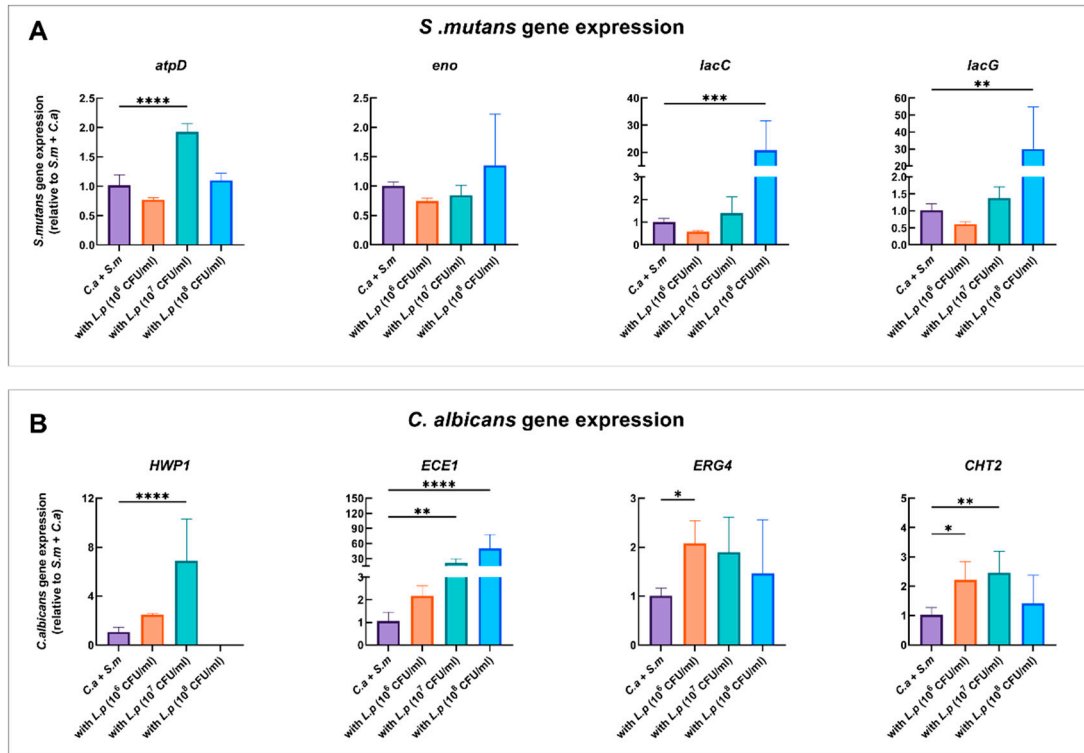
**Figure. S2. Changes of species composition in dual-species**

The composition of each microorganism in dual-species were showed. (A–E) The composition of *C. albicans* and *L. plantarum* in dual-species condition. (F–J) The composition of *S. mutans* and *L. plantarum* in dual-species condition.



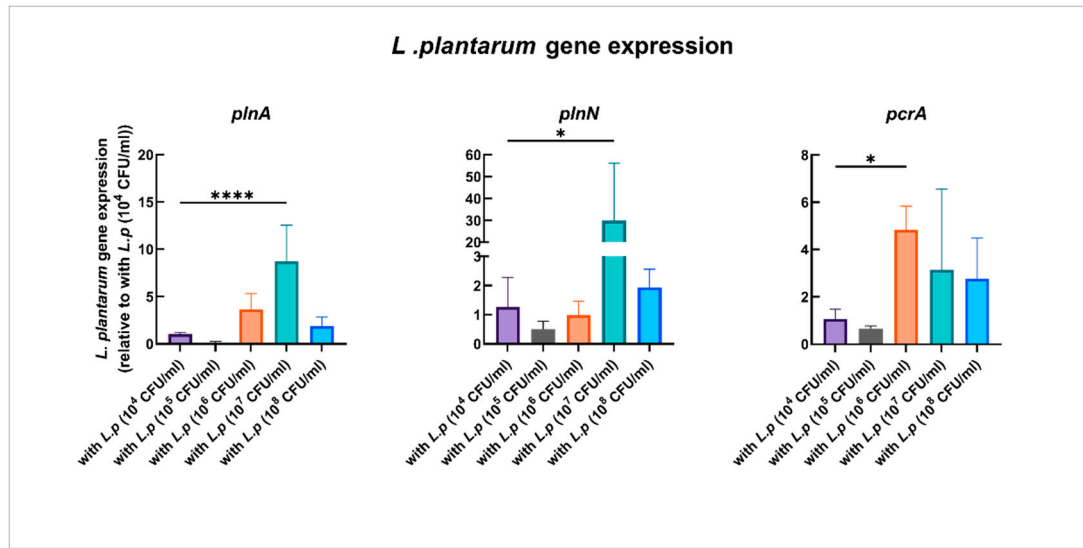
**Figure. S3. pH in culture media**

(A) pH in mono-species condition. (B) pH in *C. albicans* presence dual-species condition. (C) pH in *S. mutans* presence dual-species condition. (D) pH in multi-species condition. pH decreased faster and to lower value by adding a high concentration of  $10^8$  CFU/ml *L. plantarum*. The dotted line represents the control groups in each model. \* Indicates the pH values of other groups were significantly different from the pH values of the control group at 20 h ( $p < 0.05$ ).



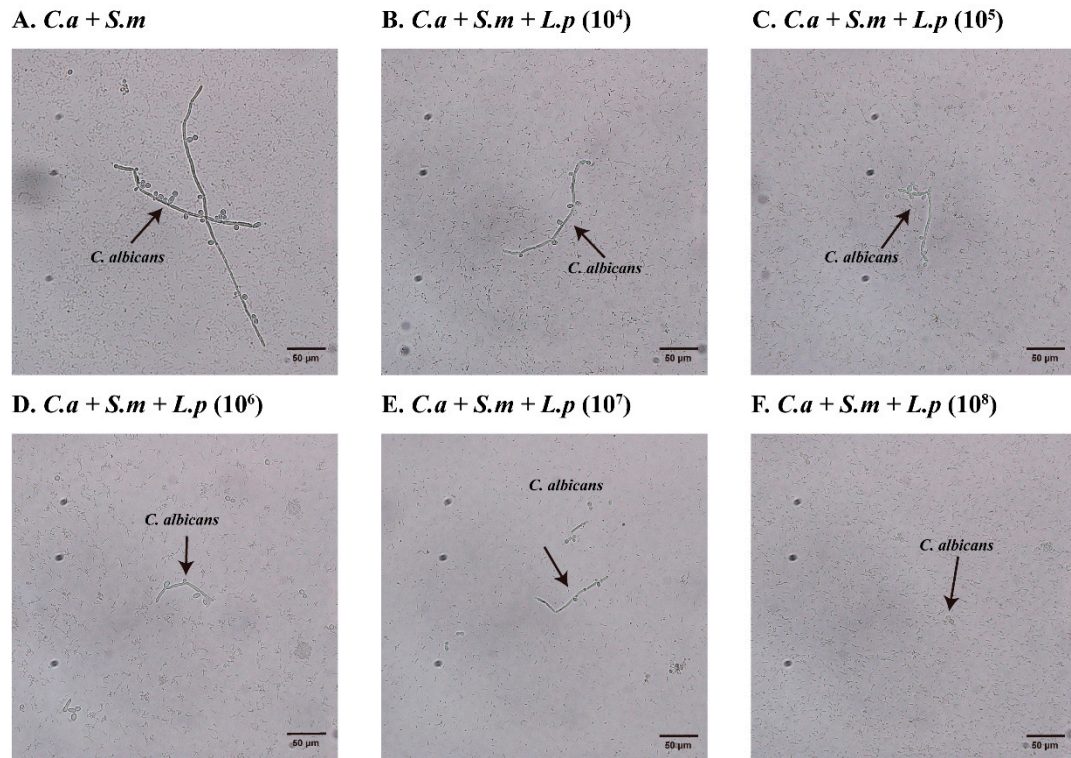
**Figure. S4. Effect of *L. plantarum* on the expression of *C. albicans* and *S. mutans* genes in multi-species model at six hours**

qRT-PCR was performed for *S. mutans* and *C. albicans* genes of interest for mixed-species culture at 6 h. *S. mutans* (A) and *C. albicans* (B) gene expression ratio was shown, the comparison was relative to *S. mutans* and *C. albicans* dual-species. p values were determined by one-way ANOVA with post hoc test. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ .



**Figure. S5. Dose-related expression of *L. plantarum* gene in multi-species model at twenty hours**

qRT-PCR was performed for *L. plantarum* genes of interest for mixed-species at 20 h. *L. plantarum* gene expression ratio was shown, the comparison was relative to  $10^4$  CFU/ml *L. plantarum* multi-species group. p values were determined by one-way ANOVA with post hoc test. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ .



**Figure S6: Dose-dependent inhibition of *C. albicans* hyphae formation by *L. plantarum* gene in multi-species model at  $\times 20$  magnification (A–F)**