

Supplementary material for the paper

Study on the microflora structure in *Litopenaeus vannamei*-*Sinonovacula constricta* tandem culture model based on high-throughput sequencing under different culture densities

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Table S1. Relative abundance of main bacterial groups in water

Genus	CS	MXS1	MXS2	MXS3	MXS4	MYS1	MYS2	MYS3	MYS4
uncultured_bacterium_									
f_Rhodobacteraceae	50.86±21.96a	21.61±1.97b	26.46±3.73b	20.10±0.24b	35.19±3.71ab	17.70±2.23b	26.98±2.59b	27.61±1.72b	19.71±14.08b
uncultured_bacterium_									
f_Cryomorphaceae	1.93±1.32c	14.20±4.59b	2.99±0.72c	2.86±0.31c	3.73±0.33c	29.23±5.61a	4.28±0.43c	4.22±0.68c	4.96±1.01c
NS3a_marine_group	1.40±0.76d	11.59±1.16ab	9.87±1.97b	5.02±0.11c	2.53±0.10cd	9.28±0.41b	14.25±2.36a	4.57±0.51c	2.00±0.24d
uncultured_bacterium_									
f_NS9_marine_group	0.47±0.34d	0.73±0.03d	4.57±0.88c	9.89±0.50a	4.21±0.80c	0.32±0.02d	4.58±0.53c	8.19±0.90b	3.51±0.68c
uncultured_bacterium_									
f_Saprospiraceae	0.22±0.14e	0.55±0.09e	3.11±1.31d	9.03±1.10a	4.80±0.38c	0.47±0.16e	4.65±0.33c	6.76±0.60b	3.17±0.84d
Nautella	0.20±0.10d	2.61±0.33c	8.10±1.23a	3.23±0.12c	0.77±0.04d	2.61±0.22c	7.66±0.87a	4.45±0.21b	0.42±0.21d
Aureimarina	0.93±0.53c	4.35±0.32a	2.67±0.79cd	3.69±0.19ab	2.00±0.06d	3.71±0.36ab	3.47±0.43abc	3.31±0.29bc	2.86±0.41bcd
uncultured_bacterium_									
f_Burkholderiaceae	0.17±0.09d	1.80±0.22c	6.78±0.53b	0.60±0.02d	1.49±0.15c	1.92±0.46c	7.64±0.08a	0.64±0.10d	1.44±0.61c
uncultured_bacterium_									
f_Flavobacteriaceae	2.10±1.20cde	4.64±0.40a	3.05±0.59cd	1.51±0.05e	1.97±0.33cde	3.53±0.19b	2.73±0.29bcd	1.19±0.14e	1.76±0.39de
Phaeodactylibacter	0.08±0.05c	0.01±0.00c	0.85±0.09c	5.76±0.52a	3.65±0.54b	0.06±0.01c	0.40±0.02c	4.80±0.48a	2.90±1.15b

Different letters in the same line represent significant differences between different groups ($p < 0.05$).

Table S2. Relative abundance of main bacterial groups in sediment

Genus	CN	MYN1	MYN2	MYN3	MYN4
uncultured_bacterium_f_Anaerolineaceae	3.51±2.15c	7.63±0.11bc	11.65±4.83ab	11.06±0.19ab	13.71±1.06a
Woeseia	3.80±2.91b	9.72±0.92a	7.99±3.19ab	11.14±0.46a	10.53±0.59a
uncultured_bacterium_f_Desulfobulbaceae	1.28±0.84d	3.82±0.28a	1.66±0.50cd	3.15±0.09ab	2.51±0.07bc
uncultured_bacterium_c_Gammaproteobacteriay	1.68±0.47c	2.67±0.19ab	2.04±0.48bc	3.22±0.09a	2.61±0.28ab
uncultured_bacterium_f_Rhodobacteraceae	2.23±1.74a	3.29±0.33a	1.87±0.67a	2.25±0.06a	2.46±0.14a
uncultured_bacterium_o_Gammaproteobacteria					
Incertae_Sedis	1.13±0.83b	2.79±0.42a	2.28±0.73ab	3.13±0.10a	2.67±0.25a
uncultured_bacterium_o_Actinomarinales	0.74±0.41b	2.06±0.13ab	3.00±1.39a	2.41±0.27ab	2.84±0.63a
uncultured_bacterium_f_Lachnospiraceae	6.64±4.18a	1.04±1.08ab	2.83±3.49ab	0.13±0.04b	0.11±0.02b
uncultured_bacterium_o_SBR1031	1.05±0.61b	1.93±0.09ab	1.93±0.70ab	2.32±0.41a	2.94±0.40a
uncultured_bacterium_o_Chloroplast	4.21±2.42a	1.37±0.43b	1.47±0.32b	1.82±0.15b	1.11±0.20b

Different letters in the same line represent significant differences between different groups ($p < 0.05$).

Table S3. Relative abundance of main flora in the visceral mass of *S. constricta*

Genus	CY	MY1	MY2	MY3	MY4
Lactococcus	10.61±3.92a	14.76±4.93a	16.97±1.37a	11.72±4.70a	16.72±1.90a
uncultured_bacterium_f_Lachnospiraceae	15.09±2.96a	5.71±1.61b	6.50±0.49b	10.43±6.02ab	6.99±1.05b

uncultured_bacterium_c_Subgroup_6	3.24±0.44a	3.28±0.73a	3.29±0.42a	4.87±1.94a	2.47±0.96a
uncultured_bacterium_f_Spirochaetaceae	0.26±0.16b	1.89±0.97b	3.95±1.31b	0.97±0.32b	8.62±4.04a
<i>Lactobacillus</i>	2.52±0.67a	3.02±0.93a	3.09±0.40a	2.75±0.67a	3.72±0.49a
<i>Alloprevotella</i>	4.45±0.93a	1.78±0.49b	2.07±0.22b	3.06±1.51ab	2.32±0.35b
uncultured_bacterium_f_Muribaculaceae	3.09±0.74a	1.98±0.21b	2.10±0.07b	3.35±0.56a	1.83±0.33b
<i>Mycoplasma</i>	0.00±0.00a	10.06±13.30a	0.06±0.04a	0.13±0.14a	0.03±0.02a
<i>Dongia</i>	1.27±0.30a	2.24±0.58a	2.26±0.25a	1.89±0.80a	1.86±0.07a
Lachnospiraceae_NK4A136_group	2.18±0.33a	1.21±0.30b	1.60±0.06ab	1.82±0.55ab	1.58±0.04ab

Different letters in the same line represent significant differences between different groups ($p < 0.05$).

Table S4. Relative abundance of major intestinal flora of *L. vannamei*

Genus	CX	MX1	MX2	MX3	MX4
<i>Lactococcus</i>	6.69±0.66a	13.92±1.26a	10.79±6.76a	16.29±4.94a	11.32±2.77a
uncultured_bacterium_f_Lachnospiraceae	9.41±0.53a	7.24±3.15a	7.40±2.76a	6.93±1.16a	7.41±3.33a
uncultured_bacterium_c_Subgroup_6	3.44±0.19a	4.66±0.85a	3.30±2.19a	3.70±1.18a	4.94±1.70a
<i>Alloprevotella</i>	3.38±0.27a	2.37±0.93a	6.21±5.92a	4.07±3.06a	2.11±0.60a
uncultured_bacterium_f_Muribaculaceae	3.21±0.27a	2.43±0.16a	5.43±4.54a	3.13±1.56a	2.94±0.93a
uncultured_bacterium_f_Flavobacteriaceae	15.81±1.25a	0.07±0.06b	0.03±0.02b	0.04±0.04b	0.05±0.01b
<i>Lactobacillus</i>	1.78±0.21b	2.52±0.14ab	2.94±1.08ab	3.48±0.52a	2.51±0.31ab
<i>Photobacterium</i>	0.86±0.33a	2.48±1.11a	0.18±0.15a	0.17±0.06a	6.99±8.90a
Lachnospiraceae_NK4A136_group	1.65±0.16a	1.49±0.26a	2.58±2.02a	1.94±0.84a	1.43±0.18a
uncultured_bacterium_o_Chloroplast	0.98±0.09a	1.87±0.23a	1.47±0.89a	1.61±0.53a	1.83±0.35a

Different letters in the same line represent significant differences between different groups ($p < 0.05$).

Table S5. Alpha diversity index of each *L. vannamei* intestinal content sample at the OTU level

	Shannon index	Simpson index	ACE index	Chao1 index
CX	7.31±0.10a	0.966±0.003a	949.40±6.01b	983.93±21.52b
MX1	7.79±0.09a	0.975±0.003a	1030.60±17.85ab	1078.29±9.88ab
MX2	7.31±0.46a	0.970±0.004a	957.77±20.21b	1069.43±111.07ab
MX3	7.60±0.15a	0.965±0.008a	1151.67±102.15a	1205.12±79.33a
MX4	7.59±0.31a	0.969±0.013a	1009.53±23.04ab	1046.91±32.40ab

Different letters in the same line represent significant differences between different groups ($p < 0.05$).

Table S6. Alpha diversity index of the visceral mass samples of each *S. constricta* at the OTU level

	Shannon index	Simpson index	ACE index	Chao1 index
CY	7.52±0.07a	0.977±0.003a	1135.98±85.18a	1173.43±97.56a
MY1	7.13±0.31a	0.957±0.006b	941.29±22.11b	985.56±36.43bc
MY2	7.62±0.08a	0.967±0.003ab	1111.05±32.08a	1136.69±19.82ab
MY3	7.60±0.17a	0.976±0.002a	892.84±11.63b	926.23±22.21c
MY4	7.24±0.05a	0.961±0.003b	1031.83±47.10ab	1070.64±35.12abc

Different letters in the same line represent significant differences between different groups ($p < 0.05$).

Table S7. Alpha diversity index of water samples at OTU level

	Shannon index	Simpson index	ACE index	Chao1 index
CS	4.90±0.84b	0.825±0.068b	1246.60±62.68ab	1226.36±57.28ab
MXS1	5.54±0.12ab	0.947±0.006a	1258.79±13.67ab	1123.76±67.85ab
MXS2	5.45±0.13b	0.942±0.005a	1030.56±92.67bc	1036.15±65.01b
MXS3	6.01±0.04ab	0.964±0.001a	1216.33±41.94abc	1016.47±24.79b
MXS4	5.78±0.19ab	0.923±0.011a	1157.07±104.93abc	1108.07±58.05ab
MYS1	4.92±0.31b	0.893±0.024ab	933.19±45.21c	964.51±46.54b
MYS2	5.13±0.06b	0.933±0.003a	1052.30±69.94bc	971.52±29.17b
MYS3	5.97±0.05ab	0.961±0.002a	1214.57±179.34abc	1159.28±188.77ab
MYS4	6.85±0.77a	0.957±0.028a	1383.79±116.80a	1322.76±21.99a

Different letters in the same line represent significant differences between different groups ($p < 0.05$).

Table S8. Alpha diversity index of sediment samples at OTU level

	Shannon index	Simpson index	ACE index	Chao1 index
CN	8.554±0.110a	0.9895±0.0002c	1475.09±9.23a	1483.92±21.03a
MYN1	8.635±0.097a	0.9935±0.0005a	1471.54±12.85a	1470.19±12.53a
MYN2	8.492±0.158a	0.9898±0.0005c	1353.14±104.85ab	1328.85±118.15ab
MYN3	8.503±0.004a	0.9927±0.0001a	1303.78±74.00ab	1272.99±47.33b
MYN4	8.395±0.026a	0.9914±0.0004b	1259.54±23.70b	1230.75±10.38b

Different letters in the same line represent significant differences between different groups ($p < 0.05$).