

Figure S1. Change in dominant rhizosphere fungal taxa at the phylum level across different nutrient treatments and melon growth stages.

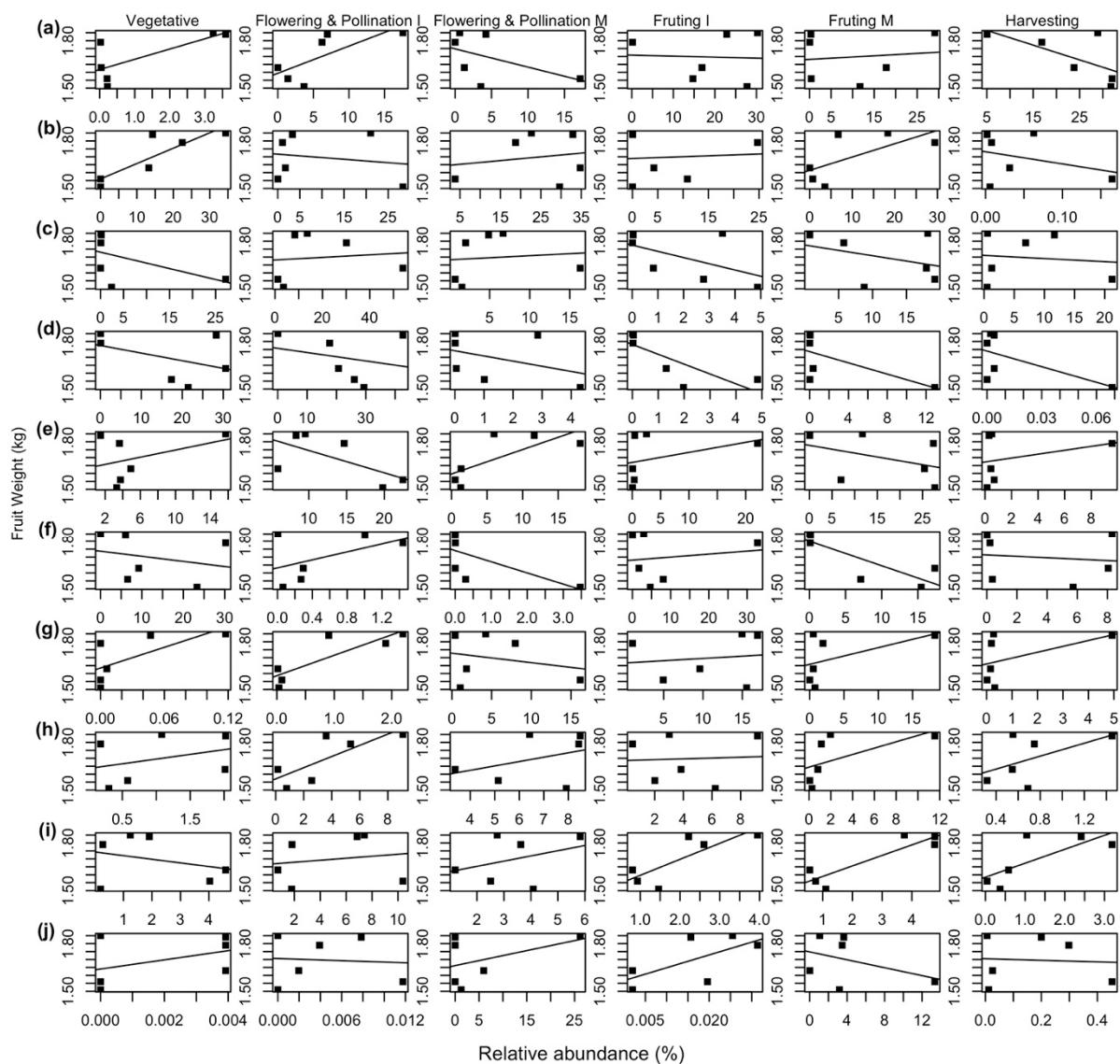


Figure S2. Linear regression between selected bacterial genera and fruit weight. (a) – (j): *Brevibacillus*, *Chryseobacterium*, *Pseudomonas*, *Massilia*, *Bacillus*, *B.C.Paraburkholderia*, *Lysobacter*, *Bosea*, *A.N.P.Rhizobium*, and *Enterobacter*

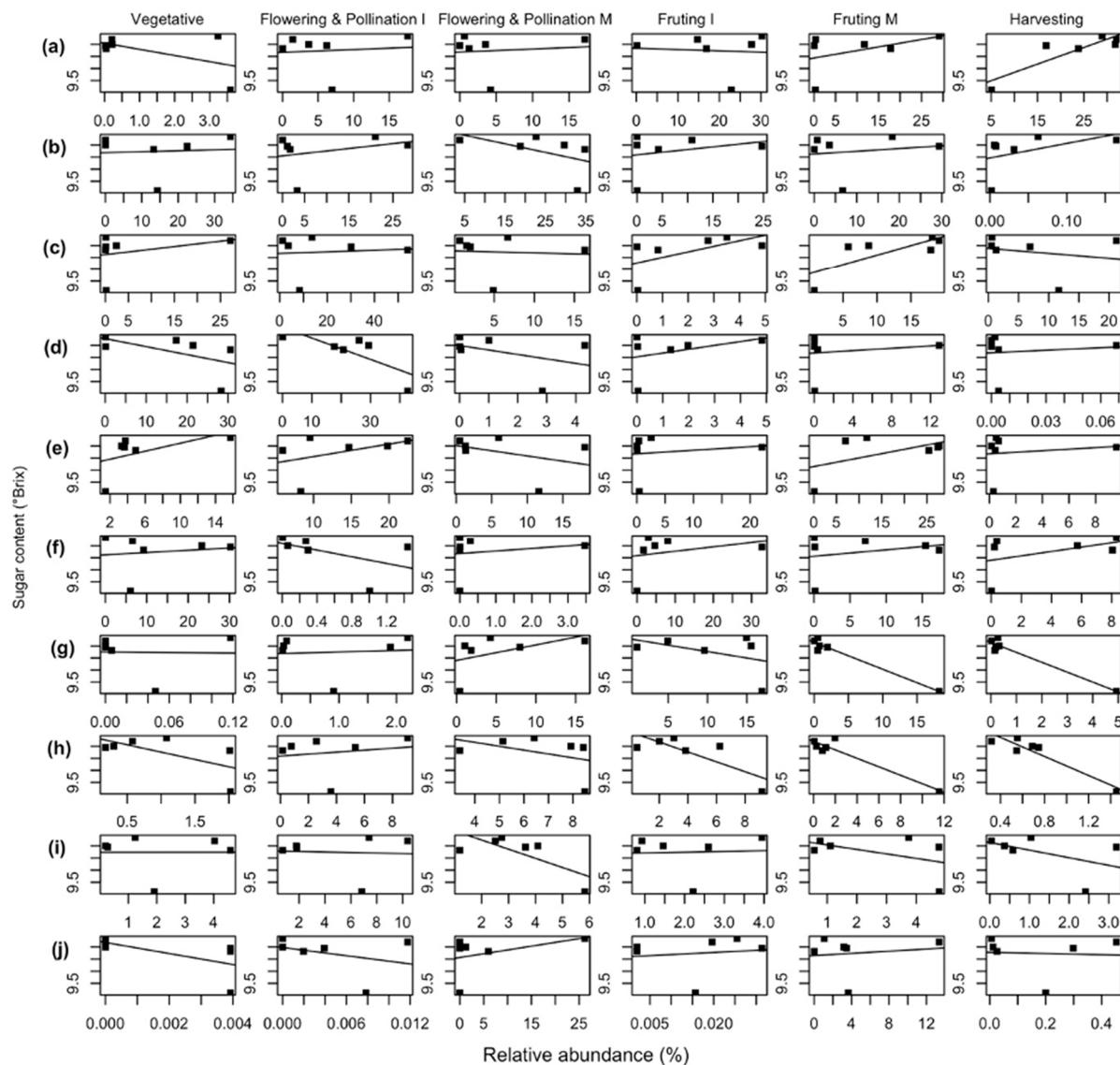


Figure S3. Linear regression between selected bacterial genera and fruit sweetness. (a) – (j): *Brevibacillus*, *Chryseobacterium*, *Pseudomonas*, *Massilia*, *Bacillus*, *B.C.Paraburkholderia*, *Lysobacter*, *Bosea*, *A.N.P.Rhizobium*, and *Enterobacter*

Table S1. Square of the correlation between relative abundance of bacteria genera and fruit weight. * $p < 0.05$.

	Vegetative	Flowering & Pollination I	Flowering & Pollination M	Fruting I	Fruting M	Harvesting
Brevibacillus	0.55	0.53	0.25	0.00	0.01	0.43
Chryseobacterium	0.75*	0.03	0.03	0.01	0.44	0.10
Pseudomonas	0.26	0.01	0.01	0.28	0.12	0.01
Massilia	0.19	0.06	0.16	0.62	0.39	0.36
Bacillus	0.15	0.40	0.54	0.14	0.15	0.10
Burkholderia_Caball eronia_Paraburkhold eria	0.06	0.24	0.44	0.02	0.70*	0.01
Lysobacter	0.48	0.72*	0.06	0.02	0.26	0.23
Bosea	0.11	0.60	0.14	0.00	0.35	0.28
Allorhizobium_Neor hizobium_Pararhizo bium_Rhizobium	0.08	0.03	0.12	0.65	0.81*	0.55
Enterobacter	0.17	0.01	0.19	0.43	0.16	0.00

Table S2. Square of the correlation between relative abundance of bacteria genera and fruit sweetness. * $p < 0.05$

	Vegetative	Flowering & Pollination I	Flowering & Pollination M	Fruting I	Fruting M	Harvesting
Brevibacillus	0.28	0.01	0.01	0.01	0.20	0.78*
Chryseobacterium	0.00	0.09	0.25	0.07	0.03	0.21
Pseudomonas	0.09	0.01	0.00	0.33	0.56	0.04
Massilia	0.29	0.58	0.17	0.13	0.02	0.01
Bacillus	0.27	0.18	0.14	0.02	0.27	0.02
Burkholderia_Caballer onia_Paraburkholderia	0.02	0.24	0.03	0.08	0.07	0.20
Lysobacter	0.00	0.01	0.22	0.18	0.96*	0.94*
Bosea	0.38	0.03	0.16	0.62	0.90*	0.88*
Allorhizobium_Neorhi zobium_Pararhizobiu m_Rhizobium	0.00	0.00	0.53	0.00	0.21	0.23
Enterobacter	0.36	0.11	0.16	0.02	0.02	0.00