

1 **Supplemental Material**

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3 **Supplemental Table 1:** Number of reads at each step of sequence data processing for

4 *Experiment 1.*

Processing Step	Number of Reads
Quality Filtering and Chimera Removal	10,250,881
OTU Picking	7,932,440
Sample Filtering	6,637,351
Rarefaction at 100,000 Reads / Sample	3,700,000

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6 **Supplemental Table 2:** Number of reads at each step of sequence data processing for

7 *Experiment 2.*

Processing Step	Number of Reads
Quality Filtering and Chimera Removal	6,487,790
OTU Picking	5,007,234
Sample Filtering	4,267,285
Rarefaction at 116,000 Reads / Sample	2,668,000

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9 **Supplemental Table 3:** Significant differences exist in rhizosphere community structure

10 between day vs. night time points based on Bray-Curtis dissimilarities and adonis tests.

	df	F Statistic	R ²	p-value
Time Point	1, 15	3.433	0.186	0.001

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12 **Supplemental Table 4:** Significant differences are observed in rhizosphere community
 13 composition between clock genotypes based on Jaccard dissimilarities and adonis tests.

	df	F Statistic	R ²	p-value
Genotype	2, 20	2.769	0.191	0.001

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 15 **Supplemental Table 5:** Significant differences are observed in rhizosphere community structure
 16 between clock genotypes based on Bray-Curtis dissimilarities and adonis tests.

	df	F Statistic	R ²	p-value
Genotype	2, 20	2.772	0.217	0.001

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 18 **Supplemental Table 6:** Effect of culling OTUs by minimum read numbers on Jaccard and Bray-
 19 Curtis dissimilarities. Column 1 indicates the minimum read number or range for OTU culling.
 20 Column 2 indicates total reads per sample once OTUs with a given read number or range are
 21 selected. P-values are provided for Jaccard and Bray-Curtis dissimilarities. Both common and
 22 rare taxa are influenced by plant genotype (df =2, 20).

Read Threshold or Range	Rarefaction	p-value (Jaccard)	p-value (Bray-Curtis)
1	116,000	0.001	0.001
10	115,000	0.001	0.001
50	113,000	0.001	0.001
100	111,000	0.001	0.001
500	103,000	0.001	0.001
1,000	98,000	0.001	0.001
Range 1-500	13,000	0.001	0.001

23 **Supplemental Table 7:** Indicator OTUs associated with the *toc1-21* rhizosphere, IndVal
 24 statistic, and p-value. OTUs often could not be identified to the species level. The lowest
 25 phylogenetic level to which we could identify an OTU is indicated by the use of o (for order), f (for
 26 family), or g (for genus).

OTU	Phylum (relative abundance)	IndVal Statistic	p-value
Gemmatimonadales;o_;f_;g_	Gemmatimonadetes	0.899	0.010
Beijerinckia	Proteobacteria	0.866	0.015
Chloracidobacteria;o_;f_;g_	Acidobacteria	0.770	0.010
Barnesiellaceae;g_	Bacteroidetes	0.707	0.010
Pseudoramibacter	Firmicutes	0.707	0.010
Lachnospira	Firmicutes	0.707	0.035
Polyangiaceae;g_	Proteobacteria	0.707	0.020
Rickettsia	Proteobacteria	0.640	0.045
Legionellales;f_;g_	Proteobacteria	0.572	0.050

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 28 **Supplemental Table 8:** Indicator OTUs associated with the *ztl-30* rhizosphere, IndVal statistic,
 29 and p-value.

OTU	Phylum (relative abundance)	IndVal Statistic	p-value
Dyella	Proteobacteria	0.935	0.005
Mycetocola	Actinobacteria	0.934	0.005
Klebsiella	Proteobacteria	0.905	0.005
Pantoea	Proteobacteria	0.789	0.035
Cytophagales;g_	Bacteroidetes	0.655	0.045

31 **Supplemental Table 9:** Indicator OTU from Lefse analysis for all rhizospheres.

OTU	LDA	Genotype
MIZ46lf;f_;g_	2.78	<i>toc1-21</i>
WD2101;f_;g_	2.84	<i>toc1-21</i>
Novosphingobium	3.38	<i>toc1-21</i>
iii1_15;f_;g_	2.39	Ws
Solibacterales;f_;g_	2.79	Ws
Chloroflexi	2.51	Ws
Acidobacteria	3.41	Ws
Xanthomonadaceae	2.98	<i>ztl-30</i>
Micrococcaceae;g_	2.70	<i>ztl-30</i>
Tatlockia	2.62	<i>ztl-30</i>
Bacteriovoracaceae;g_	3.04	<i>ztl-30</i>
Erythrobacteraceae;g_	3.16	<i>ztl-30</i>
Nocardiodaceae;g_	3.76	<i>ztl-30</i>
Azospirillum	2.95	<i>ztl-30</i>

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33 **Supplemental Table 10:** There were not significant differences in community size as measured
 34 by extracted DNA yield divided by soil mass.

	df	F Statistic	p-value
Genotype	2, 19	2.49	0.11

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37 **Supplemental Table 11:** Soil pH based on overstory history.

Overstory History	pH
<i>toc1-21</i>	5.21
Ws	5.30
<i>ztl-30</i>	5.20

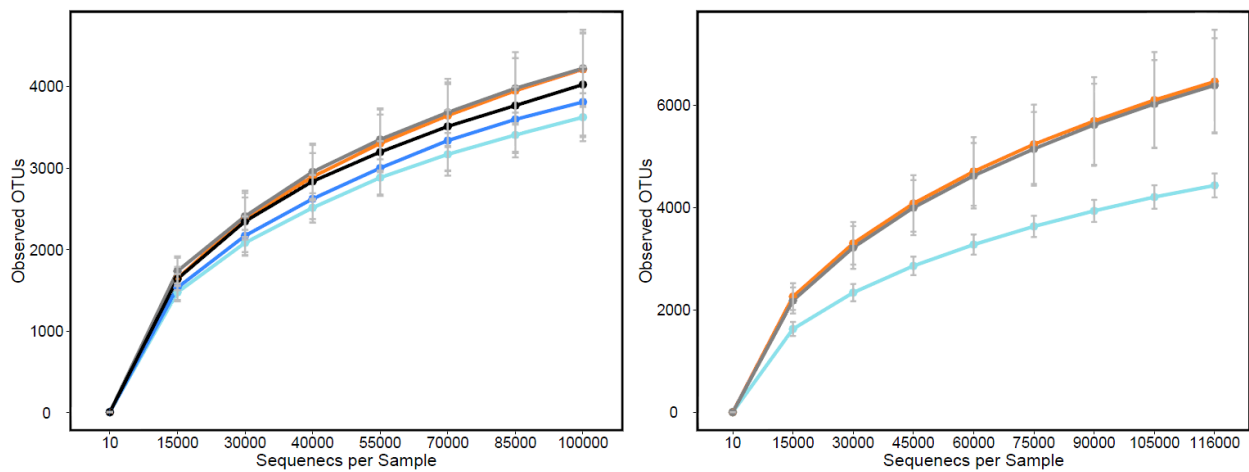
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39 **Supplemental Figure 1:** Rarefaction based on observed OTUs for *Experiments 1* and 2. A)

40 *Experiment 1:* rarefaction to 100,000 reads. The lines represent 6 A.M. (light blue), 12 P.M.

41 (orange), 6 P.M. (gray), 12 A.M. (blue), and 6 A.M. (black). (B) *Experiment 2:* rarefaction to

42 116,000 reads. The lines represent the genotypes Ws (orange), *toc1-21* (blue), and *ztl-30* (gray).



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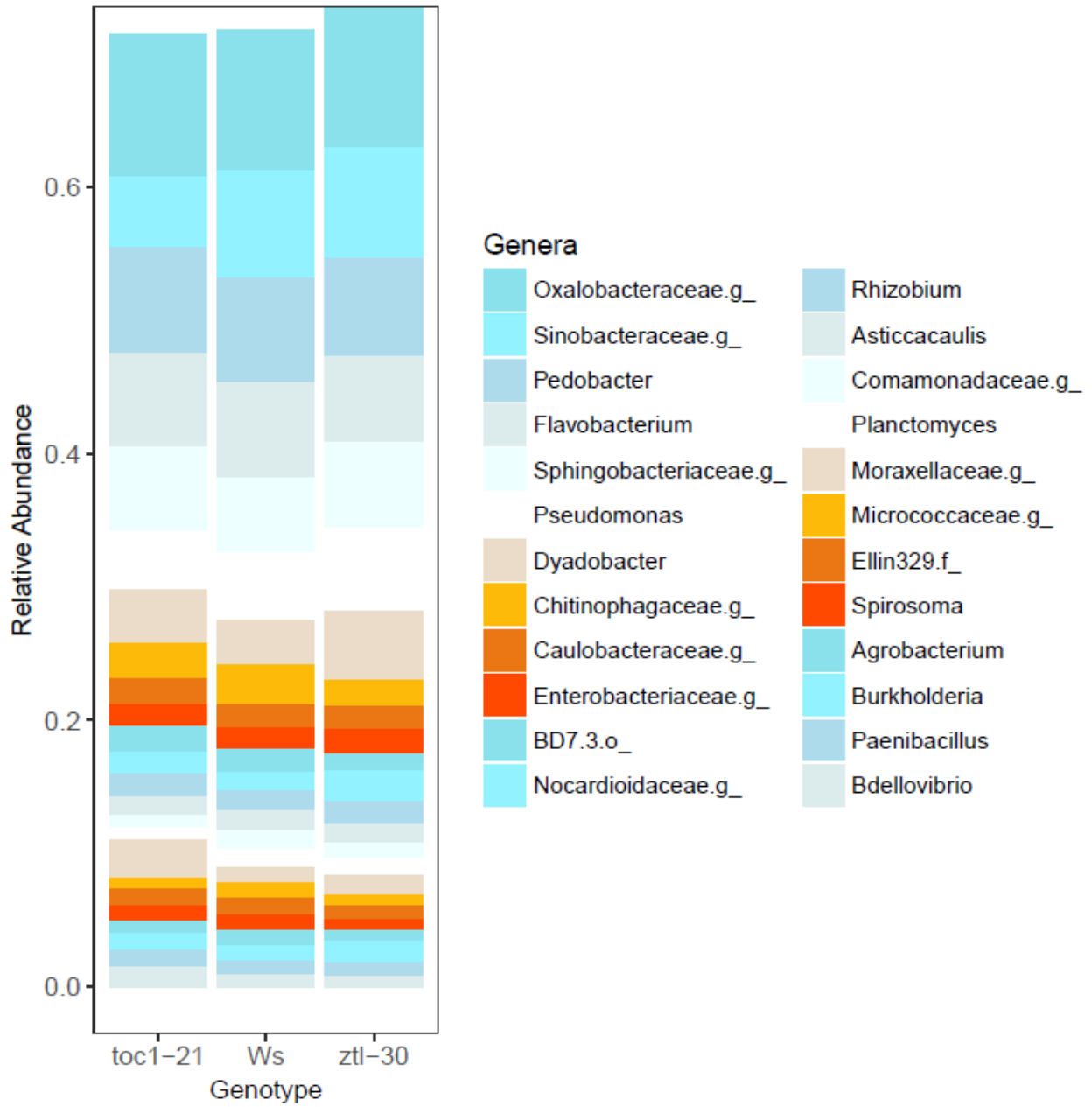
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50 **Supplemental Figure 2:** Relative abundance of taxa with greater than 1% relative abundance
 51 across genotypes.



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