

*The following supplement accompanies the article*

## **Succession of bacteria and fungi in leaf litter of tree hole habitats: responses of diversity to mosquito larvae**

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*Aquatic Microbial Ecology* 83: 237–250 (2019)

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Table S1. Community development time for replicates (separated by commas) within each treatment. Development time includes conditioning period.

<b>Treatment</b>	<b>Development time (days)</b>
3D/initial	3,3,3
3D/no larvae	51,51,51
3D/larvae	28,34,29
1M/initial	30,30,30
1M/no larvae	89,89,89
1M/larvae	52,54,56

Table S2. Relative abundance (%) of 3 most abundant bacterial OTUs from initial (I), no larvae (NL), and larvae (L) communities. Phyla (or class in the case of Proteobacteria) are in bold.

	Loosely adhered communities						Imbedded communities					
	3D			1M			3D			1M		
	I	NL	L	I	NL	L	I	NL	L	I	NL	L
<b>Bacteroidetes</b>												
<i>Flavobacterium</i>						8				12		10
Family Chitinophagaceae			19	5	30	23					12	13
<b>Cyanobacteria</b>												
Order Streptophyta									2			
<b>Firmicutes</b>												
<i>Clostridium</i>	34			31			8					
<b>Alphaproteobacteria</b>												
<i>Sphingobium</i>		6	7									
<i>Sphingomonas</i>									27			
<b>Betaproteobacteria</b>												
Family Comamonadaceae		7	15					12	20			
Family Neisseriaceae				5	11					13	8	18
<i>Methylibium</i>								7				
<b>Deltaproteobacteria</b>												
Order Myxococcales											14	
<b>Gammaproteobacteria</b>												
Family Enterobacteriaceae	45	11		6			86	9	6	14		
<i>Pseudomonas</i>	10											
Family Sinobacteraceae					9							
<b>Total Relative Abundance of 3 most abundant OTUs</b>	<b>89</b>	<b>24</b>	<b>41</b>	<b>42</b>	<b>44</b>	<b>42</b>	<b>96</b>	<b>28</b>	<b>53</b>	<b>39</b>	<b>34</b>	<b>41</b>

Table S3. Relative abundance (%) of 3 most abundant fungal OTUs from initial (I), no larvae (NL), and larvae (L) communities. Phyla are in bold. When 2 of the most abundant OTUs were given the same identity, relative abundances of both OTUs are shown separated by a comma.

	Loosely Adhered Communities						Imbedded communities							
	3D			1M			3D			1M				
	I	NL	L	I	NL	L	I	NL	L	I	NL	L		
<b>Ascomycota</b>														
Family Dothioraceae	28						34							
Family Pleosporaceae				8			16			21,11				
<i>Pleosporales unknown species</i> [SH186930.07FU]							9			19				
<i>Pseudeurotiaceae unknown species</i> [SH190079.07FU]	10													
Class Leotiomyces										9				
<i>Ascomycota unknown species</i> [SH217942.07FU]							13							
<i>Ascomycota unknown species</i> [SH186928.07FU]	11,11		10,10	13,12		14,13	17,17		21,20		13, 13		8	12,11
<b>Basidiomycota</b>														
<i>Cryptococcus wieringae</i> [SH221435.07FU]	18													
Unidentified fungi	6		31											
Unassigned				13		8								
<b>Total Relative Abundance of 3 most abundant OTUs</b>	<b>56</b>	<b>28</b>	<b>51</b>	<b>38</b>	<b>35</b>	<b>42</b>	<b>63</b>	<b>50</b>	<b>51</b>	<b>39</b>	<b>25</b>	<b>38</b>		

Table S4. Comparisons of bacterial community composition using PERMANOVA for each prediction. Bolded P values are significant ( $\leq 0.05$ ). The levels within the factor “type” are loosely adhered and imbedded communities and levels within the factor “community stage” are 3D and 1M communities. The levels of the factor “manipulation” are indicated for each prediction as initial (I), no larvae (NL), or larvae (L) communities.

Comparison of early-stage and well-developed communities (Prediction 1)						
	df	Sums of Squares	Mean Sum of squares	F Model	R <sup>2</sup>	P
<i>type</i>	1	0.405	0.405	2.921	0.125	<b>0.045</b>
<i>community stage</i>	1	1.427	1.427	10.290	0.440	<b>0.001</b>
<i>type*stage</i>	1	0.304	0.304	2.190	0.094	0.083
<i>Residuals</i>	8	1.110	0.139		0.342	
<i>Total</i>	11	3.246			1	

  

Changes in early-stage and well-established communities over succession (Prediction 2)						
	df	Sums of Squares	Mean Sum of squares	F Model	R <sup>2</sup>	P
<i>type</i>	1	0.373	0.373	2.148	0.049	<b>0.028</b>
<i>community stage</i>	1	1.491	1.491	8.588	0.196	<b>0.001</b>
<i>Manipulation (I vs NL)</i>	1	1.568	1.568	9.031	0.207	<b>0.001</b>
<i>type* stage</i>	1	0.274	0.274	1.575	0.036	0.112
<i>type*manipulation</i>	1	0.264	0.264	1.522	0.035	0.114
<i>stage *manipulation</i>	1	0.843	0.843	4.854	0.111	<b>0.001</b>
<i>type*stage*manipulation</i>	1	0.173	0.173	0.994	0.023	0.391
<i>Residuals</i>	15	2.605	0.174		0.343	
<i>Total</i>	22	7.591			1	

  

Larvae effects on succession of early-stage and well-established communities (Prediction 3)						
	df	Sums of Squares	Mean Sum of squares	F Model	R <sup>2</sup>	P
<i>type</i>	1	0.383	0.383	2.240	0.047	<b>0.028</b>
<i>community stage</i>	1	1.582	1.582	9.248	0.196	<b>0.001</b>
<i>Manipulation (I vs L)</i>	1	1.639	1.639	9.576	0.203	<b>0.001</b>
<i>type* stage</i>	1	0.294	0.294	1.718	0.036	0.098
<i>type*manipulation</i>	1	0.303	0.303	1.769	0.038	0.086
<i>stage*manipulation</i>	1	0.895	0.895	5.232	0.111	<b>0.001</b>
<i>type* stage*manipulation</i>	1	0.243	0.243	1.422	0.030	0.152
<i>Residuals</i>	16	2.738	0.171		0.339	
<i>Total</i>	23	8.077			1	

Table S5. Comparisons of fungal community composition using PERMANOVA for each prediction. Bolded P values are significant ( $\leq 0.05$ ). The levels within the factor “type” are loosely adhered and imbedded communities and levels within the factor “community stage” are 3D and 1M communities. The levels of the factor “manipulation” are indicated for each prediction as initial (I), no larvae (NL), or larvae (L) communities.

Comparison of early-stage and well-developed communities (Prediction 1)						
	df	Sums of Squares	Mean Sum of squares	F Model	R <sup>2</sup>	P
<i>type</i>	1	0.499	0.499	4.120	0.164	<b>0.012</b>
<i>community stage</i>	1	1.426	1.426	11.753	0.469	<b>0.001</b>
<i>type*stage</i>	1	0.143	0.143	1.175	0.047	0.294
<i>Residuals</i>	8	0.970	0.121		0.320	
<i>Total</i>	11	3.037			1	
Changes in early-stage and well-established communities over succession (Prediction 2)						
	df	Sums of Squares	Mean Sum of squares	F Model	R <sup>2</sup>	P
<i>type</i>	1	0.573	0.573	3.965	0.086	<b>0.002</b>
<i>community stage</i>	1	0.912	0.912	6.306	0.137	<b>0.001</b>
<i>manipulation</i>	1	1.292	1.292	8.937	0.194	<b>0.001</b>
<i>type*stage</i>	1	0.196	0.196	1.354	0.029	0.235
<i>type*manipulation</i>	1	0.306	0.306	2.115	0.046	0.068
<i>stage*manipulation</i>	1	0.866	0.866	5.985	0.130	<b>0.001</b>
<i>type*stage*manipulation</i>	1	0.194	0.194	1.338	0.029	0.202
<i>Residuals</i>	16	2.314	0.145		0.348	
<i>Total</i>	23	6.652			1	
Larvae effects on succession of early-stage and well-established communities (Prediction 3)						
	df	Sums of Squares	Mean Sum of squares	F Model	R <sup>2</sup>	P
<i>type</i>	1	0.787	0.787	6.888	0.128	<b>0.001</b>
<i>community stage</i>	1	1.105	1.105	9.669	0.180	<b>0.001</b>
<i>manipulation</i>	1	1.052	1.052	9.204	0.172	<b>0.001</b>
<i>type*stage</i>	1	0.254	0.254	2.219	0.041	<b>0.047</b>
<i>type*manipulation</i>	1	0.303	0.303	2.648	0.049	<b>0.030</b>
<i>stage*manipulation</i>	1	0.640	0.640	5.603	0.104	<b>0.001</b>
<i>type*stage*manipulation</i>	1	0.164	0.164	1.434	0.027	0.180
<i>Residuals</i>	16	1.829	0.114		0.298	
<i>Total</i>	23	6.134			1	