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Permalink
https://escholarship.org/uc/item/4t18476q

Journal
Oikos, 127(3)

ISSN
0030-1299

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Publication Date
2018-03-01

DOI
10.1111/oik.04243

Peer reviewed
Priority effects can persist across floral generations in nectar microbial metacommunities

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The order of species arrival can influence how species interact with one another and, consequently, which species may coexist in local communities. This phenomenon, called priority effects, has been observed in various types of communities, but it remains unclear whether priority effects persist over the long term spanning multiple generations of local communities in metacommunities. Focusing on bacteria and yeasts that colonize floral nectar of the sticky monkey flower, *Mimulus aurantiacus*, via hummingbirds and other flower-visiting animals, we experimentally manipulated initial microbial dominance on plants (regarded as metacommunities) to examine whether its effects persisted across multiple generations of flowers (regarded as local microbial habitats). The experimental introduction of *Neokomagataea* (= *Gluconobacter*) bacteria and *Metschnikowia* yeasts into wild flowers showed that the effects of initial dominance were observable across multiple floral generations. Three weeks after introduction, corresponding approximately to three floral generations, *Neokomagataea* introduction led to exclusion of yeasts, whereas *Metschnikowia* introduction did not result in the exclusion of *Neokomagataea*. Our results suggest that, even when local habitats are ephemeral, priority effects may influence multiple generations of local communities within metacommunities.

The order of species arrival during community assembly can promote or limit species coexistence (Palmgren 1926, Sutherland 1974, Drake 1991). These effects, termed priority effects, have been reported in a range of organisms, including plants (Grman and Suding 2010), animals (Alford and Wilbur 1985), fungi (Kennedy and Bruns 2005), protists (Louette and De Meester 2007) and bacteria (Devevey et al. 2015). These studies have shown that species that arrive early influence community development by competitively suppressing later colonizers or by modifying habitat conditions to some species’ favor and not others’ (Fukami 2015).

Although local priority effects are well studied, relatively little is known about whether priority effects persist over time across ephemeral local communities (Pu and Jiang 2015). In most previous studies of priority effects, the observed communities are persistent (i.e. they do not disappear during the period of the study), but many natural meta-communities are characterized by a high turnover of local habitat patches with frequent patch formation and extinction (e.g. pitcher plants colonized by aquatic invertebrates and animal carcasses colonized by terrestrial invertebrates) (Ellis et al. 2006, Vanschoenwinkel et al. 2008a, Ripley and Simovich 2009). Knowledge of such patch dynamics is well recognized as essential for predicting species extinction resulting from habitat destruction that creates increasingly patchy landscapes (De Meester et al. 2005, Tscharntke et al. 2007). Thus, studies that inform whether the effects of initial dominance by specific species persist across ephemeral communities over multiple generations of local habitat patches are not only of fundamental interest, but also have applied importance. To our knowledge, however, no experimental test has been conducted.

In this study, we examine whether priority effects persist across ephemeral communities of bacteria and yeasts that colonize floral nectar of wild plants. Nectar-inhabiting microbes disperse across flowers via flower-visiting animals (Brysch-Herzberg 2004, Herrera et al. 2010, Belisle et al. 2012, Jacquemyn et al. 2013, Schaeffer and Irwin 2014). Local communities of nectar microbes are highly ephemeral as the host flowers inevitably disappear as they wither, but the collection of flowers on a host plant functions as a microbial metacommunity that lasts longer than individual flowers while the plant is in bloom (Belisle et al. 2012). Previous studies have suggested that nectar microbial communities of our study plant, the sticky monkey flower *Mimulus aurantiacus* (Phrymaceae), is dominated by *Neokomagataea* bacteria (Acetobacteraceae) (formerly recognized as *Gluconobacter*) and *Metschnikowia* yeasts.
(Metschnikowiaceae) (Vannette et al. 2013, Tucker and Fukami 2014). We have also shown in an experiment that priority effects can be strong between Neokomagataea sp. and Metschnikowia reukaufii (Tucker and Fukami 2014). In this experiment, priority effects were mutually negative, and whichever species arrived first reduced the abundance of the other that arrived later, in both the presence and absence of temperature fluctuations. However, this study was conducted in laboratory microcosms with artificial nectar, and it remains unclear how strongly priority effects may influence microbes in real nectar in the field. Here we report the results of a field experiment with wild M. aurantiacus plants, in which we experimentally introduced Neokomagataea bacteria or Metschnikowia yeasts into flowers early in the flowering season. We then investigated whether these microbes persisted despite frequent turnover of local communities.

Material and methods

Experiment

The experiment was conducted at the Turchet Leaseland, land owned by Stanford University, located in the Santa Cruz Mountains of California, USA (37°38′8″N, 122°19′4″W). This site mainly consisted of oak woodland and chaparral habitats similar to those found at the nearby Jasper Ridge Biological Preserve of Stanford Univ. (JRBP), described in Belisle et al. (2012) and Vannette et al. (2013). Within a 2.4-ha area at the site, 24 individuals of Mimulus aurantiacus were tagged and monitored through the plant’s flowering season in 2013, which lasted from April to June (Supplementary material Appendix 1). Each of the 24 Mimulus individuals was assigned to one of the following three experimental treatments: Neokomagataea bacterium introduction treatment (eight individuals), Metschnikowia fungus (yeast) introduction treatment (eight individuals), and control (sham introduction of species) treatment (eight individuals).

The treatments were assigned to plants in a stratified random fashion so as to have the treatments evenly spread spatially (Supplementary material Appendix 1). We regarded plant individuals as each representing a microbial metacommunity consisting of multiple flowers each harboring a local community of nectar microbes. Bacterial and fungal species disperse among local communities (flowers) by Anna’s hummingbird Calypte anna, the primary pollinator of M. aurantiacus at the study site (Belisle et al. 2012, Vannette et al. 2013), and other flower visitors. Besides Anna’s hummingbird, Allen’s hummingbird Selasphorus sasin, Rufous hummingbird Selasphorus rufus, bees (e.g. Bombus vosnesenskii, Ceratina acanthia and Xylocopa micans), and thrips visit M. aurantiacus flowers (Vannette et al. 2013). Nectar microbes could also disperse from other external environments, e.g. pollen, phyloplane, and air (Belisle et al. 2012, Vannette and Fukami 2017). The three treatments represented metacommunities with Neokomagataea priority-effects, those with Metschnikowia priority-effects, and those with no experimental priority effects, respectively.

To examine possible effects of floral visits by hummingbirds (and other large pollinators), we divided flowers of each plant individual into two categories: caged (some branches on each plant were enclosed in a cylindrical cage covered with 2.5-cm black plastic mesh) and exposed (control) flowers. The cages were used to exclude hummingbirds in order to evaluate their effect on microbial communities in flowers. Smaller animals such as bees and thrips could enter the cages and access flowers in them. We found previously that microbial densities were lower in caged M. aurantiacus flowers than in exposed (control) flowers, indicating that the lack of hummingbird visits resulted in reduced microbial dispersal (Belisle et al. 2012). The cages were placed on the plants early in the flowering season, on 22–26 April 2013.

Before anthesis, we had tagged each harvested flower with a small piece of adhesive address label that had a unique identification number printed on it. We monitored each tagged flower bud to check when they opened. This way, we could tell the age of flowers, and in order to standardize for flower age, we harvested all flowers when they were four or five days old. The first sampling of flowers was conducted from 7 to 10 May (week 0) to compare microbial community composition between caged and exposed flowers. The harvested flowers were immediately placed in a cool box, brought to the laboratory, and nectar extracted, diluted, and plated as described below within 3 h of the harvesting. After plating, the remainder of the diluted nectar samples was stored at −80°C until DNA extraction was conducted as described below. Colony-forming units (CFUs) were recorded for the plate samples, but the CFU data did not show statistically significant differences in total or colony morphotype abundances among the inoculation treatments, presumably due to low taxonomic resolution and accuracy. In this paper, we focus on data from the Illumina sequencing.

We introduced a single strain of Neokomagataea sp. and one of Metschnikowia reukaufii into the flowers of the plants pre-assigned to Neokomagataea and Metschnikowia treatments, respectively, on 7 to 10 May, immediately after the week-0 harvesting of flowers. For this introduction, we used a strain of Neokomagataea sp. collected in 2012 at JRBP and similar to the one described in Vannette et al. (2013), which we referred to as Gluconobacter sp. in this previous paper (<www.ncbi.nlm.nih.gov/nuccore/JX437138>), and a strain of M. reukaufii collected in 2010 at JRBP and similar to the one described in Peay et al. (2012) (<www.ncbi.nlm.nih.gov/nuccore/JF809868>). For the Neokomagataea and Metschnikowia treatments, 4 µl of 10⁴ cells ml⁻¹ in 20% sucrose was added to all caged and exposed flowers on the focal plant individuals. For the control treatment, 4 µl of 20% sucrose was added to all flowers. Seven days (week 1) after the introduction treatment, up to 14 flowers were harvested per plant individual in the field, using the same procedure as for week 0. The same sampling was conducted again 21 days (week 3) after the introduction treatment (up to 11 flowers per plant individual). The flowers sampled in weeks 1 and 3 were different from the original flowers into which Neokomagataea bacteria or Metschnikowia yeasts were introduced in week 0. Flowers of M. aurantiacus usually wither 6 to 10 days after opening (Peay et al. 2012). Over the three sampling periods, a total of 513 flowers were sampled (Supplementary material Appendix 3). A widespread incidence of midge infestation of M. aurantiacus flower buds in week 3 limited flower availability as flowers did not develop once
Illumina sequencing of bacteria and fungi

From the nectar of each flower sample, microbial genomic DNA was extracted using TRizol reagents (ThermoFisher Scientific). We then PCR-amplified bacterial 16S ribosomal DNA region and fungal internal transcribed spacer 1 (ITS1) region using the specific primer pairs, 5′- GTG YCA GCM GCC GGG GTA A -3′ – 806rB (5′- GGA CTA CNV GGG TWT CTA AT -3′) (Caporaso et al. 2012) and ITS1-F KYO1 (5′- CTH GGT GCT CTA TTA GGA STA A -3′) – ITS2 KYO2 (5′- TTY RCT RCG TTC TTC ATC ATC -3′) (Toju et al. 2012), respectively. Each of the forward and reverse primers was fused with 3–6-mer Ns for improved Illumina sequencing quality (Lundberg et al. 2013) and a Illumina sequencing primer region (forward, 5′- TCG TCG GCA GCG TCA GAT GTG TAT TAT AAG AGA CAG - [3–6-mer Ns] – [515f or ITS1-F KYO1] -3′; reverse, 5′- GTC TCG TGG GCT CCG AGA TGT GTA TAA GAG ACA G [3–6-mer Ns] - [806rB or ITS2 KYO2] -3′). The multiplex PCR of the 16S and ITS regions was conducted using the MyTaq HS DNA polymerase Mastermix (Bioline) with a temperature profile of 95ºC for 2 min, followed by 37 cycles at 95ºC for 20 s, 50ºC for 20 s, 72ºC for 50 s, and a final extension at 72ºC for 10 min. The ramp rate was set to 1ºC s⁻¹ to prevent the generation of chimeric amplicons (Stevens et al. 2013). P5/P7 Illumina adaptors were then added in the subsequent PCR using fusion primers with 8-mer index sequences for sample identification (Hamady et al. 2008) (forward, 5′- AAT GAT ACG GCG ACC ACC GAG ATC AC - [8-mer tag] - TCG TCG GCA GCG TC -3′; reverse, 5′- CAA GCA GAA GAC GCC GGC ATA CGA GAT - [8-mer tag] - GTC TCG TGG GCT CGG CGG -3′). The temperature profile was 95ºC for 2 min, followed by 8 cycles at 95ºC for 20 s, 50ºC for 20 s, 72ºC for 50 s, and a final extension at 72ºC for 10 min (ramp rate=1ºC s⁻¹). The PCR amplicons of the samples were pooled with equal volume after a purification/equalization process with AMPure XP Kit (sample:AMPureXP = 1:6). The pooled library was sequenced using the Illumina MiSeq sequencer of the Stanford Functional Genomics Facility (2 × 250 cycle sequencing kit) with 15% PhiX spike-in.

The Illumina sequencing data (DNA Databank of Japan (DDBJ) BioProject, PRJDB4972) were processed through the bioinformatic pipeline detailed in Supplementary material Appendix 2. The obtained data matrix depicting samples of the Illumina sequencing primer region was rarefied to 300 reads per flower sample (an even number) by choosing the random number of reads. The sample × OTU matrix was constructed as described above (300 reads per sample). The sample × class matrix representing bacterial and fungal (yeast) density in nectar samples, therefore, the matrix varied among samples, presumably reflecting the relative abundance of bacteria and fungi in the samples.

In the sample × class matrix, the number of obtained reads varied considerably among flowers (Supplementary material Appendix 3) likely due to variation in bacterial and fungal (yeast) density in nectar samples. Therefore, the data matrix was rarefied to 300 reads per flower sample using the vegan ver. 2.2-3 package (Oksanen et al. 2012) of R ver. 3.3.1 (<www.r-project.org>). Three-hundred reads per sample were sufficient to describe the class-level composition of the bacterial and fungal communities (Supplementary material Appendix 5). The matrix contained two archaeal, 25 bacterial, and 11 fungal classes (including ‘unidentified’) (Supplementary material Appendix 3). Due to the lack of nectar or low microbe density in many flowers, the number of samples with the information of class-level community structure was reduced to 189 (Supplementary material Appendix 3).

The most frequently observed bacterial OTU belonging to the bacterial family Acetobacteraceae (1103:13204:3353_467; Supplementary material Appendix 3) was allied to the sequence of a species in a recently proposed genus, Neokomagataea (Yukphan et al. 2011) (Supplementary material Appendix 6a). In the fungal data, 18 OTUs were allied to Metschnikowia reukaufii (Supplementary material Appendix 6b).

Statistical analysis

In the sample × class matrix representing bacterial and fungal community structure (for a total of 189 samples), week-1 and week-3 flower samples were separated into two data matrices to construct models testing for priority effects in respective sampling weeks. For each of the week-1 and week-3 data, we first constructed a generalized linear mixed model (GLMM) to predict the proportion of Alphaproteobacteria reads, of which 87.8% were allied to Metschnikowia reukaufii (Supplementary material Appendix 3). The proportion of bacterial and fungal sequencing reads in the matrix varied among samples, presumably reflecting the relative abundance of bacteria and fungi in the samples.

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Additionally, to examine the effects of the introduction treatment on the composition of the entire microbial
community, we constructed GLMM models in which the axes of principal coordinate analyses (PCoAs) summarizing the microbial community structure quantified at the family level were used as response variables. In each model of PCoA1 or PCoA2 axis in week-1 or week-3 data, the same fixed and random effects as described above were incorporated. In another set of GLMM models, we also evaluated the effects of the introduction treatment on the community structure of microbes other than Alphaproteobacteria, using PCoA on all sequence reads included except Alphaproteobacteria reads. Because Gaussian family models were unavailable with the glmmML package, we used the glmmPQL function of the MASS ver 7.3-45 package of R.

Data deposition

Data available from the Dryad Digital Repository: <http://dx.doi.org/10.5061/dryad.0j4b2> (Fukami et al. 2017).

Results

The GLMMs indicated that the introduction of Neokomagataea and Metschnikowia influenced microbial community structure three weeks (but not one week) after the introduction treatment (Table 1; PCoA2 in Table 2; Fig. 1–2). In week 3, few Metschnikowia or other fungal sequences were detected from the plants to which Neokomagataea bacteria were introduced in week 0 (Fig. 1). The Neokomagataea treatment samples were dominated by Alphaproteobacteria (mostly Neokomagataea) reads. In contrast, the Metschnikowia and control treatment samples contained both Metschnikowia (Saccharomycetes) and Alphaproteobacteria (Fig. 1).

The proportion of Alphaproteobacteria reads was influenced by the presence/absence of cages, but the effects of cages (exclusion of hummingbirds) differed between week 1 and week 3: the presence of cages increased Alphaproteobacteria in week 1, whereas it reduced the relative abundance of the nectar bacterial clade in week 3 (Table 1). In addition, the GLMMs also showed that the introduction treatment influenced the community structure of microbes other than Alphaproteobacteria (PCoA 1 in Supplementary material Appendix 7) in week 3, but not in week 1 (Supplementary material Appendix 7). Effects of the caging on the entire microbial community structure were detected only in week 1 (Table 2).

We also found that the proportion of samples with Alphaproteobacteria were higher in the Neokomagataea-introduced plants and lower in the Metschnikowia-introduced plants than they were in the control plants in week 3 (Supplementary material Appendix 3 and 8). In addition, Saccharomyces reads were obtained from none of the samples of Neokomagataea-introduced plants but were present in other treatment groups in week 3 (Supplementary material Appendix 8).

Discussion

Our results indicate that the effects of initial dominance can persist across multiple generations of ephemeral local habitats in this nectar microbial system. Given our experimental design, a higher relative abundance of Neokomagataea in flowers on Neokomagataea-inoculated plants compared to those on Metschnikowia-inoculated or control plants could have simply reflected increased dispersal of Neokomagataea among flowers on Neokomagataea-inoculated plants. However, we found that both Neokomagataea and Metschnikowia were present in at least some of the flowers sampled from control plants. We also found that Metschnikowia relative abundance was lower in Neokomagataea-inoculated plants than in Metschnikowia-inoculated or control plants in week 3, though not in week 1 (Fig. 1). Together, these two findings suggest competitive suppression of Metschnikowia by Neokomagataea in Neokomagataea-inoculated plants. We do not have direct evidence for such competitive interactions occurring in wild flowers (but see Tucker and Fukami 2014). Nevertheless, our results are consistent with the hypothesis that priority effects, along with other factors influencing pollinator behavior and plant physiological status, structure nectar microbial communities within and across floral generations.

Table 1. Effects of the experimental introduction of Neokomagataea/Metschnikowia on the proportion of sequence reads mapping to Alphaproteobacteria. In each GLMM model of week-1 or week-3 data, the first three PCNM vectors of the sampling points (spatial structure), the introduction treatment, and the presence/absence of cages were included as fixed effects and plant individuals as random effects.

<table>
<thead>
<tr>
<th>Week</th>
<th>Explanatory variable</th>
<th>Coefficient</th>
<th>SE</th>
<th>z</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Week 1</td>
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<td>Treatment (Metschnikowia)</td>
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<td>0.63</td>
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<td>0.2750</td>
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<tr>
<td></td>
<td>Cage (Exposed)</td>
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<td>0.0004</td>
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<td>Week 3</td>
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<td>−5.47</td>
<td>0.25</td>
<td>−21.97</td>
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Table 2. Effects of the experimental introduction of Neokomagataea/Metschnikowia on the entire microbial community structure. In each of the week-1 and week-3 microbial community data, a principal coordinate analysis (PCoA) was performed and the resultant PCoA1 and PCoA2 axes were used as response variables of the GLMM models examining the effects of the introduction treatment and experimental cages. In each GLMM model, the first three PCNM vectors of the sampling points (spatial structure), the introduction treatment, and the presence/absence of cages were included as fixed effects and plant individuals as random effects.

<table>
<thead>
<tr>
<th>Week</th>
<th>PCoA</th>
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<td>Week</td>
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<td>Treatment (Neokomagataea)</td>
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<td>0.085</td>
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<td>0.083</td>
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<td>-0.058</td>
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<td>-0.71</td>
<td>0.4832</td>
</tr>
<tr>
<td>Week</td>
<td>PCoA 1</td>
<td>(Intercept)</td>
<td>0.167</td>
<td>0.208</td>
<td>0.80</td>
<td>0.4317</td>
</tr>
<tr>
<td></td>
<td>PCNM 1</td>
<td>Treatment (Neokomagataea)</td>
<td>-0.568</td>
<td>1.020</td>
<td>-0.56</td>
<td>0.5834</td>
</tr>
<tr>
<td></td>
<td>PCNM 2</td>
<td>Treatment (Metschnikowia)</td>
<td>-0.078</td>
<td>0.878</td>
<td>-0.09</td>
<td>0.9301</td>
</tr>
<tr>
<td></td>
<td>PCNM 3</td>
<td>Cage (Exposed)</td>
<td>-0.339</td>
<td>1.278</td>
<td>-0.27</td>
<td>0.7935</td>
</tr>
<tr>
<td>Week</td>
<td>PCNM 1</td>
<td>Treatment (Neokomagataea)</td>
<td>0.200</td>
<td>0.173</td>
<td>1.16</td>
<td>0.2746</td>
</tr>
<tr>
<td></td>
<td>PCNM 2</td>
<td>Treatment (Metschnikowia)</td>
<td>0.001</td>
<td>0.136</td>
<td>0.01</td>
<td>0.9946</td>
</tr>
<tr>
<td></td>
<td>PCNM 3</td>
<td>Cage (Exposed)</td>
<td>-0.259</td>
<td>0.185</td>
<td>-1.40</td>
<td>0.1749</td>
</tr>
<tr>
<td>Week</td>
<td>PCoA 2</td>
<td>(Intercept)</td>
<td>-0.297</td>
<td>0.157</td>
<td>-1.89</td>
<td>0.0725</td>
</tr>
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<td></td>
<td>PCNM 1</td>
<td>Treatment (Neokomagataea)</td>
<td>-0.870</td>
<td>0.767</td>
<td>-1.13</td>
<td>0.2698</td>
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<tr>
<td></td>
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<td>Treatment (Metschnikowia)</td>
<td>0.642</td>
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<td>0.97</td>
<td>0.3421</td>
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<td>PCNM 3</td>
<td>Cage (Exposed)</td>
<td>1.097</td>
<td>0.962</td>
<td>1.14</td>
<td>0.2670</td>
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<td>Treatment (Neokomagataea)</td>
<td>-0.134</td>
<td>0.130</td>
<td>-1.03</td>
<td>0.3279</td>
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<tr>
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<td>Treatment (Metschnikowia)</td>
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<td>0.102</td>
<td>2.86</td>
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<tr>
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<td>Cage (Exposed)</td>
<td>0.217</td>
<td>0.139</td>
<td>1.57</td>
<td>0.1323</td>
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The strength of priority effects was asymmetric in the sense that introduction of Neokomagataea bacteria resulted in the lowered relative abundance of yeasts and other fungi in week 3 (Fig. 1), whereas introduction of Metschnikowia yeasts had only minor effects, if any, on Metschnikowia (Supplementary material Appendix 8). The reasons for this asymmetry are uncertain, but it might reflect species-specific efficiency of dispersal. In our experiments, the effects of the exclusion of hummingbirds differed between sampling weeks (Table 1–2), suggesting idiosyncratic contributions of pollinators to Neokomagataea abundance in floral nectar. Regardless, persistent priority effects could in turn influence pollination and plant fitness, as we found previously that Neokomagataea (= Gluconobacter, but not Metschnikowia reukatii, could negatively affect pollinator foraging and seed set (Vannette et al. 2013, Good et al. 2014).

Priority effects were detected in week 3 but not in week 1 (Table 1–2), even though the larger number of samples analyzed for week 1 (Fig. 1) afforded higher statistical power compared to week 3. This result suggests that priority effects do not necessarily decrease monotonically over time, but that their magnitude can show some temporal fluctuation. Factors generating such potential fluctuation remain unclear, but one possibility is ambient temperature. If bacterial and yeast populations grow more rapidly at higher temperature (Tucker and Fukami 2014), priority effects may become stronger later in the flowering season as temperature increases. Consistent with this expectation, air temperature (daily means and maxima) appears to have been higher in week 3 than in week 1 (Supplementary material Appendix 9), although actual causality remains uncertain. Another possibility is pollinator abundance. Anecdotally, we have observed more insects visiting flowers later in the flowering season, which may increase the rate of among-flower dispersal of the nectar microbes. However, both factors remain no more than speculation at this point. Moreover, we used only one strain per species for the experimental inoculation, but strains can be phenotypically variable (Herrera 2014) and may therefore show different priority effects, which remains to be tested.

Metacommunities consisting of ephemeral local patches are found not only in nectar microbes, but are prevalent across a variety of habitats and organisms (Hanski 1998). Examples of metacommunities consisting of ephemeral habitats include aquatic insects in phytotelmata (Ellis et al. 2006), symbiotic microbes in plant hosts (Jousimo et al. 2014), freshwater plankton in rock pools (Vanschoenwinkel et al. 2008b), and epiphyllous (leaf-inhabiting) bryophytes in tropical forests (Zartman and Nascimento 2006). Because priority effects within patch generations have now been documented widely, further research on priority effects across patch generations in different systems seems
worthwhile for a better understanding of species coexistence. Moreover, habitats are becoming increasingly patchy and ephemeral because of human activity (Didham 2010). For this reason, knowledge of priority effects across multiple generations of ephemeral habitat patches will only become more important for biodiversity conservation.

Figure 1. Comparison of community composition among microbial introduction treatments. Results are shown separately for the three introduction treatments (introduction of Neokomagataea sp., introduction of Metschnikowia reukaufii, and 20% sucrose as control), each separately for weeks 0, 1, and 3. Note that Neokomagataea and Metschnikowia account for 87.8% of Alphaproteobacteria and 100% of Saccharomycetes sequencing reads, respectively. The number of flowers analyzed is shown in a parenthesis for each group.

Figure 2. Microbial community structure in flowers, as characterized by PCoA on week-1 (a) and week-3 (b) sequence reads. Treatments where Neokomagataea (blue), Metschnikowia (beige), or no microbe (control) (grey) was initially introduced in week 0 are shown. Each data point represents a flower. Circles and triangles indicate exposed and caged flowers, respectively. Data points were jittered slightly (no more than 0.03) for better presentation of overlapping points.
We thank Bill Gomez and Jerry Hearn for assistance with field work, Dino and Giselle Turchet for permission to conduct this research on the Turchet Leasehold owned by Stanford University, and Rein Brys for comments. Bill Gomez designed and made the cages to exclude hummingbirds.

Funding – This work was financially supported by Stanford University’s Terman Fellowship and Dept of Biology and the NSF (DEB 1149600) awarded to TF and the JSPS KAKENHI Grant (no. 26711026) and the Supporting Program for Interaction-based Initiative Team Studies (SPIRITS) by Kyoto University awarded to HT. The Gordon and Betty Moore Foundation supported RLV through the Life Sciences Research Fellowship (GBMF 2550.02). Statement of authorship – MPLG, RLV and TF designed the study and conducted the field work. All authors contributed to laboratory work. HT analyzed the data, and wrote the first manuscript draft with TF. All authors contributed to revising the manuscript.

Acknowledgements – We thank Bill Gomez and Jerry Hearn for assistance with field work, Dino and Giselle Turchet for permission to conduct this research on the Turchet Leasehold owned by Stanford University, and Rein Brys for comments. Bill Gomez designed and made the cages to exclude hummingbirds.

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Devey, G. et al. 2015. First arrived takes all: inhibitory priority effects dominate competition between co-infecting Borellia burgdorferi strains. – BMC Microbiol. 15: 61.


