



# Foliar fungi alter reproductive timing and allocation in *Arabidopsis* under normal and water-stressed conditions

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## ABSTRACT

Microbes influence plant phenotypes but most known examples of this are from the study of below-ground microbes and plant disease modification. To examine the potential importance of phyllosphere microbes on non-disease related plant traits, we used sterile *Arabidopsis* clones to test the effects of foliar fungi on flowering phenology and reproductive allocation under conditions of varying water stress. We inoculated the sterile plants with fully-factorial combinations of four fungal isolates, then measured flowering time and reproductive allocation for each treatment group under normal and water-stressed conditions. All plants inoculated with foliar fungi had significantly later flowering and greater seed mass than the sterile control groups. The magnitude of this effect depended on the specific fungi present, but individual fungal effects diminished as inoculum richness increased. Above-ground microbes likely influence other plant traits as well and should be considered in any study measuring plant phenotypes.

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## 1. Introduction

Plants are hosts to a diverse array of endophytic and epiphytic microorganisms that, together with the plant, make up the holobiont. Under natural conditions, many “plant” traits depend entirely, or in part, on members of the plant microbiome (Vandenkoornhuysen et al., 2015). However, the more we discover about the holobiont, the more questions arise about the relative roles of microbial community dynamics, plant genotype, and environmental factors that shape a plant's extended phenotype (Preston, 2017).

Untangling the processes of plant-microbe interactions can be very complicated, with plants shaping their microbiome and the microbes, in turn, shaping attributes of plant phenotype (Mendes et al., 2014; Edwards et al., 2015). Work that has simplified these systems by incorporating sterile model plants and manipulating the microbial constituents is, however, beginning to reveal a much needed mechanistic understanding of plant microbiome assembly and function (Panke-Buisse et al., 2015; Wolfe, 2018).

The influence of microbes on plant traits can be subtle or

dramatic. For example, that bacterial root endophytes are known to modify plant phenotypes in some cases by changing when and how carbon is allocated within plant tissues (Henning et al., 2016), and that transplantations of natural soil biota to gnotobiotic plants can alter flowering phenology (Wagner et al., 2014). Although most work has focused on below-ground microbes and plant tissues (Rossmann et al., 2017), it is clear from other efforts that microbes associated with above-ground (phyllosphere) tissues also shape plant traits (Estrada et al., 2013; Giauque et al., 2019).

Aside from modifying plant disease or herbivory (Falconi and Mendgen, 1994; Arnold et al., 2003; Busby et al., 2015), phyllosphere-associated microbes alter plant traits such as leaf wettability and xylem conductivity, (Beattie, 2011), cuticle permeability and transpiration (Ritpitakphong et al., 2016), and even the biosynthesis of plant hormones (Egamberdieva et al., 2017). Additionally, above-ground microbes can influence seed mass (Saari et al., 2010), leaf size (Davitt et al., 2000), frost sensitivity (Bertrand et al., 2007), and shoot height (Perrine-Walker et al., 2007). No doubt, many more microbially-mediated plant traits await discovery. An increased understanding of phyllosphere microbial communities and which plant traits they can alter is crucial for informing emergent agricultural (Schlaeppli and Bulgarelli, 2014), industrial (Doty, 2017), and conservation (Zahn and Amend, 2017) practices.

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In this study we investigated how foliar fungal endophytes impact flowering phenology and seed mass, important ecological traits (Westoby et al., 1992; Rosas et al., 2014) under normal and water-stressed conditions. Using gnotobiotic clones of *Arabidopsis thaliana* inoculated with a fully-factorial combination of four fungal isolates with varying phylogenetic distance from each other, we sought to uncover whether the presence and identity of foliar fungi affect reproductive timing and allocation under normal and stressed conditions.

## 2. Materials and methods

### 2.1. Overview

Replicates of sterile *Arabidopsis* seedlings were inoculated with factorial combinations of 4 fungal isolates having varying phylogenetic distance from each other. The experiment was duplicated under normal (surface soil never allowed to completely dry) and water-stressed (soil surface allowed to dry for 2 days between waterings) conditions. Flowering phenology (days to first flower) and average seed mass were measured.

### 2.2. Plant selection and growth

*Arabidopsis* bulk germplasm was generated from a single line obtained from TAIR ([www.arabidopsis.org](http://www.arabidopsis.org), Accession: CS22468). Seeds were surface sterilized by shaking in 10% bleach containing 0.05% Tween 20 detergent for 10 min, 70% ethanol for 2 min, 3 rinses of sterile DI water. After 2 weeks cold treatment at 4°C, they were sown in autoclaved soil-less potting medium (Sunshine #4, Sun Grow, Chicago, IL). Seeds were germinated in the dark at 21°C for 1 week, then transplanted into 3" pots of sterile potting medium and grown in a Percival E-41L2 growth chamber (Percival Scientific, Inc., Perry, IA, USA) at 20°C with 16 h/8 h day/night cycle. Successfully-germinated seedlings were randomly assigned to fungal and water treatments, so that sterile controls and each factorial treatment combination had 5 replicate individuals. Replicates from each group were kept together in the growth chamber to minimize the potential for cross-contamination and group locations were rotated each day. Plants were watered from below with sterile DI water when the soil surface began to dry (for normal water treatment) and 2 d after the soil surface dried (water stress treatment). The first and third waterings contained 15–5–15 fertilizer at [200 ppm N]. Plants were not allowed to sit in standing water. The date of first flowering was recorded for each plant and waterings were halted 7 d after 80% of plants in each group initiated flowering. At the end of flowering, seeds were collected from each individual and dried at 40°C for 2 weeks, after which the total mass for 50 randomly selected seeds from each individual was measured to determine the mean mass of a single seed from each plant.

### 2.3. Fungal isolate inoculum preparation and inoculation

Fungi were originally isolated from Brassicaceae (kale and broccoli cultivars grown in an outdoor garden) leaf surfaces by running a moistened sterile swab across leaf surfaces and then streaking it onto MEA agar (Malt extract [1 g/L], Yeast extract [1 g/L], Agar [10 g/L]) amended with Streptomycin [20 mg/mL] and Kanamycin [20 mg/mL]. Morphologically distinct fungal colonies were serially axenized on MEA plates. DNA was extracted from 8 fungal isolates using the Extract-N-Amp protocol (Sigma-Aldrich) and subjected to bi-directional Sanger sequencing of the ITS1–28S region using the primers ITS1F (5'-CTTGGTCATTAGAGGAAGTAA-3') and TW-13 (5'-GGTCCGTGTTCAAGACG-3'). Taxonomy was assigned by comparing consensus sequences against the NCBI

nucleotide database using BLAST. Phylogenetic relatedness was estimated as the sum of patristic branch lengths from a Jukes-Cantor model neighbor-joining tree of the 5.8S rDNA region containing a taxonomically diverse collection of 70 other fungi (Cullings and Vogler, 1998, Supporting material).

Four sporulating fungal isolates with varying levels of phylogenetic distance (SI Table 1) were chosen as inoculum sources. Phylogenetic placement was consistent with the top BLAST hit. The four fungal isolates selected were *Pleospora rosae*, *Cochliobolus* sp., *Alternaria tenuissima*, *Cladosporium macrocarpum* (Table 1). Spores from these isolates were scraped from the surfaces of cultures and centrifugally washed three times in sterile water (500 RCF for 10 min, supernatant removed from pellet, pellet resuspended in 1 mL sterile water). Spore concentrations were quantified and normalized using a hemocytometer and DIC microscopy at 40X magnification before diluting them into 200 mL of 0.1% sterile agarose solution. Each fungal inoculum had an equivalent final spore concentration of 6,944 cells/mL, regardless of the number of species present. Negative controls consisted of a heat-killed combination of all 4 fungal isolates at 6,944 cells/mL in sterile 0.1% agarose solution.

After the first true leaves appeared on at least 75% of all germinated plants (6 d) fungal inocula were sprayed to fully cover plants and soil surfaces. Plants were sprayed weekly with their respective fungal treatments until rosettes reached full size (23 d).

### 2.4. Fungal isolate growth rates

Three replicate cultures were prepared for isolates in which fungi were grown singly and in each possible combination with each other. Agar blocks (0.25 cm<sup>2</sup>) of vegetative mycelium were cut from pure cultures and placed onto the surface of MEA agar and grown at ambient temperature for 9 d. To measure baseline and competitive growth rates, replicates of pure cultures and each factorial combination were photographed and mycelium surface area was measured with ImageJ (Supporting Info) after 4 d and 9 d. Growth rates were determined as the increase in mycelial surface area over 5 d. Growth rates of isolates in competition were relativized against pure culture growth rates.

### 2.5. Statistics

All analyses were performed in R (version 3.3.3). An analysis of variance (ANOVA) test was used to determine the significance of fungal treatment and water stress on flowering time. Flowering time was regressed onto seed mass (a proxy for plant fitness) with a linear model to determine the relationship between phenology and fitness. To estimate the role of each of the four fungal isolates in altering flowering time, we used a general linear model with community matrix components as predictors. The intercept was excluded and Type-III Sums of Squares were obtained with the *car* package (Fox and Weisberg, 2011). Figures were constructed with the *ggplot2* package (Wickham, 2009).

## 3. Results

### 3.1. Flowering phenology and seed mass

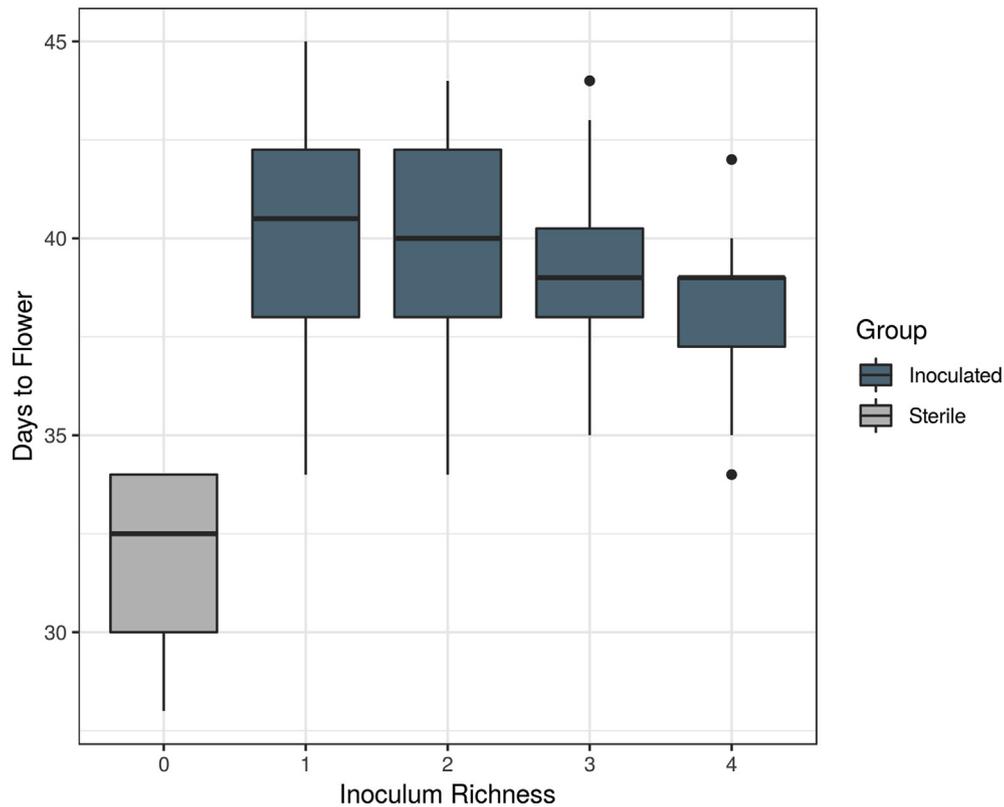
All individuals inoculated with viable fungal isolates flowered later than sterile controls, irrespective of watering levels (Fig. 1; SI Fig. 1). We observed significant changes to flowering phenology depending on fungal treatment group (ANOVA:  $F_{128, 15} = 36.734$ ;  $P < 2^{-16}$ ) and water regime (ANOVA:  $F_{128, 1} = 162.438$ ;  $P < 2^{-16}$ ).

Water stress consistently led to earlier flowering in all treatment groups, including controls. The magnitude of this change, however,

**Table 1**

Taxonomic assignments for the four fungal isolates used in this study. Sequences have been deposited at NCBI under the GenBank Accession Numbers given. Taxonomy was chosen based on the top named BLAST hit against the NCBI nr database.

Isolate ID	GenBank Accession No.	Top BLAST hit	Tentative Taxonomic Assignment
A	MH972194	NR_157531.1	<i>Pleospora rosae</i>
B	MH972195	KX641964.1	<i>Cochliobolus</i> sp.
C	MH972196	KX664408.1	<i>Alternaria tenuissima</i>
D	MH972197	KX664406.1	<i>Cladosporium macrocarpum</i>



**Fig. 1.** – Sterile plants consistently flowered earlier than plants with endophyte treatments, regardless of the richness of the fungal inoculum.

varied between fungal community treatments (ANOVA:  $F_{128, 15} = 3.292$ ;  $P = 0.000118$ ; [SI Table 2](#)). The average reduction in flowering time due to water stress was 1.6 d for plants treated with *P. rosae*, 1.8 d for those treated with *Cochliobolus* sp., 5 d for plants treated with *A. tenuissima*, and 4.4 d for those treated with *C. macrocarpum*. A related pattern was observed for these four isolates in their effects on plants' overall flowering times. Plants inoculated with isolate A flowered later on average than plants inoculated with *A. tenuissima* or *C. macrocarpum*, regardless of water stress ([SI Table 3](#)).

Inoculum community richness had no influence on the observed lengthening of flowering time ([Fig. 1](#)). Even the presence of a single fungal isolate, regardless of identity, increased the mean flowering time over sterile control plants ([Fig. 2](#)).

Mean seed mass was positively correlated with later flowering times ( $F_{1, 123} = 22.24$ ;  $P < 0.0005$ ; Adj. R-sq = 0.1462; [SI Fig. 2](#)).

### 3.2. Fungal isolate growth rates

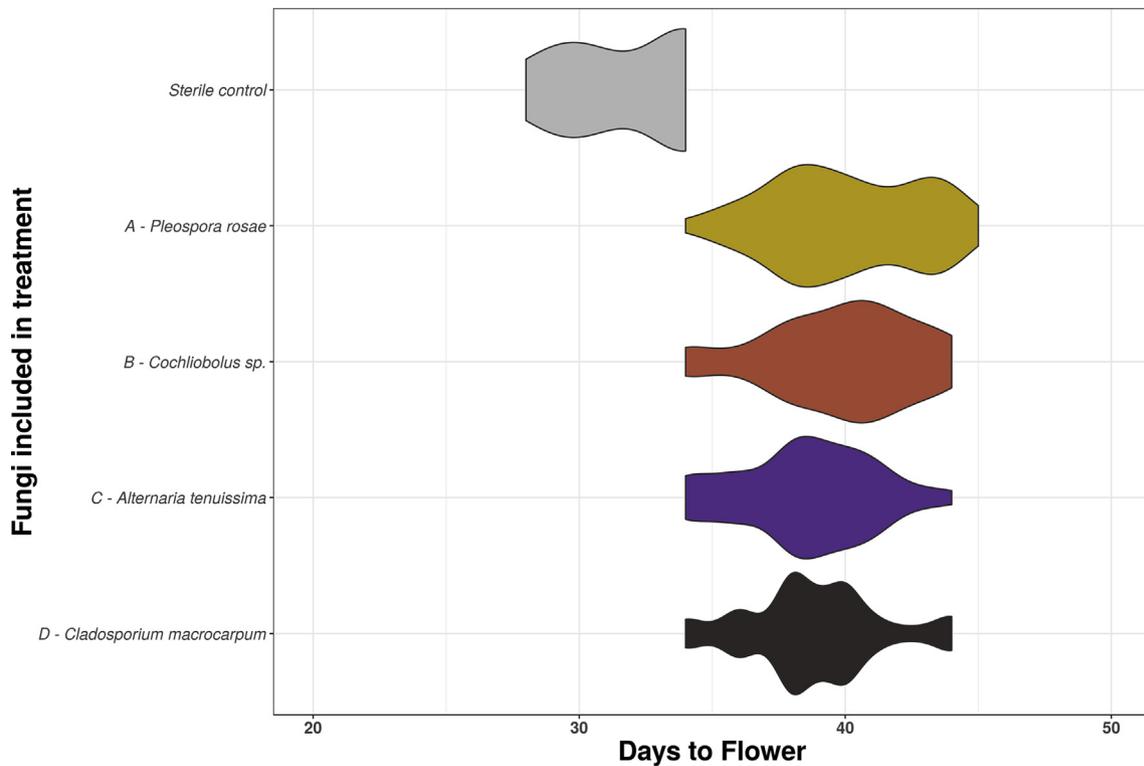
The culture-based experiment allowed us to see how the four fungal isolates behaved in combination with each other ([Fig. 3](#)). *Cochliobolus* sp. was a poor competitor under these conditions,

often growing at half (or less) of its baseline rate when in competition with any or all of the other isolates. In culture, it seemed to facilitate faster growth in the other three isolates, though it grew more slowly than the other isolates in pure culture ([SI Table 4](#)). The patterns we found in culture, however, had little predictive power for results on plants.

## 4. Discussion

Flowering timing is strongly determined by genetic ([Rosas et al., 2014](#)), and environmental ([Banta et al., 2012](#)) factors but, like other plant traits, it is also dependent on microbial members of the holobiont. Prior efforts have demonstrated important roles for soil bacteria in flowering phenology and drought response ([Lau and Lennon, 2012](#); [Wagner et al., 2016](#)). Here, we show that above-ground fungal members of the holobiont can also modify flowering phenology. Interestingly, at least for the isolates tested in this study, fungal identity was much less important than the fact that fungi were present.

In general, plants receiving inoculum with *P. rosae* and/or *Cochliobolus* sp. had later flowering times and a reduction in the deleterious effects of drought compared with plants receiving



**Fig. 2.** — The presence of any specific fungal isolate was less important than the presence of any fungus, regardless of identity. Y-axis shows the presence of a given fungal isolate in a treatment group. X-axis shows violin distributions of flowering times (in days) for plant treated with that fungus in any combination of other inocula.

inoculum with *A. tenuissima* and/or *C. macrocarpum*. However, in the higher-order interactions when more than two fungal strains were present in an inoculum, these patterns were not always maintained.

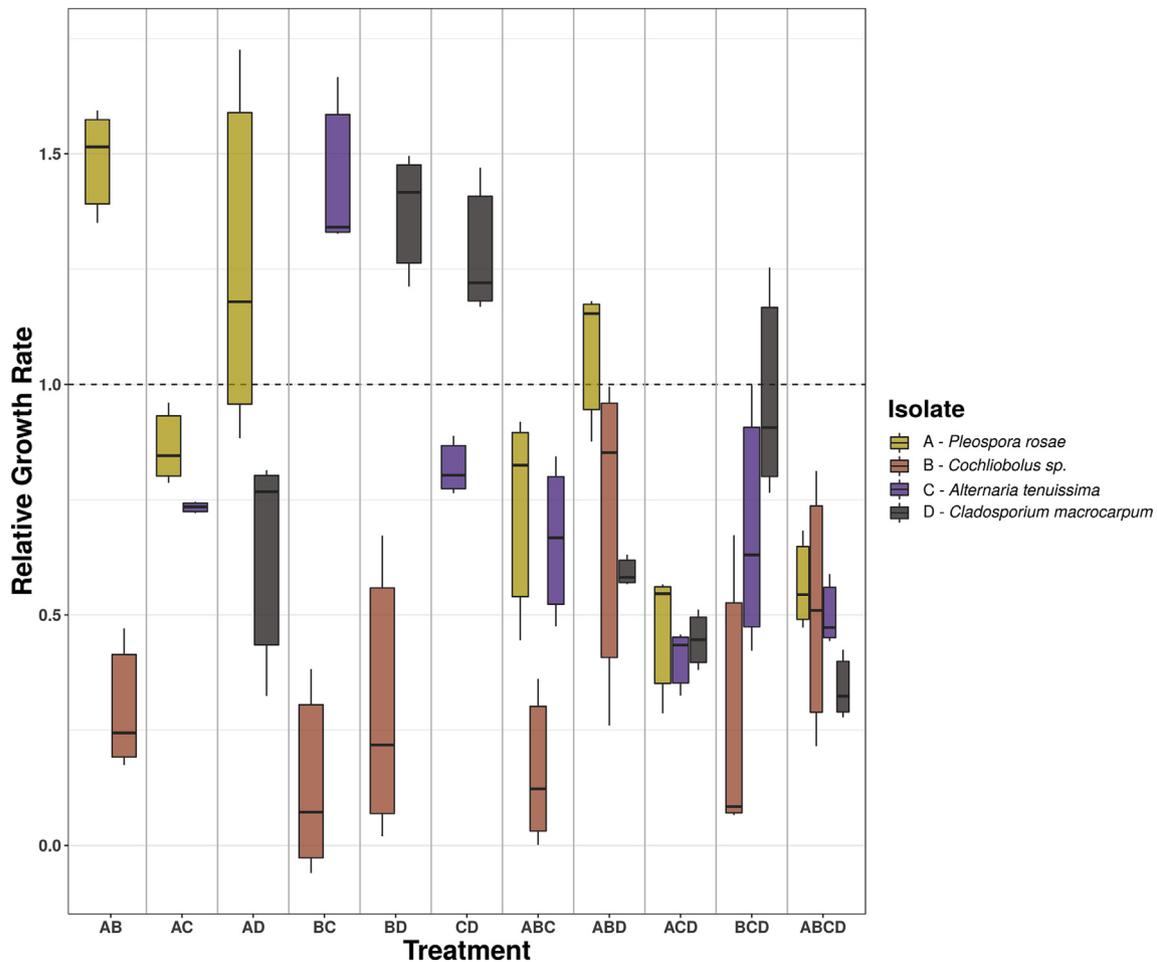
There was also an interaction between water stress and the functional benefits of harboring foliar fungi. Resources available to the phyllosphere microbial community may alter or even erase the advantages of that community for a plant (Berg and Koskella, 2018). Here we observe that drought conditions consistently resulted in earlier flowering times and reduced seed mass, but the magnitude of this effect depended on the fungal community present. Again, no consistent pattern could be found with respect to any specific isolate due to complexities in higher-order interactions.

Culture-based competition results shed little light on why simple interactions were not predictive of higher-order results. For example, both *P. rosae* and *Cochliobolus* sp. were associated with later flowering time individually and together, and *C. macrocarpum* was associated with earlier flowering time, especially under water stress. However, a mixed inoculum of *P. rosae*, *Cochliobolus* sp., and *C. macrocarpum* showed no significant changes in flowering time from the mean of all treatment groups. In culture, the growth rate of *C. macrocarpum* was reduced by both *P. rosae* and *Cochliobolus* sp., and the growth rate of *P. rosae* was increased in the presence of *C. macrocarpum* (Fig. 3). This led us to predict that, in the presence of *P. rosae* and *Cochliobolus* sp., the growth of *C. macrocarpum* would be reduced and its solitary effect on flowering time would be less pronounced, but this was not seen. This shows that there is not a clear relationship between competitiveness in a rich culture medium and effects on plant phenotype. Something more complex is taking place on the surface of plant leaves.

This higher-order unpredictability is not surprising, given that fungal community interactions and assembly processes are still not

well understood. Our system was very simple, with just four fungal isolates. In natural systems, we must consider that determinants of microbial colonization of a given plant tissue include host plant identity and attributes, local abiotic conditions, and microbe-microbe interactions (Alekkett et al., 2014). Of further importance are: priority effects (Tucker and Fukami, 2014; Toju et al., 2018), phylogenetic relatedness and trait conservatism (Maherali and Klironomos, 2007), environmental filtering (Glassman et al., 2017; Whitman et al., 2018), and the interactions between these processes (Peay et al., 2011). The specific mechanism by which fungi postponed flowering time in this study is also not known. Foliar fungi may alter photosynthetic efficiency, transpiration, and water use efficiency, particularly when plants are experiencing stress (Pinto et al., 2000; Li et al., 2012). They also produce abundant secondary metabolites that have received little attention outside of pathology applications (Suryanarayanan, 2013), which may be important for flowering phenology. Further, it has been suggested that changes to belowground microbes can alter nutrient availability and the fitness benefits of associating with mutualists (Lau and Lennon, 2011), and something similar may be taking place in aboveground tissues. Associating with endophytes might reduce stresses that lead to shorter flowering times, or could actually trigger immune responses that prime them for resistance to other stressors (Van et al., 2008).

While we currently lack a detailed mechanistic explanation for why some fungal communities generated a greater effect than others, all the foliar fungal communities tested resulted in plants with significantly later flowering times and greater seed mass than the sterile controls. This, along with other research demonstrating that belowground microbes have strong influences on plant phenotype, should add complexity to the interpretation of “plant” traits, which might actually be microbial traits in disguise.



**Fig. 3.** — Fungal competitive growth rate on MEA medium as the proportion of growth rate in pure culture ( $\text{cm}^2 \text{day}^{-1}$ ). X-axis = competition groups; Y-axis = Proportion of pure culture growth rate. Colored by fungal isolate. Values above 1.0 denote fungi that outperformed baseline growth rates in the presence of other isolate(s).

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### Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.funeco.2019.04.002>.

### Data accessibility statement

All raw data are provided along with analysis code in the Supporting Information. DNA sequences for fungal isolates used in this study have been uploaded to NCBI and are given in Table 1. Cultures of the fungi used in this study are kept at the University of Hawaii at Manoa, Botany Department.

### Author contributions

AA and GZ conceived and designed the experiments. AA provided materials, reagents, and equipment. GZ performed the experiments. AA and GZ analyzed data and wrote the manuscript.

### References

- Aleklett, K., Hart, M., Shade, A., 2014. The microbial ecology of flowers: an emerging frontier in phyllosphere research. *Botany* 92, 253–266.
- Arnold, A.E., Mejía, L.C., Kyllö, D., Rojas, E.I., Maynard, Z., Robbins, N., Herre, E.A., 2003. Fungal endophytes limit pathogen damage in a tropical tree. *Proc. Natl. Acad. Sci. Unit. States Am.* 100, 15649–15654.
- Banta, J.A., Ehrenreich, I.M., Gerard, S., Chou, L., Wilczek, A., Schmitt, J., Kover, P.X., Purugganan, M.D., 2012. Climate envelope modelling reveals intraspecific relationships among flowering phenology, niche breadth and potential range size in *Arabidopsis thaliana*. *Ecol. Lett.* 15, 769–777.
- Beattie, G.A., 2011. Water relations in the interaction of foliar bacterial pathogens with plants. *Annu. Rev. Phytopathol.* 49, 533–555.
- Berg, M., Koskella, B., 2018. Nutrient- and dose-dependent microbiome-mediated protection against a plant pathogen. *Curr. Biol.* 28, 2487–2492 e3.
- Bertrand, A., Prévost, D., Bigras, F.J., Castonguay, Y., 2007. Elevated atmospheric CO<sub>2</sub> and strain of rhizobium alter freezing tolerance and cold-induced molecular changes in alfalfa (*medicago sativa*). *Ann. Bot.* 99, 275–284.
- Busby, P.E., Ridout, M., Newcombe, G., 2015. Fungal endophytes: modifiers of plant disease. *Plant Mol. Biol.* 90, 645–655.
- Cullings, K.W., Vogler, D.R., 1998. A 5.8S nuclear ribosomal RNA gene sequence database: applications to ecology and evolution. *Mol. Ecol.* 7, 919–923.
- Davitt, A.J., Stansberry, M., Rudgers, J.A., 2000. Do the costs and benefits of fungal endophyte symbiosis vary with light availability? *New Phytol.* 188, 824–834.
- Doty, S.L., 2017. Functional importance of the plant endophytic microbiome: implications for agriculture, forestry, and bioenergy. In: *Functional Importance of the Plant Microbiome*, 1–5. Springer, Cham. Available at: [https://link.springer.com/chapter/10.1007/978-3-319-65897-1\\_1](https://link.springer.com/chapter/10.1007/978-3-319-65897-1_1). (Accessed 20 June 2018).
- Edwards, J., Johnson, C., Santos-Medellín, C., Lurie, E., Podishetty, N.K., Bhatnagar, S., Eisen, J.A., Sundaresan, V., 2015. Structure, variation, and assembly of the root-associated microbiomes of rice. *Proc. Natl. Acad. Sci. Unit. States Am.* 112, E911–E920.
- Egamberdieva, D., Wirth, S.J., Alqarawi, A.A., Abd\_Allah, E.F., Hashem, A., 2017. Phytohormones and beneficial microbes: essential components for plants to

- balance stress and fitness. *Front. Microbiol.* 8. Available at: <https://www.frontiersin.org/articles/10.3389/fmicb.2017.02104/full>. (Accessed 20 June 2018).
- Estrada, C., Wcislo, W.T., Van Bael, S.A., 2013. Symbiotic fungi alter plant chemistry that discourages leaf-cutting ants. *New Phytol.* 198 (1), 241–251.
- Falconi, C.J., Mendgen, K., 1994. Epiphytic fungi on apple leaves and their value for control of the postharvest pathogens *Botrytis cinerea*, *Monilinia fructigena* and *Penicillium expansum*/Epiphytische Pilze auf Apfelblättern und ihre Eignung für die Bekämpfung der Apfelfäuleerreger *Botrytis cinerea*, *Monilinia fructigena* und *Penicillium expansum*. *Zeitschrift für Pflanzenkrankheiten und Pflanzenschutz/J. Plant Dis. Prot.* 38–47.
- Fox, J., Weisberg, S., 2011. An {R} Companion to Applied Regression, second ed. Sage, Thousand Oaks, CA, USA. Available at: <http://socserv.socsci.mcmaster.ca/jfox/Books/Companion>.
- Giaque, H., Connor, E.W., Hawkes, C.V., 2019. Endophyte traits relevant to stress tolerance, resource use and habitat of origin predict effects on host plants. *New Phytol.* 221, 2239–2249.
- Glassman, S.I., Wang, I.J., Bruns, T.D., 2017. Environmental filtering by pH and soil nutrients drives community assembly in fungi at fine spatial scales. *Mol. Ecol.* <https://doi.org/10.1111/mec.14414>.
- Henning, J.A., Weston, D.J., Pelletier, D.A., Timm, C.M., Jawdy, S.S., Classen, A.T., 2016. Root bacterial endophytes alter plant phenotype, but not physiology. *PeerJ* 4, e2606.
- Lau, J.A., Lennon, J.T., 2011. Evolutionary ecology of plant–microbe interactions: soil microbial structure alters selection on plant traits. *New Phytol.* 192, 215–224.
- Lau, J.A., Lennon, J.T., 2012. Rapid responses of soil microorganisms improve plant fitness in novel environments. *Proc. Natl. Acad. Sci. Unit. States Am.* 109 (35), 14058–14062. <https://doi.org/10.1073/pnas.1202319109>.
- Li, X., Bu, N., Li, Y., Ma, L., Xin, S., Zhang, L., 2012. Growth, photosynthesis and antioxidant responses of endophyte infected and non-infected rice under lead stress conditions. *J. Hazard. Mater.* 213–214, 55–61. <https://doi.org/10.1016/j.jhazmat.2012.01.052>.
- Maherali, H., Klironomos, J.N., 2007. Influence of Phylogeny on Fungal Community Assembly and Ecosystem Functioning. *Science* 316 (5832), 1746–1748. <https://doi.org/10.1126/science.1143082>.
- Mendes, L.W., Kuramae, E.E., Navarrete, A.A., van Veen, J.A., Tsai, S.M., 2014. Taxonomical and functional microbial community selection in soybean rhizosphere. *ISME J.* 8, 1577–1587.
- Panke-Buisse, K., Poole, A.C., Goodrich, J.K., Ley, R.E., Kao-Kniffin, J., 2015. Selection on soil microbiomes reveals reproducible impacts on plant function. *ISME J.* 9, 980–989.
- Peay, K.G., Belisle, M., Fukami, T., 2011. Phylogenetic relatedness predicts priority effects in nectar yeast communities. *Proc. R. Soc. Lond. B Biol. Sci.* [rspb20111230](https://doi.org/10.1098/rspb.2011.1230).
- Perrine-Walker, F.M., Gartner, E., Hocart, C.H., Becker, A., Rolfe, B.G., 2007. Rhizobium-initiated rice growth inhibition caused by nitric oxide accumulation. *Mol. Plant Microbe Interact.* 20, 283–292.
- Pinto, L.S.R.C., Azevedo, J.L., Pereira, J.O., Vieira, M.L.C., Labate, C.A., 2000. Symptomless infection of banana and maize by endophytic fungi impairs photosynthetic efficiency. *New Phytol.* 147 (3), 609–615.
- Preston, G.M., 2017. Profiling the extended phenotype of plant pathogens. *Mol. Plant Pathol.* 18, 443–456.
- Ritpitakphong, U., Falquet, L., Vimoltust, A., Berger, A., Métraux, J.-P., L'Haridon, F., 2016. The microbiome of the leaf surface of *Arabidopsis* protects against a fungal pathogen. *New Phytol.* 210, 1033–1043.
- Rosas, U., Mei, Y., Xie, Q., Banta, J.A., Zhou, R.W., Seufferheld, G., Gerard, S., et al., 2014. Variation in *Arabidopsis* flowering time associated with cis-regulatory variation in *CONSTANS*. *Nat. Commun.* 5, 3651.
- Rossmann, M., Sarango-Flores, S.W., Chiaramonte, J.B., Kmit, M.C.P., Mendes, R., 2017. Plant microbiome: composition and functions in plant compartments. In: *The Brazilian Microbiome*, 7–20. Springer, Cham. Available at: [https://link.springer.com/chapter/10.1007/978-3-319-59997-7\\_2](https://link.springer.com/chapter/10.1007/978-3-319-59997-7_2). (Accessed 19 June 2018).
- Saari, S., Helander, M., Faeth, S.H., Saikkonen, K., 2010. The effects of endophytes on seed production and seed predation of tall fescue and meadow fescue. *Microb. Ecol.* 60, 928–934.
- Schlaeppli, K., Bulgarelli, D., 2014. The plant microbiome at work. *Mol. Plant Microbe Interact.* 28, 212–217.
- Suryanarayanan, T., 2013. Endophyte research: going beyond isolation and metabolite documentation. *Fungal Ecol.* 6 (6), 561–568. <https://doi.org/10.1016/j.funeco.2013.09.007>.
- Toju, H., Vannette, R.L., Gauthier, M.-P.L., Dhami, M.K., Fukami, T., 2018. Priority effects can persist across floral generations in nectar microbial meta-communities. *Oikos* 127 (3), 345–352. <https://doi.org/10.1111/oik.04243>.
- Tucker, C.M., Fukami, T., 2014. Environmental variability counteracts priority effects to facilitate species coexistence: evidence from nectar microbes. *Proc. R. Soc. Lond. B: Biol. Sci.* 281 (1778), 20132637. <https://doi.org/10.1098/rspb.2013.2637>.
- Vandenkoornhuysse, P., Quaiser, A., Duhamel, M., Le Van, A., Dufresne, A., 2015. The importance of the microbiome of the plant holobiont. *New Phytol.* 206, 1196–1206.
- Van Wees, S.C., Van Der ent, S., Pieterse, C.M., 2008. Plant immune responses triggered by beneficial microbes. *Curr. Opin. Plant Biol.* 11 (4), 443–448. <https://doi.org/10.1016/j.pbi.2008.05.005>.
- Wagner, M.R., Lundberg, D.S., Coleman-Derr, D., Tringe, S.G., Dangl, J.L., Mitchell-Olds, T., 2014. Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild *Arabidopsis* relative. *Ecol. Lett.* 17, 717–726.
- Wagner, M.R., Lundberg, D.S., del Rio, T.G., Tringe, S.G., Dangl, J.L., Mitchell-Olds, T., 2016. Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. *Nat. Commun.* 7, 12151.
- Westoby, M., Jurado, E., Leishman, M., 1992. Comparative evolutionary ecology of seed size. *Trends Ecol. Evol.* 7, 368–372.
- Whitman, T., Neurath, R., Perera, A., Chu-Jacoby, I., Ning, D., Zhou, J., Nico, P., Pett-Ridge, J., Firestone, M., 2018. Microbial community assembly differs across minerals in a rhizosphere microcosm. *Environ. Microbiol.* 0. <https://doi.org/10.1111/1462-2920.14366>.
- Wickham, H., 2009. *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag, New York.
- Wolfe, B.E., 2018. Using cultivated microbial communities to dissect microbiome assembly: challenges, limitations, and the path ahead. *mSystems* 3, e00161-17.
- Zahn, G., Amend, A.S., 2017. Foliar microbiome transplants confer disease resistance in a critically-endangered plant. *PeerJ* 5, e4020.