

Ecography

ECOG-03367

Menzel, A., Hempel, S., Davison, J., Moora, M., Pyšek, P., Rillig, M. C., Zobel, M. and Kühn, I. 2017. Widely distributed native and alien plant species differ in arbuscular mycorrhizal associations and related functional trait interactions. – Ecography doi: 10.1111/ecog.03367

Supplementary material

Appendix 1

14 **Table A1:** Summary of phylogenetically informed generalized linear models explaining the number of occupied grid cells in Germany.

15 The error probabilities for the main effect of mycorrhizal status, origin and each particular trait, as well as all possible two-way interactions and the

16 three-way interactions of all three predictors are displayed here. M=mycorrhizal status; O=origin; t=functional trait. Each cell includes degrees of

17 freedom (df), deviance (dev) and significance levels: $p \leq 0.001$ ***, $0.001 < p \leq 0.01$ **, $0.01 < p \leq 0.05$ *, $0.05 < p \leq 0.1$ +, ns – non-significant. Bold

18 rows indicate a significant three-way-interaction between mycorrhizal status, origin, and the particular functional trait; Italic rows indicate a

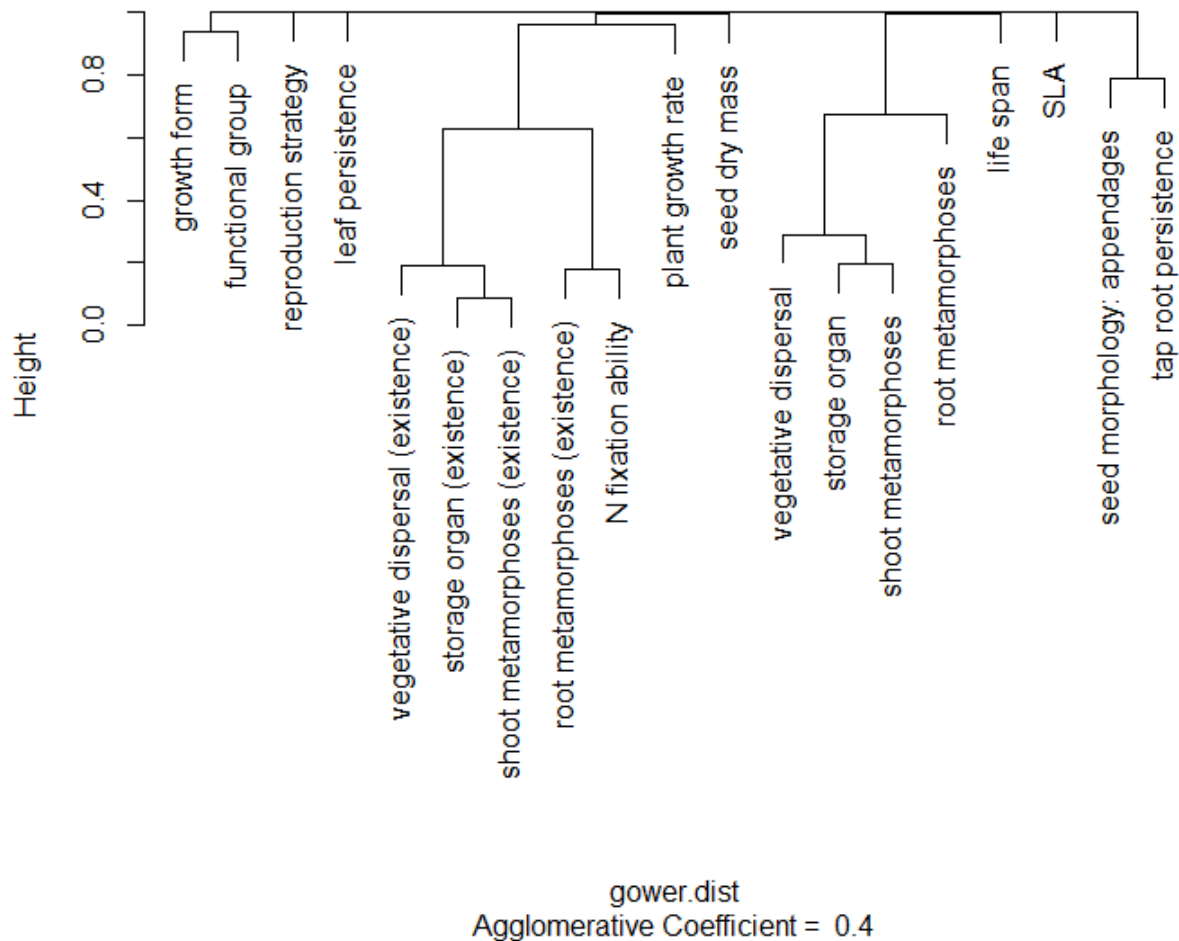
19 marginally significant three-way interaction between mycorrhizal status, origin, and the particular functional trait.

| functional trait | M×O×t | M×t | M×O | O×t | M | t | O |
|--------------------------------|-----------------------------------|------------------------------------|--|-------------------------------------|-------------------------------------|------------------------------------|--------------------------------------|
| <i>growth form</i> | <i>df=2</i> <i>dev=5</i> + | <i>df=2</i> <i>dev=6.1</i> * | <i>df=4</i> <i>dev=2.7</i> ns | <i>df=1</i> <i>dev=1.5</i> ns | <i>df=2</i> <i>dev=58</i> *** | <i>df=1</i> <i>dev=6.6</i> * | <i>df=2</i> <i>dev=104</i> *** |
| functional group | df=5 dev=12 * | df=9 dev=15 + | df=4 dev=1.5 ns | df=7 dev=18 *** | df=2 dev=58 *** | df=5 dev=12 * | df=2 dev=105 *** |
| storage organ (existence) | - | - | - | - | df=2 dev=58 *** | df=1 dev=.3 ns | df=2 dev=106 *** |
| storage organ | - | - | - | df=4 dev=9.2 + | df=2 dev=58 *** | df=8 dev=43 *** | df=2 dev=106 *** |
| root metamorphoses (existence) | - | - | - | - | df=2 dev=59 *** | df=1 dev=7.5 ** | df=2 dev=105 *** |
| root metamorphoses | - | - | - | df=3 dev=8.9 * | df=2 dev=59 *** | df=4 dev=8.5 + | df=2 dev=104 *** |
| shoot metamorphoses | - | - | - | - | df=2 | df=1 | df=2 |

| | | | | | | | |
|--|----------------------|------------------------|-----------------------|-----------------------|-----------------------|-----------------------|------------------------|
| (existence) | | | | | dev=58 *** | dev=.1 ns | dev=107 *** |
| shoot metamorphoses | df=7 dev=15 * | df=9 dev=7.5 ns | df=4 dev=4.6 ns | df=4 dev=3.6 ns | df=2 dev=57 *** | df=5 dev=19 ** | df=2 dev=94 *** |
| vegetative propagation and dispersal (existence) | df=3 dev=8 * | df=2 dev=.7 ns | df=4 dev=2.8 ns | df=2 dev=.1 ns | df=2 dev=58 *** | df=1 dev=.8 ns | df=2 dev=106 *** |
| vegetative propagation and dispersal | df=7 dev=21 ** | df=11 dev=9.4 ns | df=4 dev=3.6 ns | df=4 dev=8.1 ns | df=2 dev=56 *** | df=6 dev=18 ** | df=2 dev=99 *** |
| reproduction strategy | df=4 dev=9 + | df=4 dev=2.6 ns | df=4 dev=2.2 ns | df=2 dev=2.4 ns | df=2 dev=57 *** | df=2 dev=.5 ns | df=2 dev=109 *** |
| life span | - | - | - | - | df=2 dev=60 *** | df=2 dev=2.5 ns | df=2 dev=104 *** |
| leaf persistence | - | - | - | - | df=2 dev=53 *** | df=2 dev=8.1 * | df=2 dev=93 *** |
| nitrogen fixation ability | df=2 dev=4.8 + | df=2 dev=1.7 ns | df=4 dev=3.4 ns | df=1 dev=5.1 * | df=2 dev=59 *** | df=1 dev=2.8 + | df=2 dev=106 *** |
| tap root persistence | - | df=2 dev=5.2 + | - | - | df=2 dev=56 *** | df=1 dev=.6 ns | df=2 dev=46 *** |
| plant growth rate | - | - | - | - | df=2 dev=14 *** | df=1 dev=.8 ns | df=2 dev=44 *** |
| seed dry mass | df=4 dev=9.2 + | df=2 dev=1.2 ns | df=4 dev=2.7 ns | df=2 dev=17 *** | df=2 dev=47 *** | df=1 dev=4.2 * | df=2 dev=124 *** |

| | | | | | | | |
|---------------------------|----------------|----------------|----------------|----------------|---------------|----------------|---------------|
| <i>specific leaf area</i> | <i>df=4</i> | <i>df=2</i> | <i>df=4</i> | <i>df=2</i> | <i>df=2</i> | <i>df=1</i> | <i>df=2</i> |
| | <i>dev=8.1</i> | <i>dev=6.3</i> | <i>dev=2.7</i> | <i>dev=2.5</i> | <i>dev=32</i> | <i>dev=8.8</i> | <i>dev=67</i> |
| | + | * | <i>ns</i> | <i>ns</i> | *** | ** | *** |
| seed morphology: | df=6 | df=4 | df=4 | df=3 | df=2 | df=2 | df=2 |
| appendages | dev=16 | dev=4.6 | dev=.3 | dev=1.3 | dev=46 | dev=27 | dev=85 |
| | * | ns | ns | ns | *** | *** | *** |

Figure A1: Dendrogram illustrating correlations of the functional traits next to arbuscular mycorrhizal status, resulting of a cluster analysis based on a Gower's pairwise dissimilarity distance and agglomerative hierarchical clustering. The dendrogram was built using the package 'cluster' (Mächler et al. 2013) in R (version 3.0.2, R Development Core Team, 2013)



References:

Mächler M., Rousseeuw P., Struyf A., Hubert M. & Hornik K. (2013) *cluster: cluster analysis basics and extensions*. R package version 1.14.4.

R Development Core Team (2013) R: A Language and Environment for Statistical Computing. Tech. rep., Vienna, Austria. <https://www.r-project.org/>