**Supplemental methods**

*Extraction of beetle DNA and PCR:* For the beetles, DNA was extracted using a DNeasy DNA extraction kit (Qiagen, USA), following standard protocol for animal tissue except the sample was punctured to retain the morphology as a voucher. Vouchers of the specimens used remain in the UF Forest Entomology cryo-preserved collection. For fungi, fungal spore masses were aseptically dissected from the mycangium of female beetles that had been captured in flight, preserved in ethanol, and stored at -80 ºC. PCR was conducted on genomic DNA obtained by adding fungal spore masses to 5 µl of Sigma-Aldrich extraction solution (Extract-N-Amp, St. Louis MO.) and heating to 95 ºC for 30 m.

*Phylogenetics:* Genes were aligned using MAFFT-linsi with default settings [1]. Sequences were concatenated using Geneious R9.0.5 [2]. Regions of the alignment with less than 20% coverage, not including deletions (i.e. gaps), were eliminated from the dataset with a custom Python script. Tree topology and node support were estimated using Bayesian inference using Exabayes [3]. PLL-DPPDiv v1.0 [4, 5] was used to estimate a tree with relative node ages using default settings. Output trees were summarized to a single ultrametric tree with TreeAnnotator v1.7 [6]. For co-phylogenetic analysis, trees were trimmed of redundant taxa using Newick utilities [7].

*Artificial gallery construction and inoculation:* We chose the black twig borer, *Xylosandrus compactus*,as a model system for testing selectivity of the *Xylosandrus* mycangium for three reasons: 1) it is abundant and easily collected. 2) It can be reared on small twigs in laboratory conditions. And 3), this species is a globally invasive crop pest with increasing negative economic and ecological impacts. It is currently one of the largest concerns to coffee producers [8], and threatening to extinguish endemic island plant species [8, 9]. Female black twig borers excavate a longitudinal chamber by removing the pith from small healthy twigs, establish a fungal garden, and then lay eggs [10]. We simulated natural galleries using 4 – 8 mm diameter internode sections from healthy sweetgum twigs (*Liquidambar styraciflua*). Stems were cut to 50 mm lengths and split lengthwise. A Dremel® micro drill was used to create a longitudinal gallery by removing ~ 20 mm of pith from the center of each section, and to bore a simulated beetle entrance hole on one of the halves. The halves were rejoined with nylon cable ties, autoclave sterilized, and then inoculated with *Ambrosiella* by inserting a toothpick with fungal hyphae into the simulated beetle entrance hole. Paraffin wax was used to prevent drying by sealing each end of the stem sections. Inoculated galleries were placed individually in sterile Petri dishes and incubated at 25 ºC in the dark until the entire length was visibly colonized by *Ambrosiella* hyphae, typically 1 – 2 weeks. Galleries that failed to be fully colonized were discarded.

*Rearing laboratory broods:* Broods were reared by placing wild collected adult females individually in Petri dishes with one 50 mm section of freshly cut sweetgum stem that were sealed on both ends with paraffin wax. Females typically initiated galleries within 1 – 2 days. Stems with beetles were then incubated at 25 – 30 ºC and 90 – 100% RH, with 12 hr/d indirect full spectrum light, and opened after 19 – 22 d after gallery initiation to harvest third (ultimate) instar larvae. To minimize contamination in experimental galleries and vertical cross-contamination between developmental stages, larvae were double-separated from the native substrate: first by the incubation of pre-pupae on sterile moistened filter paper until they evacuated their gut contents and molted to pupae, and by a rapid second transfer of pupae to experimental galleries.

Literature Cited

1. Katoh K., Standley D.M. 2013 MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. *Molecular Biology and Evolution* **30**(4), 772-780. (doi:10.1093/molbev/mst010).

2. Kearse M., Moir R., Wilson A., Stones-Havas S., Cheung M., Sturrock S., Buxton S., Cooper A., Markowitz S., Duran C., et al. 2012 Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28**(12), 1647-1649. (doi:10.1093/bioinformatics/bts199).

3. Aberer A.J., Kobert K., Stamatakis A. 2014 ExaBayes: Massively Parallel Bayesian Tree Inference for the Whole-Genome Era. *Molecular Biology and Evolution* **31**(10), 2553-2556. (doi:10.1093/molbev/msu236).

4. Heath T.A., Holder M.T., Huelsenbeck J.P. 2011 A dirichlet process prior for estimating lineage-specific substitution rates. *Molecular biology and evolution* **29**(3), 939-955.

5. Flouri T., Stamatakis A. 2012 An improvement to DPPDIV. *Heidelberg Institute for Theoretical Studies, Heidelberg, Germany, Exelixis-RRDR-2012-7 Available at* [*http://sco*](http://sco) *h-its org/exelixis/pubs/Exelixis-RRDR-2012-7 pdf*.

6. Drummond A.J., Suchard M.A., Xie D., Rambaut A. 2012 Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Molecular biology and evolution* **29**(8), 1969-1973.

7. Junier T., Zdobnov E.M. 2010 The Newick utilities: high-throughput phylogenetic tree processing in the UNIX shell. *Bioinformatics* **26**(13), 1669-1670.

8. Greco E., Wright M.G. 2015 Ecology, biology, and management of Xylosandrus compactus (Coleoptera: Curculionidae: Scolytinae) with emphasis on coffee in Hawaii. *Journal of Integrated Pest Management* **6**(1).

9. Daehler C.C., Dudley N. 2002 Impact of the black twig borer, an introduced insect pest, on Acacia koa in the Hawaiian Islands. *MICRONESICA-AGANA-* **35**, 35-53.

10. Hara A.H., Beardsley J.W. 1979 The biology of the black twig borer, Xylosandrus compactus (Eichhoff), in Hawaii. *Proceedings of Hawaiian Entomological Society* **8**(1).