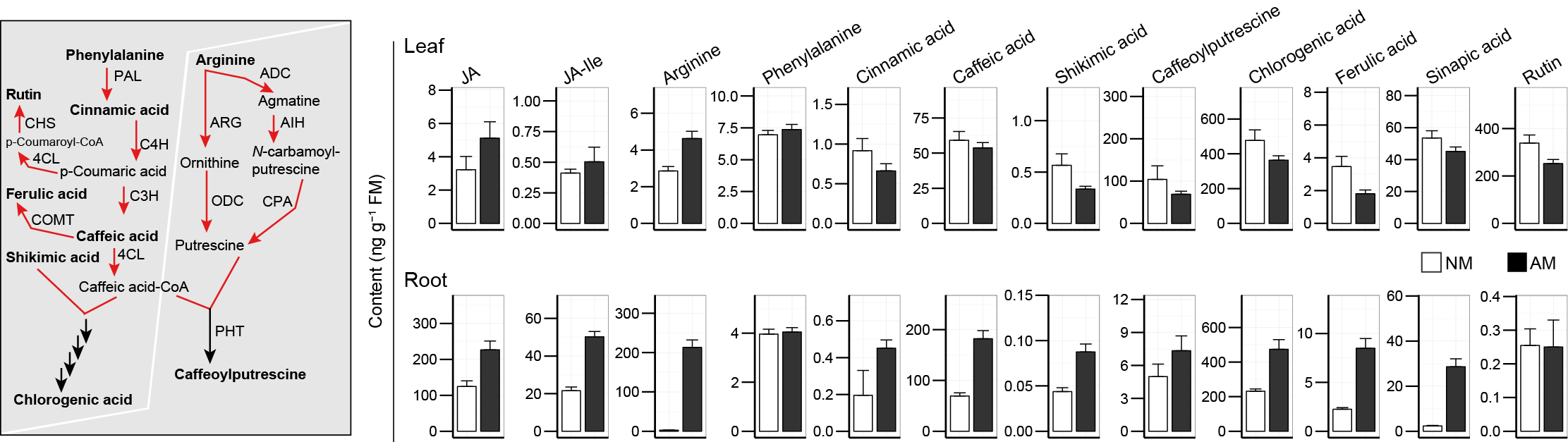
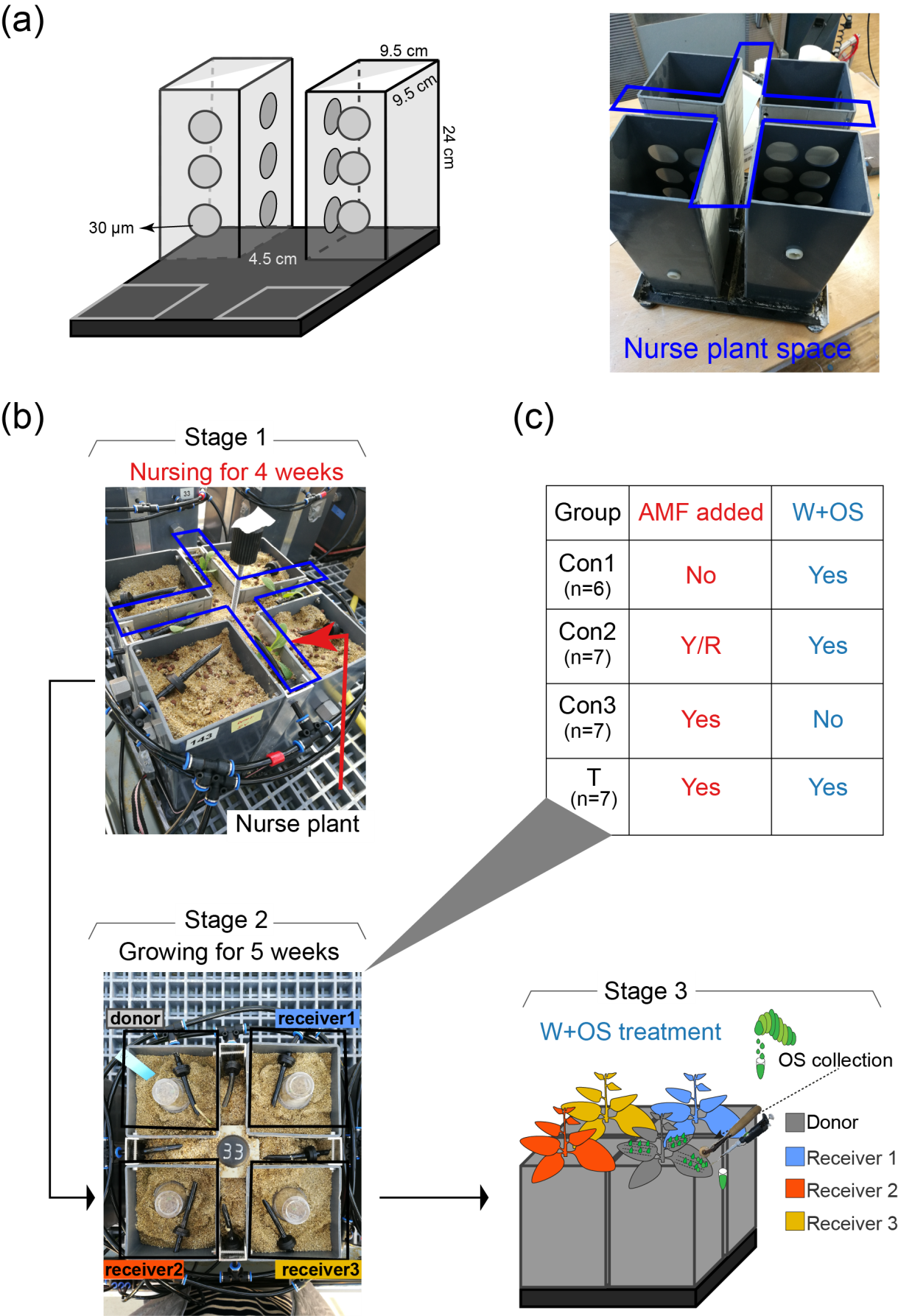
**Supporting information**

****

**Fig. S1** AMF-induced increases in constitutive jasmonates in the roots of *N. attenuata* do not translate into systemic increases in JA-dependent secondary metabolites in leaves

Representative phenolic metabolites in *N. attenuata* were induced in roots but not in leaves after inoculation with *R. irregularis.* (a) Simplified biosynthetic pathway for caffeoylputrescine and chlorogenic acid; the levels of intermediates in this pathway were quantified in both root and leaf tissues after AMF inoculation. (b) Samples were harvested from EV plants inoculated with *R. irregularis* (6 wpi). AMF inoculated groups were labeled as “AM”, and non-inoculated groups as “NM”. Data are means (± SD), statistical significance was evaluated with Student’s t tests (\**p≤*0.05, \*\**p≤*0.01, \*\*\**p≤*0.001).

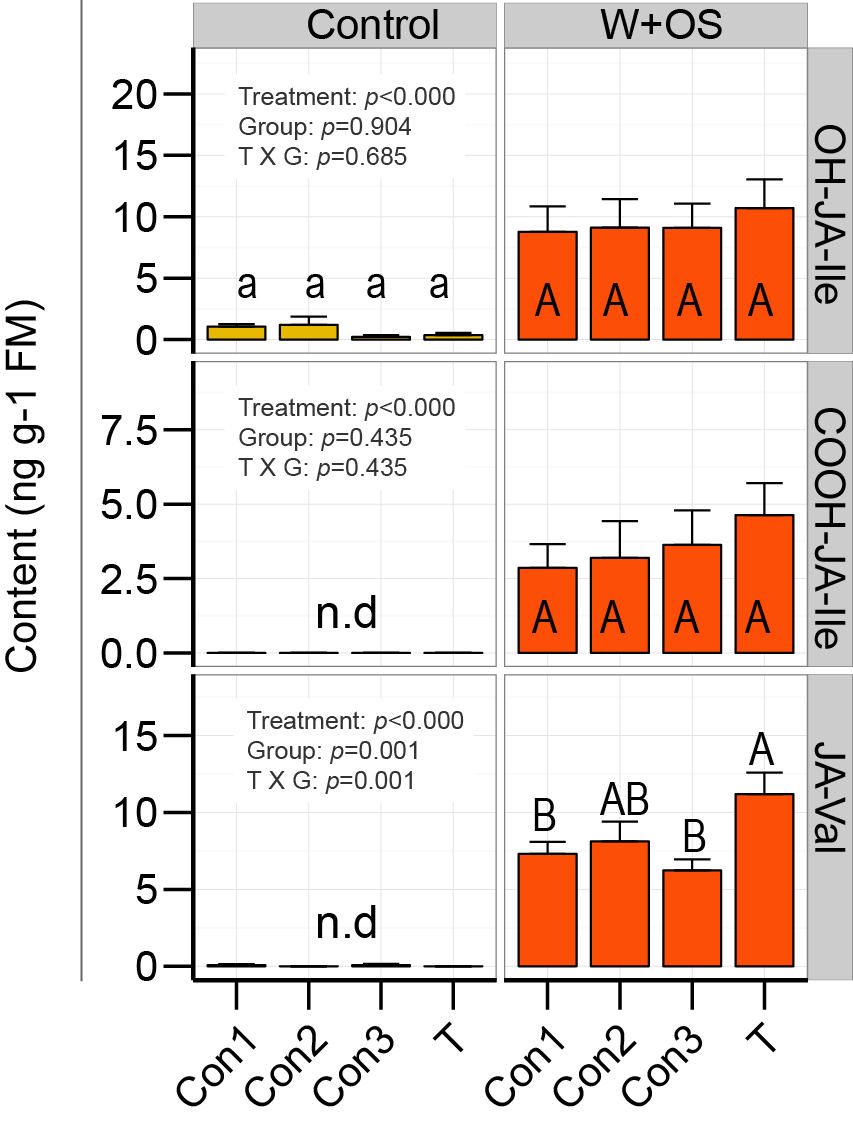


**Fig. S2** Mesocosm design, mesocosms grouping and experimental procedures.

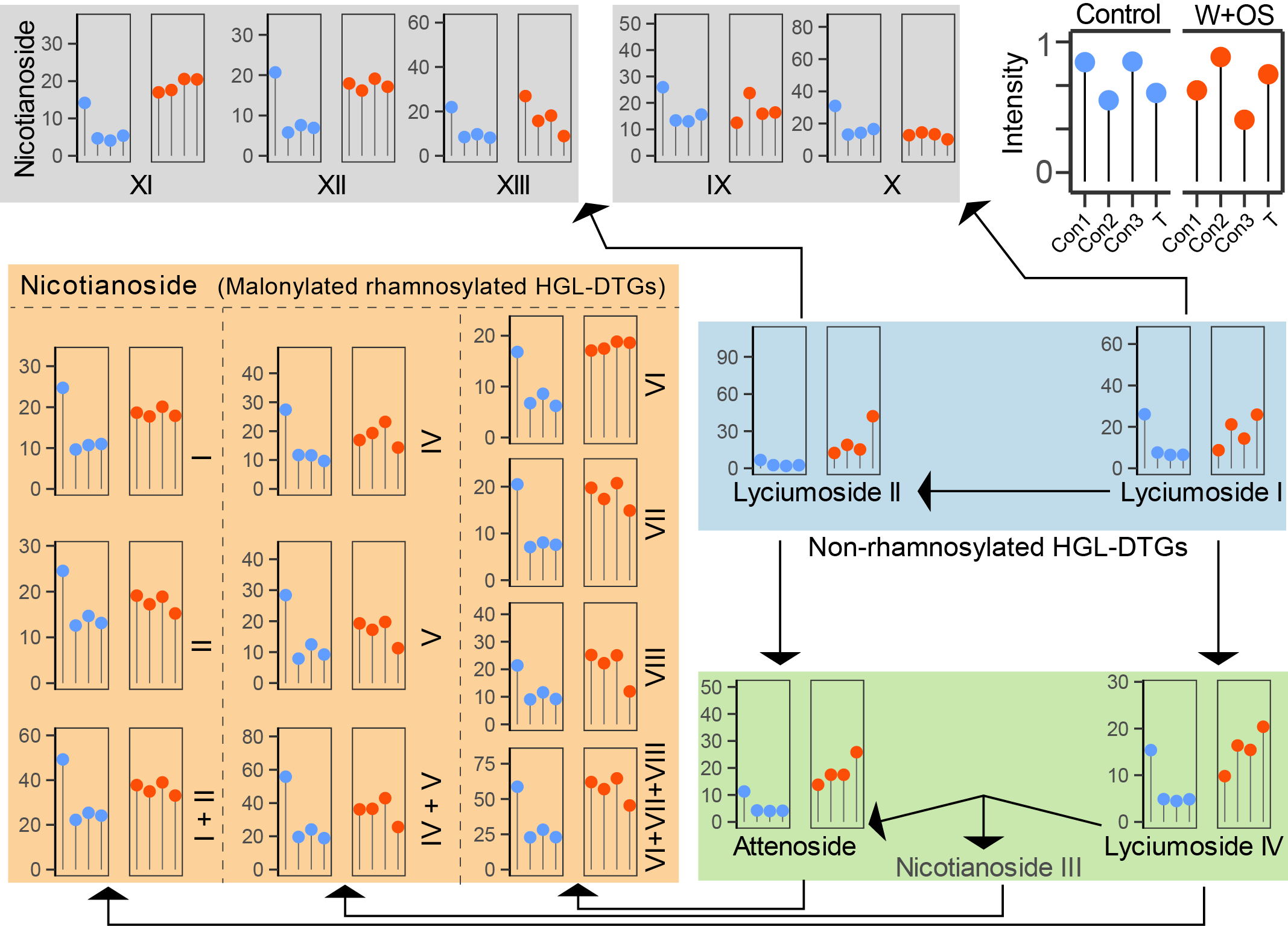
(a) Mesocosm designed to test the hypothesis of CMN-mediated OS-elicited JA signaling: 4 boxes [length: width: height=9.5: 9.5: 24 (cm)] constitute a single mesocosm, and each box is separated by metal mesh (pore diameter=30 µm), which excludes plant roots but allows mycelia to penetrate. The spaces separating the 4 boxes of each mesocosm (4.5 cm) were planted with *N. attenuata* WT nurse plants inoculated with autoclaved or live *R. irregularis* inoculum. (b) The nurse plants were grown for 4 weeks to activate AMF spores and establish an AMF network that extended into all 4 boxes of the mesocom; these nurse plants were removed just prior to the planting of the experimental plants into their individual boxes for an additional 5 weeks of growth, before plants were W+OS elicited which started the sampling sequence (detailed in Fig. 4a). The four individual plants that comprised each experimental mesocosm were named as: “donor”, “receivers” 1 to 3. (c) Mesocosms were assigned to 4 different treatments that combined AMF addition (in red) and W+OS treatment with “donors” (in blue) with the following terms defined:

If autoclaved AMF inoculum was used: “N”; active inoculum: “Y”; the AMF mycelial network connections among plants were removed by emptying the soil (just prior to first W+OS elicitation) from the spaces separating the boxes that were originally occupied by the nurse plants: (Y/R).

If “donor” plants were treated with W+OS: (Y), if not (N). Based on different combinations of these treatments, Con1, Con2, Con3 and T groups are defined.



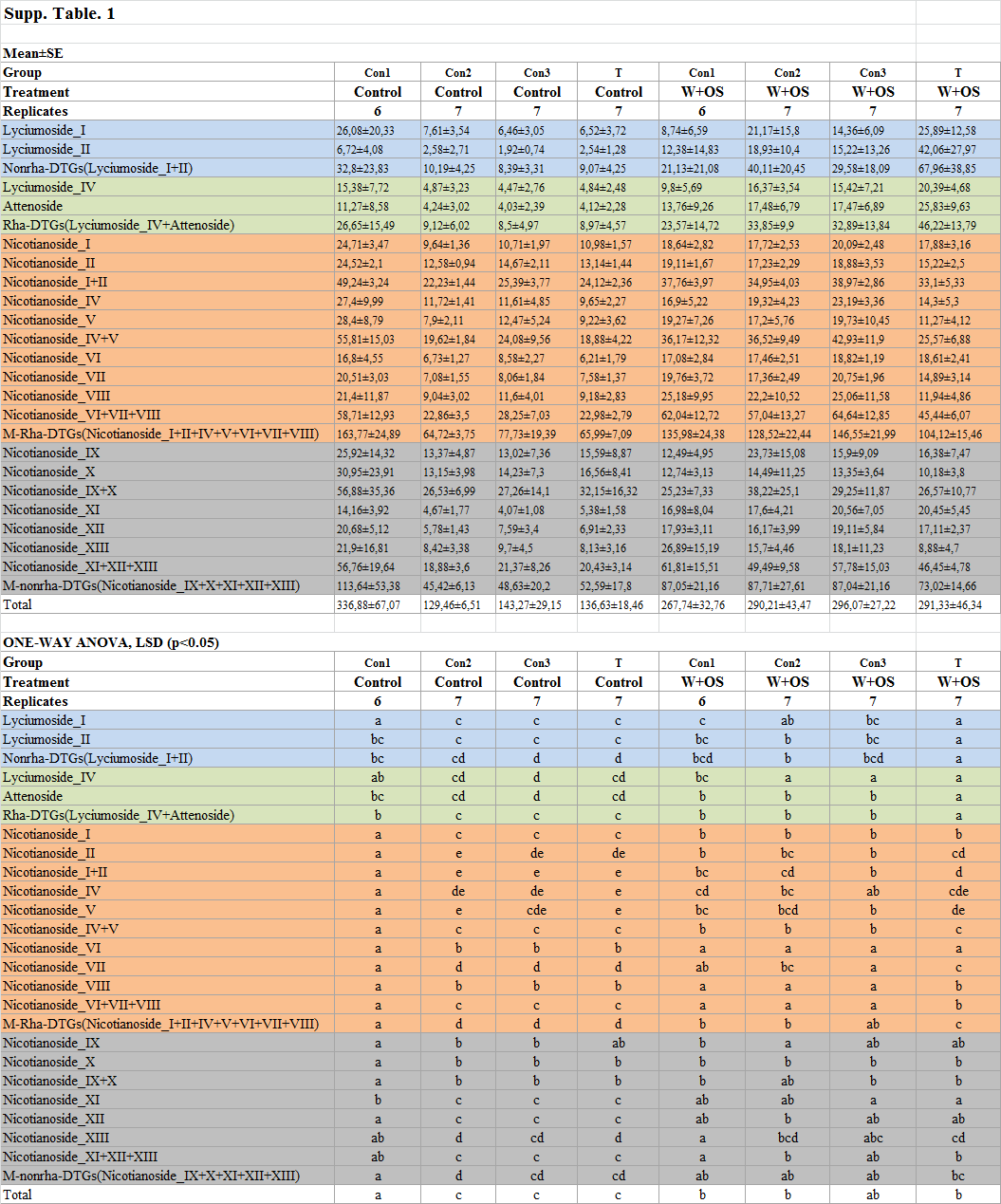
**Fig. S3** Evidence of AMF-mediated defense priming: bursts of inactive jasmonate forms are not amplified in the “receiver” plants of the AMF mycelia group (T) after the W+OS elicitation of the “donor” plants. Details are as described in Fig. 4.



**Fig. S4** Hydroxygeranyllinalool diterpene glycosides (HGL-DTGs) exhibit compound-specific increases in response to W+OS elicitation among the 4 mesocosm treatment groups.

The biological replicates used and the quantification method for HGL-DTG analysis are as described in Fig. 7. Data are means (±SE; Con1, n=6; Con2, n=7; Con3, n=7; T, n=7). For the statistical analysis see Table. S1.

**Table. S1** Numerical values of each HGL-DTG relative concentration and statistical analysis.



Data presented in Fig. 7 and Fig. S3, sampling and analysis is described in Fig. 4, and background colors are the same as in Fig. 7 and Fig. S3. Different letters indicate significant differences (*p*<0.05, one-way ANOVA followed by Fisher’s LSD)

**Table. S2** Primer sequences for Quantitative (q)PCR.

|  |  |  |  |
| --- | --- | --- | --- |
| GeneBank | Name | Forward | Reverse |
| EXX64097.1 | *Ri-tub* | TGTCCAACCGGTTTTAAAGT | AAAGCACGTTTGGCGTACAT |
| XP\_019258720.1 | *NaSTR1* | TCAGGCTTCCACCTTCAATATCT | GACTCTCCGACGTTCTCCC |
| XP\_019267066.1 | *NaPT4* | GGGGCTCGTTTCAATGATTA | AACACGATCCGCCAAACAT |
| XP\_019246749 | *NaIF-5a* | GTCGGACGAAGAACACCATT | CACATCACAGTTGTGGGAGG |