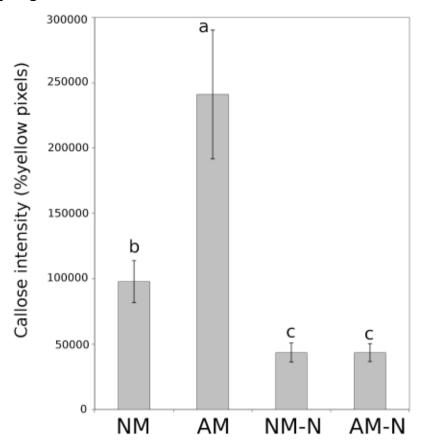
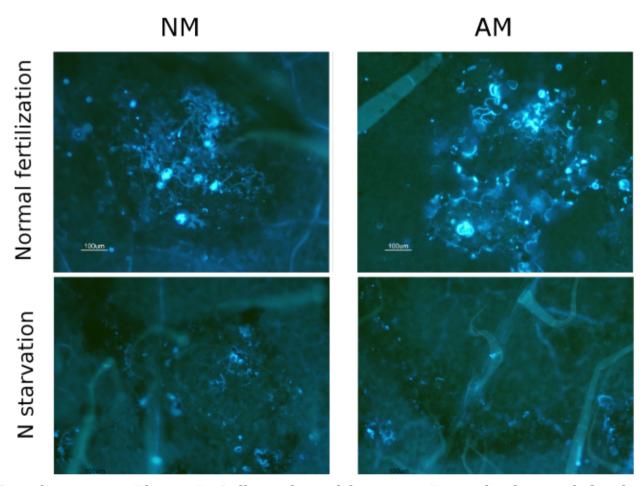
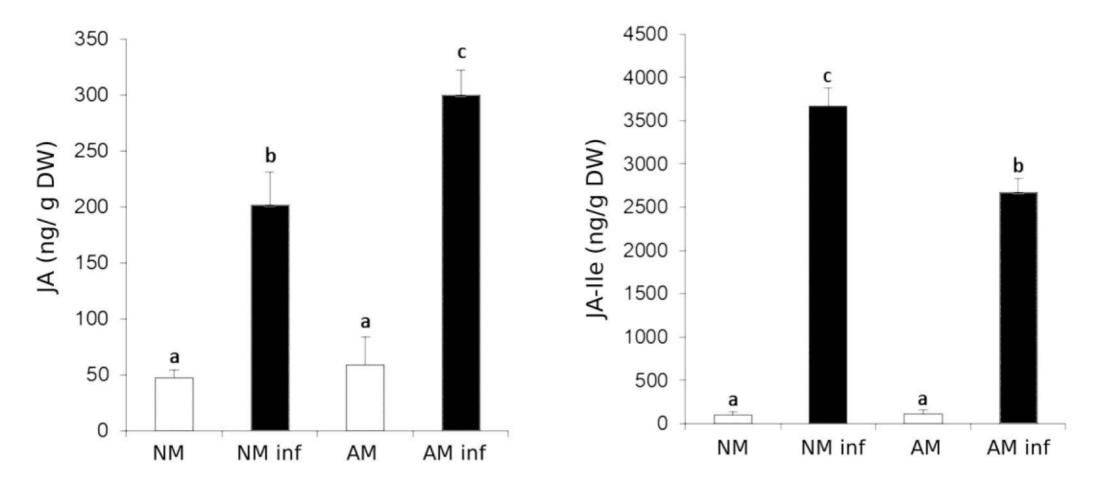
Supplementary Table 1. List of primers used for qPCR analysis.

Primer name	PCR primers sequence $(5' \rightarrow 3')$	Gene ID (NCBI)
ACT-52	F – CACCATTGGGTCTGAGCG	101263261
	R – GGGCGACAACCTTGATCT	
ATL31	F – CGTACTGCTGCTACTCG	101265719
	R – CATGAGATTTGAGCCAAGCA	
BAM1	F – TCGAGTTCTGTTATGCGTTTTG	100736451
	R – TCTCCTCAACAACCCACCTC	
BC-TUB	F – CCGTCATGTCCGGTGTTACCAC	5441652
	R – CGACCGTTACGGAAATCGGAA	
EF-1	F – GATTGGTGGTATTGGAACTGTC	101244084
	R – AGCTTCGTGGTGCATCTC	
LIN6	F – AGCACATTTATTCGCCTTCAAC	543502
	R – TTTGTGACGTGGCATAATAAGA	
PMR4	F – GCCGGCGGCGAGACAAGTTT	101243903
	R – CAGCGCCAGCCAGTCAAGCA	
SUS1	F – GGATTGAAAGCCACGGAAAGG	543961
	R – ACCAGGCCTCAACGAATAGCA	
SUS3	F – GGTTTCTGTCTGATTGTTATCC	543731
	R – ACAGAAGGGAAAAATGGCAAA	
SUT1	F – TTCCATAGCTGCTGGTGTTC	544099
	R – TACCAGAAATGGGTCCACAA	
SUT2	F – CCTACAGCGTCCCTTTCTCT	543613
	R – GGATACAACCATCTGAGGTACAA	
SUT4	F – TCTCCGCTGATATTGGATGG	543620
	R – GCAACATCGAGAAGCCAAAA	
SWEET4	F – CTGGGACGATGAAGAAAAGC	101246848
	R – GTGGCTTTAAACTGTGTCCG	
SWEET15	F – ACGCAAAGCCAGCGATAGAT	101255592
	R – ACGTCTTCGGAATCAACAGG	
SWEET17	F – GCTCGGCCCATCTTATGAAA	101255592
	R – GGCAGGCTTTTCCATTTGTG	
SYP121	F – AAGGCAAAGAATGGCATCTG	101247381
	R – TGTCCTCTTCCTTGCTCCTG	

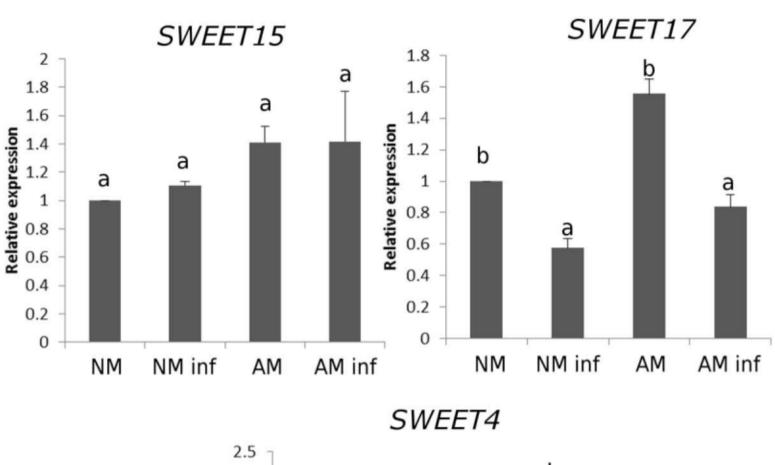


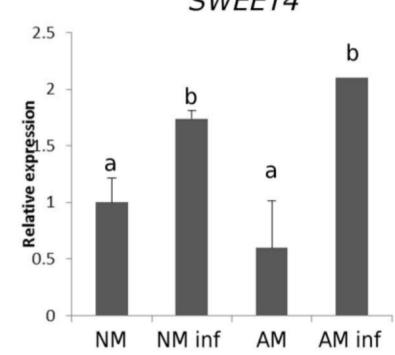


Supplementary Figure 1. Callose deposition upon *Botrytis cinerea* **infection under Nitrogen starvation**. (A) Level of callose in non-mycorrhizal (NM) and mycorrhizal (AM) infected tomato plants under normal fertilization and under 48h of nitrogen starvation (-N). Three different replicates, which consist in three pooled plants per condition, were carried out. Standard error is represented by error bars. (*) represents statistically significant differences (T-test; n = 9).



Supplementary Figure 2. **Oxylipin levels.** Targeted analysis of oxylipin hormones, JA and JA-isoleucine, in non-mycorrhizal (NM) and mycorrhizal (AM) plants 72 hpi. For each combination, infected leaves from three plants were pooled. Experiments were repeated three times to have different replicates. Letters indicate statistically significant differences (ANOVA, Fisher's least significant difference [LSD] test; p < 0.05, n = 9).





Supplementary Figure 3. Expression levels of different SWEET sugar transporter genes. Levels of SWEET sugar transporters (4, 15 and 17) gene expression in non-mycorrhizal (NM) and mycorrhizal (AM) non-infected and infected (inf) tomato plants at 72 hpi. Experiments were repeated three times to have different replicates, which consist in three pooled plants for each combination. The standard error of the mean is represented by error bars and statistically significant differences are represented by different letters (ANOVA, Fisher's least significant difference [LSD] test; p < 0.05, n = 9).