

TABLE S1 Identification of fungal strains by sequencing of ITS1-D2 rRNA gene region (rRNA) and partial sequences of actin (ACT) and translation elongation factor 1- α (TEF) genes. Reported % of identity was the highest match in BLAST search.

Strain	Highest Match	Identity %	Reference GenBank Accession numbers rRNA, ACT, TEF	Deposited GenBank Accession numbers rRNA, ACT, TEF
T1.PL.1	<i>Cladosporium pseudocladosporioides</i>	100	KJ596320.1	KU605794
		100	HM148674.1	KU605800
		100	HM148424.1	KU605786
A2.PP.5	<i>Cladosporium tenuissimum</i>	100	KJ596320.1	KU605789
		100	HM148694.1	KU605796
		99	HM148424.1	KU605782
BP8.I.3	<i>Cladosporium asperulatum</i>	100	AY251074.2	KU605793
		100	KT600576.1	KU605799
		97	LN834453.1	KU605785
A3.I.1	<i>Cladosporium tenuissimum</i>	100	AY251074.2	KU605790
		100	HM148694.1	KU605797
		99	HM148457.1	KU605783
BP3.I.2	<i>Cladosporium asperulatum</i>	99	AY251074.2	KU605791
		100	KT600576.1	KU605798
		96	LN834453.1	KU605784
A2.H.4	<i>Cladosporium montecillanum</i>	100	AY251074.2	KU605787
		100	KT600604.1	KU605795
		96	KT600504.1	KU605781
BP3.I.7*	<i>Penicillium chrysogenum</i>	100	FJ613114.1	KU605792
A2.PL.1*	<i>Aspergillus fumigatus</i>	100	FJ867935.1	KU605788

* Strains only identified by sequencing of ITS1-D2 rRNA gene region.

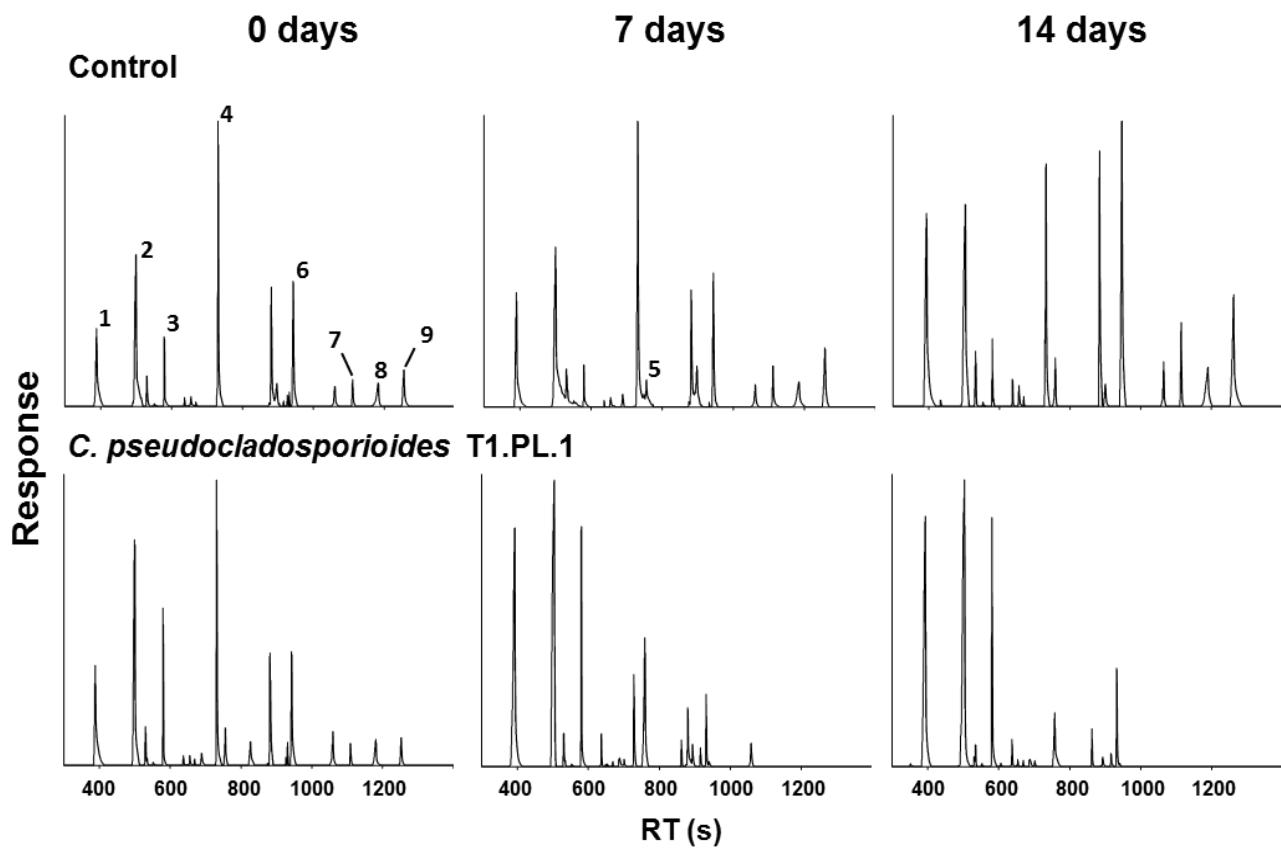
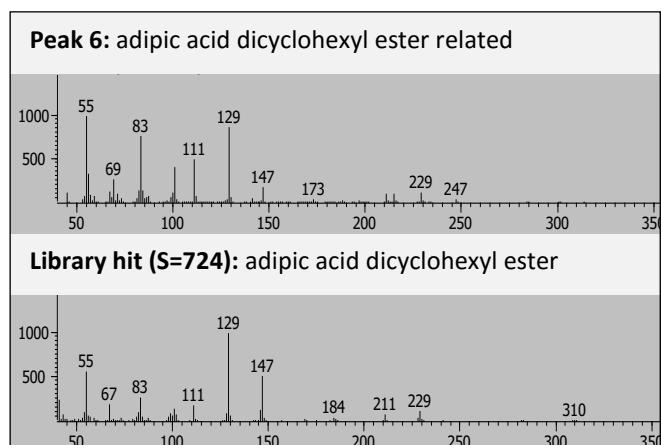
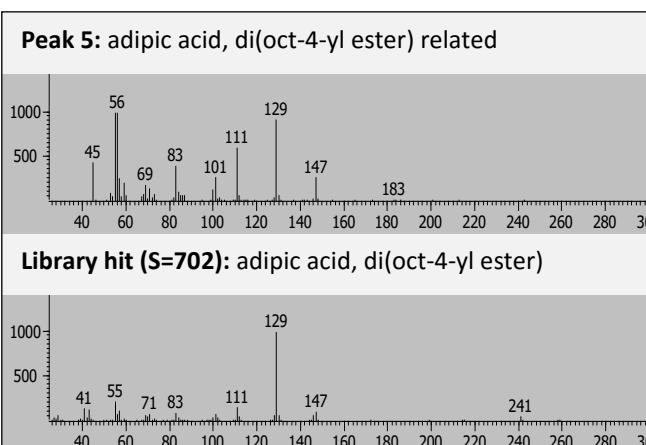
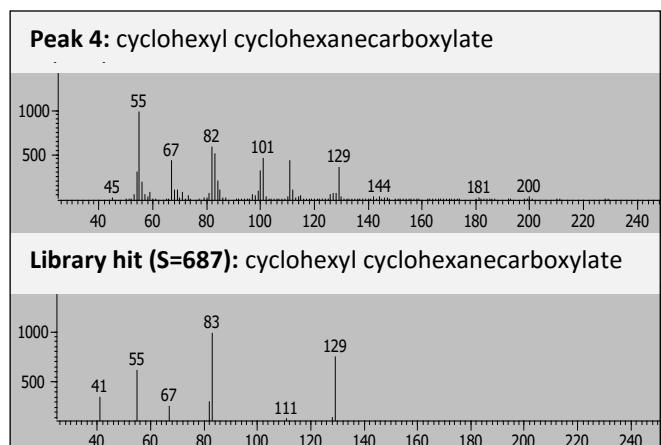
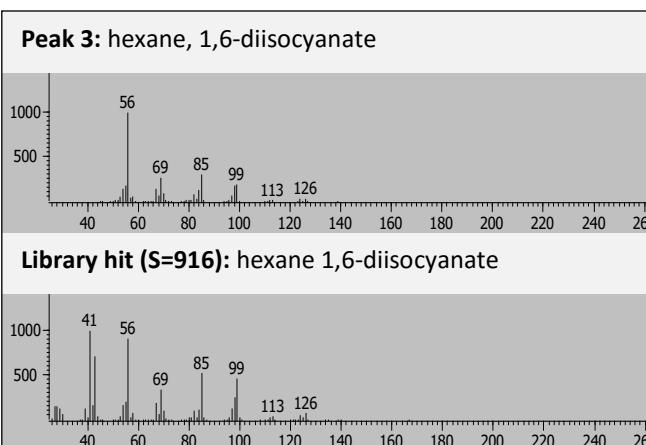
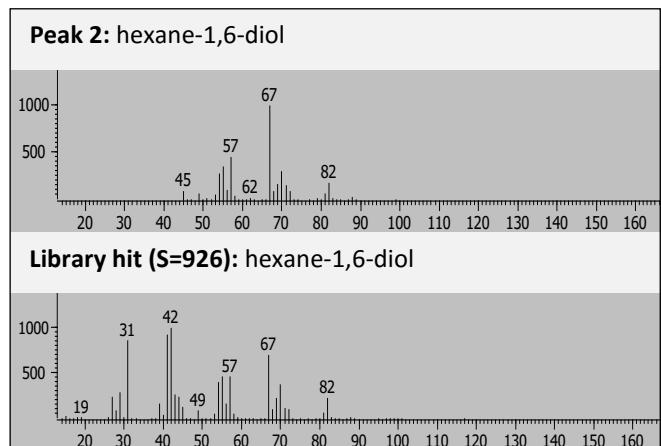
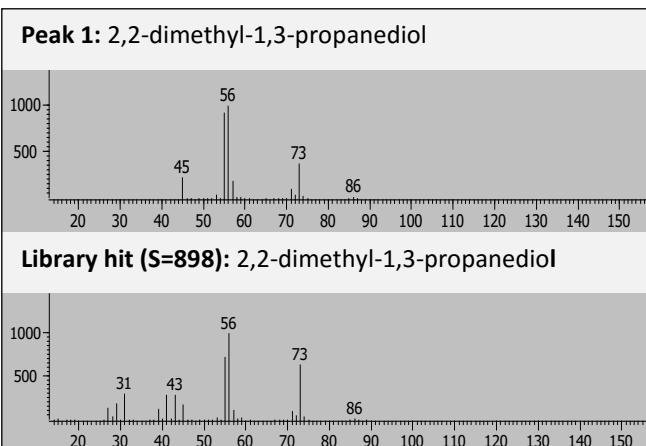


FIG S1. Gas chromatography analysis of compounds present in MM with Impranil after incubation with *Cladosporium pseudocladosporioides* strain T1.PL.1. Supernatants of non-inoculated and fungus-inoculated MM with Impranil cultures incubated at 25 °C for 0, 7, and 14 days were extracted with dichloromethane and analyzed by GC-MS. Numbers indicate representative peaks referred to tentatively identified compounds included in Table 1.



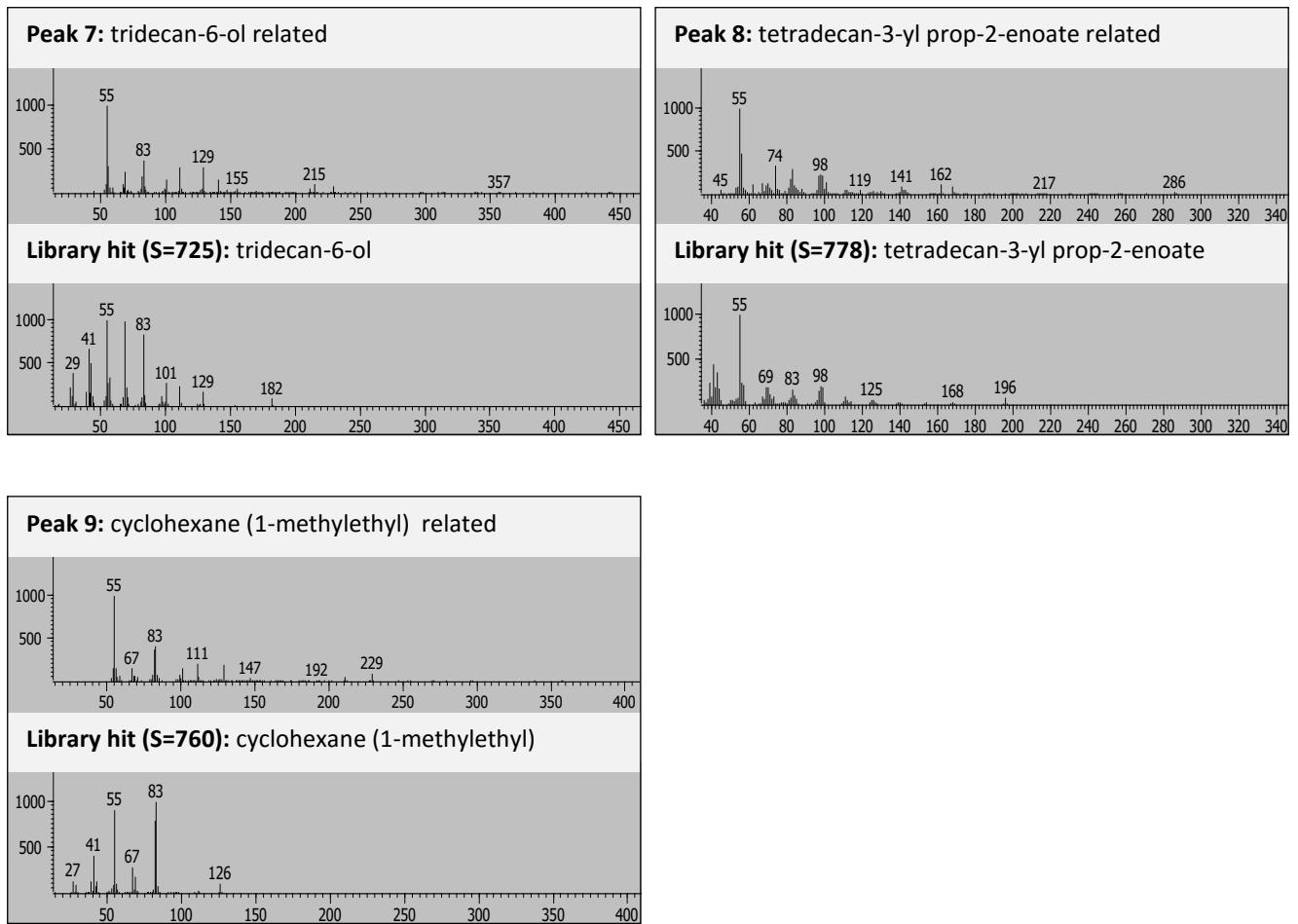


FIG S2. Mass spectra of compounds detected by GC-MS analysis of MM-Impranil supernatants incubated with *Cladosporium pseudocladosporioides* T1.PL.1. Each panel corresponds to a peak; upper image, mass spectrum of the compound detected in the sample; lower image, mass spectrum of the most similar compound from the NIST Mass Spec Data Center (2002 Library). S= similarity.