Supplemental material

(a)

(b)

(c)

Fig. S1: Alignments for identification of IAA biosynthesis genes from *T. vaccinum*. Conceptually translated sequences for *tam1*, *ipd1* and *iah1* were aligned with four most similar sequences in BLASTp using MAFFT and BioEdit alignments. Tam1 (1: KP096350) was aligned to sequences 2 (KDR75974 of *Galerina marginata*), 3 (KDQ24236 of *Pleurotus ostreatus*), 4 (KDR77824 of *Galerina marginata*) and 5 (XP_007868862 of *Gloeophyllum trabeum*) (a), Ipd1 (1: KP096351) was aligned to 2 (XP_007845706 of *Moniliophthora roreri*), 3 (KDQ25837 of *Pleurotus ostreatus*), 4 (KDR82740 of *Galerina marginata*) and 5 (XP_001875889 of *Laccaria bicolor*) (b); Iah1 (1: KP096352) was similar to 2 (KDR84180 of *Galerina marginata*), 3 (XP_007329104 of *Agaricus bisporus*), 4 (XP_006456935 of *Agaricus bisporus*) and 5 (XP_007846638 of *Moniliophthora roreri*) (c).

Tab. S1: Orthologs in mycorrhizal, plant-pathogenic/parasitic as well as saprobic fungi for the enzymes Tam1, Ipd1, Ald1 and Iah1 suggested to be involved in IAA production in *T. vaccinum* (protein-IDs, JGI http://genome.jgi-psf.org, in brackets).

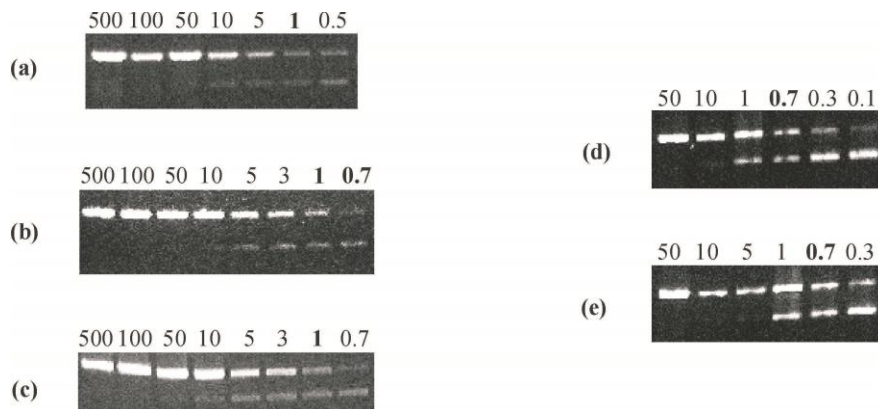| Protein	Mycorrhizal	Plant-pathogenic/parasitic	Saprobic
Tam1	*Laccaria bicolor* (191053); *Paxillus involutus* ATCC 200175 (103787); *Tricholoma matsutake* 945 (1422813); *Suillus luteus* UH-Slu-Lm8-n1 (801906)	*Armillaria mellea* (7757)	*Heterobasidion annosum* (458781); *Schizophyllum commune* H4-8 (2616666);
Ipd1	*Laccaria bicolor* (188370); *Paxillus involutus* ATCC 200175 (175618); *Tricholoma matsutake* 945 (1425307); *Suillus luteus* UH-Slu-Lm8-n1 (94806)	*Armillaria mellea* (6628)	*Heterobasidion annosum* (440059); *Schizophyllum commune* H4-8 (2626643); *Schizophyllum commune* H4-8 (2637783)
Ald1	*Laccaria bicolor* (256254); *Laccaria bicolor* (191009); *Paxillus involutus* ATCC 200175 (182543); *Paxillus involutus* ATCC 200175 (76843); *Tricholoma matsutake* 945 (1284147); *Tricholoma matsutake* 945 (1444458); *Tricholoma matsutake* 945 (1295949); *Tricholoma matsutake* 945 (1308658); *Suillus luteus* UH-Slu-Lm8-n1 (803802); *Suillus luteus* UH-Slu-Lm8-n1 (807535); *Suillus luteus* UH-Slu-Lm8-n1 (807087)	*Armillaria mellea* (9343); *Armillaria mellea* (5490); *Armillaria mellea* (3731); *Armillaria mellea* (13567)	*Heterobasidion annosum* (454399); *Schizophyllum commune* H4-8 (1156481); *Schizophyllum commune* H4-8 (2606953)
Iah1	*Tricholoma matsutake* 945 (290237)		

Fig. S2: Expression of *ald1* in *T. vaccinum* mycorrhiza. Competitive PCR was used to estimate the relative amount of the transcript using 1 ng cDNA for the control with mycelium from pure culture (a), and 0.02 ng fungal cDNA from mycorrhizal tissues Hartig' net (b) and hyphal mantle (c) from 3 weeks and (d) 3 months co-cultures with the compatible host, spruce and (e) the low compatibile host, pine; the bold numbers indicate bands of the same intensity with the competitor. 1 pg *ald1* transcript was found in the pure culture, making it 10^{-3} of cDNA. In Hartig' net 0.7 to 1 pg was found making it 1:20 of all cDNA and thus approximately 40-fold more compared to pure culture. For mantle, 50-fold and in compatible interaction (45-fold) or for low compatibility (30-fold) can be calculated.
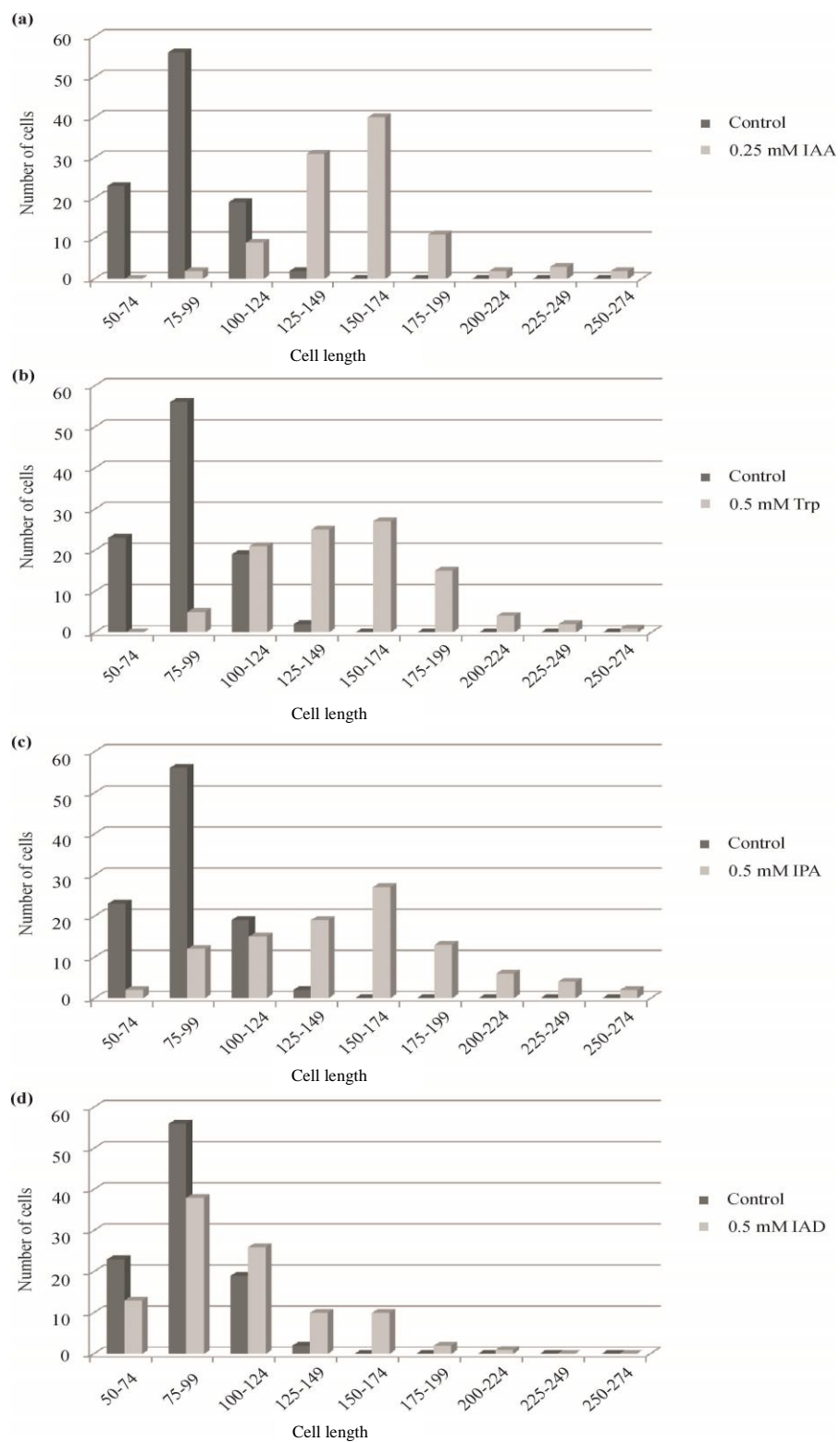
Fig. S3: Influence of IAA and precursors on cell length distribution. MMNb control was compared to 0.25 mM IAA (a), 0.5 mM Trp (b), 0.5 mM IPA (c) and 0.5 mM IAD (d) treatments.
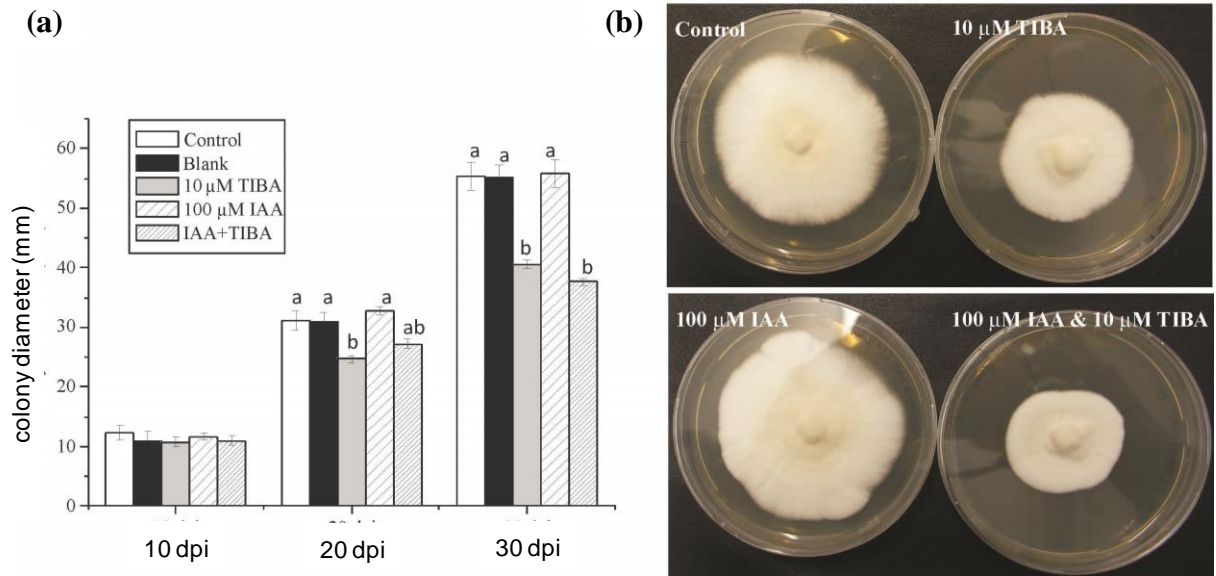
Fig. S4: Growth of *T. vaccinum* after 4-week application of IAA with or without addition of TIBA blocking IAA uptake. Fungal growth was measured as colony diameter, bars denote standard error, letters indicate significant differences (a); representative plate cultures (b).
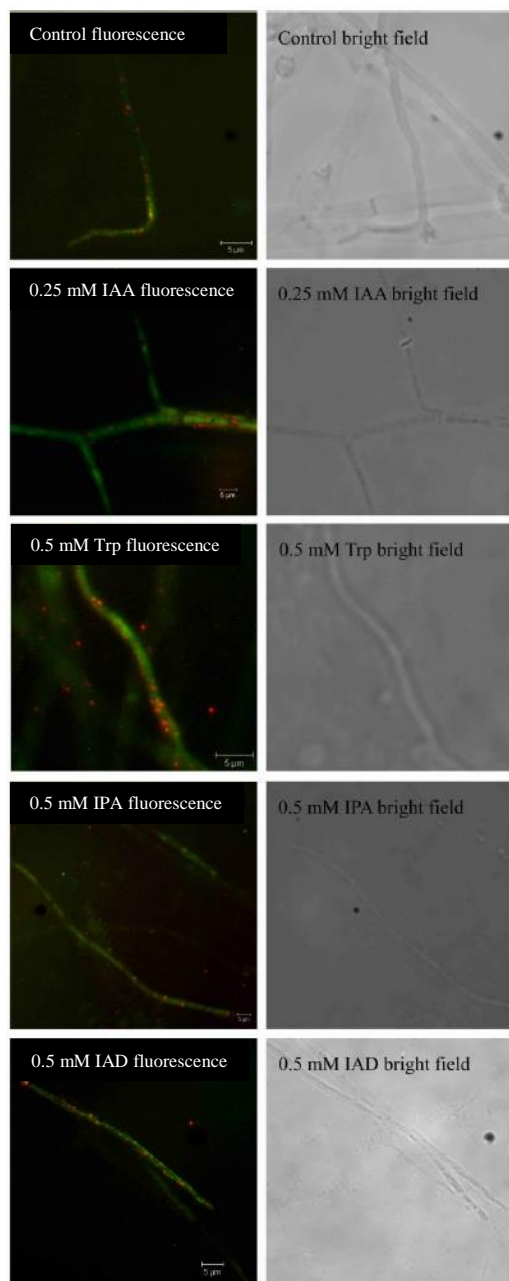
Fig. S5: Cytoskeleton of hyphae of *T. vaccinum* stained with immunofluorescence for actin (red) and tubulin (green) after treatment with 0.25 mM IAA and 0.5 mM of different IAA precursors in the tryptophan dependent pathway. Corresponding bright field picture is given on the right side.