

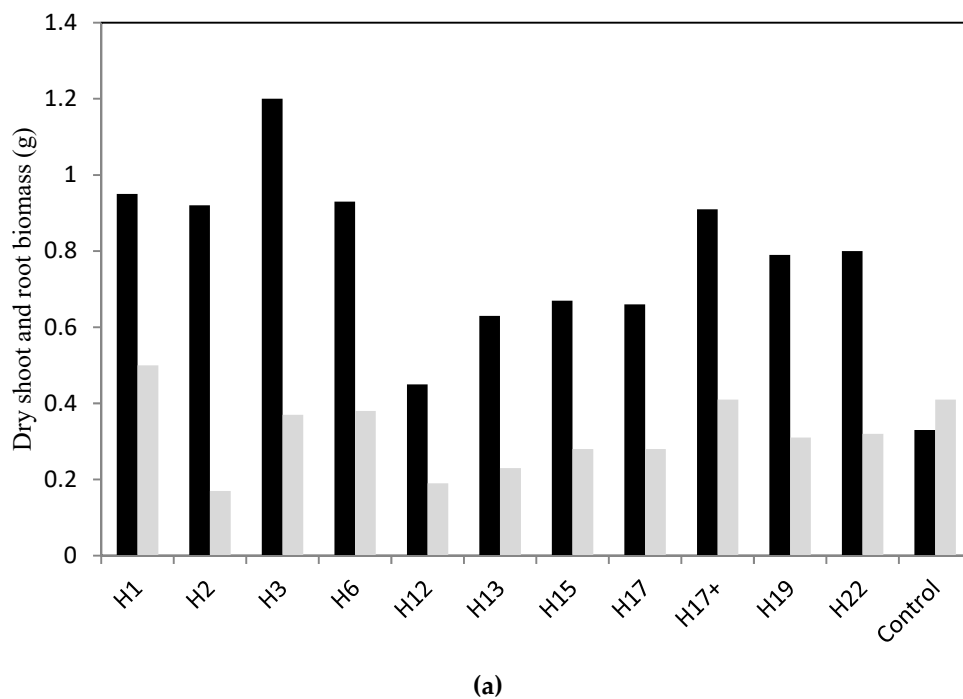
Different Green Manures (*Vicia villosa* and *Brassica juncea*) Construct Different Fungal Structures, Including Plant-Growth-Promoting Effects, after Incorporation into the Soil

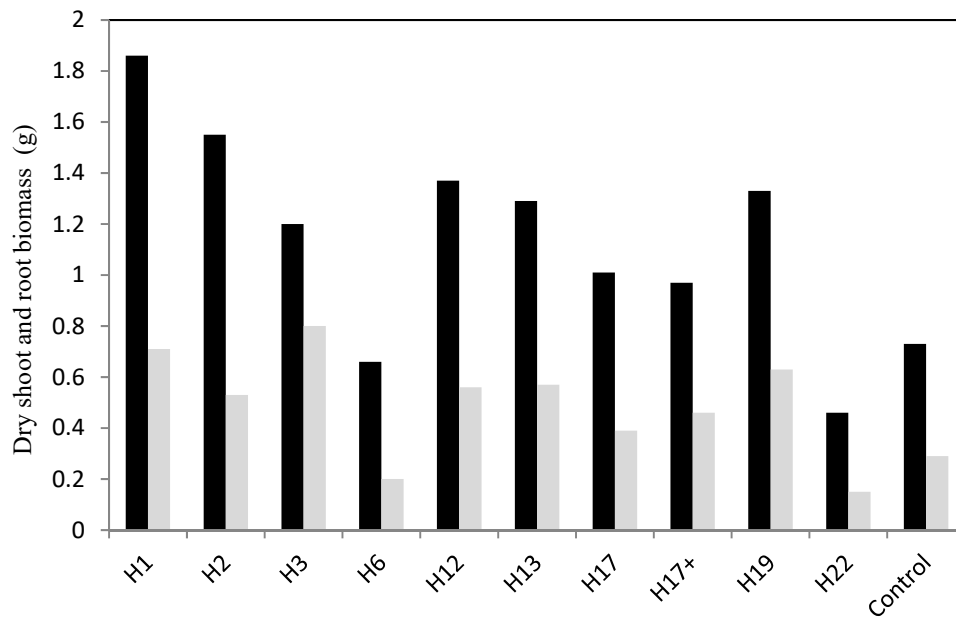
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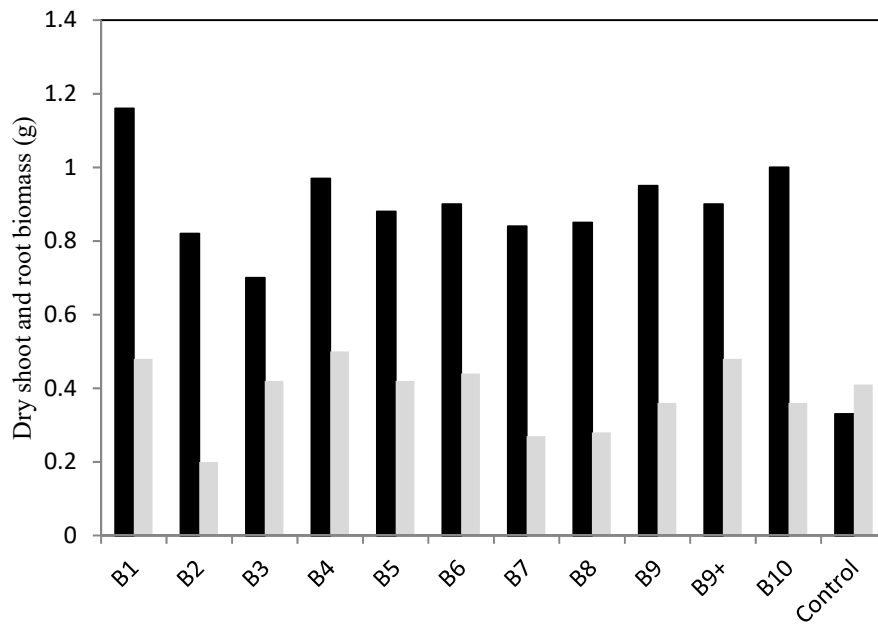
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Supplementary





(b)



(c)

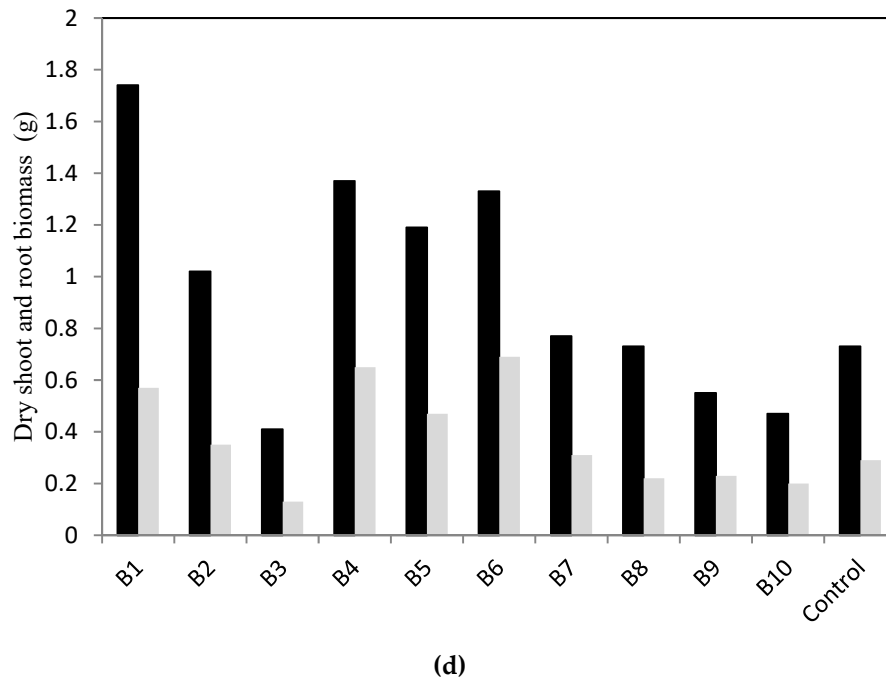
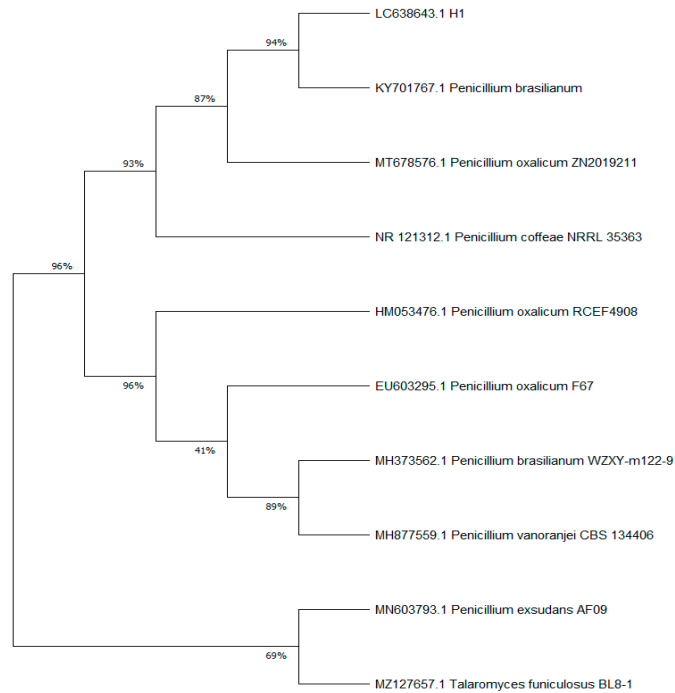
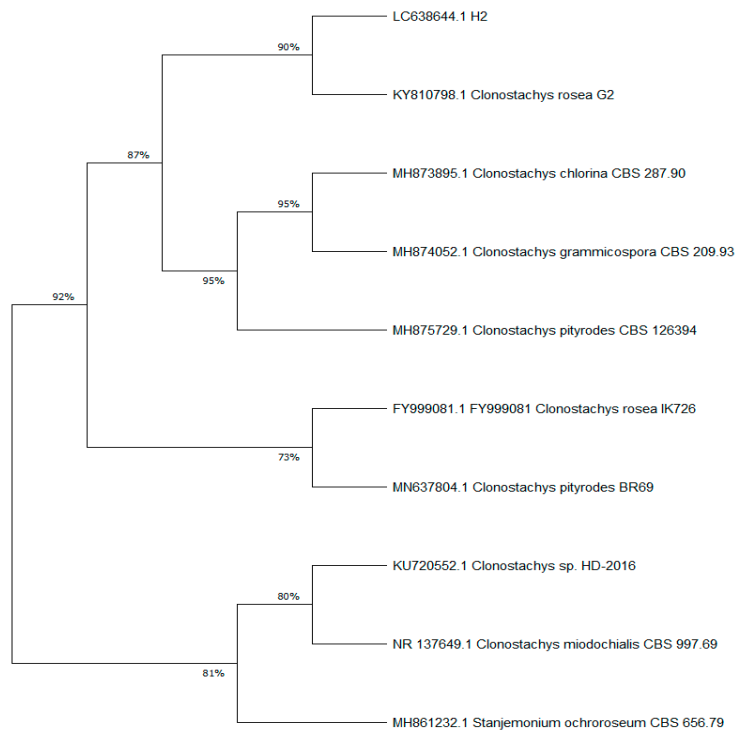


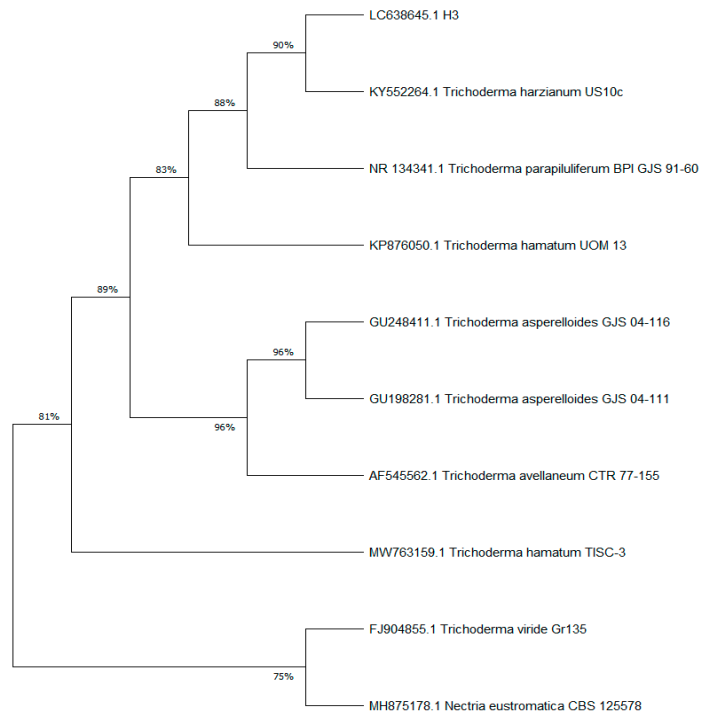
Figure S1. Pre-screening of fungal isolates: Growth response of (a) *Brassica rapa* with leguminous isolates (b) *Lactuca sativa* with leguminous isolates (c) *Brassica rapa* with non-leguminous isolates (d) *Lactuca sativa* with non-leguminous isolates. This time only one replication was used. Closed and grey bars show shoot and root biomass, respectively.



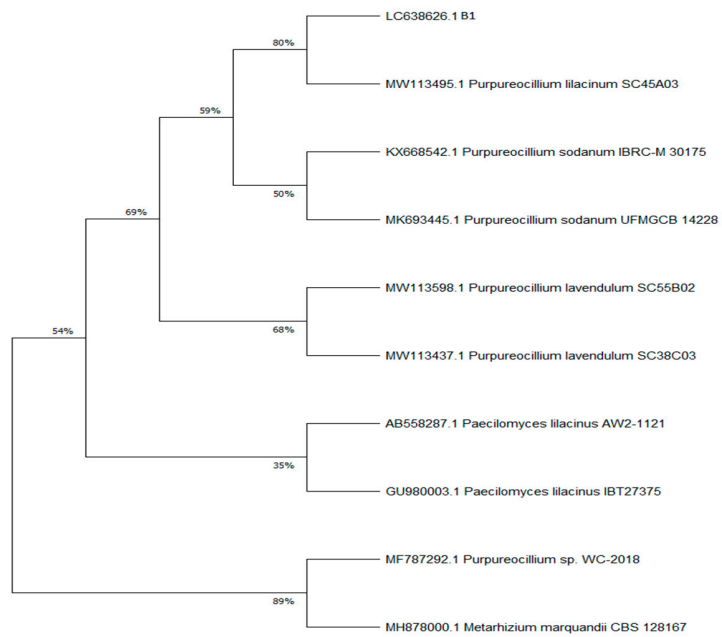
(a) H1



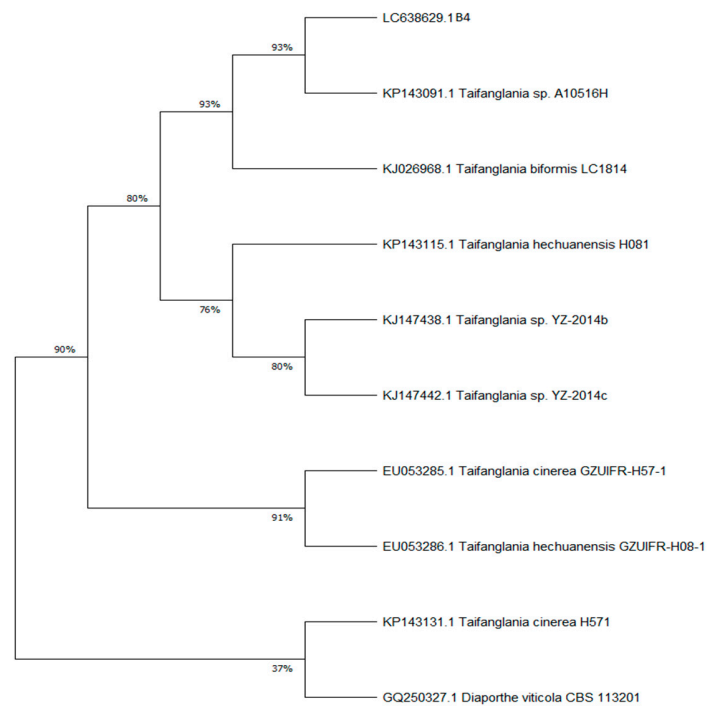
(b) H2



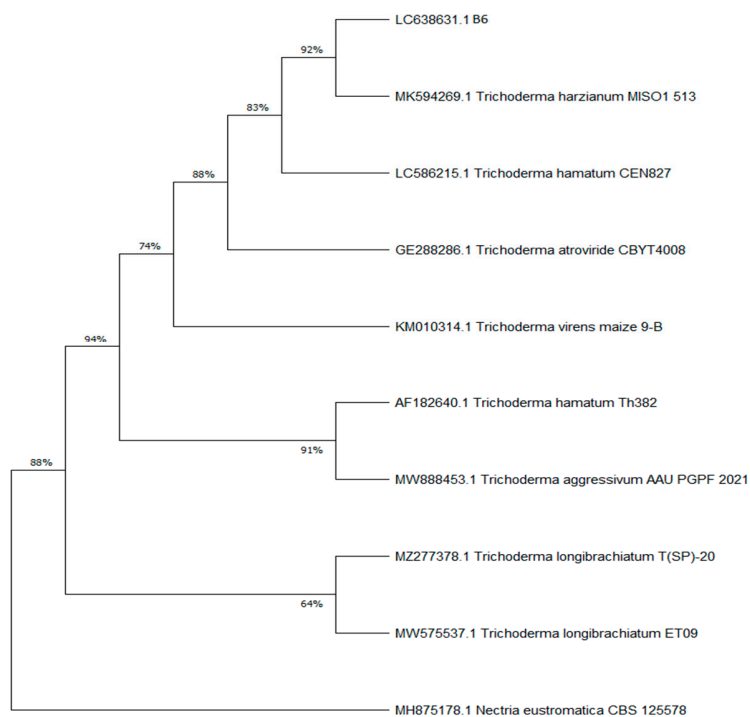
(c) H3



(d) B1



(e) B4



(f) B6

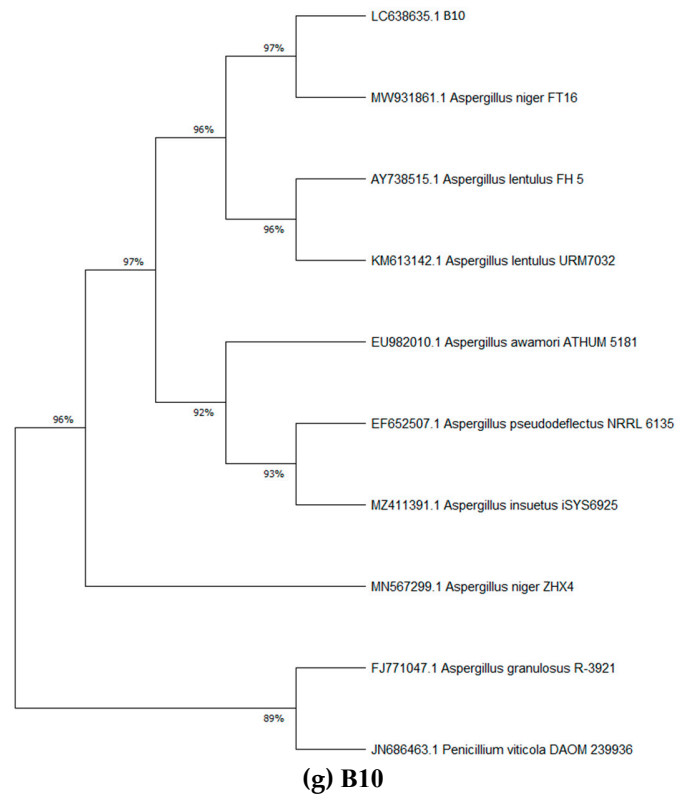


Figure S2. Phylogenetic tree of fungal isolates based on ITS rRNA gene sequences showing the evolutionary position of **(a)** H1 **(b)** H2 **(c)** H3 **(d)** B1 **(e)** B4 **(f)** B6 and **(g)** B10. *Metarhizium marquandii* for B1, *Diaporthe viticola* for B4, *Nectria eustromatica* for B6, *Penicillium viticola* for B10, *Talaromyces funiculosus* for H1, *Stanjemonium ochroroseum* for H2, *Nectria eustromatica* for H3 were used as the out-group. The phylogenetic tree and branching pattern was generated by a neighbor-joining method through the MEGA program

Table S1. Effects of green manure treatments on fungal biomass

Treatment	CFU·g ⁻¹ of soil	Average	S.D.
<i>Brassica Juncea</i> (B)	600000	1.14×10 ⁶	4.94×10 ⁵
	1860000		
	1400000		
	1000000		
	860000		
Hairy Vetch (H)	860000	2.98×10 ⁶	1.70×10 ⁶
	5400000		
	3400000		
	3260000		
	2000000		