Supplementary Information

Figure S1. Initial assessment of culture filtrate (CF) of fungal endophytes for their growth inhibitory/promotory effect on lettuce seed germination. The fungal endophytes strains were isolated from the roots of *Helianthus annuus*, *Capsicum annuum*, and *Cucumis sativus* grown in Czapek media. The CF were harvested through centrifugation, and bioassay was independently performed five times (n = 45). For convenient access the strains were given names starting with HA, CAA, CMS, referring to the strain-host plant *Helianthus annuus*, *Capsicum annuum*, or *Cucumis sativus*, respectively, followed by their isolation sequence number.

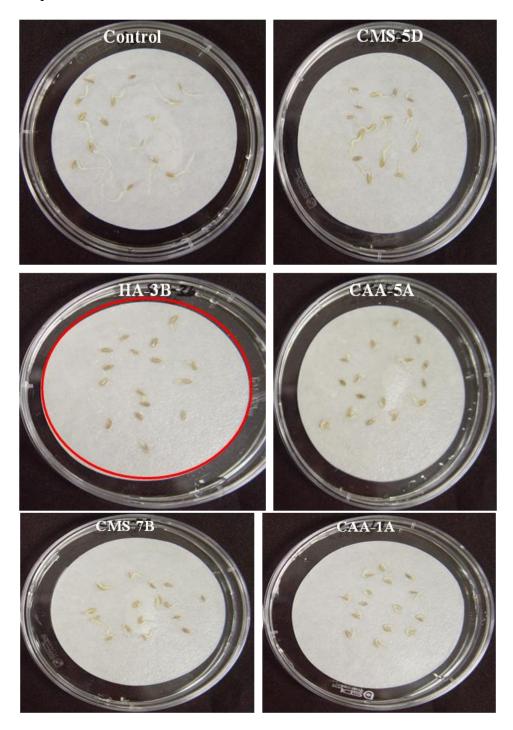


Figure S1. Cont.

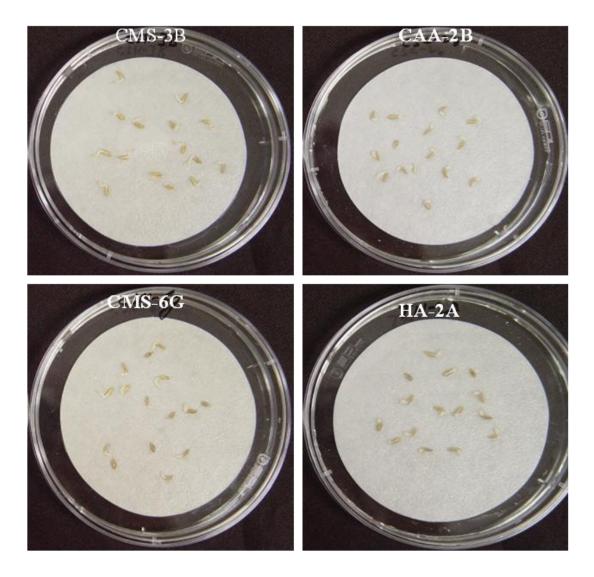
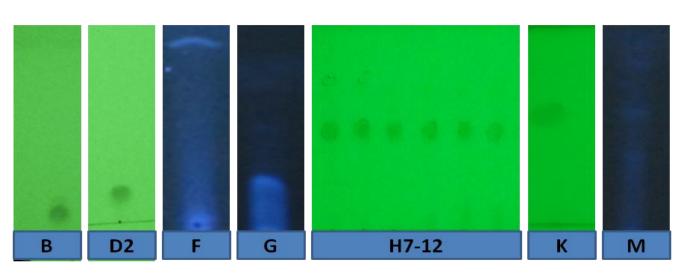


Figure S2. Phylogenetic analysis of strain HA-3B, isolated from the roots of sunflower. Phylogenetic tree was constructed by neighbor joining method of 22 clades (21 references and one clone) using MEGA software (version 5). The fungal strain HA-3B was identified as *Cladosporium cladosporiods* LWL5 as revealed by 88% bootstrap support of *C. cladosporiods*.

		Cladosporium cladosporioides 28S ribosomal RNA gene partial sequence.
		Cladosponium cladosponioides strain CPC 18230 28S ribosomal RNA gene partial sequence.
		Cladosporium cladosporioides gene for 26S rRNA partial sequence strain: IFM 41447.
		Cladosponium cladosponioides strain Cc 101 18S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ri.
		Cladosporium cladosporioides strain AMC001 28S ribosomal RNA gene partial sequence.
		Cladosporium sp.(1) P555 28S large subunit ribosomal RNA gene partial sequence.
		Cladosporium cladosporioides strain CBS 574.78A 28S large subunit ribosomal RNA gene partial sequence.
		Cladosporium uredinicola strain CPC 5390 18S ribosomal RNA gene panial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribo.
	2	Cladosporium cladosporioides strain STE-U 3683 18S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28.
		Cladosporium bruhnei strain CPC 5101 18S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosoma.
		Cladosporium cladosporioides strain CBS 109.21 28S large subunit ribosomal RNA gene partial sequence.
		Cladosporium uredinicola strain CPC 5390 28S large subunit ribosomal RNA gene partial sequence.
	43	Cladosporium silenes strain CBS 109082 28S ribosomal RNA gene partial sequence.
		Cladosporium cladosporioides isolate BM-102 28S ribosomal RNA gene partial sequence.
		Endophyte
1	88	Cladosporium cladosporioides strain STE-U 5100 18S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28.
		Cladosponium cladosponioides strain UWFP 863 28S ribosomal RNA gene partial sequence.
		Cladosporium phaenocomae strain CPC 18221 28S ribosomal RNA gene partial sequence.
		Cladosporium phaenocomae strain CBS 128769 28S ribosomal RNA gene partial sequence.
		Cladosporium cladosponioides strain CBS 109501 28S large subunit ribosomal RNA gene partial sequence.
l		Cladosporium cladosporioides partial 285 rRVA gene strain MT 9.
Aspergillus niger isolate UOAHCPF 10153 18S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence and 28S ribosomal RNA gene partial sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence internal transcribed spacer 2 complete sequence internal transcribed spacer 1 5.8S ribosomal RNA gene and internal transcribed spacer 2 complete sequence internal transcribed spacer 2 complete sequence internal transcribed spacer 2		

Figure S3. (a) TLC plates of fractions B, D, F, G, H, K and M visualized under 254 nm and 365 nm; (b) Effect of fraction B (elution with 10:80 ethyl acetate-hexane) and D (elution with 40:60 ethyl acetate-hexane) on lettuce seed germination and growth at 50, 100 and 300 ppm.



(a)



