TABLE S1. PCR primers and conditions used for the characterization of the haplotypes of *Glomus intraradices* s. l. in the large subunit of mitochondrial ribosomal DNA.

Primer name(s)	Primer sequences (5'→3')	Application	Primer concn (μM)	Annealing temp (°C)	$MgCl_2$ concn (mM)
RNL5 / RNL28a	Börstler *et al.*, 2008	1st step of nested PCR	0.2 / 0.2	59	1.5
RNL29 / GImt4510R	Börstler *et al.*, 2008 / CATCCACGCTAGTGTTAGC	2nd step of nested PCR	0.1 / 0.1	53	2
GImt1631F / GImt2234R	AACACAAGGCAGTCCTCTCC / CCCTCACCAGGCAATATACC	2nd step of nested PCR, isolate PH5	0.2 / 0.2	59	2.5
GImt2829F / GImt4510R	GAAGGAACTCGGCAAAATGAC / see above	2nd step of semi-nested PCR, isolate CH	0.2 / 0.2	56	2.5
GImt1227F	AGGTCCGTTGCAAGGGACTC	sequencing			
GImt2811F	GTGCCACTAATAAGTGGCGG	sequencing			
GImt2822R	CCCTGTTTAGTGCCGCCACTT	sequencing			

Börstler, B., P. A. Raab, O. Thiéry, J. B. Morton, and D. Redecker. 2008. Genetic diversity of the arbuscular mycorrhizal fungus *Glomus intraradices* as determined by mitochondrial large subunit rRNA gene sequences is considerably higher than previously expected. New Phytol. **180:**452-465.

TABLE S2. Root and shoot dry weight of medic plants in the experiment when non-inoculated (NM), inoculated with isolate PH5, isolate Chomutov (CH) or both isolates together (MIX).

Harvest time	Inoculation	Shoot dry weight (g)	Root dry weight (g)
6 wks	NM	0.47 (0.07)	0.20 (0.09)
	PH5	0.44 (0.09)	0.21 (0.04)
	CH	0.46 (0.07)	0.21 (0.05)
	MIX	0.54 (0.07)	0.24 (0.03)
12 wks	NM	1.19 (0.17)	0.92 (0.30)
	PH5	1.12 (0.08)	0.89 (0.21)
	CH	1.21 (0.13)	0.76 (0.19)
	MIX	1.29 (0.22)	0.83 (0.20)
26 wks	NM	6.82 (0.71)	5.41 (1.67)
	PH5	7.41 (2.06)	4.99 (1.80)
	CH	6.60 (0.48)	5.55 (2.69)
	MIX	7.77 (1.64)	5.85 (3.29)
Significance		F-values	
Harvest (A)		647.9 ***	127.8 ***
Inoculation (B)		1.5 ns	0.2 ns
A x B		1.2 ns	0.2 ns

Data are means of 9-10 replicates (SD). Effects of factors according to ANOVA: ns non-significant effect; *** $P < 0.001$.