

Target of Rapamycin, *PvTOR*, Is a Key Regulator of Arbuscule Development during Mycorrhizal Symbiosis in *Phaseolus*

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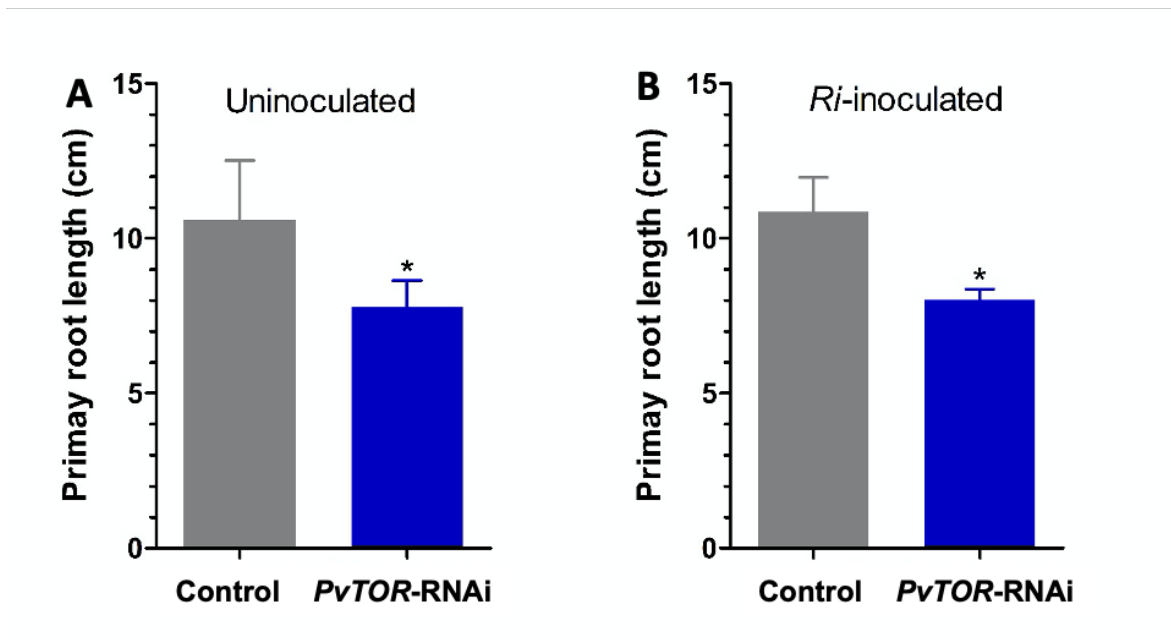


Figure S1. Knockdown of *PvTOR* inhibits primary root length in *P. vulgaris*. (A-B) Primary root length in uninoculated (A) and *Ri*-inoculated (B) transgenic roots of control and *PvTOR*-RNAi at 12 days post inoculation. The statistical significance of differences between control and *PvTOR*-RNAi roots was determined using an unpaired two-tailed Student's *t*-test (*, $P < 0.05$). Error bars refer to the SD of the mean of three biological replicates ($n > 30$). *Ri*, *R. irregularis*.

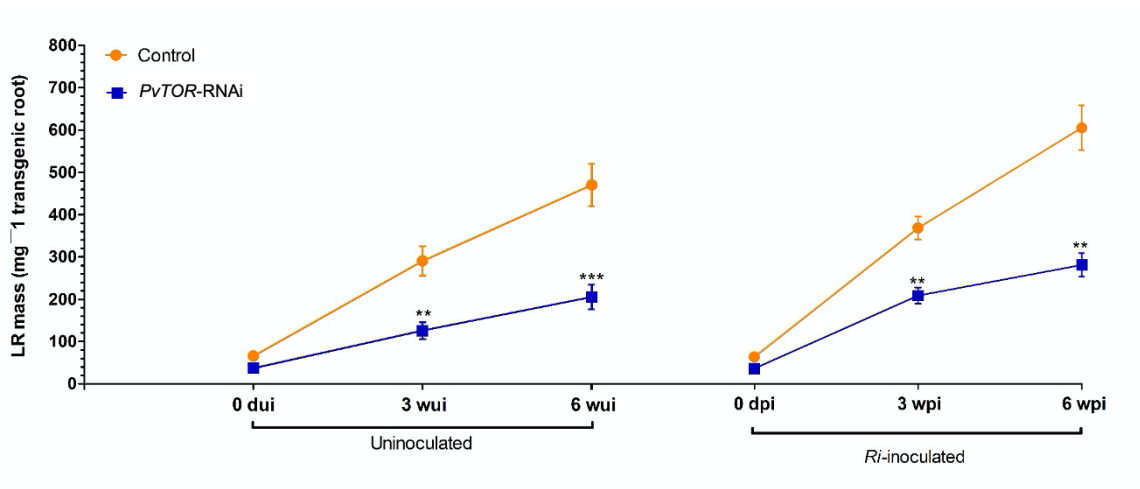


Figure S2. Quantitative analysis of lateral root mass in uninoculated and *Ri*-inoculated transgenic roots of control and *PvTOR*-RNAi at different time points. The statistical significance of differences between control and *PvTOR*-RNAi roots was determined using an unpaired two-tailed Student's *t*-test (**, $P < 0.01$; ***, $P < 0.001$). Error bars refer to the SE of the mean of three biological replicates ($n > 30$). LR, lateral root; *Ri*, *R. irregularis*; dui, day(s) uninoculated; dpi, day(s) post inoculation; wpi, week(s) post inoculation.

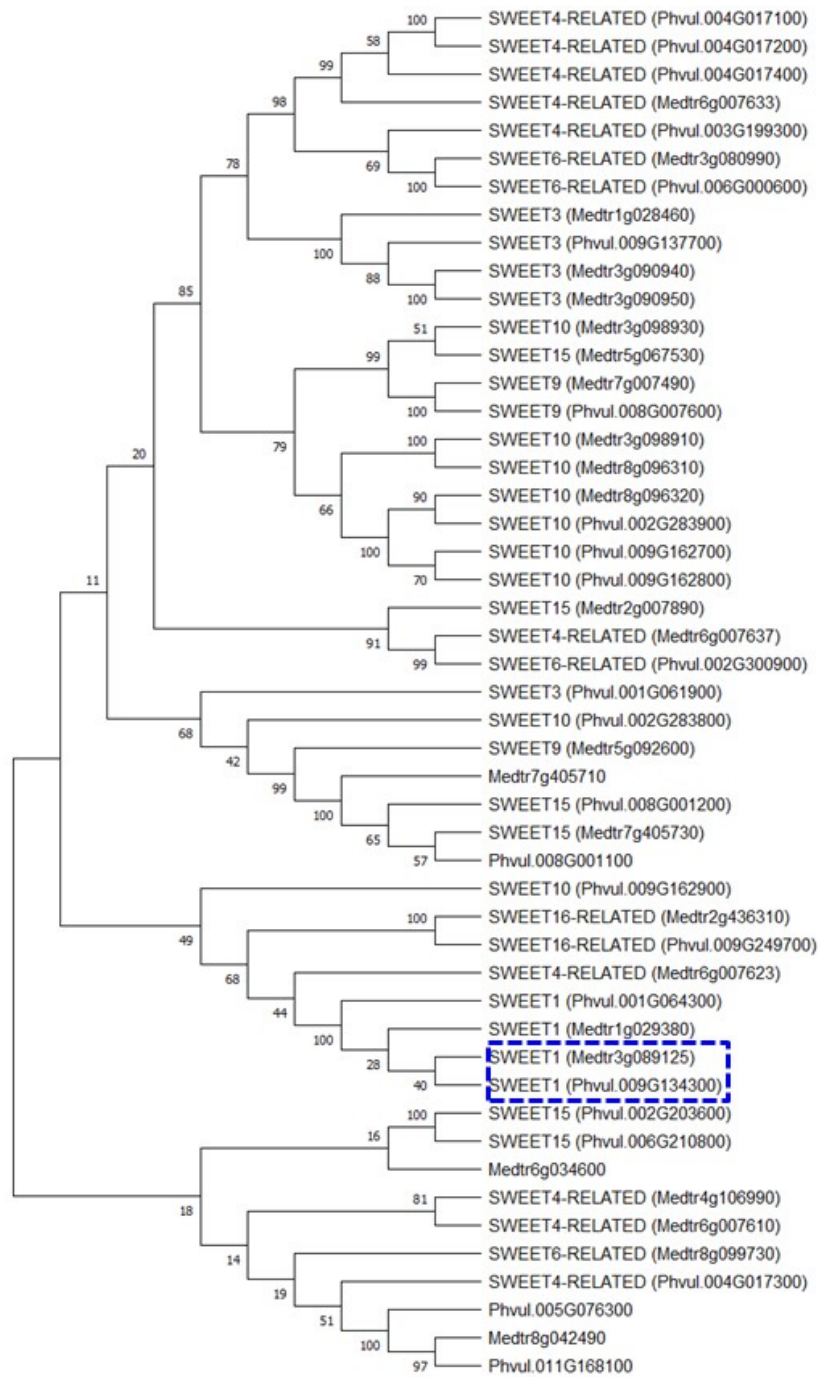


Figure S3. Phylogenetic analysis of *Phaseolus vulgaris* and *Medicago truncatula* SWEET genes. Protein sequences of SWEET homologs were identified in the Phytozome database. The phylogenetic tree was constructed using MEGA-X-10.1.1 software with the neighbor-joining (NJ) tree method with 1000 bootstrap values.

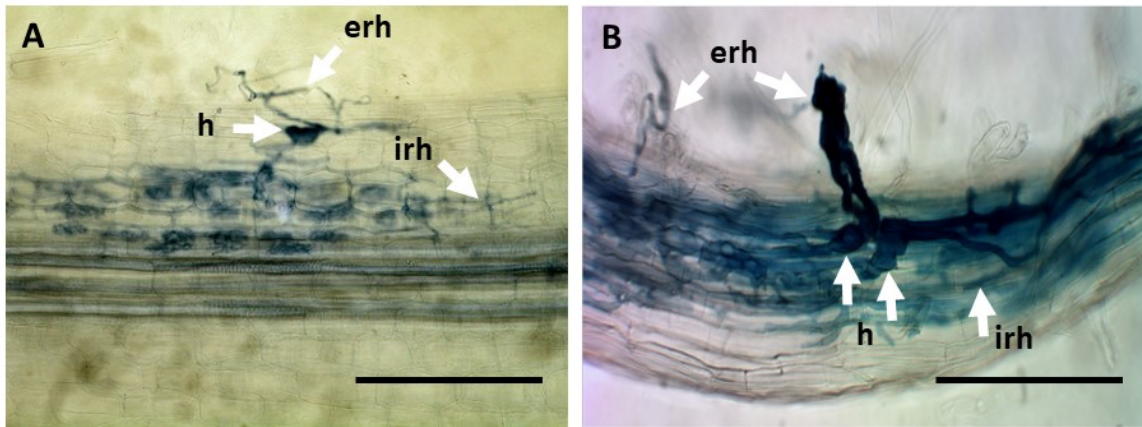


Figure S4. Micrograph of *R. irregularis*-inoculated transgenic roots showing hyphopodia at 3wpi. (A) Control and (B) *PvTOR*-RNAi. wpi, week(s) post inoculation; erh, extraradical hyphae; irh, intraradical hyphae; h, hyphopodia. Bars = 1 mm.

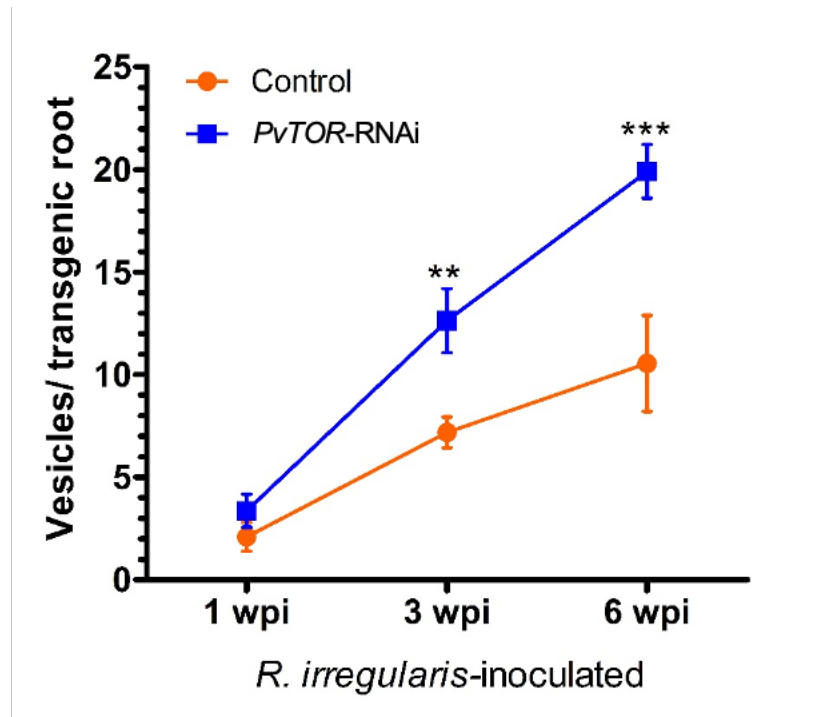


Figure S5. Quantification of vesicles in mycorrhized *P. vulgaris* control and *PvTOR*-RNAi roots at 1, 3 and 6 wpi. The statistical significance of differences between control and *PvTOR*-RNAi roots was determined using an unpaired two-tailed Student's *t*-test (**, $P < 0.01$; ***, $P < 0.001$). Error bars refer to the SD of the mean of three biological replicates ($n > 30$). wpi, week(s) post inoculation.

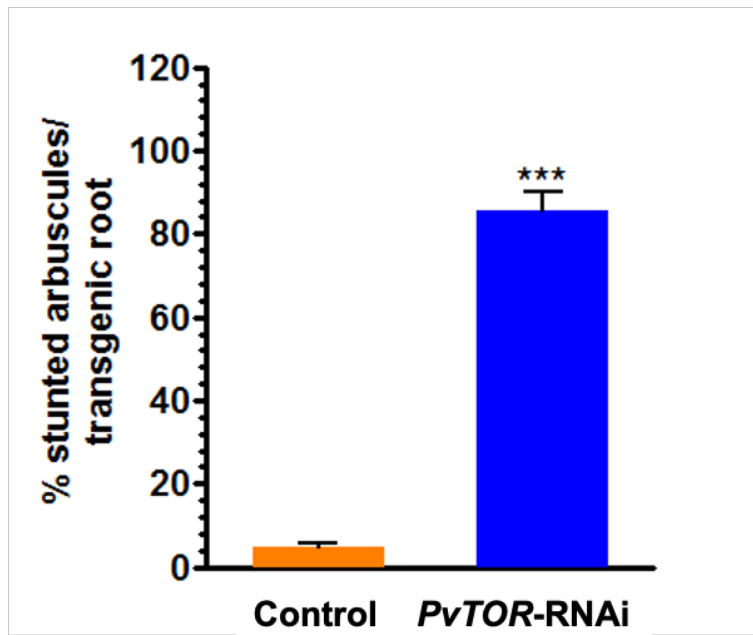


Figure S6. Quantification of stunted arbuscules per transgenic root of control and *PvTOR*-RNAi at 6 wpi with *R. irregularis*. The statistical significance of differences between control and *PvTOR*-RNAi roots was determined using an unpaired two-tailed Student's *t*-test (***, $P < 0.001$). Error bars refer to the SE of the mean of three biological replicates ($n > 30$). wpi, weeks post inoculation.

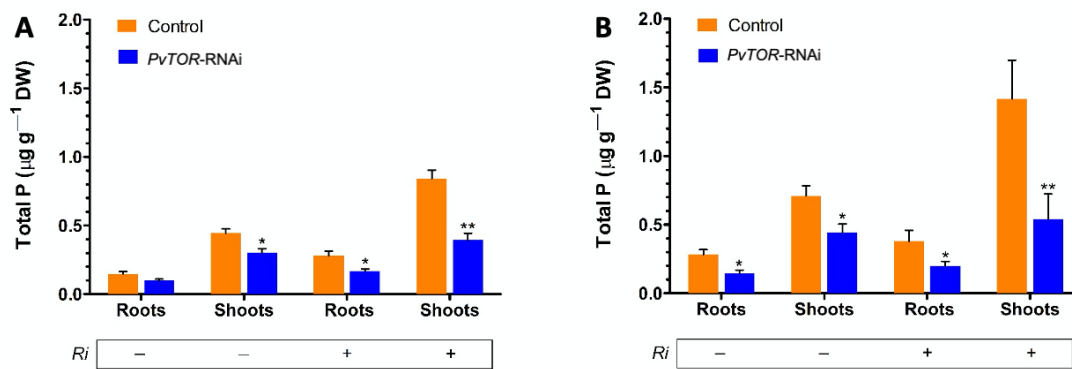


Figure S7. Total root and shoot phosphorus (P) concentration in mycorrhized composite plants of control and *PvTOR*-RNAi at (A) 3 wpi and (B) 6 wpi. The statistical significance of differences between control and *PvTOR*-RNAi samples was determined using an unpaired two-tailed Student's *t*-test (*, $P < 0.05$; **, $P < 0.01$). Error bars refer to the SD of the mean of three biological replicates ($n > 12$). wpi, week(s) post inoculation, Ri, *R. irregularis*.

Table S1: Primer sequences of *Phaseolus vulgaris* genes used to generate constructs and perform quantitative RT-PCR.

Gene		Oligonucleotide sequence (5' – 3')
<i>EIF4a</i>	F	GGTGTCCACACTGTTGTTGG
<i>Phvul.010G136300</i>	R	CGGCATTGTAGCAGAGAACA
<i>IDE</i>	F	GCAACCAACCTTTCATCAGC
<i>Phvul.001G133200</i>	R	AGAAATGCCTCAACCCTTTG
<i>PvTOR-RNAi</i>	F	CTTTCTGGTAATTCGCAAGGGAGCAGTA
<i>Phvul.002G049900</i>	R	AGCTAATTGAGGCATGCCCTTTCATCTG
<i>PvTOR</i>	F	GCTAGCCGTTTGTATTTTGGTGAGC
<i>Phvul.002G049900</i>	R	AGCAATTCCGTGTCGATAGGCCTCA
<i>UPB1</i>	F	CAAAGAAGGGTGTTAGGAGGCCAAG
<i>Phvul.007G089100</i>	R	TGACACTCACTCTCGTTTGTAAAGG
<i>RGF6</i>	F	GCTACAGGAAAATCAACAGCAGCAAG
<i>Phvul.002G062100</i>	R	CTGACCAGCTCCCAGCATTGACC
<i>RGF9</i>	F	AGGCCATGTCTTGTGCAAGTGCC
<i>Phvul.002G267404</i>	R	TTGTTGTGCAGCTTCATGTTGTGGC
<i>GSS</i>	F	GCATTGTTGCCGACGCCGTTTC
<i>Phvul.006G094700</i>	R	GACCGATGTAACCCCAATCGTATTTCCCTC
<i>APK2</i>	F	GAAGGTTTTCAAGGTCATAAAGAGTGTT
<i>Phvul.002G089100</i>	R	CCAATAGCCACTTTCATCCTCACTGA
<i>SIR</i>	F	TTGCTGACCAGTTTGGGATCGG
<i>Phvul.011G021800</i>	R	GATAATCCTTTCTCACGAGGGGAGC
<i>APSI</i>	F	TCTCCAAAACCTTCGACACC
<i>Phvul.007G062900</i>	R	AACCCACTGCAAGTCGATTC
<i>APR3</i>	F	GGCCTGTTTTACCTGGACAA
<i>Phvul.003G079800</i>	R	ATTTGCATGGGATTGGGATA
<i>ORC5</i>	F	CAACGGTGGACTGATGTCTG
<i>Phvul.008G061800</i>	R	CTCCTTGCAACCTTCAAAGC
<i>ETG1</i>	F	TCGCGGAATGATACAAGACA
<i>Phvul.009G142700</i>	R	CCGGGACACAGTAAAGCAGT
<i>MCM7</i>	F	GAAATGGCTAGGCACGTTGT
<i>Phvul.001G212600</i>	R	GAATGTGGAGCATTGGACCT
<i>CDC6</i>	F	AAAATCTCCCCACAGCTCCT
<i>Phvul.006G064300</i>	R	CTTGGCTCCACGAAAGTGAT
<i>SUCS1</i>	F	GGAAGCATGTGACCAACCTT
<i>Phvul.009G223800</i>	R	GTGAAAGCTGCATGAGACCA
<i>SUCS2</i>	F	CAAGTGAACCGTGCTCGTAA
<i>Phvul.009G250800</i>	R	AGGGCCACCATGACAAGTAG
<i>CINV1</i>	F	CTGGCTGTGATCCCAAAAAT
<i>Phvul.007G091300</i>	R	GCCACCAGATAACCTGCAAT

<i>SWEET1</i>	F	TGGAGTTCATGCCCTTCTTC
<i>Phvul.009G134300</i>	R	TCCATGAATTCCTCCTCTGC
<i>SWEET6</i>	F	CGCTTCTCTCCATTCTCACC
<i>Phvul.006G000600</i>	R	TGAAGGGATCAAAAGGGATG
<i>SYMRK</i>	F	GAAGATTTATGGTACTAGGT
<i>Phvul.002G143400</i>	R	TGTCAAGGCTACTCTGGA
<i>CCAMK</i>	F	GTGCATCACCAAGGAAGAAGTAG
<i>Phvul.011G186900</i>	R	TCACTGTTGGCATCCATTCTGTC
<i>IPD3</i>	F	GAAGAGGTGTGAAACCCTTGAGAA
<i>Phvul.002G128600</i>	R	AATCTCTTCAAGCAGACGCTCCTT
<i>NSP2</i>	F	ACTATTCGGCGGTGTTTGAC
<i>Phvul.009G122700</i>	R	TAGAAGCTTCGCTTGGCAAT
<i>RAM1</i>	F	GATATTGACCAAACCTACCCTAACCCACCA
<i>Phvul.001G089900</i>	R	CTAATTGGTCAGCAAAAAGGATTCCCAC
<i>RAM2</i>	F	GCTTTTTCCACCTTCCAACCGT
<i>Phvul.007G233600</i>	R	AACCCACAGCTTCAAAGG
<i>VPY</i>	F	ATCAAAGAACCCTCCTCCATGTTC
<i>Phvul.001G113900</i>	R	GAGCTTCTCTGATTTTCATCTATGGAG
<i>VAMP713</i>	F	GGACTCACCGTTCTCTGCAT
<i>Phvul.008G201600</i>	R	ATTGATCCTGTGCGGCGTTAG
<i>STR</i>	F	GGCCTGTACCTGATGGAGAA
<i>Phvul.002G331200</i>	R	CTTGGCTGCGTAGGCTAATC
<i>STR2</i>	F	TCGAGAAAGTGCACGACATC
<i>Phvul.002G143300</i>	R	TTCTCTCCCTTGGGGACTTT
<i>PT-4</i>	F	GCGGTGACTAACATGTTAGGG
<i>Phvul.004G007300</i>	R	CCTGTGCCCTAGTATTGTTGG
<i>AM-1</i>	F	GATGCAAGGTCAAAGGCCAC
<i>Phvul.003G143400</i>	R	AACACCAACCCTTCCAACCT
<i>HA-1</i>	F	TGGTAAACCAAAGGACCGCA
<i>Phvul.010G050900</i>	R	GCAGAGTGGAGGCCATGTAA