Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.

Supporting Material legends

Fig. S1: Systemic effect on wheat seeds nutrient and amino acid composition exerted by *F. mosseae*. A) The picture shows the greenhouse seeds collected from control (C) and mycorrhizal plants (M). B) Changes in the mineral content in greenhouse seeds. Ratios of the mean values of 3 replicate samples (μ g/g dry weight; two-tailed t test *P < 0.05) are given. C) Changes in levels of free amino acids in roots and shoots samples (two-tailed t test *P < 0.05)

Fig. S2: Venn diagrams of control and AM fungal-modulated genes and proteins (DEGs and DEPs) in roots and leaves.

Venn diagram showing the relationships between DEPs and DEGs in response to arbuscular mycorrhizal (AM) symbiosis in the roots (A) and leaves (B). The number of DEPs and DEGs commonly expressed is shown in the overlapping portion. Functional distribution of the common DEGs and DEPs in the roots (C) and leaves (D) of wheat colonized by *F. mosseae*; genes and proteins were grouped in comprehensive groups on the basis of their gene ontology (GO) annotation.

Fig. S3: The evolutionary history of the mycorrhiza-induced phosphate transporter (PT) genes. The amino acid sequences were aligned using Clustal Omega (Sievers et al., 2011) and the LG + G substitution model was selected under the Akaike criterion using ProtTest 3.4.2 (Darriba et al., 2011). Maximum likelihood was estimated with PhyML 3.0 (Guindon and Gascuel, 2003) and the resulting neighbour joining tree was visualized with FigTree (http://tree.bio.ed.ac.uk/software/figtree/). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Abbreviations for plant species: Le, *Licopersicum esculentum*; Lj, *L. japonicus*; Mt, *Medicago truncatula*, Os, O. *sativa*, Ta, *Triticum aestivum*. Asteric indicate the ID of a non-annotated PT gene of *Triticum aestivum*.

Fig. S4: Relative gene expression of ten differentially expressed genes. qRT-PCR analysis was done on genes selected from DEGs identified in the comparison between control (RC) and mycorrhizal (RM) roots. The y-axis represents relative expression. Values are means of three replicates. Error bars represent standard deviation. Asterisks indicates significant difference at p-value < 0.01, according to the one-way ANOVA with Tukey's post-hoc test.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.

Supporting Material legends

Fig. S5: Plots illustrating enriched GO terms specific for RM vs RC contrast. The enriched GO terms (y axis labels; FDR threshold for GO enrichment \leq 0.1) associated to DEGs in the contrast are shown. Reference set was defined as all genes with expression above 0.1 RPKM. X-axis displays the reciprocal of Enrichment p value as calculated with the Goseq R package. Enriched GO terms belong to the category biological process.

Fig. S6: Plots illustrating enriched GO terms specific for LM vs LC contrast. The enriched GO terms (y axis labels; FDR threshold for GO enrichment ≤ 0.1) associated to DEGs in the contrast are shown. Reference set was defined as all genes with expression above 0.1 RPKM. X-axis displays the reciprocal of Enrichment p value as calculated with the Goseq R package. Enriched GO terms belong to the category biological process.

Fig. S7: Single enrichment analysis of protein GO terms specific for RM vs RC and LM vs LC contrasts. The enriched GO terms (FDR threshold for GO enrichment \leq 0.05) associated to DEPs in the contrasts are shown. Reference set was defined as Uniprot 2016 database. Enriched GO terms belong to biological process term.

Fig. S7: Single enrichment analysis of protein GO terms specific for RM vs RC and LM vs LC contrasts. The enriched GO terms (FDR threshold for GO enrichment \leq 0.05) associated to DEPs in the contrasts are shown. Reference set was defined as Uniprot 2016 database. Enriched GO terms belong to biological process term.

Fig. S9: Plots illustrating enriched GO terms specific for RMX vs RM contrast. The enriched GO terms (y axis labels; FDR threshold for GO enrichment ≤ 0.1) associated to DEGs in the contrast are shown. Reference set was defined as all genes with expression above 0.1 RPKM. X-axis displays the reciprocal of Enrichment p value as calculated with the Goseq R package. Enriched GO terms belong to biological process term.

В

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.

M/C

1.03 1.39*

1.04

0.82

1.32*

1.08

1.19*

M/C

0.82

0.73

0.85

1.07

1.29*

1.22

1.15

1.37

1.17

1.12

0.88

1.32 0.84

0.58* 1.31*

1.30*

Mineral Са Mg К Μ Fe А Zn Cu Ρ С AA Aspartic acid Glutamic acid Alanine Arginine Asparagine Cystine Citrulline Phenylalanine GABA Glycine Glutamine Histidine Leucine Lysine Metionine Ornitine Proline Serine Tyrosine Threonine



Fig. S1. Systemic effect on wheat seeds nutrient and amino acid composition exerted by *F. mosseae*.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.



Fig. S2: Venn diagrams of control and AM fungal-modulated genes and proteins (DEGs and DEPs) in roots and leaves.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.



Fig. S3: The evolutionary history of the mycorrhiza-induced phosphate transporter (PT) genes.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.



Fig. S4: Relative gene expression of ten differentially expressed genes.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.



Fig. S5: Plots illustrating enriched GO terms specific for RM vs RC contrast.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.



Fig. S6: Plots illustrating enriched GO terms specific for LM vs LC contrast.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.

Biological process	RM/RC up	RM/RC down	LM/LC up	LM/LC down	
translation					
amide biosynthetic process					
organonitrogen compound metabolic process					Significant
protein metabolic process					levels
biosynthetic process					
gene expression					- Level9
metabolic process					- Level8
nitrogen compound metabolic process					_ Level7
primary metabolic process					Level6
macromolecule metabolic process					- Level5
protein folding					_ Level4
macromolecular complex asseMXly					_ Level3
nucleotide biosynthetic process					_ Level2
carboxylic acid biosynthetic process					_ Level1
monosaccharide metabolic process					
alpha-amino acid metabolic process					
hexose metabolic process					
aspartate family amino acid biosynthetic process					
methionine biosynthetic process					
carbohydrate metabolic process					
S-adenosylmethionine metabolic process					
cofactor metabolic process					
nicotinamide nucleotide metabolic process					
cellular aldehyde metabolic process					
oxidoreduction coenzyme metabolic process					
fatty acid metabolic process					
intracellular transport					
phosphate-containing compound metabolic process					
pentose-phosphate shunt					
protein localization					
protein catabolic process					
nucleotide metabolic process					
glucose metabolic process					
cellular metabolic compound salvage					
catabolic process					
pyruvate metabolic process					
NADP metabolic process					
coenzyme biosynthetic process					
serine family amino acid metabolic process					
monocarboxylic acid biosynthetic process					
disaccharide metabolic process					
lipid metabolic process					
ribose phosphate metabolic process					
proteolysis					
vesicle-mediated transport					
oligosaccharide metabolic process					
cellular homeostasis					
glycosyl compound metabolic process					
seed development					
glycolytic process					
ATP generation from ADP					
posttranscriptional regulation of gene expression					
response to stress					
response to oxidative stress					
cellular catabolic process					
response to stimulus					

Fig.S7: Single enrichment analysis of protein GO terms specific for RM vs. RC and LM vs. LC contrasts.

Fiorilli Valentina, Vannini Candida, Ortolani Francesca, Garcia-Seco Daniel, Chiapello Marco, Novero Mara, Domingo Guido, Terzi Valeria, Morcia Caterina, Bagnaresi Paolo, Moulin Lionel, Bracale Marcella, Bonfante Paola.

A	Biological process	LMX/LX up	LMX/LX down	Significant levels
	carboxylic acid metabolic process			_ Level9
	oxoacid metabolic process			- Level8
	organic acid metabolic process			Level7
	small molecule metabolic process			- Level5
	cellular amino acid metabolic process			_ Level3
	carbohydrate metabolic process			_ Level2
				_ Level1

В

Biological process	RMX/RM up	RMX/RM down
alpha-amino acid biosynthetic process		
aspartate family amino acid metabolic process		
carboxylic acid biosynthetic process		
cellular amino acid metabolic process		
chromatin organization		
coenzyme metabolic process		
dicarboxylic acid metabolic process		
metabolic process		
organic acid biosynthetic process		
oxylipin metabolic process		
small molecule biosynthetic process		
organonitrogen compound metabolic process		
organic acid metabolic process		
phosphate-containing compound metabolic process		
carboxylic acid metabolic process		
carbohydrate derivative metabolic process		
nucleotide metabolic process		
ATP metabolic process		
glycosyl compound metabolic process		
protein folding		
purine ribonucleoside monophosphate metabolic process		
ribonucleoside triphosphate biosynthetic process		
ribonucleotide biosynthetic process		
ATP synthesis coupled proton transport		

Fig. S8: Single enrichment analysis of protein GO terms specific for LMX vs. LX (A) and RMX vs. RM (B) contrasts.