**Table S1.** Scoring scale and calculating of mycorrhizal colonization and arbuscule abundance

|  |  |  |
| --- | --- | --- |
| **A. Scaling scale \*** | | |
| Degree of colonization | Explanation | |
| 0 | No structures of arbuscular fungi have formed within the root segment | |
| 1 | Structures of arbuscular fungi have formed which occupy less than 1% of the root segment | |
| 2 | Structures of arbuscular fungi occupy less than 10% of the root segment | |
| 3 | Structures of arbuscular fungi occupy less than 50% of the root segment | |
| 4 | Structures of arbuscular fungi occupy more than 50% of the root segment | |
| 5 | Structures of arbuscular fungi occupy more than 90% of the root segment | |
| Arbuscule of abundance | Explanation | |
| A0 | No arbuscular structures | |
| A1 | Single arbuscular structures observed | |
| A2 | Small groups of arbuscular structures observed | |
| A3 | Large groups of arbuscular structures observed | |
| **B. Calculating Formulae \*\*** | | |
| Parameters | Formulae | where |
| Frequency of mycorrhizal in the root system (F%) |  | F – mycorrhizal frequency  lm – total number of root segments in which mycelium had formed  lt – total number of the segments examined. |
| Intensity of the mycorrhizal colonization in the root system (M%) |  | M – relative mycorrhizal frequency,  n5 – n1 – total number of root segments in which the degree of colonization by mycorrhizal structures was 5-1  lt – total number of the segments examined. |
| Intensity of the mycorrhizal colonization in the root fragments (m%) |  | m – absolute mycorrhizal intensity  M – relative mycorrhizal frequency  lm – total number of root segments in which mycelium had formed  lt – total number of the segments examined. |
| Arbuscule abundance in mycorrhizal parts of root fragments (a%) |  | where:  a – absolute abundance of arbuscules  m – absolute mycorrhizal intensity  lm – total number of root segments in which mycelium had formed  n5 –n1– total number of root segments in which the degree of colonization by mycorrhizal structures was 5-1 |
| Arbuscule abundance in the root system (A%) |  | A – relative abundance of arbuscules,  M– relative mycorrhizal intensity  a – absolute abundance of arbuscules. |

\* adapted from mycorrhiza manual (https://www2.dijon.inra.fr/mychintec/Protocole/Workshop\_Procedures.html#1.5), Session 1.5 Estimation of AMF colonization

\*\* adapted from Derkowska, E., Sas-Paszt, L., Sumorok, B., Szwonek, E., and Gluszek, S. 2008. The influence of mycorrhization and organic mulches on mycorrhizal frequency in apple and strawberry roots. Journal of Fruit and Ornamental Plant Research, 16, 227-242.

**Table S2.** Influence of SUT47 on *Acaulospora tuberculata* root establishment at different sample dates.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Interactions** | **% F** | **%M** | **%A** | **%V** | **%m** |  | **%a** | **%v** |
| Sampling date | \* | \*\* | \*\* | \*\* | \*\* |  | \*\* | \*\* |
| Inoculated plant | ns | ns | \* | \* | \* |  | \*\* | \* |
| Sampling date × Inoculated plant | ns | ns | \*\* | \*\* | ns |  | \*\* | \* |

\*  *p <* *0.05*; \*\* *p* *< 0.01*; ns, not significant

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Protein spot No.** | **Intensity** | | | | **p <0.05** | **> 2 folds** |
| **Control** | **AM** | **SUT47** | **AM+SUT47** |
| 1 | n | 5.67^ | n | 36.00^ | + | + |
| 2 | n | 24.33^ | n | 31.67^ | + | + |
| 15 | n | 5.33^ | 15.33^ | 21.67^ | + | + |
| 7 | n | 18.00^ | 18.66^ | 19.67^ | + | + |
| 6 | n | 5.67^ | n | 15.33^ | + | + |
| 11 | n | 11.67^ | n | 13.67^ | + | + |
| 12 | n | 5.67^ | n | 12.67^ | + | + |
| 5 | n | 28.00^ | n | 31.33^ | + | + |
| 4 | n | 9.33^ | n | 11.33^ | + | + |
| 9 | n | 4.00^ | n | 9.00^ | + | + |
| 8 | 16.33 | 8.67 | 6.66 | 8.00 | + | + |
| 10 | n | 8.00^ | n | 8.00^ | + | + |
| 13 | n | 3.00^ | n | 7.67^ | + | + |
| 16 | n | 6.67^ | n | 6.00^ | + | + |
| 14 | n | 10.00^ | n | 5.00^ | + | + |
| 3 | n | 6.33^ | n | 3.67^ | + | + |
| 0 | n | 44.67^ | n | 3.00^ | + | + |
| 19 | 11.00 | 15.67^ | 57.00^ | n | + | + |
| 24 | n | 6.67^ | 32.66^ | n | + | + |
| 20 | 16.00 | 10.00 | 32.00^ | n | + | + |
| 23 | n | 8.00^ | 9.33^ | n | + | + |
| 18 | 7.67 | 32.66^ | 7.00 | n | + | + |
| 22 | n | 6.00^ | 6.33^ | n | + | + |
| 17 | 2.00 | 3.33^ | 5.33^ | n | + | + |
| 21 | 15.33 | 8.99 | 4.67 | n | + | + |
| 26 | 5.33 | 12.33^ | n | n | + | + |
| 28 | 12.67 | 2.00 | n | n | + | + |
| 30 | 14.67 | 2.33 | n | 11.00 | + | + |
| 29 | 10.67 | 4.33 | n | n | + | + |
| 27 | 11.33 | 4.67 | n | n | + | + |
| 31 | 11.67 | 3.33 | n | n | + | + |
| 25 | 10.67 | 2.33 | n | n | + | + |

**Table S3.** The intensity of protein spots from different treatments that show at list 2 folds spot intensitydifferent when compared with non-inoculated maize (control).

^ = up regulated protein when compare with control

n = none detected protein spot, ^ = up-regulated protein spots when compared with control

+ = significant differentially expressed protein spots

**Figure S2. AM root establishment of maize root inoculated with AM and AM+SUT47 at different time tested 7, 14, 21, and 30 dai.**  (a, b, e, f, i, j, m and n) AM root, (c, d, g, h, k, l, o and p) AM+SUT47 root, (b, f, j, n, d, h, l and p) zoom picture; v = vesicle, arrow = arbuscular.

**Table S4.** Influence of AM and SUT47 on antioxidative enzymes activity and the content of SA and H2O2 at different sample dates.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Interactions** | **H2O2** | **SA** | **T-SOD** | **APX** | **POD** |
| Sampling date | \*\* | \*\* | \*\* | \*\* | \*\* |
| AM | \*\* | \*\* | \*\* | \*\* | \*\* |
| SUT47 | \*\* | \*\* | \*\* | ns | \*\* |
| AM × SUT47 | \*\* | \* | \*\* | \*\* | ns |
| Sampling date × AM | \*\* | \* | \*\* | \*\* | \*\* |
| Sampling date × SUT47 | \*\* | ns | \*\* | \*\* | \*\* |
| Sampling date × AM × SUT47 | \*\* | \*\* | \*\* | ns | ns |

\*  *p <* *0.05*; \*\* *p* *< 0.01*; ns, not significant

**Figure S1**

****

AM root establishment of maize root inoculated with AM and AM+SUT47 at different times tested 7, 14, 21, and 30 dai. (a, b, e, f, i, j, m and n) AM root, (c, d, g, h, k, l, o and p) AM+SUT47 root, (b, f, j, n, d, h, l and p) zoom picture; v = vesicle, arrow = arbuscular.

**Figure S2**

**The protein-protein interaction**

The 15 selected spot proteins were analyzed the protein-protein interaction network using STRING system, and only 13 proteins were matched with this database (Show in below figure). The first group contains two proteins, BX9 and PR1, which did not have the protein-protein interaction between them. However, these two proteins were linked with the reduced form of nicotinamide adenine dinucleotide (NADH). Although NADH was not significantly altered in our proteomics analysis, this protein has a common function in energy production. It was found that this protein interacted with all other proteins in different groups. Especially in the group of energy metabolism, a network of NADH, GLXI, GLN4, MDH, and TPI interacted among themselves. Interestingly, the TPI protein interacted with the SOD\_Mn presence in the ROS-scavenging enzyme group. However, other proteins including CPN20, CPN60, and actin showed the protein interaction and also interacted with several proteins in ROS-scavenging enzyme group. Our result of the protein-protein interaction network predicted the information which supports the possible functional relationship among them.

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**The protein-protein interaction network of the identified differentially expressed proteins.** The network containing 13 identified differentially expressed proteins was mapped using the STRING system based on evidence with different types. The links between proteins represent possible interaction. Different line colors represent the types of evidence for the associations, which are shown in the legend. (Red line - indicates the presence of fusion evidence, Green line - neighborhood evidence, Blue line - cooccurrence evidence, Purple line - experimental evidence, Yellow line - textmining evidence, Light blue line - database evidence, and Black line - coexpression evidence)