**Supplementary Table S1.** Soil chemical properties of the 0 to 40 cm topsoil layer at different treatments in each of two field experiments (Assis and Serra Azul)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chemical properties** | **Assis (Zinc addition)** | | | |  | **Serra Azul (Zinc addition)** | | | |
| **0 kg ha-1** | **5 kg ha-1** | **10 kg ha-1** | **20 kg ha-1** |  | **0 kg ha-1** | **5 kg ha-1** | **10 kg ha-1** | **20 kg ha-1** |
| pH | 4.4† a§A¶± 0.1‡ | 4.3 aB± 0.3 | 4.2 aB± 0.3 | 4.2 aA± 0.2 |  | 5.3 aA± 0.3 | 5.0 aA± 0.4 | 5.0 aA± 0.4 | 4.8 aA± 0.1 |
| OM | 13.0 aA± 1.0 | 12.0 aB± 1.0 | 11.7 aA± 0.6 | 12.3 aB± 0.6 |  | 17.3 aA± 1.2 | 19.7 aA± 3.2 | 13.7 bA± 2.3 | 19.0 aA± 1.0 |
| P | 21.7 aA± 5.5 | 17.0 aA± 1.7 | 22.0 aA± 4.6 | 26.0 aA± 11.5 |  | 16.0 aA± 1.0 | 26.7 aA± 8.5 | 22.0 aA± 7.2 | 17.3 aA± 2.9 |
| K | 0.9 aA± 0.2 | 0.7 aA± 0.2 | 0.8 aA± 0.2 | 0.8 aA± 0.1 |  | 0.5 aA± 0.2 | 0.7 aA± 0.1 | 0.7 aA± 0.2 | 0.7 aA± 0.3 |
| Ca | 20.0 aA± 9.5 | 18.3 aA± 3.1 | 15.0 aA± 7.2 | 15.7 aA± 3.1 |  | 22.3 aA± 2.9 | 18.7 aA± 4.2 | 17.0 aA± 3.0 | 21.3 aA± 5.9 |
| Mg | 5.0 aA± 1.0 | 6.3 aA± 0.6 | 4.3 aA± 1.5 | 5.0 aA± 1.0 |  | 4.7 aA± 0.6 | 4.0 aA± 1.0 | 4.0 aA±1.0 | 4.3 aA± 2.3 |
| Al | 1.3 aA± 0.6 | 0.7 aA± 0.6 | 2.0 aA± 2.0 | 1.0 aA± 0 |  | 0.3 aA± 0.6 | 0.7 aA± 0.6 | 0.3 aA± 0.6 | 1.0 aA± 0 |
| H+Al | 22.0 aA± 2.6 | 19.0 aA± 6.1 | 25.7 aA± 8.6 | 22.0 aA± 3.6 |  | 19.0 aA± 4.6 | 27.0 aA± 8.9 | 20.0 aA± 2.0 | 28.0 aA± 7.5 |
| SB | 25.9 aA± 9.5 | 25.4 aA± 3.2 | 20.1 aA± 8.6 | 21.5 aA± 3.9 |  | 27.5 aA± 3.5 | 23.3 aA± 5.0 | 21.7 aA± 2.4 | 26.4 aA± 8.3 |
| CEC | 47.9 aA± 11.0 | 44.4 aA± 2.9 | 45.8 aA± 3.3 | 43.5 aA± 5.0 |  | 46.5 aA± 1.6 | 50.3 aA± 7.3 | 41.7 aA± 1.6 | 54.4 aA± 15.3 |
| V | 53.0 aA± 7.0 | 57.7 aA± 11.0 | 44.0 aA± 17.5 | 49.3 aA± 6.0 |  | 59.0 aA± 8.9 | 47.0 aA± 13.2 | 52.3 aA± 4.9 | 48.3 aA± 4.7 |
| S | 2.3 aA± 1.5 | 0.3 aA± 0.1 | 1.0 aA± 1.0 | 1.0 aA± 0 |  | 3.0 aA± 1.7 | 4.3 aB± 2.5 | 1.7 aA± 1.5 | 2.3 aA± 0.6 |
| B | 0.1 aA± 0 | 0.1 aA± 0 | 0.1 aA± 0 | 0.1 aA± 0 |  | 0.1 aA± 0 | 0.3 aA± 0.1 | 0.1 aA± 0 | 0.1 aA± 0 |
| Cu | 0.3 aA± 0.1 | 0.4 aA± 0.2 | 0.3 aA± 0 | 0.3 aB± 0 |  | 0.7 aA± 0.1 | 0.8 aA± 0.2 | 0.5 aA± 0.2 | 0.9 aA± 0.3 |
| Fe | 31.3 aA± 9.3 | 26.3 aA± 3.1 | 34.3 aA± 4.5 | 36.0 aA± 3.6 |  | 30.7 aA± 6.4 | 39.7 aA± 8.7 | 35.3 aA± 2.1 | 41.7 aA± 9.2 |
| Mn | 3.2 aA± 0.8 | 2.1 aA± 0.6 | 3.3 aA± 0.9 | 3.7 aA± 1.3 |  | 2.5 aA± 1.4 | 2.4 aA± 1.0 | 1.6 aA± 1.0 | 1.7 aA± 0.2 |
| Density | 1.6 aA± 0 | 1.6 aA± 0 | 1.6 aA± 0 | 1.6 aA± 0.1 |  | 1.4 aA± 0.2 | 1.4 aA± 0.2 | 1.4 aA± 0.1 | 0.8 aB± 0.7 |
| Moisture | 10.1 aA± 0.6 | 10.7 aA± 0.1 | 10.8 aA± 0.5 | 10.5 aA± 1.1 |  | 7.3 aA± 0 | 8.8 aA± 1.8 | 10.3 aA± 1.9 | 9.6 aA± 2.1 |

K, Ca, Mg, Al, potential acidity (H+Al), sum of bases (SB), and cation exchange capacity (CEC) are expressed in mmolc.dm-3; organic matter (OM) is expressed in g.dm-3; P is expressed in mg.dm-3; S, B, Cu, and Fe are expressed in mg.dm-3. P-K – Mehlich 1 extractor. Ca-Mg-Al – KCl 1N. H+Al – SMP extractor. V – base saturation index.

† Average for each of three replicates of soil.

‡ Standard deviation based on three replicates of soil.

§ Tukey’s honestly significant difference (HSD) test was performed separately for each of the two field experiments. Values with the same lower-case letters were not significantly different (*P* < 0.05) based on Tukey’s test.

¶ Tukey’s honestly significant difference (HSD) test was performed for both field experiments across all soil cores for each of the four treatments. Samples were contrasted for treatments equally supplied with zinc. Values with the same upper-case letters were not significantly different (*P* < 0.05) based on Tukey’s test between contrasted samples.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Kingdom/Domain** | **Phylum** |
| **Zinc transport** | | |
| MSC2 | Fungi | Ascomycota |
| Yiip (FieF) | Bacteria | Proteobacteria |
| *Znt*A | Archaea | Euryarchaeota |
| Bacteria | Acidobacteria, Actinobacteria, Bacteroidetes, Cyanobacteria, Firmicutes, Planctomycetes, Proteobacteria |
| Fungi | Ascomycota |
| *Znu*C | Archaea | Euryarchaeota |
| Bacteria | Actinobacteria, Bacteroidetes, Caldiserica, Chlamydiae, Chlorobi, Chloroflexi, Cyanobacteria, Deinococcus, Firmicutes, Proteobacteria, Verrucomicrobia |
| *Zrt*2 | Fungi | Ascomycota, Basidiomycota |
| **Secondary metabolism** | | |
| per arc | Archaea | Crenarchaeota, Euryarchaeota |
| per fun | Fungi | Ascomycota, Basidiomycota |
| V BPO | Bacteria | Bacteroidetes |
| mg chelatase | Bacteria | Cyanobacteria |
| methoxyneurosporene desaturase | Bacteria | Proteobacteria |
| IPyA | Bacteria | Actinobacteria, Planctomycetes, Proteobacteria, Verrucomicrobia |
| **Oxidative stress** | | |
| *sod*A | Archaea | Crenarchaeota, Euryarchaeota |
| Bacteria | Actinobacteria, Bacteroidetes, Chlorobi, Chloroflexi, Chlamydiae, Cyanobacteria, Deinococcus, Firmicutes, Gemmatimonadetes, Ignavibacteriae, Planctomycetes, Proteobacteria, Verrucomicrobia |
| Fungi | Ascomycota, Basidiomycota |
| **Oxygen limitation** | | |
| Arca | Bacteria | Proteobacteria |
| **Glucose limitation** | | |
| ccpA | Bacteria | Actinobacteria, Bacteroidetes, Firmicutes, Proteobacteria, Spirochaetes |
| **Phosphate limitation** | | |
| *pho*B | Bacteria | Actinobacteria, Deinococcus, Firmicutes, Planctomycetes, Proteobacteria |
| **Stress (others)** | | |
| *Rse*A | Bacteria | Proteobacteria |
| tre fun | Fungi | Ascomycota, Basidiomycota |
| CpxR | Archaea | Euryarchaeota |
|  | Bacteria | Actinobacteria, Cyanobacteria, Firmicutes, Proteobacteria |
| *Psp*B | Bacteria | Proteobacteria |
| **Infection** | | |
| pilin | Bacteria | Acidobacteria, Cyanobacteria, Deinococcus, Elusimicrobia, Firmicutes, Proteobacteria |
| pap | Bacteria | Proteobacteria |
| *bfp*B | Bacteria | Proteobacteria |
| srt | Bacteria | Actinobacteria, Firmicutes |
| *hys*A | Bacteria | Firmicutes |

**Supplementary Table S2.** Gene probes origin for the gene families significantly correlated with zinc concentration in soil

**Supplementary Table S2.** Continued.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Kingdom/Domain** | **Phylum** |
| **Secretion system** | | |
| *hrp*Q | Bacteria | Proteobacteria |
| YopM | Bacteria | Proteobacteria |
| lcrD | Bacteria | Proteobacteria |
| **Survival of host response** | | |
| *sia*C | Bacteria | Proteobacteria |
| lip | Bacteria | Proteobacteria |
| Fungi | Basidiomycota |
| *zmp*A | Bacteria | Proteobacteria |
| *ams*G | Bacteria | Planctomycetes |
| **Virulence (others)** | | |
| Vip | Bacteria | Proteobacteria |
| ler | Bacteria | Proteobacteria |
| patulin (6MSAS) | Fungi | Ascomycota |
| **Carbon degradation** | | |
| *Ace*A | Archaea | Euryarchaeota |
| Bacteria | Acidobacteria, Actinobacteria, Chloroflexi, Deinococcus, Firmicutes, Proteobacteria, Verrucomicrobia |
| Fungi | Ascomycota |
| endopolygalacturonase | Fungi | Ascomycota, Basidiomycota |
| exopolygalacturonase | Fungi | Ascomycota, Basidiomycota |
| GLX | Bacteria | Actinobacteria, Proteobacteria |
| Fungi | Ascomycota, Basidiomycota |
| phospholipase C | Fungi | Ascomycota, Basidiomycota |
| **Carbon fixation** | | |
| C CoA hydratase DiC4HB | Archaea | Crenarchaeota |
| FBPase | Bacteria | Cyanobacteria, Proteobacteria |
| *frd*A (rTCA) | Bacteria | Aquificae, Chlorobi, Nitrospirae, Proteobacteria |
| mdh | Bacteria | Aquificae, Chlorobi, Proteobacteria |
| MMCE | Bacteria | Chloroflexi |
| rubisco | Bacteria | Actinobacteria, Chlorobi, Cyanobacteria, Firmicutes, Verrucomicrobia |
| *sdh*A | Bacteria | Chloroflexi |
| *suc*A | Archaea | Crenarchaeota |
| **Methanogenesis** | | |
| *mrt*H | Archaea | Euryarchaeota |
| Bacteria | Firmicutes, Proteobacteria |
| MtaB | Archaea | Euryarchaeota |
| Bacteria | Firmicutes |
| **Denitrification** | | |
| *nir*S | Bacteria | Aquificae, Proteobacteria |
| **Dissimilatory N reduction** | | |
| *Nap*a | Bacteria | Proteobacteria |
| **Phosphorus utilization** | | |
| 5f1 (*ptx*D) | Bacteria | Proteobacteria |
| 5f1 (ppn) | Fungi | Ascomycota |