**Supplementary Table 1.** Differentially abundant proteins in mite susceptible *Oryza barthii* (control x early infested condition).

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| ***Oryza barthii* Control x Early infested - Proteins unique or more expressed in control leaves** |
| **Functional categories** | **Description** | **Uniprot** | **Locus** | **Reported peptides** | **t-Test** | **Log2 Fold Change** |
| **Antioxidant system** | ferredoxin--nitrite reductase, chloroplastic | Q0JMV6\_ORYSJ | LOC\_Os01g25484 | 11 | 0.046 | -0.825 |
| **Translation** | 60S ribosomal protein L6 | Q6YY64\_ORYSJ | LOC\_Os02g37862 | 2 | 0.018 | -0.747 |
| **Cytoskeleton** | actin-7 | Q94DL4\_ORYSJ | LOC\_Os01g73310 | 11 | Unique Control | Unique Control |
| ***Oryza barthii* Control x Early infested - Proteins unique or more expressed in early infested leaves** |
| **Functional categories** | **Description** | **Uniprot** | **Locus** | **Reported peptides** | **t-Test** | **Log2 Fold Change** |
| **Antioxidant system** | peroxidase 2 | Q7F1U0\_ORYSJ | LOC\_Os07g48020 | 7 | 0.003 | 1.561 |
| peroxidase 2-like | Q7F1U1\_ORYSJ | LOC\_Os07g48010 | 2 | 0.004 | 1.477 |
| glutathione transferase GST 23 | Q93WY5\_ORYSJ | LOC\_Os09g29200 | 3 | 0.018 | 1.307 |
| peroxidase 1 | Q654S0\_ORYSJ | LOC\_Os01g22230 | 4 | 0.019 | 0.940 |
| cationic peroxidase SPC4-like | Q5JMS4\_ORYSJ | LOC\_Os01g73170 | 5 | 0.017 | 0.838 |
| glutathione S-transferase 1 | GSTF2\_ORYSJ | LOC\_Os01g55830 | 4 | 0.012 | 0.821 |
| anionic peroxidase | Q7XSV2\_ORYSJ | LOC\_Os04g59150 | 3 | 0.038 | 0.779 |
| lactoylglutathione lyase | LGUL\_ORYSJ | LOC\_Os08g09250 | 10 | 0.022 | 0.764 |
| catalase | CATA2\_ORYSJ | LOC\_Os06g51150 | 7 | 0.047 | 0.574 |
| monodehydroascorbate reductase | MDAR3\_ORYSJ | LOC\_Os09g39380 | 5 | 0.046 | 0.535 |
| **Stress response** | momilactone A synthase-like | Q0D3V0\_ORYSJ | LOC\_Os07g46930 | 6 | 0.009 | 1.638 |
| momilactone A synthase-like | A0A0P0X9T1\_ORYSJ | LOC\_Os07g46830 | 2 | 0.031 | 1.250 |
| cysteine-rich repeat secretory protein 55-like | Q75L18\_ORYSJ | LOC\_Os05g02200 | 2 | 0.002 | 1.179 |
| PLAT domain-containing protein 3 | Q7XRE7\_ORYSJ | LOC\_Os04g38390 | 4 | 0.013 | 1.126 |
| heat shock cognate 70 kDa protein | Q10NA1\_ORYSJ | LOC\_Os03g16920 | 10 | 0.003 | 1.022 |
| stress-response A/B barrel domain-containing protein UP3 | A0A0P0X8Q0\_ORYSJ | LOC\_Os07g41820 | 2 | 0.049 | 0.694 |
| chalcone--flavonone isomerase | CFI\_ORYSJ | LOC\_Os03g60509 | 5 | 0.001 | 0.694 |
| Grx\_C2.2 - glutaredoxin subgroup I | GRXC6\_ORYSJ | LOC\_Os04g42930 | 2 | 0.038 | 0.527 |
| **Protein modification/degradation** | probable carboxylesterase 15 | Q8GSJ3\_ORYSJ | LOC\_Os07g06830 | 4 | 0.011 | 1.082 |
| serine carboxypeptidase 2 | Q5W6C6\_ORYSJ | LOC\_Os05g18604 | 2 | 0.003 | 0.903 |
| serine carboxypeptidase II-2 | Q5SMV5\_ORYSJ | LOC\_Os06g08720 | 2 | 0.030 | 0.861 |
| oryzain alpha chain | ORYA\_ORYSJ | LOC\_Os04g55650 | 4 | 0.000 | 0.806 |
| subtilisin-like protease SBT1.9 | Q8S1N3\_ORYSJ | LOC\_Os01g64860 | 5 | 0.017 | 0.748 |
| probable carboxylesterase 15 | Q8GSE8\_ORYSJ | LOC\_Os07g06840 | 4 | 0.018 | 0.647 |
| serine carboxypeptidase-like 50 | Q75HY2\_ORYSJ | LOC\_Os05g50600 | 7 | 0.037 | 0.640 |
| **General metabolic processes** | putative Tryptophan synthase beta chain | Q67VM2\_ORYSJ | LOC\_Os06g42560 | 3 | 0.028 | 1.049 |
| primary amine oxidase | A0A0P0W896\_ORYSJ | LOC\_Os04g20164 | 2 | 0.049 | 0.697 |
| nucleoside diphosphate kinase 2, chloroplastic | A0A0P0YB67\_ORYSJ | LOC\_Os12g36194 | 2 | 0.010 | 0.620 |
| glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic | G3PC1\_ORYSJ | LOC\_Os08g03290 | 13 | 0.019 | 0.537 |
| **Lipid metabolism** | lipid-transfer protein | NLTP1\_ORYSJ | LOC\_Os12g02320 | 2 | 0.015 | 2.117 |
| lipid transfer protein | NLT2A\_ORYSJ | LOC\_Os11g02369 | 4 | 0.043 | 1.785 |
| 3-ketoacyl-CoA thiolase 2, peroxisomal-like | Q84P96\_ORYSJ | LOC\_Os02g57260 | 6 | 0.002 | 0.576 |
| **Carbohydrate metabolism and energy production** | NADP-dependent malic enzyme isoform X1 | A0A0P0V7M3\_ORYSJ | LOC\_Os01g52500 | 6 | 0.016 | 0.798 |
| thiamine thiazole synthase 2, chloroplastic | A0A0N7KNK4\_ORYSJ | LOC\_Os07g34570 | 4 | 0.014 | 0.691 |
| transaldolase 2 | Q5JK10\_ORYSJ | LOC\_Os01g70170 | 13 | 0.029 | 0.538 |
| **Photosynthesis** | protochlorophyllide reductase A, chloroplastic | PORA\_ORYSJ | LOC\_Os04g58200 | 4 | 0.032 | 0.923 |
| ruBisCO large subunit-binding protein subunit beta, chloroplastic | Q6ZFJ9\_ORYSJ | LOC\_Os02g01280 | 5 | 0.004 | 0.717 |
| **Hormone-related** | allene oxide cyclase, chloroplastic | AOC\_ORYSJ | LOC\_Os03g32314 | 3 | 0.032 | 0.523 |
| **Amino acid metabolism** | peptide methionine sulfoxide reductase A4, chloroplastic | MSRA4\_ORYSJ | LOC\_Os10g41400 | 2 | 0.042 | 0.511 |
| **Translation** | putative RNase S-like protein precursor | Q69JF3\_ORYSJ | LOC\_Os09g36700 | 3 | 0.045 | 1.169 |
| **Cytoskeleton** | actin-2 | ACT2\_ORYSJ | LOC\_Os10g36650 | 13 | Unique Infected | Unique Infected |
|  | chitin elicitor-binding protein-like | CEBIP\_ORYSJ | LOC\_Os03g04110 | 3 | 0.001 | 0.958 |
| **Others** | amidase 1 | A3AQC6\_ORYSJ | LOC\_Os04g02754 | 5 | 0.008 | 0.910 |
|  | PLAT domain-containing protein 3 | Q6ZGP5\_ORYSJ | LOC\_Os02g51710 | 5 | 0.043 | 0.765 |
|  | dirigent protein 21 | Q2R0H3\_ORYSJ | LOC\_Os11g42550 | 5 | 0.028 | 0.684 |