**Supplementary Table 1. Rice defense genes used for the qPCR analysis and their function**

|  |  |  |
| --- | --- | --- |
| **Gene** | **Characteristics and function** | **Reference** |
| *OsCEBiP*(Chitin Elicitor Binding Protein) | It is a Pattern Recognition Receptor (PRR) that detects the pathogen PAMP molecule chitin and activates plant defense system. It is a plasma membrane protein that forms a receptor complex essential for fungal chitin-driven immune responses in rice. | Akamatsu et al. 2013 |
| *OsCERK1*(Chitin Elicitor Receptor Kinase) | It is a rice receptor-like kinase (RLK) that mediates the signal of a fungal cell wall component chitin. It indispensable for chitin perception and participates in innate immunity. It can mediate the signaling pathways of both fungal and bacterial PAMP molecules. | Kouzai et al. 2014 |
| *OsPAD4* (Phytoalexin deficient 4) | Phytoalexin deficient 4 (PAD4) induces JA-dependent induced systemic resistance. It also plays an important role in accumulation of JA and a terpenoid-type phytoalexin momilactone A (MOA). | Ke et al. 2014 |
| *OsEDS1*(Enhanced disease susceptibility 1) | Enhanced disease susceptibility 1 (EDS1) induces JA-dependent induced systemic resistance. | Ke et al. 2019 |
| *OsNPR1* (Non Repressor of Pathogenesis related Protein) | A central regulator of salicylic-acid (SA)-mediated defense signalingReallocation of energy and resources during defense responses | Sugano et al. 2010 |
| *OsPDF2.2* (Plant Defensin-like protein 2) | Plant defensin inhibit the growth of a broad range of fungi | Thomma et al. 2002 |
| *OsFMO1* (Favin-dependent Monooxygenase 1) | An essential component for induced systemic acquired resistance (SAR) | Mishina et al 2006; Koch et al 2006 |
| *OsPR1.1* (Pathogenesis related protein 1) | Acidic pathogenesis related protein 1, among the most abundant antimicrobial protein. It is also a marker for salicylic acid mediated SAR | Breen et al 2017 |

**Supplementary Table 2. List of the PCR primers used in the gene expression studies**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **SN** | **Gene**  |  | **Primer sequence(5→3)** | **Number of bases** | **Product size** |
| 1 | *Os*PAD4 | Forward  | TGCCGACTACCACCGAAAC | 19 | 61 |
| Reverse  | CCGGCCATGGGTGATGTA | 18 |  |
| 2 | *Os*EDS1 | Forward  | TTGAATTTTGTCGTGCCAGTAGA | 23 | 63 |
| Reverse  | GGCAGATGCAAGCGGAGTAA | 20 |  |
| 3 | *Os*CEBiP | Forward  | GTGCGGAGAAGTCTGGAAAG | 20 | 131 |
|  | Reverse  | TCCTGATTTCGCTTGCTTTT | 20 |  |
| 4 | *Os*CERK1 | Forward  | AAGAACTACCGGGCAAAGGT | 20 | 244 |
| Reverse  | GCCCCTTTGAATCACTTGAA | 20 |  |
| 5 | *Os*PDF2.2 | Forward  | CCACAGGTTCAAGGGCATGT | 20 | 63 |
| Reverse  | CTCTCCGTCCTGCACACGTT | 20 |  |
| 6 | *Os*NPR1 | Forward  | AAACAAAGGAGCAGCTGTATCACA | 24 | 66 |
| Reverse  | CTCCGGCAGATACTCATTGCA | 21 |  |
| 7 | *Os*FMO1 | Forward  | CAGTGGAGTGCCCAACATACC | 21 | 65 |
| Reverse  | CCTGGCCATCAAATGCTTCT | 20 |  |
| 8 | *Os* PR1.1 | Forward  | GGAGGCATCCAAGCTAGCAA | 20 | 80 |
| Reverse  | GGGCATCGGAGCAGTGAA | 18 |  |
| 9 | *Os*Actin | Forward  | CAGCCACACTGTCCCCATCTA | 21 | 67 |
| Reverse  | AGCAAGGTCGAGACGAAGGA | 20 |  |

Primers designed using online platform Primer3Plus <http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi>

**Supplementary Table 3. Metagenome read statistics of phyllomicrobiome of rice genotypes grown in two contrasting climatic zone**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Location** | **Sample Name** | **\*MG-RAST accession No****(Project ID mgp94842)** | **\*\*NCBI-Genbank accession No. (Bio Project ID PRJNA681302)** | **Number of base pairs (bp)** | **Total number of sequences** | **Mean Sequence Length (bp)** |
| **Palampur (HP), 2016** | **PRR78\_Plm1** | mgm4895994.3 | SRR13171790 | 20,127,006  | 43,818 | 459 ± 18  |
| **PRR78\_Plm2** | mgm4895995.3 | SRR13355773 | 12,296,139  | 26,794 | 459 ± 17  |
| **Pusa1602\_Plm1** | mgm4895999.3 | SRR13171789 | 17,306,479  | 38,369 | 451 ± 22  |
| **Pusa1602\_Plm2** | mgm4896000.3 | SRR13355772 | 10,617,288  | 23,552 | 451 ± 21  |
| **Port Blair****Andaman Island, 2017** | **PRR78\_ANI1** | mgm4895998.3 | SRR13171788 | 43,236,085  | 96,317 | 449 ± 23  |
| **PRR78\_ANI2** | mgm4896001.3 | SRR13355771 | 8,316,792  | 18,933 | 439 ± 46  |
| **Pusa1602\_ANI1** | mgm4895997.3 | SRR13171787 | 58,289,850  | 129,470 | 450 ± 22  |
| **Pusa1602\_ANI2** | mgm4895996.3 | SRR13355770 | 11,173,095  | 25,340 | 441 ± 45  |

 \*<https://www.mg-rast.org/>

\*\* <https://www.ncbi.nlm.nih.gov/>

**Supplementary Table 4. Network analysis of rice phyllospheric microbiome using SparCC correlation coefficients**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Genus** | ***Positively Correlated Genus*** | **Correlation** | ***Negatively Correlated Genus*** | **Correlation** |
| **Acidovorax** | ***Macrococcus*** | 0.743 | ***Asaia*** | -0.739 |
|  | ***Sphingopyxis*** | 0.829 | ***Enterococcus*** | -0.774 |
|  | ***unclassified-(derived-from-Alphaproteobacteria)*** | 0.944 | ***Leptolyngbya*** | -0.652 |
|  |  |  | ***unclassified-(derived-from-Bacteria)*** | -1.000 |
|  |  |  | ***Xenococcus*** | -0.729 |
|  |  |  |  |  |
| **Acinetobacter** | ***Arthrobacter*** | 0.743 | ***Bacillus*** | -0.790 |
|  | ***Exiguobacterium*** | 0.781 | ***Citrobacter*** | -0.743 |
|  | ***Flavobacterium*** | 0.853 | ***Tetrasphaera*** | -0.798 |
|  | ***Pseudomonas*** | 0.805 |  |  |
|  | ***Riemerella*** | 0.811 |  |  |
|  |  |  |  |  |
| **Agrobacterium** | ***Leucobacter*** | 0.885 | ***Chryseobacterium*** | -0.696 |
|  |  |  |  |  |
| **Agromyces** | ***Clavibacter*** | 0.851 | ***Paenibacillus*** | -0.845 |
|  | ***Kineococcus*** | 1.000 | ***Sphingobacterium*** | -0.755 |
|  | ***Lactobacillus*** | 0.710 |  |  |
|  | ***Leifsonia*** | 0.903 |  |  |
|  | ***Okibacterium*** | 0.847 |  |  |
|  |  |  |  |  |
| **Arthrobacter** | ***Acinetobacter*** | 0.743 | ***Bacillus*** | -0.975 |
|  | ***Erwinia*** | 0.826 | ***Citrobacter*** | -0.714 |
|  | ***Pseudoalteromonas*** | 0.761 | ***Clostridium*** | -0.802 |
|  | ***Pseudomonas*** | 0.736 | ***Lactobacillus*** | -0.859 |
|  | ***Shewanella*** | 0.952 | ***unclassified-(derived-from-Oscillatoriales)*** | -0.753 |
|  | ***Sphingopyxis*** | 0.801 |  |  |
|  |  |  |  |  |
| **Arthrospira** | ***Clostridium*** | 0.644 | ***Shewanella*** | -0.647 |
|  | ***Kurthia*** | 0.819 |  |  |
|  | ***Lyngbya*** | 0.777 |  |  |
|  | ***Mycetocola*** | 0.770 |  |  |
|  |  |  |  |  |
| **Asaia** | ***Enterococcus*** | 0.713 | ***Acidovorax*** | -0.739 |
|  | ***Leptolyngbya*** | 0.732 | ***unclassified-(derived-from-Alphaproteobacteria)*** | -0.912 |
|  | ***unclassified-(derived-from-Bacteria)*** | 1.000 |  |  |
|  | ***Xanthomonas*** | 0.798 |  |  |
|  | ***Xenococcus*** | 0.901 |  |  |
|  |  |  |  |  |
| **Azorhizobium** |  |  | ***Rhizobium*** | -0.670 |
|  |  |  | ***Spirosoma*** | -0.691 |
|  |  |  |  |  |
| **Bacillus** | ***Bifidobacterium*** | 0.852 | ***Acinetobacter*** | -0.790 |
|  | ***Citrobacter*** | 0.747 | ***Arthrobacter*** | -0.975 |
|  | ***Clostridium*** | 0.952 | ***Erwinia*** | -0.943 |
|  | ***Lactobacillus*** | 0.864 | ***Flavobacterium*** | -0.749 |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.814 | ***Pseudoalteromonas*** | -0.756 |
|  |  |  | ***Shewanella*** | -0.889 |
|  |  |  | ***unclassified-(derived-from-unclassified-sequences)*** | -0.896 |
|  |  |  |  |  |
| **Bifidobacterium** | ***Bacillus*** | 0.852 | ***Erwinia*** | -0.812 |
|  | ***Clostridium*** | 0.835 | ***Pseudoalteromonas*** | -0.843 |
|  | ***Lactobacillus*** | 0.965 | ***Shewanella*** | -0.931 |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.948 | ***Sphingopyxis*** | -0.825 |
|  | ***Xenococcus*** | 0.672 |  |  |
|  |  |  |  |  |
| **Burkholderia** | ***Micrococcus*** | 0.878 |  |  |
|  |  |  |  |  |
| **Candidatus-Aquiluna** | ***Sphingomonas*** | 0.753 | ***Sphingobacterium*** | -0.696 |
|  | ***unclassified-(derived-from-Bacteria)*** | 1.000 | ***unclassified-(derived-from-Alphaproteobacteria)*** | -0.825 |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.702 |  |  |
|  | ***Xenococcus*** | 0.635 |  |  |
|  |  |  |  |  |
| **Chryseobacterium** | ***Pedobacter*** | 0.880 | ***Agrobacterium*** | -0.696 |
|  | ***Rhodococcus*** | 0.805 | ***Clavibacter*** | -0.842 |
|  | ***Spirosoma*** | 0.866 | ***Cronobacter*** | -0.841 |
|  |  |  | ***Leifsonia*** | -0.720 |
|  |  |  | ***Leucobacter*** | -0.863 |
|  |  |  | ***Okibacterium*** | -0.776 |
|  |  |  |  |  |
|  |  |  | ***unclassified-(derived-from-Enterobacteriaceae)*** | -0.802 |
| **Citrobacter** | ***Bacillus*** | 0.747 | ***Acinetobacter*** | -0.743 |
|  | ***Cronobacter*** | 0.751 | ***Arthrobacter*** | -0.714 |
|  | ***Staphylococcus*** | 0.694 | ***Exiguobacterium*** | -0.930 |
|  | ***Tetrasphaera*** | 0.701 | ***Flavobacterium*** | -0.876 |
|  |  |  | ***Pseudomonas*** | -0.820 |
|  |  |  |  |  |
| **Clavibacter** | ***Agromyces*** | 0.851 | ***Chryseobacterium*** | -0.842 |
|  | ***Cronobacter*** | 0.778 | ***Deinococcus*** | -0.873 |
|  | ***Kineococcus*** | 1.000 | ***Paenibacillus*** | -0.872 |
|  | ***Leifsonia*** | 0.943 | ***Sphingobacterium*** | -0.795 |
|  | ***Leucobacter*** | 0.944 | ***Spirosoma*** | -0.816 |
|  | ***Okibacterium*** | 0.790 |  |  |
|  |  |  |  |  |
| **Clostridium** | ***Arthrospira*** | 0.644 | ***Arthrobacter*** | -0.802 |
|  | ***Bacillus*** | 0.952 | ***Erwinia*** | -0.848 |
|  | ***Bifidobacterium*** | 0.835 | ***Pseudoalteromonas*** | -0.772 |
|  | ***Lactobacillus*** | 0.855 | ***Shewanella*** | -0.819 |
|  | ***Mycetocola*** | 0.754 |  |  |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.810 |  |  |
|  |  |  |  |  |
| **Cronobacter** | ***Citrobacter*** | 0.751 | ***Chryseobacterium*** | -0.841 |
|  | ***Clavibacter*** | 0.778 | ***Enterococcus*** | -0.754 |
|  | ***Escherichia*** | 0.735 | ***Flavobacterium*** | -0.623 |
|  | ***Leucobacter*** | 0.822 | ***Paenibacillus*** | -0.781 |
|  | ***Serratia*** | 0.775 | ***Pseudomonas*** | -0.767 |
|  |  |  |  |  |
| **Curtobacterium** | ***Rhizobium*** | 0.775 | ***Pseudoalteromonas*** | -0.714 |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.844 | ***Sphingopyxis*** | -0.791 |
|  |  |  |  |  |
| **Deinococcus** | ***Frankia*** | 0.772 | ***Clavibacter*** | -0.873 |
|  | ***Hymenobacter*** | 0.892 | ***Kineococcus*** | -1.000 |
|  | ***Rhodococcus*** | 0.846 | ***Leucobacter*** | -0.819 |
|  | ***Sphingobacterium*** | 0.716 | ***Methylocella*** | -0.802 |
|  | ***Spirosoma*** | 0.840 | ***Okibacterium*** | -0.799 |
|  |  |  |  |  |
| **Enterococcus** | ***Asaia*** | 0.713 | ***Acidovorax*** | -0.774 |
|  | ***Leptolyngbya*** | *0.771* | ***Cronobacter*** | *-0.754* |
|  | ***Xenococcus*** | 0.782 | ***Serratia*** | -0.741 |
|  |  |  |  |  |
| **Erwinia** | ***Arthrobacter*** | 0.826 | ***Bacillus*** | -0.943 |
|  | ***Pseudoalteromonas*** | 0.801 | ***Bifidobacterium*** | -0.812 |
|  | ***Shewanella*** | 0.858 | ***Clostridium*** | -0.848 |
|  | ***Sphingopyxis*** | 0.708 | ***Lactobacillus*** | -0.774 |
|  |  |  | ***Microcoleus*** | -0.664 |
|  |  |  | ***unclassified-(derived-from-Oscillatoriales)*** | -0.796 |
|  |  |  |  |  |
| **Escherichia** | ***Cronobacter*** | 0.735 |  |  |
|  | ***Serratia*** | 0.851 |  |  |
|  |  |  |  |  |
| **Exiguobacterium** | ***Acinetobacter*** | 0.781 | ***Citrobacter*** | -0.930 |
|  | ***Flavobacterium*** | 0.924 | ***Staphylococcus*** | -0.858 |
|  |  |  | ***Tetrasphaera*** | -0.829 |
|  |  |  |  |  |
| **Flavobacterium** | ***Acinetobacter*** | 0.853 | ***Bacillus*** | -0.749 |
|  | ***Exiguobacterium*** | 0.924 | ***Citrobacter*** | -0.876 |
|  | ***Pedobacter*** | 0.688 | ***Cronobacter*** | -0.623 |
|  | ***Pseudomonas*** | 0.710 | ***Staphylococcus*** | -0.741 |
|  |  |  | ***Tetrasphaera*** | -0.778 |
|  |  |  | ***unclassified-(derived-from-Bacteria)*** | -1.000 |
|  |  |  |  |  |
| **Frankia** | ***Deinococcus*** | 0.772 | ***Methylocella*** | -0.698 |
|  | ***Hymenobacter*** | 0.778 |  |  |
|  | ***Janibacter*** | 0.966 |  |  |
|  | ***Methylobacterium*** | 0.793 |  |  |
|  |  |  |  |  |
| **Hymenobacter** | ***Deinococcus*** | 0.892 | ***Okibacterium*** | -0.787 |
|  | ***Frankia*** | 0.778 |  |  |
|  | ***Kineococcus*** | 0.860 |  |  |
|  | ***Methylobacterium*** | 0.859 |  |  |
|  | ***Rhodococcus*** | 0.799 |  |  |
|  | ***Spirosoma*** | 0.802 |  |  |
|  |  |  |  |  |
| **Janibacter** | ***Frankia*** | 0.966 | ***Methylocella*** | -0.737 |
|  | ***Methylobacterium*** | 0.829 |  |  |
|  |  |  |  |  |
| **Kineococcus** | ***Agromyces*** | 1.000 | ***Deinococcus*** | -1.000 |
|  | ***Clavibacter*** | 1.000 | ***Rhodococcus*** | -1.000 |
|  | ***Hymenobacter*** | 0.860 | ***Sphingobacterium*** | -1.000 |
|  | ***Leifsonia*** | 1.000 | ***Spirosoma*** | -1.000 |
|  | ***Leucobacter*** | 1.000 |  |  |
|  | ***Okibacterium*** | 1.000 |  |  |
|  | ***Pedobacter*** | 0.882 |  |  |
|  |  |  |  |  |
| **Klebsiella** | ***Pseudomonas*** | 0.699 |  |  |
|  | ***Sphingomonas*** | 0.805 |  |  |
|  |  |  |  |  |
| **Kurthia** | ***Arthrospira*** | 0.819 | ***Renibacterium*** | -0.686 |
|  | ***Lactobacillus*** | 0.751 |  |  |
|  | ***Leifsonia*** | 0.819 |  |  |
|  | ***Mycetocola*** | 0.728 |  |  |
|  |  |  |  |  |
| **Lactobacillus** | ***Agromyces*** | 0.710 | ***Arthrobacter*** | -0.859 |
|  | ***Bacillus*** | 0.864 | ***Erwinia*** | -0.774 |
|  | ***Bifidobacterium*** | 0.965 | ***Macrococcus*** | -0.744 |
|  | ***Clostridium*** | 0.855 | ***Pseudoalteromonas*** | -0.848 |
|  | ***Kurthia*** | 0.751 | ***Shewanella*** | -0.927 |
|  | ***Leifsonia*** | 0.832 | ***Sphingopyxis*** | -0.789 |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.889 |  |  |
|  |  |  |  |  |
| **Leifsonia** | ***Agromyces*** | 0.903 | ***Chryseobacterium*** | -0.720 |
|  | ***Clavibacter*** | 0.943 | ***Paenibacillus*** | -0.873 |
|  | ***Kineococcus*** | 1.000 | ***Sphingobacterium*** | -0.822 |
|  | ***Kurthia*** | 0.819 |  |  |
|  | ***Lactobacillus*** | 0.832 |  |  |
|  | ***Leucobacter*** | 0.799 |  |  |
|  | ***unclassified-(derived-from-Bacteria)*** | 1.000 |  |  |
|  |  |  |  |  |
| **Leptolyngbya** | ***Asaia*** | 0.732 | ***Acidovorax*** | -0.652 |
|  | ***Enterococcus*** | 0.771 | ***Chryseobacterium*** | -0.863 |
|  | ***Rhizobium*** | 0.683 | ***Deinococcus*** | -0.819 |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.821 | ***Paenibacillus*** | -0.865 |
|  | ***Xenococcus*** | 0.923 | ***Sphingobacterium*** | -0.722 |
|  | ***Agrobacterium*** | 0.885 | ***Spirosoma*** | -0.754 |
|  | ***Clavibacter*** | 0.944 |  |  |
|  | ***Cronobacter*** | 0.822 |  |  |
|  | ***Kineococcus*** | 1.000 |  |  |
|  | ***Leifsonia*** | 0.799 |  |  |
|  | ***Okibacterium*** | 0.736 |  |  |
|  | ***Serratia*** | 0.717 |  |  |
|  |  |  |  |  |
| **Lyngbya** | ***Arthrospira*** | 0.777 |  |  |
|  | ***Rothia*** | 0.813 |  |  |
|  | ***unclassified-(derived-from-Alphaproteobacteria)*** | 0.783 |  |  |
|  |  |  |  |  |
| **Macrococcus** | ***Acidovorax*** | 0.743 | ***Lactobacillus*** | -0.744 |
|  | ***Nocardioides*** | 0.798 | ***unclassified-(derived-from-Oscillatoriales)*** | -0.717 |
|  | ***Pseudoalteromonas*** | 0.667 |  |  |
|  | ***Shewanella*** | 0.731 |  |  |
|  | ***Sphingobacterium*** | 0.651 |  |  |
|  | ***Sphingopyxis*** | 0.748 |  |  |
|  | ***Staphylococcus*** | 0.753 |  |  |
|  |  |  |  |  |
| **Massilia** |  |  | ***unclassified-(derived-from-Enterobacteriaceae)*** | -0.770 |
|  |  |  |  |  |
| **Methylobacterium** | ***Frankia*** | 0.793 | ***Methylocella*** | -0.745 |
|  | ***Hymenobacter*** | 0.859 | ***unclassified-(derived-from-unclassified-sequences)*** | -0.884 |
|  | ***Janibacter*** | 0.829 |  |  |
|  | ***Nocardioides*** | 0.827 |  |  |
|  | ***Staphylococcus*** | 0.784 |  |  |
|  |  |  |  |  |
| **Methylocella** |  |  | ***Deinococcus*** | -0.802 |
|  |  |  | ***Frankia*** | -0.698 |
|  |  |  | ***Janibacter*** | -0.737 |
|  |  |  | ***Methylobacterium*** | -0.745 |
|  |  |  | ***Sphingobacterium*** | -0.782 |
|  |  |  | ***unclassified-(derived-from-Bacteria)*** | -0.763 |
|  |  |  |  |  |
| **Micrococcus** | ***Burkholderia*** | 0.878 | ***Xenococcus*** | -0.646 |
|  |  |  |  |  |
| **Microcoleus** |  |  | ***Erwinia*** | -0.664 |
|  |  | ***unclassified-(derived-from-unclassified-sequences)*** | -0.950 |
|  |  |  |  |  |
| **Mycetocola** | ***Arthrospira*** | 0.770 | ***Pseudomonas*** | -0.671 |
|  | ***Clostridium*** | 0.754 |  |  |
|  | ***Kurthia*** | 0.728 |  |  |
|  |  |  |  |  |
| **Nocardioides** | ***Macrococcus*** | 0.798 |  |  |
|  | ***Methylobacterium*** | 0.827 |  |  |
|  | ***Renibacterium*** | 0.629 |  |  |
|  | ***Staphylococcus*** | 0.716 |  |  |
|  |  |  |  |  |
| **Okibacterium** | ***Agromyces*** | 0.847 | ***Chryseobacterium*** | -0.776 |
|  | ***Clavibacter*** | 0.790 | ***Deinococcus*** | -0.799 |
|  | ***Kineococcus*** | 1.000 | ***Hymenobacter*** | -0.787 |
|  | ***Leucobacter*** | 0.736 | ***Paenibacillus*** | -0.743 |
|  |  |  | ***Pedobacter*** | -0.672 |
|  |  |  | ***Rhodococcus*** | -0.767 |
|  |  |  | ***Spirosoma*** | -0.804 |
|  |  |  |  |  |
| **Oscillatoria** |  |  | ***Staphylococcus*** | -0.749 |
|  |  |  |  |  |
| **Paenibacillus** |  |  | ***Agromyces*** | -0.845 |
|  |  |  | ***Clavibacter*** | -0.872 |
|  |  |  | ***Cronobacter*** | -0.781 |
|  |  |  | ***Leifsonia*** | -0.873 |
|  |  |  | ***Leucobacter*** | -0.865 |
|  |  |  | ***Okibacterium*** | -0.743 |
|  |  |  | ***unclassified-(derived-from-Enterobacteriaceae)*** | -0.830 |
|  |  |  |  |  |
| **Pedobacter** | ***Chryseobacterium*** | 0.880 | ***Okibacterium*** | -0.672 |
|  | ***Flavobacterium*** | 0.688 | ***unclassified-(derived-from-Bacteria)*** | -1.000 |
|  | ***Kineococcus*** | 0.882 |  |  |
|  | ***Rhodococcus*** | 0.714 |  |  |
|  |  |  |  |  |
| **Pseudoalteromonas** | ***Arthrobacter*** | 0.761 | ***Bacillus*** | -0.756 |
|  | ***Macrococcus*** | 0.667 | ***Bifidobacterium*** | -0.843 |
|  | ***Shewanella*** | 0.861 | ***Clostridium*** | -0.772 |
|  | ***Sphingopyxis*** | 0.692 | ***Curtobacterium*** | -0.714 |
|  |  |  | ***Erwinia*** | 0.801 |
|  |  |  | ***Lactobacillus*** | -0.848 |
|  |  |  | ***unclassified-(derived-from-Oscillatoriales)*** | -0.821 |
| **Pseudomonas** | ***Acinetobacter*** | 0.805 | ***Citrobacter*** | -0.820 |
|  | ***Arthrobacter*** | 0.736 | ***Cronobacter*** | -0.767 |
|  | ***Flavobacterium*** | 0.710 | ***Mycetocola*** | -0.671 |
|  | ***Klebsiella*** | 0.699 |  |  |
|  |  |  |  |  |
| **Renibacterium** | ***Nocardioides*** | 0.629 | ***Kurthia*** | -0.686 |
|  | ***Sphingopyxis*** | 0.777 |  |  |
|  |  |  |  |  |
| **Rhizobium** | ***Curtobacterium*** | 0.775 | ***Azorhizobium*** | -0.670 |
|  | ***Leptolyngbya*** | 0.683 | ***Serratia*** | -0.777 |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.619 |  |  |
|  |  |  |  |  |
| **Rhodococcus** | ***Chryseobacterium*** | 0.805 | ***Kineococcus*** | -1.000 |
|  | ***Deinococcus*** | 0.846 | ***Okibacterium*** | -0.767 |
|  | ***Hymenobacter*** | 0.799 |  |  |
|  | ***Pedobacter*** | 0.714 |  |  |
|  | ***Spirosoma*** | 0.878 |  |  |
|  |  |  |  |  |
| **Riemerella** | ***Acinetobacter*** | 0.811 | ***Staphylococcus*** | -0.891 |
|  |  |  |  |  |
| **Rothia** | ***Lyngbya*** | 0.813 | ***Xanthomonas*** | -0.666 |
|  | ***unclassified-(derived-from-Alphaproteobacteria)*** | 0.833 |  |  |
|  |  |  |  |  |
| **Salmonella** | ***Staphylococcus*** | 0.746 |  |  |
|  |  |  |  |  |
| **Serratia** | ***Cronobacter*** | 0.775 | ***Enterococcus*** | -0.741 |
|  | ***Escherichia*** | 0.851 | ***Rhizobium*** | -0.777 |
|  | ***Leucobacter*** | 0.717 | ***Spirosoma*** | -0.786 |
|  |  |  |  |  |
| **Shewanella** | ***Arthrobacter*** | 0.952 | ***Arthrospira*** | -0.647 |
|  | ***Erwinia*** | 0.858 | ***Bacillus*** | -0.889 |
|  | ***Macrococcus*** | 0.731 | ***Bifidobacterium*** | -0.931 |
|  | ***Pseudoalteromonas*** | 0.861 | ***Clostridium*** | -0.819 |
|  | ***Sphingobacterium*** | 0.712 | ***Lactobacillus*** | -0.927 |
|  | ***Sphingopyxis*** | 0.840 | ***unclassified-(derived-from-Oscillatoriales)*** | -0.871 |
|  |  |  |  |  |
| **Sphingobacterium** | ***Deinococcus*** | 0.716 | ***Agromyces*** | -0.755 |
|  | ***Macrococcus*** | 0.651 | ***Candidatus-Aquiluna*** | -0.696 |
|  | ***Shewanella*** | 0.712 | ***Clavibacter*** | -0.795 |
|  |  |  | ***Kineococcus*** | -1.000 |
|  |  |  | ***Leifsonia*** | -0.822 |
|  |  |  | ***Leucobacter*** | -0.722 |
|  |  |  | ***Methylocella*** | -0.782 |
| **Sphingomonas** | ***Candidatus-Aquiluna*** | 0.753 |  |  |
|  | ***Klebsiella*** | 0.805 |  |  |
|  | ***unclassified-(derived-from-Alphaproteobacteria)*** | 1.000 |  |  |
|  | ***unclassified-(derived-from-Bacteria)*** | 1.000 |  |  |
|  |  |  |  |  |
| **Sphingopyxis** | ***Acidovorax*** | 0.829 | ***Bifidobacterium*** | -0.825 |
|  | ***Arthrobacter*** | 0.801 | ***Curtobacterium*** | -0.791 |
|  | ***Erwinia*** | 0.708 | ***Lactobacillus*** | -0.789 |
|  | ***Macrococcus*** | 0.748 | ***unclassified-(derived-from-Oscillatoriales)*** | -0.784 |
|  | ***Pseudoalteromonas*** | 0.692 |  |  |
|  | ***Renibacterium*** | 0.777 |  |  |
|  | ***Shewanella*** | 0.840 |  |  |
|  |  |  |  |  |
| **Spirosoma** | ***Chryseobacterium*** | 0.866 | ***Azorhizobium*** | -0.691 |
|  | ***Deinococcus*** | 0.840 | ***Clavibacter*** | -0.816 |
|  | ***Hymenobacter*** | 0.802 | ***Kineococcus*** | -1.000 |
|  | ***Rhodococcus*** | 0.878 | ***Leucobacter*** | -0.754 |
|  |  |  | ***Okibacterium*** | -0.804 |
|  |  |  | ***Serratia*** | -0.786 |
|  |  |  |  |  |
| **Staphylococcus** | ***Citrobacter*** | 0.694 | ***Exiguobacterium*** | -0.858 |
|  | ***Macrococcus*** | 0.753 | ***Flavobacterium*** | -0.741 |
|  | ***Methylobacterium*** | 0.784 | ***Oscillatoria*** | -0.749 |
|  | ***Nocardioides*** | 0.716 | ***Riemerella*** | -0.891 |
|  | ***Salmonella*** | 0.746 |  |  |
|  | ***Tetrasphaera*** | 0.894 |  |  |
|  |  |  |  |  |
| **Tetrasphaera** | ***Citrobacter*** | 0.701 | ***Acinetobacter*** | -0.798 |
|  |  |  | ***Exiguobacterium*** | -0.829 |
|  |  |  | ***Flavobacterium*** | -0.778 |
|  |  |  |  |  |
|  | ***Staphylococcus*** | 0.894 |  |  |
|  |  |  |  |  |
| **unclassified-(derived-from-Alphaproteobacteria)** | ***Acidovorax*** | 0.944 | ***Asaia*** | -0.912 |
|  | ***Lyngbya*** | 0.783 | ***Candidatus-Aquiluna*** | -0.825 |
|  | ***Rothia*** | 0.833 |  |  |
|  | ***Sphingomonas*** | 1.000 |  |  |
|  |  |  |  |  |
| **unclassified-(derived-from-Bacteria)** | ***Asaia*** | 1.000 | ***Acidovorax*** | -1.000 |
|  | ***Candidatus-Aquiluna*** | 1.000 | ***Flavobacterium*** | -1.000 |
|  | ***Leifsonia*** | 1.000 | ***Methylocella*** | -0.763 |
|  | ***Sphingomonas*** | 1.000 | ***Pedobacter*** | -1.000 |
|  |  |  | ***Chryseobacterium*** | -0.802 |
|  |  |  | ***Massilia*** | -0.770 |
|  |  |  | ***Paenibacillus*** | -0.830 |
|  |  |  |  |  |
| **unclassified-(derived-from-Oscillatoriales)** | ***Bacillus*** | 0.814 | ***Arthrobacter*** | -0.753 |
|  | ***Bifidobacterium*** | 0.948 | ***Erwinia*** | -0.796 |
|  | ***Candidatus-Aquiluna*** | 0.702 | ***Macrococcus*** | -0.717 |
|  | ***Clostridium*** | 0.810 | ***Pseudoalteromonas*** | -0.821 |
|  | ***Curtobacterium*** | 0.844 | ***Shewanella*** | -0.871 |
|  | ***Lactobacillus*** | 0.889 | ***Sphingopyxis*** | -0.784 |
|  | ***Leptolyngbya*** | 0.821 |  |  |
|  | ***Rhizobium*** | 0.619 |  |  |
|  | ***Xenococcus*** | 0.787 |  |  |
|  |  |  |  |  |
| **unclassified-(derived-from-unclassified-sequences)** |  |  | ***Bacillus*** | -0.896 |
|  |  |  | ***Methylobacterium*** | -0.884 |
|  |  |  | ***Microcoleus*** | -0.950 |
|  |  |  |  |  |
| **Xanthomonas** | ***Asaia*** | 0.798 | ***Rothia*** | -0.666 |
|  |  |  |  |  |
|  |  |  |  |  |
| **Xenococcus** | ***Asaia*** | 0.901 | ***Acidovorax*** | -0.729 |
|  | ***Bifidobacterium*** | 0.672 | ***Micrococcus*** | -0.646 |
|  | ***Candidatus-Aquiluna*** | 0.635 |  |  |
|  | ***Enterococcus*** | 0.782 |  |  |
|  | ***Leptolyngbya*** | 0.923 |  |  |
|  | ***unclassified-(derived-from-Oscillatoriales)*** | 0.787 |  |  |

**Supplementary Table 5. Population size of epiphytic bacteria (Log CFU g\_1) on phyllosphere of 15 and 30 days aged rice genotypes grown in Mountain zone**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  **Isolate** | **Colony morphology** | **PRR78** | **Pusa 1602** | **Isolate** | **Colony morphology** | **PRR78** | **Pusa 1602** |
| 15P1 | Punctiform, red without hallow | 5.91 | 6.00 | 30P1 | Punctiform, red without hallow | 5.83 | 5.83 |
| 15P2 | Punctiform, red with hallow | 6.27 | 6.24 | 30P2 | Punctiform, red with hallow | 5.62 | 5.64 |
| 15P3 | Small dot like, dark red  | 6.16 | 5.59 | 30P3 | Small dot like, dark red  | 5.68 | 5.48 |
| 15P4 | Small dot like, dark red with hallow | 4.39 | 2.48 | 30P4 | Small dot like, dark red with hallow | 6.40 | 5.67 |
| 15P5 | Small dark red with yellow hallow | 1.47 | 4.01 | 30P5 | Small dark red with yellow hallow | 5.33 | 3.74 |
| 15P6 | Small dark red with while hallow | 5.35 | 4.10 | 30P6 | Small dark red with cream margin | 3.18 | 5.09 |
| 15P7 | Small, pink red with 3D structure inside media | 4.76 | 2.56 | 30P7 | Small, maroon red, round with smooth margin | 2.64 | 0.00 |
| 15P8 | Small dark maroon with white hallow, convex surface | 5.01 | 4.40 | 30P8 | Small, pink red with 3D structure inside media | 1.91 | 5.02 |
| 15P9 | Small point center with a large cream margin | 3.53 | 0.00 | 30P9 | Moderate, orange red, rough with white filiform margin | 2.62 | 3.11 |
| 15P10 | Moderate, red center with white hallow and entire margin | 3.53 | 2.00 | 30P10 | Moderate, white circular with a red dot like center | 2.90 | 0.00 |
| 15P11 | Moderate, translucent white slimy, irregular shape  | 5.21 | 2.00 | 30P11 | Moderate, slimy white, oval to round with entire margin | 3.45 | 0.00 |
| 15P12 | Moderate, maroon red, convex slimy surface  | 5.79 | 1.43 | 30P12 | Large, creamy white with red center, smooth margin | 1.43 | 1.47 |
| 15P13 | Moderate rough surface oval with irregular margin  | 3.88 | 2.97 | 30P13 | Moderate, maroon red, convex slimy surface with irregular margin | 1.47 | 3.05 |
| 15P14 | Moderate maroon red, oval to round with white smooth margin  | 2.00 | 2.48 | 30P14 | Large, pinkish red with filiform margin | 5.32 | 4.22 |
| 15P15 | Large, flat surface with irregular white margin | 1.47 | 3.50 | 30P15 | Large, slimy rose red, wavy margin | 0.00 | 2.46 |
| - | - | - | - | 30P16 | Large, yellow, flat surface with irregular margin  | 0.00 | 3.94 |
| - | - | - | - | 30P17 | Small 3D light red submerged inside the media | 3.08 | 1.47 |
| - | - | - | - | 30P18 | Small, rose red with rough surface, irregular margin | 1.95 | 2.90 |
| - | - | - | - | 30P19 | Small, dark red, submerged with a disc like structure  | 2.93 | 2.52 |
| - | - | - | - | 30P20 | Small, violate red, submerged, flat on the bottom of plate | 1.91 | 3.05 |
| - | - | - | - | 30P21 | Moderate, red center with white background, circular with smooth margin | 3.38 | 1.47 |
| - | - | - | - | 30P22 | Small red center with yellow margin, entire circular | 1.43 | 0.96 |
| - | - | - | - | 30P23 | Large, rose red big center with white background and filiform margin  | 3.48 | 2.90 |
|  | **Mean (Cultivar)** | **4.313** | **3.317** |  | **Mean (Cultivar)** | **3.127** | **3.042** |
|  |  | Cultivar | Bacteria |  |  | Cultivar | Bacteria |
|  | *F cal* | 23.85 | 12.58 |  | *F cal* | 0.25 | 15.21 |
|  | *F tab* | 3.88 | 1.73 |  | *F tab* | 3.8 | 1.57 |

CFU/ml= (Number of colonies) X (Dilution factor)/Volume plated in mL

**Supplementary Table 6. Population size of epiphytic bacteria (Log CFU g-1) on phyllosphere of rice genotypes grown in Island zone**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  **Isolate** | **Colony morphology** | **PRR78** | **Pusa 1602** | **Isolate** | **Colony morphology** | **PRR78** | **Pusa 1602** |
| 15A1 | Punctiform, light red | 5.11 | 6.55 | 30A1 | Punctiform, light red | 6.75 | 6.36 |
| 15A2 | Punctiform, dark red  | 6.10 | 6.00 | 30A2 | Punctiform, dark red  | 6.04 | 5.90 |
| 15A3 | Punctiform, light red with white hallow | 3.87 | 5.41 | 30A3 | Punctiform, light red with white hallow | 5.71 | 5.77 |
| 15A4 | Moderate, pink center like a dot and white periphery  | 2.72 | 4.49 | 30A4 | Small, wine red,  | 3.41 | 3.29 |
| 15A5 | Moderate, dark red center like a dot and white periphery  | 5.34 | 4.28 | 30A5 | Small, pinkish white disc like 3D structure submerged in media | 3.84 | 3.16 |
| 15A6 | Small orange center with yellow hallow | 0.00 | 3.17 | 30A6 | Small submerged close to bottom of plate, violate red with entire margin | 2.69 | 4.17 |
| 15A7 | Small red center with white hallow | 4.21 | 2.42 | 30A7 | Small submerged close to bottom of plate, pinkish red with filiform margin | 3.47 | 1.47 |
| 15A8 | Moderate, cherry red with double ring structure | 0.00 | 2.49 | 30A8 | Small, dark red, with metallic shine, entire | 5.20 | 4.10 |
| 15A9 | Moderate dark red with raised center | 0.00 | 2.60 | 30A9 | Small, orange yellow round with smooth margin | 5.57 | 4.15 |
| 15A10 | Moderate, blood red center with creamy hallow and entire margin | 3.42 | 2.51 | 30A10 | Small, light yellow round with smooth margin | 4.41 | 2.48 |
| 15A11 | Moderate, wine red with metallic shine, round smooth margin | 5.04 | 0.00 | 30A11 | Small white with pink dot at the center | 4.32 | 0.00 |
| 15A12 | Moderate, opaque white, irregular, with filamentous margin | 1.98 | 4.97 | 30A12 | Moderate, candy red slimy round to oval with entire margin | 1.87 | 0.00 |
| 15A13 | Large, creamy white, filiform border | 2.39 | 3.19 | 30A13 | Moderate, dark wine red, round, with metallic shine and entire margin | 4.15 | 2.95 |
| 15A14 | Large, slimy white with wavy margin | 1.50 | 2.46 | 30A14 | Moderate light pink watery colony with concentric rings | 2.93 | 3.98 |
| 15A15 | Large, light red, oval to round with smooth margin | 2.03 | 2.48 | 30A15 | Moderate, red center with large yellow hallow | 2.63 | 0.00 |
| 15A16 | Small wine red with entire smooth margin | 2.49 | 0.00 | 30A16 | Large, opaque white, rhizoidal margin with red shades at the base  | 0.00 | 1.91 |
| 15A17 | Moderate glossy yellow, oval with entire margin  | 5.21 | 0.00 | 30A17 | Large, maroon red with creamy white hallow | 0.00 | 2.42 |
| 15A18 | Small, rose red with 3 dimensional structure submerged in the media | 5.75 | 0.00 | 30A18 | Moderate cherry red with yellow white hallow | 0.00 | 3.47 |
| - | - | - | - | 30A19 | Small boat shape dark red with brown hallow | 2.42 | 1.95 |
| - | - | - | - | 30A20 | Moderate, violate red, entire | 4.18 | 1.95 |
| - | - | - | - | 30A21 | Small, slimy colony with irregular margin | 4.64 | 3.50 |
| - | - | - | - | 30A22 | Large creamy white, wavy margin | 2.51 | 3.98 |
|  | **Mean (Cultivar)** | 3.175 | 2.945 |  | **Mean (Cultivar)** | 3.488 | 3.043 |
|  |  | Cultivar | Bacteria |  |  | Cultivar | Bacteria |
|  | *F cal* | 1.54 | 14.14 |  | *F cal* | 7.37 | 17.35 |
|  | *F tab* | 3.87 | 1.66 |  | *F tab* | 3.87 | 1.58 |

CFU/ml= (Number of colonies) X (Dilution factor)/Volume plated in mL

**Supplementary Table 7. Identification of bacterial isolates by 16S rRNA gene sequencing**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sequence ID | Organism | Seq. length (bp) | Host | Geographicalorigin | GenBank Accession  |
| OsEp\_Plm\_30P1 | *Acidovorax avenae* | 1433 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367817 |
| OsEp\_Plm\_30P6 | *Acidovorax avenae* | 1396 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367820 |
| OsEp\_Plm\_30P23 | *Acidovorax avenae* | 1378 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367833 |
| OsEp\_Plm\_30P11 | *Acinetobacter baumannii* | 1430 |  PRR78 | Palampur (HP) | MT367824 |
| OsEp\_Plm\_30P17 | *Acinetobacter baumannii* | 1401 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367827 |
| OsEp\_A&N\_30A17 | *Acinetobacter junii* | 1386 |  Pusa 1602 | Port Blair (A&N) | MT367859 |
| OsEp\_Plm\_30P2 | *Acinetobacter soli* | 1419 |  PRR78 & Pusa 1602 | Palampur (HP) | MT394056 |
| OsEp\_Plm\_30P4 | *Acinetobacter soli* | 1429 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367819 |
| OsEp\_Plm\_30P22 | *Acinetobacter soli* | 1417 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367832 |
| OsEp\_Plm\_30P19 | *Agrobacterium larrymoorei* | 1359 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367829 |
| OsEp\_A&N\_30A11 | *Aureimonas phyllosphaerae* | 1390 |  PRR78 | Port Blair (A&N) | MT367855 |
| OsEp\_Plm\_30P7 | *Aureimonas* sp. | 1369 |  PRR78 | Palampur (HP) | MT367821 |
| OsEp\_Plm\_15P1 | *Curtobacterium albidum*  | 1391 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367807 |
| OsEp\_Plm\_30P20 | *Curtobacterium albidum*  | 1401 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367830 |
| OsEp\_A&N\_30A1 | *Curtobacterium citreum* | 1395 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367846 |
| OsEp\_Plm\_15P7 | *Curtobacterium luteum*  | 1390 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367812 |
| OsEp\_Plm\_30P9 | *Curtobacterium luteum*  | 1393 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367822 |
| OsEp\_Plm\_30P16 | *Enterobacter asburiae* | 1410 |  Pusa 1602 | Palampur (HP) | MT367826 |
| OsEp\_A&N\_30A22 | *Enterobacter asburiae* | 1406 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367864 |
| OsEp\_Plm\_30P18 | *Enterobacter cloacae* | 1425 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367828 |
| OsEp\_A&N\_15A7 | *Enterobacter cloacae* | 1409 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367840 |
| OsEp\_A&N\_30A20 | *Enterobacter mori* | 1409 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367862 |
| OsEp\_A&N\_15A12 | *Enterobacter sichuanensis* | 1404 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367844 |
| OsEp\_A&N\_15A5 | *Erwinia tasmaniensis* | 1412 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367838 |
| OsEp\_Plm\_15P3 | *Exiguobacterium acetylicum*  | 1438 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367809 |
| OsEp\_Plm\_30P14 | *Exiguobacterium indicum* | 1431 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367825 |
| OsEp\_A&N\_30A4 | *Exiguobacterium indicum* | 1413 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367849 |
| OsEp\_A&N\_30A6 | *Exiguobacterium indicum* | 1430 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367851 |
| OsEp\_A&N\_15A2 | *Microbacterium* sp. | 1387 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367835 |
| OsEp\_A&N\_30A2 | *Microbacterium testaceum* | 1409 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367847 |
| OsEp\_A&N\_15A1 | *Micrococcus luteus* | 1400 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367834 |
| OsEp\_A&N\_15A8 | *Pantoea agglomerans* | 1418 |  Pusa 1602 | Port Blair (A&N) | MT367841 |
| OsEp\_A&N\_30A14 | *Pantoea agglomerans* | 1408 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367857 |
| OsEp\_A&N\_30A21 | *Pantoea agglomerans* | 1413 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367863 |
| OsEp\_Plm\_15P9 | *Pantoea ananatis* | 1410 |  PRR78 | Palampur (HP) | MT367813 |
| OsEp\_Plm\_30P3 | *Pantoea ananatis* | 1419 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367818 |
| OsEp\_Plm\_30P21 | *Pantoea ananatis* | 1405 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367831 |
| OsEp\_A&N\_15A10 | *Pantoea ananatis* | 1401 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367843 |
| OsEp\_A&N\_30A5 | *Pantoea ananatis* | 1402 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367850 |
| OsEp\_A&N\_30A8 | *Pantoea ananatis* | 1403 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367852 |
| OsEp\_A&N\_30A19 | *Pantoea ananatis* | 1408 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367861 |
| OsEp\_A&N\_30A18 | *Pantoea dispersa* | 1412 |  Pusa 1602 | Port Blair (A&N) | MT367860 |
| OsEp\_Plm\_15P14 | *Pantoea eucrina* | 1421 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367816 |
| OsEp\_Plm\_30P10 | *Pantoea eucrina* | 1414 |  PRR78 | Palampur (HP) | MT367823 |
| OsEp\_A&N\_15A4 | *Pantoea eucrina* | 1409 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367837 |
| OsEp\_A&N\_15A9 | *Pantoea* sp. | 1402 |  Pusa 1602 | Port Blair (A&N) | MT367842 |
| OsEp\_A&N\_15A15 | *Pantoea* sp. | 1400  |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367845 |
| OsEp\_Plm\_15P6 | *Pseudomonas oryzihabitans* | 1398 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367811 |
| OsEp\_Plm\_15P12 | *Pseudomonas parafulva* | 1407 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367815 |
| OsEp\_A&N\_15A6 | *Pseudomonas psychrotolerans* | 1383 |  Pusa 1602 | Port Blair (A&N) | MT367839 |
| OsEp\_A&N\_30A13 | *Pseudomonas psychrotolerans* | 1396 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367856 |
| OsEp\_Plm\_15P11 | *Pseudomonas putida*  | 1401 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367814 |
| OsEp\_A&N\_15A3 | *Sphingomonas paucimobilis* | 1390 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367836 |
| OsEp\_A&N\_30A9 | *Sphingomonas paucimobilis* | 1377 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367853 |
| OsEp\_Plm\_15P2 | *Sphingomonas pseudosanguinis* | 1389 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367808 |
| OsEp\_A&N\_30A10 | *Sphingomonas pseudosanguinis* | 1378 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367854 |
| OsEp\_Plm\_15P5 | *Sphingomonas* sp. | 1378 |  PRR78 & Pusa 1602 | Palampur (HP) | MT367810 |
| OsEp\_A&N\_30A15 | *Sphingomonas* sp. | 1362 |  PRR78 | Port Blair (A&N) | MT367858 |
| OsEp\_A&N\_30A3 | *Sphingomonas yabuuchiae* | 1362 |  PRR78 & Pusa 1602 | Port Blair (A&N) | MT367848 |

**Supplementary Table 8. Analysis of nature of BVC mediated mycelial inhibition of *Magnaporthe oryzae***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Isolate** | **Bacterial Species** | **Inhibition by BVC (%)** | **Re-growth of *Magnaporthe oryzae* (%)** | **Nature of BVC** |
| OsEp-Plm-30P11 | *Acinetobacter baumannii* | 25.7 | 74.3 | Fungistatic |
| OsEp-Plm-30P17 | *Acinetobacter baumannii* | 17.1 | 82.9 | Fungistatic |
| OsEp-Plm-30P4 | *Acinetobacter soli* | 9.5 | 90.5 | Fungistatic |
| OsEp-Plm-30P7 | *Aureimonas* sp. | 11.4 | 88.6 | Fungistatic |
| **OsEp-AN-30A14** | ***Pantoea agglomerans*** | **100.0** | **0.0** | **Fungicidal** |
| **OsEp-Plm-15P9** | ***Pantoea ananatis*** | **100.0** | **0.0** | **Fungicidal** |
| **OsEp-Plm-30P21** | ***Pantoea ananatis*** | **100.0** | **0.0** | **Fungicidal** |
| **OsEp-AN-30A5** | ***Pantoea ananatis*** | **100.0** | **0.0** | **Fungicidal** |
| **OsEp-AN-30A8** | ***Pantoea ananatis*** | **100.0** | **0.0** | **Fungicidal** |
| OsEp-AN-30A18 | *Pantoea dispersa* | 21.9 | 78.1 | Fungistatic |
| OsEp-Plm-15P14 | *Pantoea eucrina* | 31.4 | 68.6 | Fungistatic |
| OsEp-Plm-30P10 | *Pantoea eucrina* | 24.8 | 75.2 | Fungistatic |
| OsEp-AN-15A4 | *Pantoea eucrina* | 58.1 | 41.9 | Fungistatic |
| OsEp-Plm-15P12 | *Pseudomonas parafulva* | 69.5 | 30.5 | Fungistatic |
| OsEp-Plm-15P11 | *Pseudomonas putida*  | 5.7 | 94.3 | Fungistatic |
|  | Mock | 0.0 | 100.0 |  |
|  | C.D. | 10.93 | 3.79 |  |
|  | SE(m) | 3.79 | 5.37 |  |
|  | SE(d) | 5.37 | 10.93 |  |
|  | C.V. (%) | 13.56 | 12.75 |  |
|  | F (calc.) | 110.82 | 110.82 |  |
|  | F (tab.) | 1.99 | 1.99 |  |

**Supplementary Table 9. qPCR analysis of transcriptional response of defense genes in rice seedlings upon phyllobacterization**

|  |  |
| --- | --- |
| ***Gene*** | **Fold change** |
| **Time line** |
|  | **24 h** | **48 h** | **72 h** |
| ***OsPAD4*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | 0.86 | **1.165** | **1.04** |
| *Aureimonas* sp. OsEp-Plm-30P7 | 0.56 | **1.005** | **1.065** |
| *Pantoea eucrina* OsEp-Plm-30P10 | **1.03** | **1.075** | 1 |
| *Pantoea ananatis* OsEp-Plm-30P21 | 0.835 | 0.77 | 0.71 |
| *Pseudomonas putida* OsEp-Plm-15P11 | 0.855 | 0.63 | 1 |
| *Pantoea ananatis* OsEp-AN-30A8 | **1.54** | **3.51** | 0.655 |
| ***OsEDS1*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | 0.91 | 0.845 | **1.085** |
| *Aureimonas sp.* OsEp-Plm-30P7 | 0.765 | 0.685 | **1.235** |
| *Pantoea eucrina* OsEp-Plm-30P10 | 0.825 | **1.145** | 0.905 |
| *Pantoea ananatis* OsEp-Plm-30P21 | 0.78 | 0.6 | **1.165** |
| *Pseudomonas putida* OsEp-Plm-15P11 | 0.81 | 0.645 | **1.395** |
| *Pantoea ananatis* OsEp-AN-30A8 | 1 | 0.915 | **1.12** |
| ***OsNPR1*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | 0.815 | 0.78 | **1.18** |
| *Aureimonas sp.* OsEp-Plm-30P7 | 0.53 | 0.48 | **1.275** |
| *Pantoea eucrina* OsEp-Plm-30P10 | 0.785 | 0.495 | **1.03** |
| *Pantoea ananatis* OsEp-Plm-30P21 | 0.72 | 0.455 | **1.31** |
| *Pseudomonas putida* OsEp-Plm-15P11 | 0.675 | 0.535 | **1.505** |
| *Pantoea ananatis* OsEp-AN-30A8 | 0.94 | 0.805 | 0.9 |
| ***OsPDF2.2*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | 0.51 | **1.435** | **1.465** |
| *Aureimonas sp.* OsEp-Plm-30P7 | 0.605 | 0.845 | **1.1** |
| *Pantoea eucrina* OsEp-Plm-30P10 | **1.42** | 0.76 | **1.07** |
| *Pantoea ananatis* OsEp-Plm-30P21 | 0.545 | 0.88 | **1.05** |
| *Pseudomonas putida* OsEp-Plm-15P11 | 0.6 | 0.745 | **1.095** |
| *Pantoea ananatis* OsEp-AN-30A8 | 0.58 | 0.925 | **1.09** |
| ***OsCERK1*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | 0.7 | 0.94 | 0.665 |
| *Aureimonas sp.* OsEp-Plm-30P7 | 0.48 | 0.825 | **1.22** |
| *Pantoea eucrina* OsEp-Plm-30P10 | 0.615 | 0.655 | 0.91 |
| *Pantoea ananatis* OsEp-Plm-30P21 | 0.5 | 0.595 | 1 |
| *Pseudomonas putida* OsEp-Plm-15P11 | 0.46 | **1.055** | **1.43** |
| *Pantoea ananatis* OsEp-AN-30A8 | **1.06** | **3.735** | 0.845 |
| ***OsCEBiP*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | **1.15** | **1.695** | **1.225** |
| *Aureimonas* sp.OsEp-Plm-30P7 | **2.55** | **8.235** | **5.075** |
| *Pantoea eucrina* OsEp-Plm-30P10 | **1.22** | **1.7** | 0.945 |
| *Pantoea ananatis* OsEp-Plm-30P21 | **1.36** | **1.965** | **1.14** |
| *Pseudomonas putida* OsEp-Plm-15P11 | **1.085** | **2.425** | **1.705** |
| *Pantoea ananatis* OsEp-AN-30A8 | **1.415** | **4.59** | **1.275** |
| ***OsFMO*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | **1.794** | **1.168** | 0.836 |
| *Aureimonas sp.* OsEp-Plm-30P7 | **1.350** | 0.834 | 0.743 |
| *Pantoea eucrina* OsEp-Plm-30P10 | **1.453** | 0.637 | 0.616 |
| *Pantoea ananatis* OsEp-Plm-30P21 | 0.994 | 0.569 | 0.559 |
| *Pseudomonas putida* OsEp-Plm-15P11 | **1.298** | 0.754 | 0.782 |
| *Pantoea ananatis* OsEp-AN-30A8 | **2.333** | 0.633 | 0.554 |
| ***OsPR1.1*** |  |  |  |
| *Pantoea ananatis* OsEp-Plm-30P3 | 0.947 | 0.858 | **1.284** |
| *Aureimonas sp.* OsEp-Plm-30P7 | **1.252** | 0.469 | **2.109** |
| *Pantoea eucrina* OsEp-Plm-30P10 | **1.643** | 0.521 | **1.149** |
| *Pantoea ananatis* OsEp-Plm-30P21 | **1.565** | 0.494 | **1.614** |
| *Pseudomonas putida* OsEp-Plm-15P11 | **1.797** | 0.680 | **1.861** |
| *Pantoea ananatis* OsEp-AN-30A8 | **1.416** | 0.561 | **1.580** |

**\*Bold= Up- regulated; Red font= Significant up-regulation**

1. *OsCEBiP* was found induced in all time points by bacterization; significant induction by *Aureimonas sp.* OsEp-Plm-30P7for all three time points and *Pseudomonas putida* OsEp-Plm-15P11 or  *Pantoea ananatis* OsEp-AN-30A848 hour post bacterization
2. *OsPR1.1* was also found induced by 72 hour post bacterization with significant induction by *Aureimonas* sp.OsEp-Plm-30P7
3. *OsNPR1* and *OsPDF2.2* showed induction at 72 hour post inoculation for all the bacterial treatments.
4. Other genes induced were *OsFMO* in *Pantoea ananatis* OsEp-AN-30A8, *OsCERK1* and *OsPAD4* in *Pantoea ananatis* OsEp-AN-30A8