**Supplementary file 2a. Comparison of *in vitro* traits between mutants belonging to three clusters using unpaired two-samples Wilcoxon test.** Significant effects (p < 0.05) are highlighted in bold.

|  |  |  |  |
| --- | --- | --- | --- |
| **Mutant trait measured *in vitro*** | **Comparison** | **W** | **P** |
| Swarming motility | Cluster1 (n=265) VS Cluster2 (n=112) | **11125** | **<0.001** |
| Cluster1 (n=265) VS Cluster3 (n=103) | **26874** | **<0.001** |
| Cluster2 (n=112) VS Cluster3 (n=103) | **11517** | **<0.001** |
| Biomass production | Cluster1 (n=265) VS Cluster2 (n=112) | **10869** | **<0.001** |
| Cluster1(n=265) VS Cluster3 (n=103) | **7754** | **<0.001** |
| Cluster2 (n=112) VS Cluster3 (n=103) | 4931 | 0.0664 |
| Biofilm formation | Cluster1 (n=265) VS Cluster2 (n=112) | **23061** | **<0.001** |
| Cluster1 (n=265) VS Cluster3 (n=103) | **18268** | **<0.001** |
| Cluster2 (n=112) VS Cluster3 (n=103) | **4238** | **<0.001** |
| Pathogen suppression | Cluster1 (n=265) VS Cluster2 (n=112) | **28464** | **<0.001** |
| Cluster1 (n=265) VS Cluster3 (n=103) | **27253** | **<0.001** |
| Cluster2 (n=112) VS Cluster3 (n=103) | **10300** | **<0.001** |

**Supplementary file 2b. Comparison of root colonization and plant protection between mutants belonging to three clusters using unpaired two-samples Wilcoxon test.** Significant effects (p < 0.05) are highlighted in bold and dpi denotes for days post-pathogen inoculation.

|  |  |  |  |
| --- | --- | --- | --- |
| **Mutant trait measured *in vivo*** | **Comparison** | **30 dpi** | |
| **W** | **P** |
| Root colonization  (*B. amyloliquefaciens* T-5 abundance; log10 cells g-1 rhizosphere soil) | Cluster1 (n=27) VS Cluster2 (n=11) | **233.5** | **0.0065** |
| Cluster1 (n=27) VS Cluster3 (n=10) | **193.5** | **0.0472** |
| Cluster2 (n=11) VS Cluster3 (n=10) | 42 | 0.3867 |
| Plant protection  (Disease incidence; % of wilted plants) | Cluster1 (n=27) VS Cluster2 (n=11) | **85.5** | **0.0442** |
| Cluster1 (n=27) VS Cluster3 (n=10) | **24.5** | **<0.001** |
| Cluster2 (n=11) VS Cluster3 (n=10) | 31.5 | 0.1052 |

**Supplementary file 2c. Comparison of trait values of eight mutants used for the assembly of consortia richness gradient relative to the wild-type strain based on students’ t-test.** Significant differences are shown in bold and arrows show increase (upwards) and decrease (downwards) in trait values.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Mutant strain** | **P-values and changes in trait value relative to wild-type strain** | | | |
|  | Swarming  motility | Biomass  production | Biofilm  formation | Pathogen  suppression |
| M38 | 0.3486 | **0.0262↓** | **0.0298↓** | **0.0408↑** |
| M54 | 0.1836 | **0.0035↓** | **0.0193↑** | 0.5513 |
| M59 | **< 0.001↓** | **< 0.001↑** | **0.0084↓** | **< 0.001↓** |
| M78 | **< 0.001↓** | **< 0.001↓** | 0.3608 | **0.0128↑** |
| M108 | **0.0016↑** | **0.0181↓** | **0.0176↓** | 0.7541 |
| M109 | **0.0147↓** | **0.0014↑** | **0.0069↓** | 0.8217 |
| M124 | **< 0.001↑** | **0.0125↓** | **0.0033↓** | **0.0206↓** |
| M143 | **< 0.001↓** | **< 0.001↓** | **< 0.001↑** | 0.7541 |

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Growing** | **Supernatant source** | | | | | | | | |
| **mutant strain** |
|  | **M38** | **M54** | **M59** | **M78** | **M108** | **M109** | **M124** | **M143** | **WT** |
| **M38** | **0.0489↓** | **0.0202** | **0.0092↓** | 0.7062 | **0.0085↓** | **0.0023↓** | 0.6659 | **0.0441↓** | 0.0521 |
| **M54** | **0.0098↓** | 0.1632 | **0.0051↓** | **0.0299↓** | **0.0251↓** | **0.0125↓** | **0.0060↓** | **0.0136↓** | **0.0028↓** |
| **M59** | 0.7637 | **0.0028↓** | 0.0739 | **<0.001↓** | 0.0589 | **0.0152↓** | **<0.001↓** | **0.0021↓** | **0.0014↓** |
| **M78** | **0.0011↓** | **0.0166↓** | **0.0065↓** | 0.9239 | **0.0080↓** | **0.0032↓** | **0.0255↓** | **0.0065↓** | **0.0026↓** |
| **M108** | 0.1515 | 0.0917 | **0.0113↓** | 0.6877 | **0.0271↓** | **0.0213↓** | 0.8150 | 0.2301 | **0.0154↓** |
| **M109** | 0.1709 | 0.1517 | 0.6975 | 0.4325 | 0.1562 | 0.0522 | 0.2466 | 0.9747 | **0.0363↓** |
| **M124** | **0.0227↓** | **0.0015↓** | 0.5282 | 0.4584 | 0.1536 | **0.0233↓** | **<0.001↑** | **0.0023↑** | 0.0710 |
| **M143** | 0.7815 | 0.3179 | 0.0630 | 0.4702 | 0.2432 | 0.2227 | **0.0246↓** | 0.0606 | 0.4774 |
| **WT** | **0.0148↓** | **0.0010↓** | **0.0012↓** | **<0.001↓** | **0.0446↓** | **<0.001↓** | **0.0013↓** | **0.0016↓** | **0.0045↓** |

**Supplementary file 2d. P-values for comparing the biomass production of each mutant strain on its own or other strains’ supernatant compared to fresh 50% LB based on student’s t-test.** Significant differences are shown in bold and arrows show facilitative (upwards) and antagonistic (downwards) interactions between the mutants. The magnitude of these interactions is shown in Figure 3–figure supplement 1 as a heatmap.



**Supplementary file 2e. Comparison of mutant identity effects on consortia root colonization and plant protection based on the absence and presence of each mutant in consortia.** Significant effects (p < 0.05) are highlighted in bold based on unpaired two-samples Wilcoxon test.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | **Root colonization**  **(*Bacillus* abundance)** | |  | **Plant protection**  **(Disease incidence)** | |
| **Mutant**  **strain**  **identity** | **Phenotype** | **Comparison** | **W** | **P** |  | **W** | **P** |
| M38 | Pathogen suppression+ | Included (n=12) VS Excluded (n=25) | 197 | 0.1314 |  | 116 | 0.2815 |
| M54 | Biofilm formation+ | Included (n=12) VS Excluded (n=25) | **266** | **0.0143** |  | 128 | 0.4909 |
| M59 | Biomass production+ | Included (n=12) VS Excluded (n=25) | 192.5 | 0.1729 |  | **78** | **0.0188** |
| M78 | Pathogen suppression+ | Included (n=12) VS Excluded (n=25) | 139 | 0.7333 |  | 113 | 0.2401 |
| M108 | Swarming motility+ | Included (n=12) VS Excluded (n=25) | 154 | 0.9096 |  | 120 | 0.3435 |
| M109 | Biomass production+ | Included (n=12) VS Excluded (n=25) | 166.5 | 0.6037 |  | 105 | 0.1507 |
| M124 | Swarming motility+ | Included (n=12) VS Excluded (n=25) | 177 | 0.3899 |  | 97 | 0.0887 |
| M143 | Biofilm production+ | Included (n=12) VS Excluded (n=25) | 155 | 0.8839 |  | **78** | **0.0188** |

**Supplementary file 2f. Comparison of the mutant identity effects and consortia richness on root colonization and plant protection.** Richness was ﬁtted sequentially after mutant identity effects (presence or absence in consortia). Both response variables were treated as continuous variables and *Bacillus* abundance data was log-transformed before the analysis. Significant effects (p < 0.05) are highlighted in bold.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | **Root colonization (*Bacillus* abundance)** | |  | **Plant protection (Disease incidence)** | |
| **Mutant**  **strain**  **identity** | **Phenotype** | ***Df*** | ***F*** | ***P*** |  | ***F*** | ***P*** |
| M38 | Pathogen suppression+ | 1 | **4604.70** | **<0.001** |  | **652.86** | **<0.001** |
| M54 | Biofilm formation+ | 1 | **3413.15** | **<0.001** |  | **476.77** | **<0.001** |
| M59 | Biomass production+ | 1 | **2665.22** | **<0.001** |  | **433.88** | **<0.001** |
| M78 | Pathogen suppression+ | 1 | **1719.05** | **<0.001** |  | **269.91** | **<0.001** |
| M108 | Swarming motility+ | 1 | **2021.15** | **<0.001** |  | **272.12** | **<0.001** |
| M109 | Biomass production + | 1 | **1515.47** | **<0.001** |  | **215.33** | **<0.001** |
| M124 | Swarming motility+ | 1 | **1431.96** | **<0.001** |  | **185.12** | **<0.001** |
| M143 | Biofilm formation + | 1 | **1035.52** | **<0.001** |  | **126.80** | **<0.001** |
| Richness |  |  | **9.07** | **0.0048** |  | **22.24** | **<0.001** |
| Linear term |  | 1 |  |  |  |  |  |
| *Error* |  | 29 |  |  |  |  |  |

**Supplementary file 2g. Bacterial strains and plasmid used in this study.**

|  |  |  |
| --- | --- | --- |
| **Strain or plasmid** | **Characteristics** | **Source** |
| *Ralstonia solanacearum* QL-Rs1115 | Causative agent of Bacterial wilt | Z. Wei *et al*. 2011 (76) |
| *Bacillus amyloliquefaciens* T-5 | Rhizosphere isolate capable of suppressing the growth of *Ralstonia solanacearum* | S. Y. Tan *et al*. 2013 (45), X. F. Wang *et al*. 2017 (94) |
| pMarA plasmid | promoter σA, kmR ApR EmR pUC19 carrying TnYLB-1 transposon, mariner-Himar1 transposase | Y. Le Breton *et al*. 2006 (47) |

**Supplementary file 2h. Primers used in this study.**

|  |  |  |
| --- | --- | --- |
| **Primer** | **Sequence (5’ to 3’ end)** | **Source or reference** |
| oIPCR1 | GCTTGTAAATTCTATCATAATTG | Y. Le Breton *et al*. 2006 (47) |
| oIPCR2 | AGGGAATCATTTGAAGGTTGG |
| oIPCR3 | GCATTTAATACTAGCGACGCC |