**Supplementary Information (8 pages):**

* **Five supplementary tables**
* **Four supplementary figures**

**Table S1.** Oligonucleotide sequences (in the 5’ to 3’ direction) were employed for the amplification of genes encoding lipopeptides from the DNA of bacterial isolates.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Lipopeptides | Primers | Primer sequences | PCP length (bp) | Annealing T° | References |
| Bacillomycin | Bacc1FBacc1R | GAAGGACACGGCAGAGAGTCCGCTGATGACTGTTCATGCT | 875  | 60 °C | [1] |
| Fengycin | Fend1FFend1R | TTTGGCAGCAGGAGAAGTTGCTGTCCGTTCTGCTTTTTC | 964 | 62 °C | [1] |
| Iturin | Itup1FItuo2R | AGCTTAGGGAACAATTGTCATCGGGGCTTCTCAGATAGGCCGCCATATCGGAATGATTCG | 2000 | 45 °C | [2] |
| Surfactin | P17P18 | ATGAAGATTTACGGAATTTATTATAAAAGCTCTTCGTACG | 675 | 53 °C   | [3] |

**Table S2.** Diverse biochemical analyses were performed, encompassing both the aspect of revelation and the evaluation of activity indices. [References are shown at the end of SI].

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Biochemical test  | Media reference | Revelation aspect | Activity indexevaluation  | Activity index evaluation reference |
| Cellulase | [4] | clear circular area around the bacteria colony | (Clear zone+ colony diameter (mm)/colony diameter (mm)) | [5] |
| Pectinase | [6] | clear circular area around the bacteria colony | (Clear zone+ colony diameter (mm)/colony diameter (mm)) | [5] |
| Amylase | [7] | clear circular area around the bacteria colony | (Clear zone+ colony diameter (mm)/colony diameter (mm)) | [8] |
| Protease | [4] | clear circular area around the bacteria colony | (Clear zone+ colony diameter (mm)/colony diameter (mm)) | [9] |
| Chitinase | [10] | clear circular area around the bacteria colony | (Clear zone+ colony diameter (mm)/colony diameter (mm)) | [5] |
| Phosphate solubilisation  | [5] | clear circular area around the bacteria colony | (Clear zone+ colony diameter (mm)/colony diameter (mm)) | [11] |
| HCN | [12] | change of coloration from yellow to reddish-brown  | (-) negative; light brown (+); brown (++) dark brown (+++)  | [13] |
| AIA | [14] | change of coloration from yellow to red  | (-) negative; light red (+); red (++) dark red (+++)  | - |

**Table S3.** Application of treatments with varying concentrations against C. beticola in the field experiment.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Treatments | Active ingredient  | Concentration g/(l-kg) | Active ingredient/ha | Code  |
| SCORE 250 EC (SYNGENTA) | Difenoconazole | 250 | 125 | DF |
| BGH 1-6 | *Pantoea sp.* | 1x10^8 CFU/ml | 4x10^12 CFU | BGH 1-6 |
| BGH 2-2 | *Serratia sp.*  | 1x10^8 CFU/ml | 4x10^12 CFU | BGH 2-2 |
| BGH 1-3 | *Serratia sp.* | 1x10^8 CFU/ml | 4x10^12 CFU | BGH 1-3 |
| BGH 2-7 | *Bacillus sp.* | 1x10^8 CFU/ml | 4x10^12 CFU | BGH 2-7 |
| untreated control |   |   |   | UC |

**Table S4.** The impact of bacterial inoculation on the growth of sugar beet plants in a greenhouse experiment.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Bacterial isolates  | Root dry weighta (g) | Shoot dry weighta (g) | Root lengtha (mm) | shoot lengtha (mm) | Gain of root lenght (%) | Gain of shoot lengthb (%) | Gain of Shoot dry weightb (%) | Gain of root dry weightb (%) | Total gain of root dry weightb (%) | Root hair development c |
| BGH 1-5 | 1.09±0.04 | 1.70±0.02 | 44.13±1.79 | 22.28±0.30 | 72.70% | 389% | 78% | 107% | 86% | + |
|  G1b | 1.22±0.02 | 1.49±0.03 | 31.13±1.26 | 18.74±0.65 | 45.30% | 245% | 56% | 131% | 81% | ++ |
|  BGH 2-1 | 1.06±0.072 | 1.62±0.10 | 38.12±4.93 | 21.81±0.80 | 69.10% | 322% | 70% | 101% | 79% | + |
|  BGH 4-1 | 0.93±0.07 | 1.72±0.02 | 17.68±0.42 | 23.01±0.40 | 78.40% | 96% | 80.50% | 77% | 77% | ++ |
|  BGH 1-6 | 1.15±0.17 | 1.44±0.13 | 25.12±9.46 | 18.58±2.06 | 44.00% | 178% | 51% | 118% | 73% | + |
|  BGH 2-3 | 1.11±0.02 | 1.36±0.05 | 47.43±1.23 | 16.83±0.45 | 30.50% | 425% | 43% | 111% | 65% | ++ |
|  G3f | 1.12±0.05 | 1.34±0.10 | 34.59±0.83 | 16.13±0.66 | 25.10% | 283% | 41% | 113% | 64% | +++ |
|  G2c | 1.12±0.06 | 1.22±0.30 | 26.48±0.95 | 15.29±2.55 | 18.50% | 193% | 29% | 114% | 57% | +++ |
|  G2b | 0.94±0.07 | 1.31±0.02 | 16.29±1.12 | 16.25±0.39 | 26.00% | 80% | 37% | 79% | 50% | ++++ |
|  BGH 2-2 | 0.89±0.07 | 1.26±0.10 | 18.01±0.85 | 15.9±0.74 | 23.30% | 99% | 33% | 70% | 44% | ++ |
|  BGH 1-3 | 0.82±0.06 | 1.26±0.05 | 14.23±0.23 | 16.0±0.43 | 24.00% | 58% | 32% | 56% | 39% | + |
|  BGH 2-7 | 0.56±0.03 | 1.51±0.15 | 9.43±1.03 | 19.675±2 | 52.50% | 4% | 59% | 6% | 38% | + |
|  G1d | 0.76±0.07 | 1.22±0.06 | 13.5±0.4 | 15.73±0.76 | 22.00% | 49% | 28% | 44% | 32% | ++++ |
|  G3d | 0.77±0.12 | 1.20±0.060 | 13.33±1.03 | 15.38±0.77 | 19.30% | 48% | 26% | 47% | 32% | ++ |
|  BGH 2-5 | 0.74±0.07 | 1.19±0.04 | 14.36±0.50 | 15.28±0.86 | 18.50% | 59% | 25% | 41% | 29% | ++ |
|  G1a | 0.50±0.04 | 1.28±0.07 | 8.52±0.47 | 16.60±0.27 | 28.70% | -6% | 34% | -4% | 19% | ++ |
|  G3c | 0.50±0.01 | 1.04±0.05 | 8.80±0.47 | 13.77±1.16 | 6.80% | -3% | 10% | -4% | 3% | ++++ |
|  TNT | 0.52±0.01 | 0.95±0.13 | 9.03±0.70 | 12.91±0.56 | 0% | 0% | 0% | 0% | 0% | +++ |
|  G4a | 0.61±0.02 | 0.87±0.18 | 11.45±0.47 | 12.60±0.26 | -2.30% | 27% | -8% | 16% | -1% | ++++ |

**a** The values represent the mean of three independent assay replicates, expressed as the mean ± standard error, with units in grams (g) and millimeters (mm).

**b** Percentages are derived by comparing inoculated versus non-inoculated samples.

**c** The gradation of responses for the trait of root hair development, ranging from strong to weak, is denoted as (+ + ++), (+ + +), (+ +), and (+).

Figure S1.



**Figure S1.** A map showing the 6 sites that have been sampled in Morocco in three regions: G, Gharb; D, Doukkala; and T, Tadla.

Figure S2.



**Figure S2**. Panel a displays seeds of sugar beet with a coating, whereas Panel b illustrates seeds that have been washed to eliminate the coated reagents.

Figure S3.



**Figure S3.** The field trial site's location and the experimental setup, including treatments, are shown. The four bacterial isolates (BGH1-6, *Pantoea* sp.; BGH 2-2, *Serratia* sp.; BGH 2-7, *Bacillus* sp.; and BGH 1-3, *Serratia* sp.), along with DF (Difenoconazole) and UC (untreated control), were employed. The experiment included four replicates. The dimensions of the plots are presented in meters.

Figure S4.



Figure S4. Fourier Transform Infrared (FTIR) Spectroscopy used to perform qualitative and quantitative analysis the bacterial isolate BGH2-2 supernatant.

Figure S5.



Figure S4**.** Principal components analysis was conducted for the simultaneous assessment of hydrolytic enzyme production, bacterial antagonism, and the presence of lipopeptide encoding genes (ipe: pectinase index; IC: cellulase index; Iam: amylase index; IPR: protease index; hcn: hydrogen cyanide production). Bacterial isolates highlighted in red exhibited a high inhibition rate in dual culture, while those with a blue background demonstrated a high indirect inhibition rate.

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