**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 | Bacc1F  Bacc1R | GAAGGACACGGCAGAGAGTC  CGCTGATGACTGTTCATGCT | 875 | 60 °C | [1] | |
| Fengycin | Fend1F  Fend1R | TTTGGCAGCAGGAGAAGTT  GCTGTCCGTTCTGCTTTTTC | 964 | 62 °C | [1] | |
| Iturin | Itup1F  Ituo2R | AGCTTAGGGAACAATTGTCATCGGGGCTTC  TCAGATAGGCCGCCATATCGGAATGATTCG | 2000 | 45 °C | [2] | |
| Surfactin | P17  P18 | ATGAAGATTTACGGAATTTA  TTATAAAAGCTCTTCGTACG | 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  index  evaluation | 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 (+).

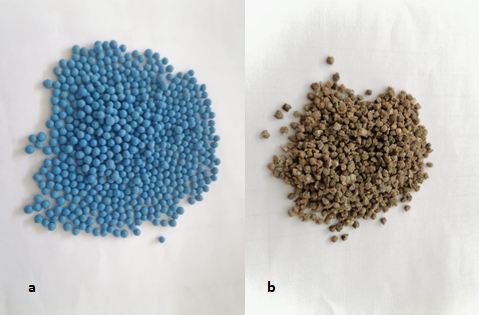
Figure S1.

A map of africa with a yellow and green area

Description automatically generated

**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.

A map of a country

Description automatically generated

**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.

A graph showing a wave number

Description automatically generated with medium confidence

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

Figure S5.

A diagram with numbers and circles

Description automatically generated with medium confidence

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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