

# Root-hair endophyte stacking in finger millet creates a physicochemical barrier to trap the fungal pathogen *Fusarium graminearum*

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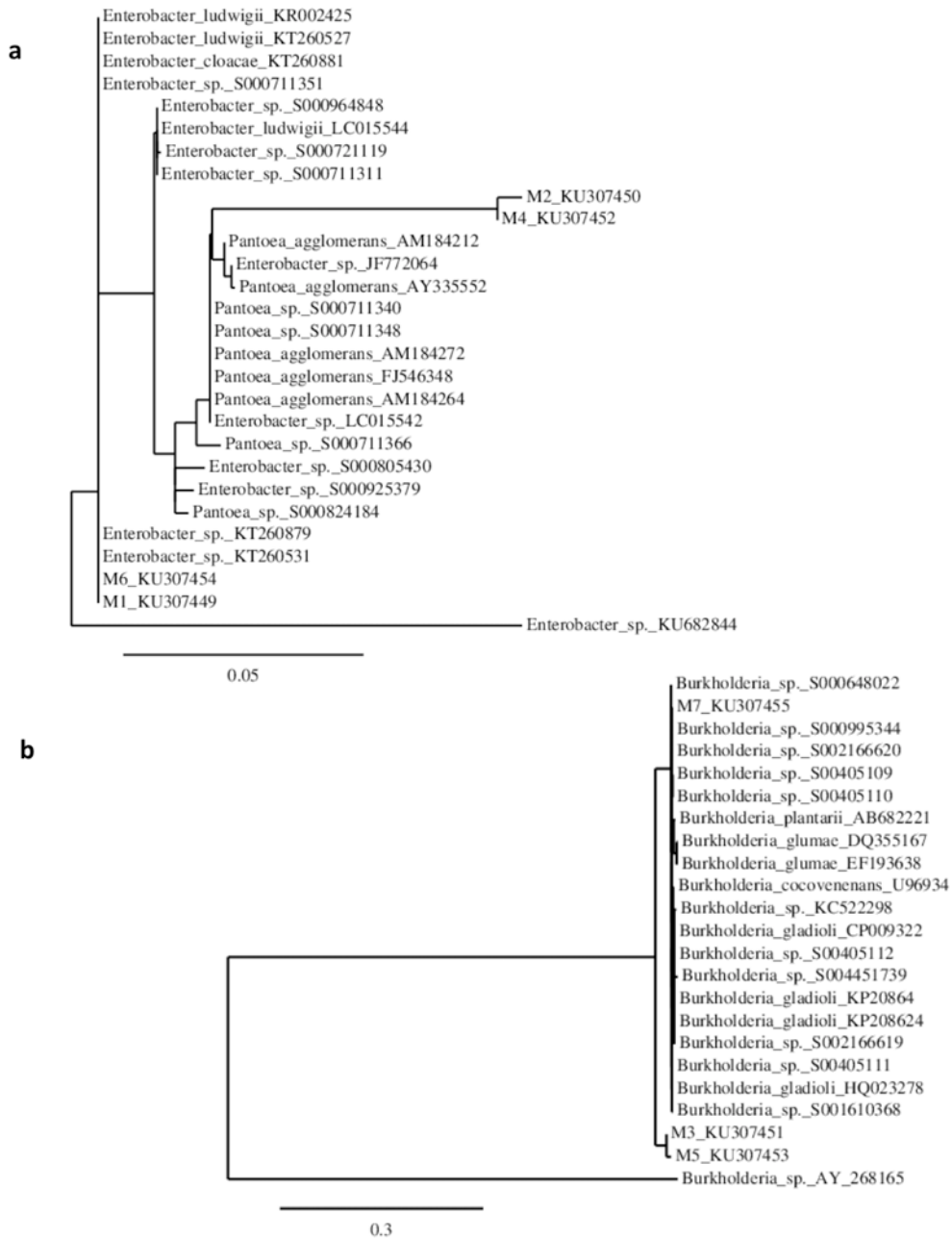
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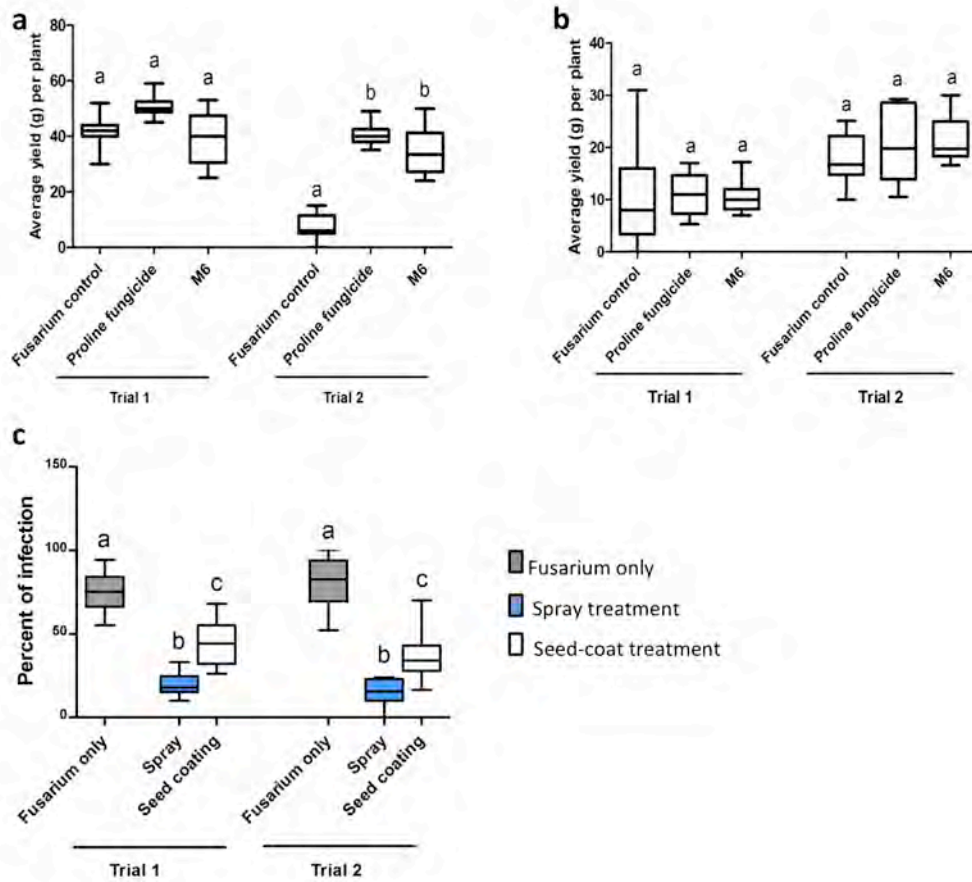
**(1) Supplementary Figures**



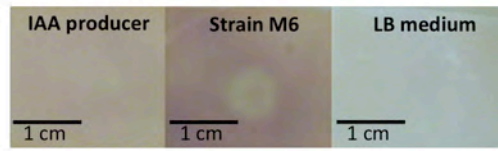
**Supplementary Figure 1 | 16S rDNA based phylogenetic tree of finger millet endophytes based on Phylogeny.fr software. a, tree with endophytes M1, M2, M4, M6. b, tree with endophytes M3, M5, M7.**



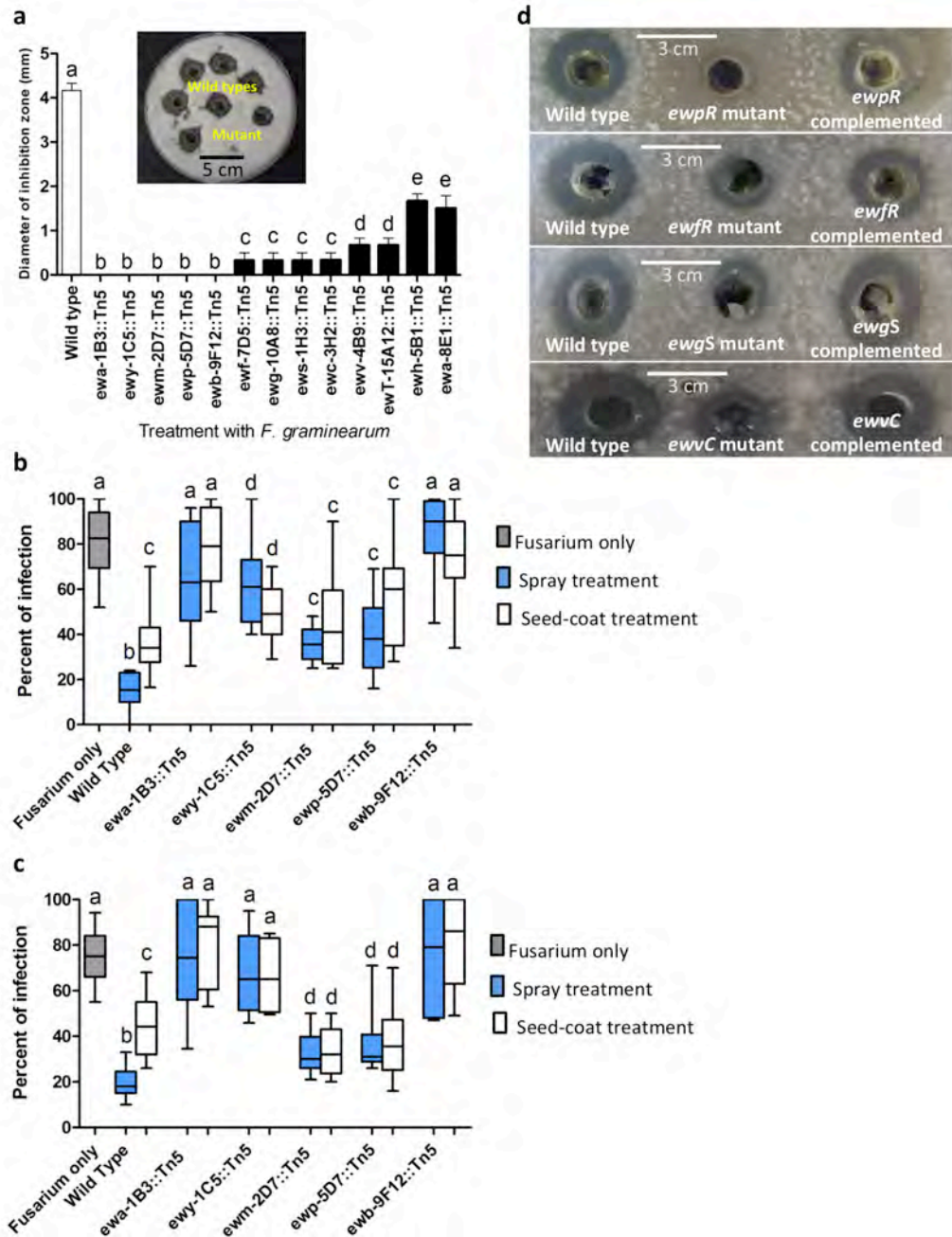
**Supplementary Figure 2 | Image of finger millet seedlings previously seed-coated with GFP-tagged M6 showing no pathogenic symptoms, consistent with the strain behaving as an endophyte.**



**Supplementary Figure 3 | Suppression of *F. graminearum* (Fg) by M6 and its effect on grain yield in greenhouse trials. a-b**, Effect of endophyte M6 on grain yield per plant in two greenhouse trials for (a) maize and (b) wheat. **c**, Effect of treatment with endophyte M6 on Fg disease symptoms in maize ears when the endophyte was applied as a seed coat or foliar spray compared to a *Fusarium* only control treatment. For greenhouse disease trials, n=20 biological replicates for M6 and 10 biological replicates for controls. Letters that are different from one another within a trial indicate that their means are statistically different ( $P \leq 0.05$ ). The whiskers indicate the range of data.

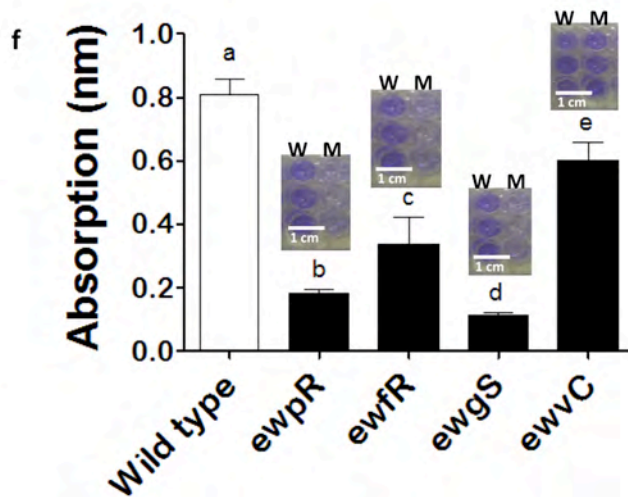
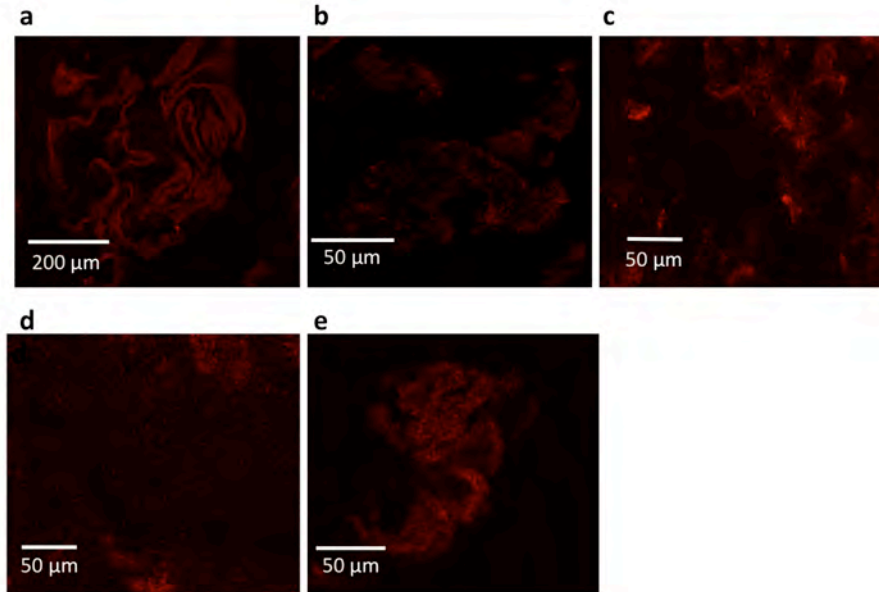


**Supplementary Figure 4 | Assay for production of indole-3-acetic acid (IAA, auxin) by wild type strain M6.** Production of indole-3-acetic acid (IAA) *in vitro* by wild type strain M6 compared to a positive control (bacterial endophyte strain 3E10) using the Salkowski reagent colorimetric assay.



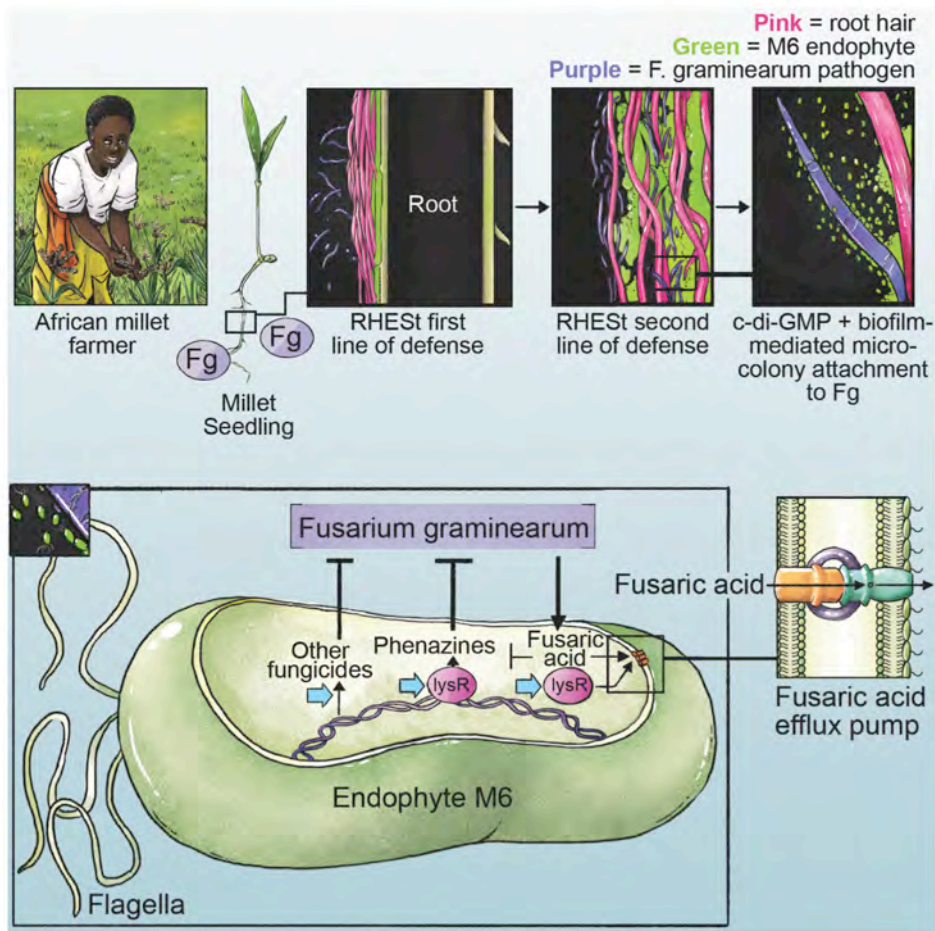
**Supplementary Figure 5 | Tn5 mutagenesis-mediated discovery, validation and complementation of genes required for the anti-*Fusarium* activity of strain M6. a,** Loss of anti-*F. graminearum* activity associated with each Tn5 insertion mutant using the *in vitro* dual culture diffusion assay, along with a representative image (inset) of the mutant screen. **b-c,** *In planta* validation of loss of anti-fungal activity of M6 mutant strains based on quantification of *F. graminearum* disease symptoms on maize ears, in **(b)** greenhouse trial 1, and **(c)** greenhouse trial 2. Only mutant strains that completely lost anti-fungal activity *in vitro* were selected for *in planta* validation. The whiskers indicate the range of data points. Letters that are different from one another indicate that their means are statistically different ( $P \leq 0.05$ ). **d,** Genetic complementation of Tn5 mutants

with the predicted, corresponding wild type coding sequences. Shown are representative images.

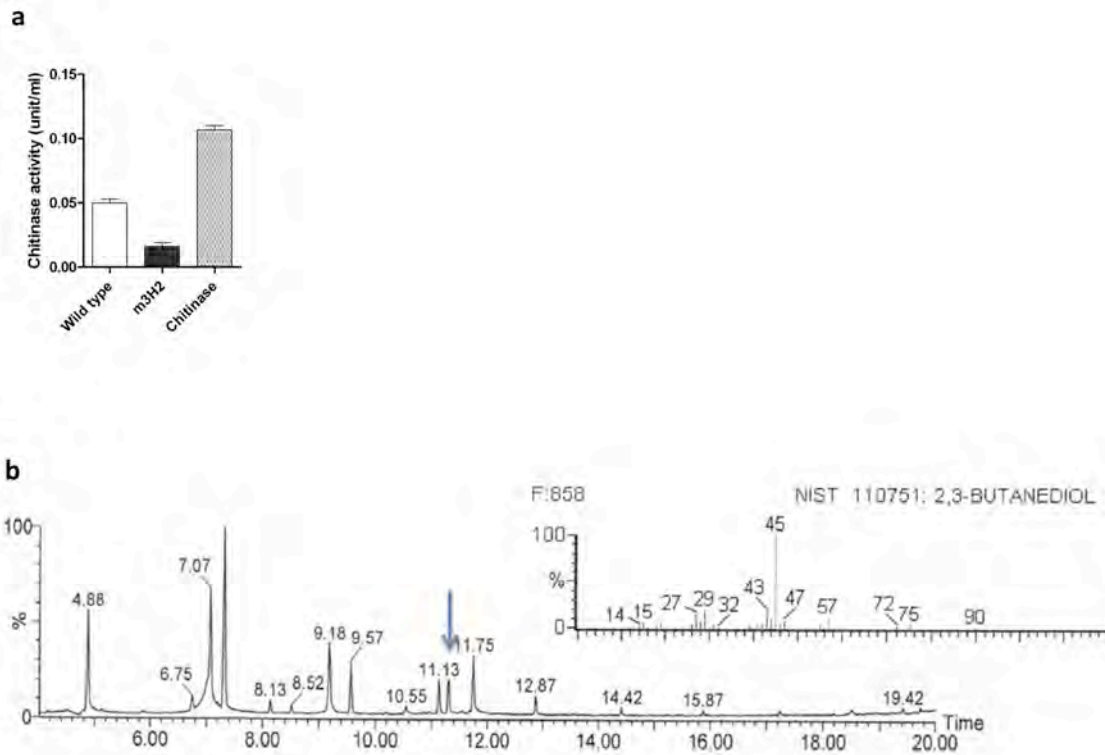


**Supplementary Figure 6** | Supporting data on biofilm formation. **a-e**, Confocal microscopy images showing the proteinaceous biofilm matrix stained with Ruby film tracer (red) associated with: **a**, the wild type M6 strain, and **b-e**, mutant strains *in vitro*. Shown are mutant strains, **(b)** *ewpR*-5D7::Tn5C (LysR-phenazine biosynthesis), **(c)** *ewfR*-7D5::Tn5 (LysR-fusaric acid resistance), **(d)** *ewvC*-4B9::Tn5 (c-di-GMP biosynthesis), and **(e)** *ewvC*-4B9::Tn5 (colicin V production). **f**, Quantification of the average light absorption ( $n=3$ ) of crystal violet indicator in wild type M6 and each mutant, along with corresponding images from the colorimetric assay (W denotes wild type and M denotes mutant). Letters that are different from one another indicate that their means are statistically different ( $P \leq 0.05$ ).





**Supplementary Figure 7 | Model to illustrate the interaction between strain M6, the host plant and *F. graminearum* pathogen.** Following pathogen sensing, M6 swarm towards invading *Fusarium* hyphae. It then creates two lines of defence. First M6 forms a dense layer of microcolonies on the root surface (rhizoplane). Second, M6 is associated with induced root hair growth, then forms microcolony stacks between the elongated and bent root hairs resulting in root hair-endophyte stack (RHESt) formation, likely mediated by biofilm. The RHESt-associated barriers prevent entry and/or trap *F. graminearum* for subsequent killing. M6 killing requires diverse antimicrobial compounds including phenazines. *Fusarium* will produce fusaric acid toxin which interferes with phenazine biosynthesis. However, M6 has a specialized fusaric acid-resistance pump system which is predicted to pump the mycotoxin outside the endophyte cell.



**Supplementary Figure 8 | Assays for production of chitinase and butanediol by strain M6.** **a**, Quantification of chitinase production by an M6 mutant strain carrying a Tn5 insertion in a chitinase encoding gene (*ewc-3H2::Tn5*, Supplementary Table 5) compared to wild type M6. **b**, Entire GC chromatogram showing an arrow pointing to a peak with RT 11.13 with a molecular weight and fragmentation pattern (inset) that matches 2, 3 butanediol when searched against the NIST 2008 database.

## (2) Supplementary Tables

**Supplementary Table 1. Taxonomic classification of finger millet bacterial endophytes based on 16S rDNA sequences and BLAST analysis**

<b>ID (Genbank Accession)</b>	<b>Tissue source</b>	<b>BLAST analysis</b>	<b>% of max. identity</b>	<b>Length of aligned sequence</b>
M1(KU307449)	Roots	<i>Enterobacter</i> sp. (CP015227)	99	646
M2 (KU307450)	Seeds	<i>Pantoea</i> sp. (FN796868)	99	701
M3(KU307451)	Seeds	<i>Burkholderia</i> sp. (KC522298)	99	587
M4 (KU307452)	Shoots	<i>Pantoea</i> sp. (KT075171)	95	751
M5 (KU307453)	Shoots	<i>Burkholderia</i> sp. (KP455296)	99	586
M6 KU307454	Roots	<i>Enterobacter</i> sp. (KU935452)	99	586
M7 (KU307455)	Shoots	<i>Burkholderia</i> sp. (HQ023278)	100	644

**Supplementary Table 2. Effect of endophyte strain M6 isolated from finger millet on the growth of diverse fungal pathogens *in vitro*.**

Target fungal species	Diameter of growth inhibition zone in mm		
	Nystatin (10.0 U/ml)	Amphotericin (250 µg/ml)	M6
<i>Alternaria alternata</i>	0.0±0.0	0.0±0.0	0.0±0.0
<i>Alternaria arborescens</i>	0.0±0.0	0.0±0.0	0.0±0.0
<i>Aspergillus flavus</i>	2.0±0.2	0.0±0.0	3.6±0.2
<i>Aspergillus niger</i>	0.0±0.0	2.0±0.0	0.0±0.0
<i>Bionectria ochroleuca</i>	2.0±0.2	0.5±0.2	0.0±0.0
<i>Davidiella tassiana</i>	1.5±0.2	0.5±0.3	0.0±0.0
<i>Diplodia pinea</i>	2.5±0.2	3.0±0.2	0.0±0.0
<i>Diplodia seriata</i>	3.0±0.2	2.0±0.2	0.0±0.0
<i>Epicoccum nigrum</i>	0.0±0.0	0.0±0.0	0.0±0.0
<i>Fusarium avenaceum</i> (isolate 1)	2.5±0.3	3.0±0.6	1.8±0.2
<i>Fusarium graminearum</i>	1.5±1.6	0.0±0.0	5.0±0.3
<i>Fusarium lateritium</i>	0.0±0.0	1.0±0.2	0.0±0.0
<i>Fusarium sporotrichioides</i>	1.0±0.2	1.0±0.2	2.8±0.2
<i>Fusarium avenaceum</i> (isolate 2)	0.0±0.0	0.0±0.0	0.0±0.0
<i>Nigrospora oryzae</i>	0.0±0.0	0.0±0.0	1.83±0.2
<i>Nigrospora sphaerica</i>	0.0±0.0	0.0±0.0	0.0±0.0
<i>Paraconiothyrium brasiliense</i>	0.0±0.0	0.0±0.0	0.0±0.0
<i>Penicillium afellutanum</i>	3.0±0.2	3.0±0.2	0.0±0.0
<i>Penicillium expansum</i>	2.0±0.2	5.0±0.2	4.9±0.1
<i>Penicillium olsonii</i>	1.5±0.3	3.5±0.3	0.0±0.0
<i>Rosellinia corticium</i>	2.0±0.2	4.5±0.3	0.0±0.0

**Supplementary Table 3. Suppression of *F. graminearum* disease symptoms in maize and wheat by endophyte M6 in replicated greenhouse trials.**

<b>Treatment</b>	<b>% Infection (mean ± SEM)*</b>	<b>% Disease reduction relative to <i>Fusarium</i> only treatment</b>	<b>Average yield per plant*</b>	<b>% Yield increase relative to <i>Fusarium</i> only treatment</b>
<b>Greenhouse trial 1 in maize</b>				
<i>Fusarium</i> only	33.69±2.3	0.0	41.77±1.4	0.0
Proline fungicide	23.10±2.0	31.4	50.9±1.2	21.85
M6	10.13±0.9	69.93	39.58±2.6	-5.2
<b>Greenhouse trial 2 in maize</b>				
<i>Fusarium</i> only	85.11±4.5	0.0	7.8±1.1	0.0
Proline fungicide	41.42±4.5	51.33	40.8±1.2	423
M6	6.9±0.9	91.89	34.70±2.7	344
<b>Greenhouse trial 1 in wheat</b>				
<i>Fusarium</i> only	51.8±6.3	0.0	10.5±2.6	0.0
Proline fungicide	31.70±2.6	38.8	10.9±1.3	3.8
M6	41.1±2.6	20.6	10.6±0.8	0.95
<b>Greenhouse trial 2 in wheat</b>				
<i>Fusarium</i> only	54.0±2.6	0.0	17.7±1.5	0.0
Proline fungicide	31.5±4.1	41.6	20.1±2.1	13.5
M6	30.7±3.6	43.1	21.1±1.3	19.2%

\*SEM is the standard error of the mean.

**Supplementary Table 4. Reduction of DON mycotoxin accumulation during prolonged seed storage following treatment with endophyte M6.**

<b>Treatment</b>	<b>DON content (ppm) (mean ± SEM)*</b>	<b>% DON reduction relative to Fusarium only treatment*</b>
<b>Greenhouse trial 1 in maize</b>		
<i>Fusarium</i> only	3.4±0.4	0.0
Proline fungicide	0.7±0.4	79.4
M6	0.1±0.0	97
<b>Greenhouse trial 2 in maize</b>		
<i>Fusarium</i> only	3.5±0.3	0.0
Proline fungicide	0.1±0.0	97.1
M6	0.1±0.0	97.1
<b>Green house trial 1 in wheat</b>		
<i>Fusarium</i> only	7.6±0.3	0.0
Proline fungicide	0.5±0.1	94.6
M6	1.5±0.6	81.33
<b>Green house trial 2 in wheat</b>		
<i>Fusarium</i> only	5.5±0.7	0.0
Proline fungicide	1.3±0.9	76.3
M6	2.0±0.4	63.6

**\*SEM is the standard error of the mean.**

**Supplementary Table 5. Complete list of strain M6 Tn5 insertion mutants showing loss of antifungal activity against *F. graminearum* in vitro.**

ID	Gene prediction	Swarming assay	Motility assay (mean ± SEM)*	Presence of flagella (%)	Biofilm (mean ± SEM)*
Wild type		+++	4.2±0.3	70%	0.8
<i>ewa-1B3::Tn5</i> <i>ewa-4B8::Tn5</i>	Transcription regulator, AraC	---	0.6±0.02	50%	0.11±0.00
<i>ewy-1C5::Tn5</i> <i>ewy-5D2::Tn5</i>	YjbH outer-membrane protein	++	0.5±0.03	10%	0.3±0.08
<i>ewm-2D7::Tn5</i>	4-hydroxyphenyl acetate 3-monoxygenase  May catalyze production of phenylacetic acid (PAA)	---	0.8±0.05	20%	0.07±0.00
<i>ewpR-5D7::Tn5</i>	Transcription regulator, LysR	---	0.5±0.03	30%	0.18±0.01
<i>ewb-9F12::Tn5</i> <i>ewb-7C5::Tn5</i>	Fatty acid biosynthesis	---	0.6±0.05	30%	0.3±0.11
<i>ewvC-4B9::Tn5</i>	Colicin V production	+	1.8±0.30	60%	0.6±0.05
<i>ewT-15A12::Tn5</i>	Transport permease protein  Within operon for biosynthesis of P-amino-phenyl-alanine antibiotics (PAPA).	+	1.5±0.00	30%	0.6±0.04

<i>ews-1H3::Tn5</i>	Sensor histidine kinase	+	0.8±0.16	50%	0.8±0.2
<i>ewc-3H2::Tn5</i>	Chitinase	---	1.0±0.00	20%	0.4±0.15
<i>ewfR-7D5::Tn5</i>	Transcription regulator, LysR	+	1.5±0.20	50%	0.3±0.08
<i>ewgS-10A8::Tn5</i>	Di-guanylate cyclase	---	0.8±0.30	40%	0.1±0.01
<i>ewh-5B1::Tn5</i>	Hig A protein	+++	1.6±0.30	30%	0.6±0.10
<i>ewa-8E1::Tn5</i>	Hypothetical protein	++	2.3±0.40	20%	0.5±0.09

\*SEM is the standard error of the mean.



**Supplementary Table 6. M6 wild type nucleotide coding sequences corresponding to Tn5 insertion mutants that showed loss of antifungal activity against *F. graminearum* in vitro**

ID	Gene sequence
<i>ewa-1B3::Tn5</i>	<p>gtgaataccattggcataaacagcgagcccatcctgacgcacagtggcttagcattaccgccgatacc  actcttgccgcagacaggcactatgacgttatctatctctctgcccgtggcgcaatcctcgtgcagtggc  agacaacagcctgaactcctggcatggcttagcgaaacagggcggcgagggaccgccatcgcgcc  gtcggaaacgggctgctgtttcctggcggaaatcgggattgctcaacgggaaaccgccaccaccactg  gcactactcaaacagttctcgcgtgactaccccaacgtaaaattacaacaaaacatttctcagcgag  gccgataatatttactgtgccgcccagcgtcaaagccctctcagatctgaccatccatttcagaaacgat  atacgggaaacgtgtagccacacatacccaacggaccttttccatgaaatcgggagtcagttgatcgc  cagtgttacagtgaagaaaacaaaccccatccggatgaagataattgtcaaattcaaatctggataaaa  gccaactcgcctcggatataatccatgcaaaatctgcccgataggctggcatgagttgcgcaactttaa  cgccgtttaaaaatgccaccgatataccccctgcagatattataaccgccagaatgaatccgcat  gacaatgtgcaatccaccaatctgagcattcaggagattgcgaatgcgggggatcaggatattgc  gcactttaatcgccagtttaagcataaaacaacggttcaccgggggattaccgtaagaccgtccgggc  aaagatgtttagtcataa</p>
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<p><i>ewf-7D5::Tn5</i></p>	<p>atgatgaatctttacactggcgtgctggtgccgtggccgatgccagtaataattcccgtgcccgtgaag  aggtcggatgacgcagtcaggtgccagccaggcgatcgctcagtagaggcctcattagattgcccgt  attcagcgcgagagcgcagccacatcggcgtgactgcccggcgagcgggtgtcaagaagcaag  gagtagtctggcgcggctggatgcatccgtgactggcggatgagagccgggggctgagcggcggga  cgattcgtctgcccagtttctcgggtgacatccagttttgcccgggctgctgcgcgactaaagcgcct  gcatcctgaaatcgaggtggctgctcgaaggcacggaccaggaggtcgaagagtggtggcggca  gatacgggtgatcggcgtggtcatgaacctgtcccggcgctgtaagcagatcttagggcaggatg  catgggtcgtggtgtgcccagccagtcaccgtcaggctcgttatacagctacgcggcatcaccttga  ggaactggcagaccagccctcgtgctcgaaccggcgggtgcccgtcaatggaaaaagcctgatgg  aacaggctggcctgacgtgctgacgtgcccgtgaccgtccgcgactggatcagcgcctgctgctg  gtgcccgaaggcatggcgtgcccgtgatacctgaatccgcccctcgggatgaattacgcggtttgtg  gtcgtaccctgacgcctcgtgctgcccgggaattgggctggtatgttcgaggtgggcaaatattccc  gcgacgcagcgttattagaaggggtgctcaaatgaaaaggctgctgctga</p>
<p><i>ewg-10A8::Tn5</i></p>	<p>atgaccacaacatttctcagaaatagggtgtgcatgaacaaaagtgtcatctcagcctgcccgtttt  acgttccagggatcgtctgttccctaacagatcgggaatacaggcttcgcatattcatttggatgggatg  aggatcgcacaggatgaaaaatccttataaatcagaatgctcatgttgggtttctcggaaaa  ggtatcctaagtctcctggagagcctgaagcagctggcgtccgtgctcaatgctgtcccgttattcagcgc  gtcacgctgtatggcgacataccggatggctgctatcgcaccctgggagctctttaaataatagttat  caattatcattgactagcccgcgttccgatgctgctcactggttctcatacaccatcatgtatttaa  ggaaactgctactattacgcgcatcgtacagggataattctcgaagacaacgtcaagtggcctaaca  aaaagagagattgacgttttataaattctaccggcgtgctcgtgaaagaaatgtgcatgaaatgg  gactatctaataaaacggtttataaccaccgtaaggaaggcgtgctgaaattacgcttaataagcggg  gctacacgattcgacaatatcaatcggaagaagatcaagcggcggagtagcaaacacgggaattt  acggataaggaagcagagatttttaagcattatataaaaaagagatcttccctgcttaccagatcattacc  gatcgtgacaaaaaggcgtaggctttgagatactgatccgctggaacaaaaacggtaaaattgtcaa  gccgaccagtttctcacggatattcaaatcatgagatatggtgaaaattaccgctgatttattcatgcc  gcccgtgcccgaataataagataatggtaaatactatttctgtgaatattccacctgcctggcctccgg  aaatgcattgctgatattgcaaggaaagctatcgacatgctgctcaaacgcagtgggccgagaagc  tggctttgaattcgcagaagatattgacgtgacgaaggacaaagggatcccagaaaccatgcccatt  tgcgtaatacaggggtgctgattttctggatgactgcttctcaatcaccaaaccatgttcccgggtgcccga  ggtagcattttagtgactcaagctggatccggatcgttgagcattttgtggcaaacgacaatgactataa  cctgatcaaaagcagacagattatagcagatgaccggaacggactgtattgagagggagtagaca  gtgaggaaaaattgaaaaattagtcgctggcgtcaaaaacttccagggatattttatcgcgagcc  gtgaaagaggacgagttggatcgcagatggtcagaatttttagttaa</p>

<i>ewh-5B1::Tn5</i>	<p>Atgacacttcaacaggcactccgcaaaccaccacgccggcgacgtgttcagtagatgatcttgaacc  gctcaatctgaaaatcagcgatctggcggagatgctcaatgtcaccgcaacaccatcagcgctgtgca  ataacaatcgaaaactactgccgatatggcgatcaaaactggcaaaagccttgataccacgattgaatttgg  ctgaacttacagctgaacgctgatatctgggaagcgcaatctaactccaggactcaggaggagctaagccg  tataaagaccggttcggaagtattggctaagcgaaaatctggccagccggatgttcctga</p>
<i>ewa-8E1::Tn5</i>	<p>gtgatccgcaaagagaaagggcgctggatgtctatggcgaccgcttcgcgacgtgcatcagct  gacgccgctgctgacggtgcacgctataatcagcaaccggaagcggatggaacagaccg  caatggagattgcgacgctgtgaaaacgctggatgccacggtggtccgcccattcaggcgtgggtt  cgccgggctgcgcatctaagcaaacgctggagcagtggttggccgggtggtcacctccagcga  agatgtccactacggtgaatacgtcgcagcgacgtcaacgcgagcattgattcgtgctggaggggc  atcagcacacctgcgaggttatccgagcccacaaccgctacgcaatggcccaggcggctctctgc  tggcgaggcgaggcaggtcgccatattggcattggcgctccggcattctggccagtataccgcca  ggctgtcagccgatggggtaaccgccacgccgttaaccgtaaccggaatagggctgcccagcagc  tgattgcgctcagcgggcgacgtgctggatgatggcgagaaatccgcgaccgggaggggca  aaccacgctgctgaagcaaacgctggcattcccaccatctgctgaccaacgccctcgattcgc  gttcagcaaggaggccagcgtggtgatccagttccgcgggcggaagcaaaatccgct  ccacggcaggtgctgctgtgctggagatgatatttatccgctcctccaccgagccgagcgacc  atcaagtcgatgaagcgcatcaacgagttacaccgtgggttaaagccgggaagaaaagtaccta</p>

**Supplementary Table 7. Gene-specific primers used in quantitative real-time PCR analysis.**

Gene ID	PCR primers
ewpR	5D7F: 5'- GGCATAACTTCCTGCGCTAC - 3' 5D7R: 5': CAGTACGCCATCAATCATCG - 3'
ewpF1	PhzF1F: 5'- TTTTCTCACCGGGCGTTTC- 3' PhzF1R: 5'- GTATGTGCGGAGCCGGTAA- 3'
ewpF2	PhzF2F: 5'- AAATGGCGCAGCAGCATAA- 3' PhzF2R: 5'- GTCGGTGCGCACGAAAA- 3'
ewfR	D5F : 5'- GGGGACAGTAACGACGAAAC - 3' D5R : 5'- CGGCAATCTGTCGATATGAA - 3'
ewfD	FusE/MFPF: 5'- TGGCCGTGCGGGATAAT- 3' FusE/MFPR: 5'- GGATCGATGGTGTAAGCACATC- 3'
ewfE	FusEF: 5'- CGTCGAGCCCACCTTTAGC- 3' FusER: 5'- TCCGGCAATCTGTCGATATG- 3'
ewgS	A8F 5: GGAGTCAAAACACGGAATTTACG - 3' A8R 5: ATCTGATAAGCAGGGAAGATCTCTTT - 3'
ewvC	B9F 5: TGTTTTATGCTTAAACTGGCGATT - 3' B9R 5: CGAATGCGGTGGGATATCA - 3'
16SrDNA (housekeeping gene)	799F: 5'- AACMGGATTAGATACCKG- 3' 1492R: 5'- GGTTACCTTGTTACGACTT- 3'



### (3) Supplementary video legends

**Supplementary video 1 | 3D video showing RHESt.** A 62  $\mu\text{m}$  confocal stack with 46 sections was imaged from a 12 day old finger millet root previously seed-coated with GFP-tagged endophyte M6 (green colour) then inoculated with *F. graminearum* (*Fg*) at a distance of 0.5 cm to the left-hand side of the image followed by a 72 h incubation. On the right side of the image is the root (purple red) oriented downward. M6 cells (green, right of the root) stack to form a deep physical barrier on the rhizoplane on the same side as *Fg* inoculation. Root hairs (purple) unusually elongate on the same side (left) as *Fg* inoculation, bend parallel to the rhizoplane and become intercalated with M6 cells, in contrast to the side of the root that is distal to *Fg* (right). In this video, few *Fg* mycelia (purple threads) are observed, perhaps because most mycelia had not yet reached the root system (mycelia were clearly visible  $\sim 1$  mm away), were obscured or due to earlier death by the RHESt complex.

**Supplementary video 2 | 3D imaging of a biofilm associated with endophyte M6 *in vitro*.** Shown is a 45  $\mu\text{m}$  confocal stack rendered as a 3D video. The biofilm was grown on a microscopic slide immersed in LB liquid medium inoculated with M6 at 37 °C and 50 rpm for 5 days, then stained with Ruby Film Tracer.