

Table S1Functional cluster of orthologous genes (COG) classification of predicted genes in the *P. fluorescens* BRZ63 strain

Code	Description	CDS	%CDS
A	RNA processing and modification	2	0.03
B	Chromatin structure and dynamics	2	0.03
C	Energy production and conversion	354	5.95
D	Cell cycle control, cell division, chromosome partitioning	54	0.91
E	Amino acid transport and metabolism	586	9.85
F	Nucleotide transport and metabolism	151	2.54
G	Carbohydrate transport and metabolism	324	5.45
H	Coenzyme transport and metabolism	213	3.58
I	Lipid transport and metabolism	252	4.24
J	Translation, ribosomal structure and biogenesis	226	3.80
K	Transcription	582	9.79
L	Replication, recombination and repair	181	3.04
M	Cell wall/membrane/envelope biogenesis	357	6.00
N	Cell motility	174	2.93
O	Posttranslational modification, protein turnover, chaperones	163	2.74
P	Inorganic ion transport and metabolism	451	7.58
Q	Secondary metabolites biosynthesis, transport and catabolism	178	2.99
S	Function unknown	1090	18.33
T	Signal transduction mechanisms	356	5.99
U	Intracellular trafficking, secretion, and vesicular transport	177	2.98
V	Defense mechanisms	74	1.24
Z	Cytoskeleton	2	0.03

Table S2

Secondary metabolite gene clusters identified in the *P. fluorescens* BRZ63 strain using antiSMASH v. 5.1.2

Cluster	Type	From	To	Most similar known cluster	Similarity
Cluster 1	LAP	85.954	107.934		
Cluster 2	NAGGN	330.566	345.306		
Cluster 3	NRPS	373.569	426.477	pyoverdin	9%
Cluster 4	siderophore	512.834	524.762		
Cluster 5	bacteriocin	326.216	337.061		
Cluster 6	arylpolyyene	232.497	276.072	APE Vf	45%
Cluster 7	bacteriocin	41.058	51.936		
Cluster 8	NRPS	1	24.586	viscosin	37%
Cluster 9	betalactone	45.049	73.349	fengycin	13%
Cluster 10	terpene	131.565	152.575		
Cluster 11	NRPS	64.606	101.624	taiwachelin	11%
Cluster 12	NRPS-like	51.064	77.559	L-2-amino-4-methoxy-trans-3-butenoic acid	40%
Cluster 13	NRPS	1	7.725		
Cluster 14	NRPS	1	3.435		

Table S3. Genes attributed to biocontrol, plant growth promotion and colonization traits identified in the *P. fluorescens* BRZ63 genome

Gene	Accession number	Gene product	Activity
<i>entD</i>	TFW40873.1	enterobactin synthetase component D [EC:6.3.2.14 2.7.8.-]	Siderophore biosynthesis
<i>iucB</i>	TFW45226.1	acetyl CoA:N6-hydroxylysine acetyl transferase [EC:2.3.1.102]	
<i>bfr</i>	TFW40338.1	bacterioferritin [EC:1.16.3.1]	
<i>bfd</i>	TFW42906.1	bacterioferritin-associated ferredoxin	
<i>fiu</i>	TFW43421.1	catecholate siderophore receptor	Siderophore uptake
<i>exbB</i>	TFW41374.1	biopolymer transport protein ExbB	
<i>exbD</i>	TFW41375.1	biopolymer transport protein ExbD	
<i>tonB</i>	TFW40662.1	periplasmic protein TonB	
<i>pvdA</i>	TFW44939.1	L-ornithine N5-monooxygenase [EC:1.14.13.195 1.14.13.196]	Pyoverdin biosynthesis
<i>pvdE</i>	TFW42495.1	putative pyoverdin transport system ATP-binding/permease protein belongs to the class-III pyridoxal-phosphate-dependent	
<i>pvdH</i>	TFW45216.1	aminotransferase family	
<i>pvdL</i>	TFW45223.1	COG0318 Acyl-CoA synthetases (AMP-forming) AMP-acid ligases II	
<i>pvdG</i>	TFW45224.1	thioesterase	
<i>pvdS</i>	TFW45225.1	belongs to the sigma-70 factor family. ECF subfamily	
<i>pvdJ</i>	TFW42491.1	AA-adenyl-dom amino acid adenylation domain protein	
<i>pvdO</i>	TFW42496.1	Chromophore maturation protein PvdO	
<i>pvdN</i>	TFW42497.1	class V aminotransferase	
<i>pvdM</i>	TFW42498.1	membrane dipeptidase (Peptidase family M19)	
<i>pvdP</i>	TFW42499.1	PvdJ PvdD PvdP-like protein	
<i>pvdI</i>	TFW40457.1	peptide synthetase	
<i>pvdQ</i>	TFW42063.1	protein related to penicillin acylase	
<i>menF</i>	TFW35465.1	isochorismate synthase	Salicylic acid production
<i>pchB</i>	TFW41741.1	isochorismate pyruvate lyase [EC:4.2.99.21]	
<i>afuA</i>	TFW44456.1	iron(III) transport system substrate-binding protein	Iron transport, receptors and related protein
<i>afuB</i>	TFW44457.1	iron(III) transport system permease protein	

<i>afuC</i>	TFW44458.1	iron(III) transport system ATP-binding protein [EC:7.2.2.7]	
-	TFW43370.1	TC.FEV.OM; iron complex outermembrane receptor protein	
-	TFW40302.1	ABC.FEV.S; iron complex transport system substrate-binding protein	
<i>pqqE</i>	TFW42428.1	PqqA peptide cyclase [EC:1.21.98.4]	Phosphate
<i>pqqD</i>	TFW42429.1	pyrroloquinoline quinone biosynthesis protein D	solubilization
<i>pqqC</i>	TFW42430.1	pyrroloquinoline-quinone synthase [EC:1.3.3.11]	
<i>pqqB</i>	TFW42431.1	pyrroloquinoline quinone biosynthesis protein B	
<i>pqqA</i>	TFW42489.1	pyrroloquinoline quinone biosynthesis protein A	
<i>phnA</i>	TFW40776.1	protein PhnA	
<i>ppk2</i>	TFW45161.1	polyphosphate kinase (ADP) [EC:2.7.4.-]	
<i>phoU</i>	TFW44677.1	phosphate transport system protein	
<i>pstB</i>	TFW44678.1	phosphate transport system ATP-binding protein [EC:7.3.2.1]	
<i>pstA</i>	TFW44679.1	phosphate transport system permease protein	
<i>pstC</i>	TFW44680.1	phosphate transport system permease protein	
<i>pstS</i>	TFW44681.1	phosphate transport system substrate-binding protein	
<i>phoQ</i>	TFW40870.1	two-component system. OmpR family. sensor histidine kinase PhoQ [EC:2.7.13.3]	
<i>phoP</i>	TFW40871.1	two-component system. OmpR family. response regulator PhoP	
<i>Pit</i>	TFW42726.1	low-affinity inorganic phosphate transporter	
<i>pqqL</i>	TFW37848.1	zinc protease [EC:3.4.24.-]	
<i>gcd</i>	TFW42967.1	quinoprotein glucose dehydrogenase [EC:1.1.5.2]	
-	TFW41813.1	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	Production volatile organic
-	TFW41814.1	acetolactate synthase I/III small subunit [EC:2.2.1.6]	compounds
<i>bdh</i>	TFW40243.1	(R,R)-butanediol dehydrogenase / meso-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4 1.1.1.- 1.1.1.303]	
<i>acdS</i>	TFW41243.1	1-aminocyclopropane-1-carboxylate deaminase [EC:3.5.99.7]	ACC deaminase activity
-	TFW41148.1	nitrilase [EC:3.5.5.1]	IAA production
<i>oxd</i>	TFW40578.1	aldoxime dehydratase [EC:4.99.1.5]	
-	TFW44414.1	oxidoreductase	
<i>trpE</i>	TFW42468.1	anthranilate synthase component I [EC:4.1.3.27]	Antibiotics
<i>trpG</i>	TFW42469.1	anthranilate synthase component II [EC:4.1.3.27]	and secondary metbolites
<i>trpD</i>	TFW42470.1	anthranilate phosphoribosyltransferase [EC:2.4.2.18]	

<i>trpC</i>	TFW42471.1	indole-3-glycerol phosphate synthase [EC:4.1.1.48]	
<i>trpA</i>	TFW44799.1	tryptophan synthase alpha chain [EC:4.2.1.20]	
<i>trpB</i>	TFW44800.1	tryptophan synthase beta chain [EC:4.2.1.20]	
<i>phzF</i>	TFW40232.1	trans-2,3-dihydro-3-hydroxyanthranilate isomerase	
<i>prtB</i>	TFW41941.1	oligopeptidase B [EC:3.4.21.83]	
<i>ubiC</i>	TFW44667.1	chorismate--pyruvate lyase [EC:4.1.3.40]	
<i>ubiA</i>	TFW44668.1	4-hydroxybenzoate polyprenyltransferase [EC:2.5.1.39]	
<i>gapP</i>	TFW43975.1	GABA permease	
<i>pys2</i>	TFW42890.1	pyocin	
-	TFW40521.1	endoglucanase [EC:3.2.1.4]	Lytic enzymes production
<i>bglX</i>	TFW39167.1	beta-glucosidase [EC:3.2.1.21]	
<i>nagAl</i>	TFW43285.1	N-acetylglucosamine-6-phosphate deacetylase (Chitinase activity)	
<i>pvdQ</i>	TFW42063.1	acyl-homoserine-lactone acylase [EC:3.5.1.97]	Quorum quenching
<i>iscU</i>	TFW39818.1	nitrogen fixation protein NifU and related proteins	Nitrogen fixation
<i>manD</i>	TFW41120.1	mannitol 2-dehydrogenase [EC:1.1.1.67]	Mannitol dehydrogenase
<i>rhlB</i>	TFW43588.1	ATP-dependent RNA helicase RhlB [EC:3.6.4.13]	Rhamnolipide production
<i>rhlE</i>	TFW42321.1	ATP-dependent RNA helicase RhlE [EC:3.6.4.13]	
<i>rhlA</i>	TFW42353.1	Alpha beta hydrolase	
<i>algA</i>	TFW43571.1	mannose-1-phosphate guanylyltransferase / mannose-6-phosphate isomerase [EC:2.7.7.13 5.3.1.8]	Exopolisacharydes biosynthesis
<i>algF</i>	TFW43572.1	alginate O-acetyltransferase complex protein AlgF	<i>Alginate</i>
<i>algJ</i>	TFW43573.1	alginate O-acetyltransferase complex protein AlgJ	
<i>algI</i>	TFW43574.1	alginate O-acetyltransferase complex protein AlgI	
<i>algL</i>	TFW43575.1	poly(beta-D-mannuronate) lyase [EC:4.2.2.3]	
<i>algX</i>	TFW43576.1	alginate biosynthesis protein AlgX	
<i>algG</i>	TFW43577.1	mannuronan 5-epimerase [EC:5.1.3.37]	
<i>algE</i>	TFW43578.1	alginate production protein	
<i>alg44</i>	TFW43579.1	mannuronan synthase [EC:2.4.1.33]	
<i>alg8</i>	TFW43580.1	mannuronan synthase [EC:2.4.1.33]	
<i>algD</i>	TFW43581.1	GDP-mannose 6-dehydrogenase [EC:1.1.1.132]	
<i>algI</i>	TFW40983.1	alginate O-acetyltransferase complex protein AlgI	

<i>flhG</i>	TFW45253.1	flagellar biosynthesis protein FlhG	Cell Motility
<i>flhF</i>	TFW45254.1	flagellar biosynthesis protein FlhF	Flagellar assembly
<i>flhA</i>	TFW45255.1	flagellar biosynthesis protein FlhA	
<i>flhB</i>	TFW45258.1	flagellar biosynthetic protein FlhB	
<i>fliR</i>	TFW45259.1	flagellar biosynthetic protein FliR	
<i>fliQ</i>	TFW45260.1	flagellar biosynthetic protein FliQ	
<i>fliP</i>	TFW45261.1	flagellar biosynthetic protein FliP	
<i>fliOZ</i>	TFW45262.1	flagellar protein FliO/FliZ	
<i>fliNY</i>	TFW45263.1	flagellar motor switch protein FliN/FliY	
<i>fliM</i>	TFW45264.1	flagellar motor switch protein FliM	
<i>fliL</i>	TFW45265.1	flagellar FliL protein	
<i>fliK</i>	TFW45266.1	flagellar hook-length control protein FliK	
<i>fliJ</i>	TFW45270.1	flagellar FliJ protein	
<i>flil</i>	TFW45271.1	flagellum-specific ATP synthase [EC:7.4.2.8]	
<i>fliH</i>	TFW45272.1	flagellar assembly protein FliH	
<i>fliG</i>	TFW45273.1	flagellar motor switch protein FliG	
<i>fliF</i>	TFW45274.1	flagellar M-ring protein FliF	
<i>fliE</i>	TFW45275.1	flagellar hook-basal body complex protein FliE	
<i>fliS</i>	TFW45279.1	flagellar protein FliS	
<i>fliD</i>	TFW45280.1	flagellar hook-associated protein 2	
<i>fliC</i>	TFW45282.1	flagellin	
<i>flrC</i>	TFW45276.1	two-component system. response regulator FlrC	
<i>fleQ</i>	TFW45277.1	sigma-54 dependent transcriptional regulator. flagellar regulatory protein	
<i>flgL</i>	TFW45284.1	flagellar hook-associated protein 3 FlgL	
<i>flgK</i>	TFW45285.1	flagellar hook-associated protein 1 FlgK	
<i>flgJ</i>	TFW45286.1	flagellar protein FlgJ	
<i>flgI</i>	TFW45287.1	flagellar P-ring protein precursor FlgI	
<i>flgH</i>	TFW45288.1	flagellar L-ring protein precursor FlgH	
<i>flgG</i>	TFW45289.1	flagellar basal-body rod protein FlgG	
<i>flgF</i>	TFW45290.1	flagellar basal-body rod protein FlgF	
<i>motB</i>	TFW43788.1	chemotaxis protein MotB	

<i>motA</i>	TFW43789.1	chemotaxis protein MotA	
<i>pilO</i>	TFW43881.1	type IV pilus assembly protein PilO	<i>Pilus assembly</i>
<i>pilN</i>	TFW43882.1	type IV pilus assembly protein PilN	
<i>pilM</i>	TFW43883.1	type IV pilus assembly protein PilM	
<i>fimA</i>	TFW43898.1	fimA; major type 1 subunit fimbrin (pilin)	
<i>pilQ</i>	TFW43990.1	type IV pilus assembly protein PilQ	
<i>pilV</i>	TFW43387.1	type IV pilus assembly protein PilV	
<i>pilE</i>	TFW43390.1	type IV pilus assembly protein PilE	
<i>pilD</i>	TFW43404.1	leader peptidase (prepilin peptidase) / N-methyltransferase [EC:3.4.23.43 2.1.1.-]	
<i>pilC</i>	TFW43405.1	type IV pilus assembly protein PilC	
<i>pilA</i>	TFW43652.1	type IV pilus assembly protein PilA	
<i>pilL</i>	TFW44166.1	type IV pili sensor histidine kinase and response regulator	
<i>pilT</i>	TFW42281.1	twitching motility protein PilT	
<i>pilG</i>	TFW42290.1	twitching motility two-component system response regulator PilG	
<i>pilH</i>	TFW42291.1	twitching motility two-component system response regulator PilH	
<i>pilI</i>	TFW42292.1	twitching motility protein PilI	
<i>pilJ</i>	TFW42293.1	twitching motility protein PilJ	
<i>pilL</i>	TFW42294.1	type IV pili sensor histidine kinase and response regulator	
<i>pilF</i>	TFW39810.1	type IV pilus assembly protein PilF	<i>Chemotaxis</i>
<i>cheR</i>	TFW42220.1	chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	
<i>cheB</i>	TFW42221.1	two-component system. chemotaxis family. protein-glutamate methylesterase/glutaminase [EC:3.1.1.61 3.5.1.44]	
<i>cheW</i>	TFW45243.1	purine-binding chemotaxis protein CheW	
<i>cheB</i>	TFW45248.1	two-component system. chemotaxis family. protein-glutamate methylesterase/glutaminase [EC:3.1.1.61 3.5.1.44]	
<i>cheA</i>	TFW45249.1	two-component system. chemotaxis family. sensor kinase CheA [EC:2.7.13.3]	
<i>cheZ</i>	TFW45250.1	chemotaxis protein CheZ	
<i>cheY</i>	TFW45251.1	two-component system. chemotaxis family. chemotaxis protein CheY	
<i>cheV</i>	TFW43560.1	cheV; two-component system. chemotaxis family. chemotaxis protein CheV	
<i>aer</i>	TFW45380.1	aer; aerotaxis receptor	
<i>mcp</i>	TFW42247.1	methyl-accepting chemotaxis protein	

<i>lpxL</i>	TFW45209.1	Kdo2-lipid IVA lauroyltransferase/acyltransferase [EC:2.3.1.241 2.3.1.-]	Lypopolysaccharides
<i>lpxO</i>	TFW44377.1	lpxO; beta-hydroxylase [EC:1.14.11.-]	
<i>lpxC</i>	TFW43550.1	lpxC; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [EC:3.5.1.108]	
<i>lpxB</i>	TFW42797.1	lpxB; lipid-A-disaccharide synthase [EC:2.4.1.182]	
<i>lpxA</i>	TFW42798.1	lpxA; UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]	
<i>lpxD</i>	TFW42800.1	lpxD; UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [EC:2.3.1.191]	
<i>lpxO</i>	TFW41929.1	lpxO; beta-hydroxylase [EC:1.14.11.-]	
<i>lpxH</i>	TFW41277.1	lpxH; UDP-2.3-diacylglucosamine hydrolase [EC:3.6.1.54]	
<i>oxyR</i>	TFW44636.1	LysR family transcriptional regulator. hydrogen peroxide-inducible genes activator	Oxidative/Stress response
<i>sod2</i>	TFW43483.1	superoxide dismutase. Fe-Mn family [EC:1.15.1.1]	
<i>grxC</i>	TFW43955.1	glutaredoxin 3	
<i>ggt</i>	TFW43320.1	gamma-glutamyltranspeptidase / glutathione hydrolase [EC:2.3.2.2 3.4.19.13]	
<i>soxR</i>	TFW41413.1	MerR family transcriptional regulator. redox-sensitive transcriptional activator SoxR	
<i>gst</i>	TFW45096.1	glutathione S-transferase [EC:2.5.1.18]	
<i>katE</i>	TFW44834.1	catalase [EC:1.11.1.6]	
<i>gpx</i>	TFW45311.1	glutathione peroxidase [EC:1.11.1.9]	
<i>gsr</i>	TFW42192.1	glutathione reductase (NADPH) [EC:1.8.1.7]	
<i>gshB</i>	TFW42289.1	glutathione synthase [EC:6.3.2.3]	

Table S4

Genes related to carbohydrate-active enzymes (CAZymes) in the *P. fluorescens* BRZ63 strain

Family of enzymes	CBM	GH	GT	PL	AA	CE
Number of genes	14	51	61	2	6	8

CBM. Carbohydrate-Binding Module; GH. Glycoside Hydrolase; GT. Glycosyl Transferase; PL. Polysaccharide lyases; AA. Auxiliary Activity; CE. Carbohydrate Esterase;

Table S5

CAZymes involved in plant and fungal cell wall degradation identified in the *P. fluorescens* BRZ63 genome

Substrate	Family enzymes	Annotation	Copy number
Beta-1-3-glucan	GH17	glucan endo-1.3- β -glucosidase (EC 3.2.1.39)	2
Cellulose	GH3	β -glucosidase (EC 3.2.1.21)	4
Cellulose	GH6	endoglucanase (EC 3.2.1.4)	4
Hemicellulose	GH36	α -galactosidase (EC 3.2.1.22)	1
Pectin	GH28	polygalacturonase (EC 3.2.1.15)	2
Polysaccharides	GH13	α -amylase (EC 3.2.1.1)	11
Polysaccharides	GH15	glucoamylase (EC 3.2.1.3)	1

Figure S1

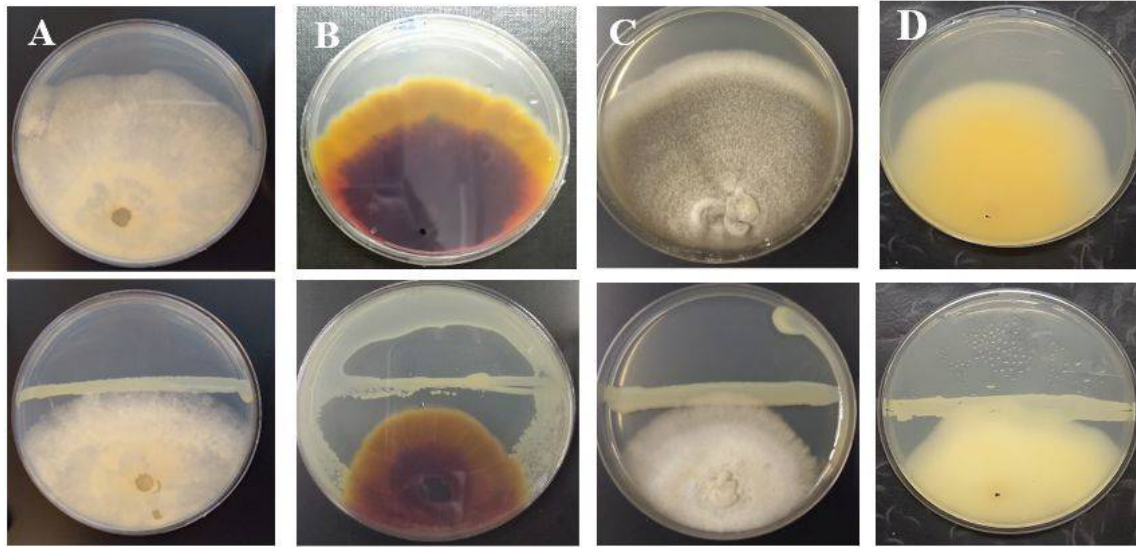


Figure S1. *In vitro* inhibition of mycelial growth of *Rhizoctonia solani* W70 (A), *Colletotrichum dematium* K (B), *Sclerotinia sclerotiorum* K2291 (C), and *Fusarium avenaceum* (D) by *P. fluorescens* BRZ63. Upper panel – control - pathogenic fungi grown on PDA medium; bottom panel – dual culture assay on PDA medium - growth of fungi in the presence of BRZ63.

Figure S2

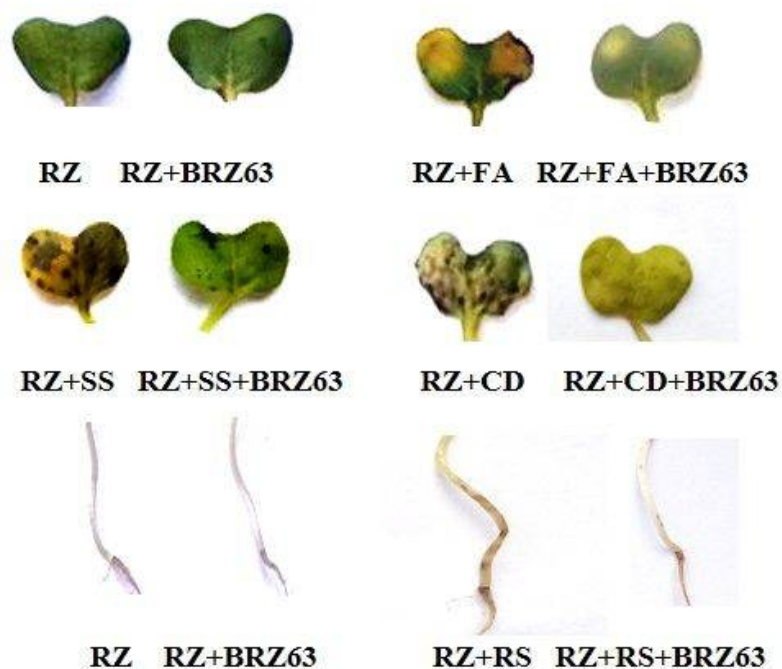


Figure S2. Effects of the BRZ63 strain on disease protection of oilseed rape. The leaves and roots of seedlings emerged from the uninoculated seeds (RZ) and seeds inoculated with the BRZ63 strain (RZ+BRZ63). The leaves of seedlings emerged from the uninoculated seeds dipped in the inoculum of *F. avenaceum* (RZ+FA) and seeds preinoculated with strain BRZ63 and dipped in the inoculum of the pathogen (RZ+BRZ63+FA). The leaves of seedlings emerged from the uninoculated seeds dipped in the inoculum of *S. sclerotiorum* K2291 (RZ+SS) and seeds preinoculated with strain BRZ63 and dipped in the inoculum of the pathogen (RZ+BRZ63+SS). The leaves of seedlings emerged from the uninoculated seeds dipped in the inoculum of *C. dematium* K (RZ+CD) and seeds preinoculated with strain BRZ63 and dipped in the inoculum of the pathogen (RZ+BRZ63+CD). The roots of seedlings emerged from the uninoculated seeds dipped in the inoculum of *R. solani* W70 (RZ+RS) and seeds preinoculated with strain BRZ63 and dipped in the inoculum of the pathogen (RZ+BRZ63+RS).