

Title page- supplementary information

Rare earth oxide nanoparticles promote soil microbial antibiotic resistance by selectively enriching antibiotic resistance genes

Lin Qi,^{#abc} Yuan Ge,^{#*ab} Tian Xia,^d Ji-Zheng He,^{ab} Congcong Shen,^{ab} Jianlei Wang^{ab} and Yong-Jun Liu^e

^aState Key Laboratory of Urban and Regional Ecology, Research Center for Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China

^bUniversity of Chinese Academy of Sciences, Beijing 100049, China

^cAgricultural College, Henan University of Science and Technology, Luoyang, Henan 471023, China

^dDivision of NanoMedicine, Department of Medicine, University of California, Los Angeles, California 90095, United States

^eDepartment of Honeybee Protection and Biosafety, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences, Beijing 100093, China

[#] Lin Qi and Yuan Ge contributed equally to this work.

Corresponding Author

* Phone: (+86) 10 6291 3536. E-mail: yuange@rcees.ac.cn.

The supplementary information has 43 pages including 6 tables and 3 figures.

Table S1. The basic properties of soils used in this study.

Property	Soil type		
	Black soil	Fluvo-aquic soil	Red soil
pH	6.25 ± 0.05	7.89 ± 0.02	5.80 ± 0.03
Total carbon (g kg ⁻¹)	10.49 ± 0.03	7.11 ± 0.01	7.17 ± 0.01
Total nitrogen (g kg ⁻¹)	1.02 ± 0.01	1.06 ± 0.01	0.94 ± 0.01
NH ₄ ⁺ -N (mg kg ⁻¹)	11.31 ± 0.25	2.31 ± 0.17	9.63 ± 0.02
NO ₃ ⁻ -N (mg kg ⁻¹)	25.32 ± 1.02	9.25 ± 0.18	10.87 ± 0.38

Values represent mean ± s.d., n=4

Table S2. Physiochemical properties of the nanoparticles used in this study.

Property	Nanoparticle type		
	Nano-La ₂ O ₃	Nano-Nd ₂ O ₃	Nano-Gd ₂ O ₃
Size (nm)	25 ± 5	35 ± 7	27 ± 2
Size in deionized H ₂ O (nm)	589 ± 16	308 ± 8	532 ± 100
Zeta potential in deionized H ₂ O (mV)	9 ± 1	26 ± 1	11 ± 1

Values represent mean ± s.d.

Table S3. 202 sets of primers used in this study.

	Assay Name	Forward primer	Reverse primer	Antibiotic resistance	Resistance mechanism
1	16S rRNA	GGGTTGCGCTCGTTG C	ATGGYTGTCGTCAGC TCGTG		
2	aac	CCCTGCGTTGTGGCT ATGT	TTGGCCACGCCAATC C	Aminoglycoside	Antibiotic deactivation
3	aac(6')-Ib-01	GTTTGAGAGGCAAGG TACCGTAA	GAATGCCTGGCGTGT TTGA	Aminoglycoside	Antibiotic deactivation
4	aac(6')-Ib-02	CGTCGCCGAGCAACT TG	CGGTACCTTGCCTCT CAAACC	Aminoglycoside	Antibiotic deactivation
5	aac(6')-Ib-03	AGAAGCACGCCCCGA CACTT	GCTCTCCATTTCAGCA TTGCA	Aminoglycoside	Antibiotic deactivation
6	aac(6')-II	CGACCCGACTCCGAA	GCACGAATCCTGCCT	Aminoglycoside	Antibiotic

		CAA	TCTCA		deactivation
7	aacC	CGTCACTTATTCGAT	GTCGGGCGCGGCATA	Aminoglycoside	Antibiotic
		GCCCTTAC			deactivation
8	aacC1	GGTCGTGAGTTCGGA	GCAAGTTCCCGAGGT	Aminoglycoside	Antibiotic
		GACGTA	AATCG		deactivation
9	aacC2	ACGGCATTCTCGATT	CCGAGCTTCACGTAA	Aminoglycoside	Antibiotic
		GCTTT	GCATT		deactivation
10	aacC4	CGGCGTGGGACACG	AGGGAACCTTTGCCA	Aminoglycoside	Antibiotic
		AT	TCAACT		deactivation
11	aadA-01	GTTGTGCACGACGAC	GGCTCGAAGATACCT	Aminoglycoside	Antibiotic
		ATCATT	GCAAGAA		deactivation
12	aadA-02	CGAGATTCTCCGCGC	GCTGCCATTCTCCAA	Aminoglycoside	Antibiotic
		TGTA	ATTGC		deactivation
13	aadA1	AGCTAAGCGCGAACT	TGGCTCGAAGATACC	Aminoglycoside	Antibiotic

		GCAAT	TGCAA		deactivation
14	aadA2-01	ACGGCTCCGCAGTGG	GGCCACAGTAACCAA	Aminoglycoside	Antibiotic
		AT	CAAATCA		deactivation
15	aadA2-02	CTTGTCGTGCATGAC	TCGAAGATACCCGCA	Aminoglycoside	Antibiotic
		GACATC	AGAATG		deactivation
16	aadA2-03	CAATGACATTCTTGC	GACCTACCAAGGCAA	Aminoglycoside	Antibiotic
		GGGTATC	CGCTATG		deactivation
17	aadA5-01	ATCACGATCTTGCGA	CTGCGGATGGGCCTA	Aminoglycoside	Antibiotic
		TTTTGCT	GAAG		deactivation
18	aadA5-02	GTTCTTGCTCTTGCTC	GATGCTCGGCAGGCA	Aminoglycoside	Antibiotic
		GCATT	AAC		deactivation
19	aadA9-01	CGCGGCAAGCCTATC	CAAATCAGCGACCGC	Aminoglycoside	Antibiotic
		TTG	AGACT		deactivation
20	aadA9-02	GGATGCACGCTTGGA	CCTCTAGCGGCCGGA	Aminoglycoside	Antibiotic

		TGAA	GTATT		deactivation
21	aadD	CCGACAACATTTCTA	ACCGAAGCGCTCGTC	Aminoglycoside	Antibiotic
		CCATCCTT	GTATA		deactivation
22	aph(2')-Id	TGAGCAGTATCATAA	GACAGAACAATCAAT	Aminoglycoside	Antibiotic
		GTTGAGTGAAAAG	CTCTATGGAATG		deactivation
23	aphA1	TGAACAAGTCTGGAA	CCTATTAATTTCCCCT	Aminoglycoside	Antibiotic
		AGAAATGCA	CGTCAAAAA		deactivation
24	aphA3-01	AAAAGCCCGAAGAG	CATCTTTCACAAAGA	Aminoglycoside	Antibiotic
		GAACTTG	TGTTGCTGTCT		deactivation
25	aphA3-02	CGGAATTGAAAAAA	ATACCGGCTGTCCGT	Aminoglycoside	Antibiotic
		CTGATCGAA	CATTT		deactivation
26	strA	CCGGTGGCATTGAG	GTGGCTCAACCTGCG	Aminoglycoside	Antibiotic
		AAAAA	AAAAG		deactivation
27	strB	GCTCGGTCGTGAGAA	CAATTCGGTCGCCT	Aminoglycoside	Antibiotic

		CAATCT	GGTAGT		deactivation
28	catA1	GGGTGAGTTTCACCA	CACCTTGTCGCCTTG	FCA	Antibiotic
		GTTTTGATT	CGTATA		deactivation
29	catB3	GCACTCGATGCCTTC	AGAGCCGATCCAAAC	FCA	Antibiotic
		CAAAA	GTCAT		deactivation
30	catB8	CACTCGACGCCTTCC	CCGAGCCTATCCAGA	FCA	Antibiotic
		AAAG	CATCATT		deactivation
31	cfr	GCAAAATTCAGAGCA	AAAATGACTCCCAAC	FCA	Antibiotic
		AGTTACGAA	CTGCTTTAT		deactivation
32	cmlA1-01	TAGGAAGCATCGGA	CAGACCGAGCACGA	FCA	Efflux pump
		ACGTTGAT	CTGTTG		
33	cmlA1-02	AGGAAGCATCGGAA	ACAGACCGAGCACG	FCA	Efflux pump
		CGTTGA	ACTGTTG		
34	cmx(A)	GCGATCGCCATCCTC	TCGACACGGAGCCTT	FCA	Efflux pump

		TGT	GGT		
35	floR	ATTGTCTTCACGGTG	CCGCGATGTCGTCGA	FCA	Efflux pump
		TCCGTTA	ACT		
36	qnrA	AGGATTTCTCACGCC	CCGCTTTCAATGAAA	FCA	Other
		AGGATT	CTGCAA		
37	ereA	CCTGTGGTACGGAGA	ACCGCATTCGCTTTG	MLSB	Antibiotic
		ATTCATGT	CTT		deactivation
38	ereB	GCTTTATTTACAGGAG	TTTAAATGCCACAG	MLSB	Antibiotic
		GCGGAAT	CACAGAATC		deactivation
39	lnuA	TGACGCTCAACACAC	TTCATGCTTAAGTTC	MLSB	Antibiotic
		TCAAAAA	CATACGTGAA		deactivation
40	mphA-01	CTGACGCGCTCCGTG	GGTGGTGCATGGCGA	MLSB	Antibiotic
		TT	TCT		deactivation
41	mphA-02	TGATGACCCTGCCAT	TTCGCGAGCCCCTCT	MLSB	Antibiotic

		CGA	TC		deactivation
42	mphB	CGCAGCGCTTGATCT	TTACTGCATCCATAC	MLSB	Antibiotic
		TGTAG	GCTGCTT		deactivation
43	vatC	CGGAAATTGGGAAC	GCAATAATAGCCCCG	MLSB	Antibiotic
		GATGTT	TTTCCTA		deactivation
44	vatE-01	GGTGCCATTATCGGA	TTGGATTGCCACCGA	MLSB	Antibiotic
		GCAAAT	CAAT		deactivation
45	vatE-02	GACCGTCCTACCAGG	TTGGATTGCCACCGA	MLSB	Antibiotic
		CGTAA	CAATT		deactivation
46	vgb	AGGGAGGGTATCCAT	ACCAAATGCGCCCGT	MLSB	Antibiotic
		GCAGAT	TT		deactivation
47	matA/mel	TAGTAGGCAAGCTCG	CCTGTGCTATTTTAA	MLSB	Efflux pump
		GTGTTGA	GCCTTGTTTCT		
48	mefA	CCGTAGCATTGGAAC	AAACGGAGTATAAG	MLSB	Efflux pump

		AGCTTTT	AGTGCTGCAA		
49	msrA	CTGCTAACACAAGTA	TCAAGTAAAGTTGTC	MLSB	Efflux pump
		CGATTCCAAAT	TTACCTACACCATT		
50	oleC	CCCGGAGTCGATGTT	GCCGAAGACGTACAC	MLSB	Efflux pump
		CGA	GAACAG		
51	vgaA	CGAGTATTGTGGAAA	CCCGTACCGTTAGAG	MLSB	Efflux pump
		GCAGCTAGTT	CCGATA		
52	vgaB	TAAAAGAGAATAAG	TGTTTAGTAGCATGT	MLSB	Efflux pump
		GCGCAAGGA	TGCATTTTCC		
53	erm(34)	GCGCGTTGACGACGA	TGGTCATACTCGACG	MLSB	Cellular
		TTT	GCTAGAAC		protection
54	erm(36)	GGCGGACCGACTTGC	TCTGCGTTGACGACG	MLSB	Cellular
		AT	GTTAC		protection
55	ermA	TTGAGAAGGGATTTG	ATATCCATCTCCACC	MLSB	Cellular

		CGAAAAG	ATTAATAGTAAACC		protection
56	ermA/ermTR	ACATTTTACCAAGGA	GTGGCATGACATAAA	MLSB	Cellular
		ACTTGTGGAA	CCTTCATCA		protection
57	ermB	TAAAGGGCATTTAAC	TTTATACCTCTGTTTG	MLSB	Cellular
		GACGAAACT	TTAGGGAATTGAA		protection
58	ermC	TTTGAAATCGGCTCA	ATGGTCTATTTCAAT	MLSB	Cellular
		GGAAAA	GGCAGTTACG		protection
59	ermF	CAGCTTTGGTTGAAC	AAATTCCTAAAATCA	MLSB	Cellular
		ATTTACGAA	CAACCGACAA		protection
60	ermK	GTTTGATATTGGCAT	ACCATTGCCGAGTCC	MLSB	Cellular
		TGTCAGAGAAA	ACTTT		protection
61	ermX	GCTCAGTGGTCCCCA	ATCCCCCGTCAACG	MLSB	Cellular
		TGGT	TTT		protection
62	ermY	TTGTCTTTGAAAGTG	TAACGCTAGAGAACG	MLSB	Cellular

		AAGCAACAGT	ATTTGTATTGAG		protection
63	pikR2	TCGTGGGCCAGGTGA	TTCCCCTTGCCGGTG	MLSB	Cellular
		AGA	AA		protection
64	acrA-01	CAACGATCGGACGG	TGGCGATGCCACCGT	Multidrug	Efflux pump
		GTTC	ACT		
65	acrA-02	GGTCTATCACCTAC	GCGCGCACGAACATA	Multidrug	Efflux pump
		GCGCTATC	CC		
66	acrA-03	CAGACCCGCATCGCA	CGACAATTCGCGCT	Multidrug	Efflux pump
		TATT	CATG		
67	acrA-04	TACTTTGCGCGCCAT	CGTGCGCGAACGAAC	Multidrug	Efflux pump
		CTTC	AT		
68	acrA-05	CGTGCGCGAACGAAC	ACTTTGCGCGCCATC	Multidrug	Efflux pump
		A	TTC		
69	acrB	AGTCGGTGTTGCGCG	CAAGGAAACGAACG	Multidrug	Efflux pump

		TTAAC	CAATACC		
70	acrF	GCGGCCAGGCACAA	TACGCTCTTCCCACG	Multidrug	Efflux pump
		AA	GTTTC		
71	acrR	GCGCTGGAGACACG	GCCTTGCTGCGAGAA	Multidrug	Efflux pump
		ACAAC	CAAA		
72	adeA	CAGTTCGAGCGCCTA	CGCCCTGACCGACCA	Multidrug	Efflux pump
		TTTCTG	AT		
73	ceoA	ATCAACACGGACCAG	GGAAAGTCCGCTCAC	Multidrug	Efflux pump
		GACAAG	GATGA		
74	emrD	CTCAGCAGTATGGTG	ACCAGGCGCCGAAG	Multidrug	Efflux pump
		GTAAGCATT	AAC		
75	marR	GCGGCGTACTGGTGA	TGCCCTGGTCGTTGA	Multidrug	Efflux pump
		AGCTA	TGA		
76	mdet11	ATACAGCAGTGGATA	TGCATAAGGTGAATG	Multidrug	Efflux pump

		TTGGTTTAATTGT	TTCCATGA		
77	mdtE/yhiU	CGTCGGCGCACTCGT	TCCAGACGTTGTACG	Multidrug	Efflux pump
		T	GTAACCA		
78	mepA	ATCGGTCGCTCTTCG	ATAAATAGGATCGAG	Multidrug	Efflux pump
		TTCAC	CTGCTGGAT		
79	mexA	AGGACAACGCTATGC	CCGGAAAGGGCCGA	Multidrug	Efflux pump
		AACGAA	AAT		
80	mexE	GGTCAGCACCGACAA	AGCTCGACGTAATTG	Multidrug	Efflux pump
		GGTCTAC	AGGAACAC		
81	mexF	CCGCGAGAAGGCCA	TTGAGTTCGGCGGTG	Multidrug	Efflux pump
		AGA	ATGA		
82	mtrD	TGCGCGTAGTCGTTC	CGTTCCAATTCCTG	Multidrug	Efflux pump
		ATCTC	ATGATTG		
83	oprD	ATGAAGTGGAGCGCC	GGCCACGGCGAACTG	Multidrug	Efflux pump

		ATTG	A		
84	oprJ	ACGAGAGTGGCGTCG	AAGGCGATCTCGTTG	Multidrug	Efflux pump
		ACAA	AGGAA		
85	qacEΔ1-01	TCGCAACATCCGCAT	ATGGATTTCAGAACC	Multidrug	Efflux pump
		TAAAA	AGAGAAAGAAA		
86	qacEΔ1-02	CCCCTTCCGCCGTTG	CGACCAGACTGCATA	Multidrug	Efflux pump
		T	AGCAACA		
87	qacH-01	GTGGCAGCTATCGCT	CCAACGAACGCCCAC	Multidrug	Efflux pump
		TGGAT	AA		
88	qacH-02	CATCGTGCTTGTGGC	TGAACGCCCAGAAGT	Multidrug	Efflux pump
		AGCTA	CTAGTTTT		
89	rarD	GCGGGTGTGGTCACT	AGCGTTGGGCCGATA	Multidrug	Efflux pump
		ACGAT	TACTG		
90	sdeB	CACTACCGCTTCCGC	TGAAAAAACGGGAA	Multidrug	Efflux pump

		ACTTAA	AAGTCCAT		
91	tolC-01	GGCCGAGAACCTGAT	AGACTTACGCAATTC	Multidrug	Efflux pump
		GCA	CGGGTTA		
92	tolC-02	CAGGCAGAGAACCT	CGCAATTCCGGGTTG	Multidrug	Efflux pump
		GATGCA	CT		
93	tolC-03	GCCAGGCAGAGAAC	CGCAATTCCGGGTTG	Multidrug	Efflux pump
		CTGATG	CT		
94	ttgA	ACGCCAATGCCAAAC	GTCACGGCGCAGCTT	Multidrug	Efflux pump
		GATT	GA		
95	ttgB	TCGCCCTGGATGTAC	ACCATTGCCGACATC	Multidrug	Efflux pump
		ACCTT	AACAAC		
96	yceE/mdtG	TGGCACAAAATATCT	TTGTGTGGCGATAAG	Multidrug	Efflux pump
		GGCAGTT	AGCATTAG		
97	yceL/mdtH-01	TCGGGATGGTGGGCA	CGATAACCGAGCCGA	Multidrug	Efflux pump

		AT	TGTAGA		
98	yceL/mdtH-02	CGCGTGAAACCTTAA	AGACGGCTAAACCCC	Multidrug	Efflux pump
		GTGCTT	ATATAGCT		
99	yidY/mdtL	GCAGTTGCATATCGC	CTTCCCGGCAAACAG	Multidrug	Efflux pump
		CTTCTC	CAT		
100	bacA	CGGCTTCGTGACCTC	ACAATGCGATACCAG	Other	Antibiotic
		GTT	GCAAAT		deactivation
101	sat4	GAATGGGCAAAGCA	CCGATTTTGAAACCA	Other	Antibiotic
		TAAAAACTTG	CAATTATGATA		deactivation
102	pncA	GCAATCGAGGCGGTG	TTGCCGCAGCCAATT	Other	Unkown
		TTC	CA		
103	uidA	AACCACGCGTCTGTT	CCCGGTTGCCAGAGG	Other	Unkown
		GACTG	TG		
104	dfrA1	GGAATGGCCCTGATA	AGTCTTGCGTCCAAC	Sulfonamide	Antibiotic

		TTCCA	CAACAG		deactivation
105	dfrA12	CCTCTACCGAACCGT	GCGACAGCGTTGAAA	Sulfonamide	Antibiotic
		CACACA	CAACTAC		deactivation
106	folA	CGAGCAGTTCCTGCC	CCCAGTCATCCGGTT	Sulfonamide	Antibiotic
		AAAG	CATAATC		deactivation
107	sul1	CAGCGCTATGCGCTC	ATCCCGCTGCGCTGA	Sulfonamide	Cellular
		AAG	GT		protection
108	sul2	TCATCTGCCAAACTC	GTCAAAGAACGCCGC	Sulfonamide	Cellular
		GTCGTTA	AATGT		protection
109	tetA	GCTGTTTGTTCCTGCC	GGTTAAGTTCCTTGA	Tetracycline	Efflux pump
		GGAAA	ACGCAAAC		
110	tetB-01	AGTGCGCTTTGGATG	AGCCCCAGTAGCTCC	Tetracycline	Efflux pump
		CTGTA	TGTGA		
111	tetB-02	GCCCAGTGCTGTTGT	TGAAAGCAAACGGC	Tetracycline	Efflux pump

		TGTCAT	CTAAATACA		
112	tetC-01	CATATCGCAATACAT	AAAGCCGCGGTAAAT	Tetracycline	Efflux pump
		GCGAAAAA	AGCAA		
113	tetC-02	ACTGGTAAGGTAAAC	ATGCATAAACCAGCC	Tetracycline	Efflux pump
		GCCATTGTC	ATTGAGTAAG		
114	tetD-01	TGCCGCGTTTGATTA	CACCAGTGATCCCGG	Tetracycline	Efflux pump
		CACA	AGATAA		
115	tetD-02	TGTCATCGCGCTGGT	CATCCGCTTCCGGGA	Tetracycline	Efflux pump
		GATT	GAT		
116	tetE	TTGGCGCTGTATGCA	CGACGACCTATGCGA	Tetracycline	Efflux pump
		ATGAT	TCTGA		
117	tetG-01	TCAACCATTGCCGAT	TGGCCCGGCAATCAT	Tetracycline	Efflux pump
		TCGA	G		
118	tetG-02	CATCAGCGCCGGTCT	CCCCATGTAGCCGAA	Tetracycline	Efflux pump

		TATG	CCA		
119	tetH	TTTGGGTCATCTTAC	TTGCGCATTATCATC	Tetracycline	Efflux pump
		CAGCATTA	GACAGA		
120	tetL	AGCCCGATTATTCA	CAAATGCTTTCCCCC	Tetracycline	Efflux pump
		AGGAATTG	TGTTCT		
121	tetR-01	CGCGATAGACGCCTT	TCCTGACAACGAGCC	Tetracycline	Efflux pump
		CGA	TCCTT		
122	tetR-02	CGCGATGGAGCAAA	AGTGAAAAACCTTGT	Tetracycline	Efflux pump
		AGTACAT	TGGCATAAAA		
123	tetV	GCGGGAACGACGAT	CCGCTATCTCACGAC	Tetracycline	Efflux pump
		GTATATC	CATGAT		
124	tet(32)	CCATTACTTCGGACA	CAATCTCTGTGAGGG	Tetracycline	Cellular
		ACGGTAGA	CATTTAACA		protection
125	tet(36)-01	AGAATACTCAGCAGA	TGGTAGGTCGATAAC	Tetracycline	Cellular

		GGTCAGTTCCT	CCGAAAAT		protection
126	tet(36)-02	TGCAGGAAAGACCTC	CTTTGTCCACACTTC	Tetracycline	Cellular
		CATTACAG	CACGTACTATG		protection
127	tetM-01	CATCATAGACACGCC	CGCCATCTTTTGCAG	Tetracycline	Cellular
		AGGACATAT	AAATCA		protection
128	tetM-02	TAATATTGGAGTTTT	CCTCTCTGACGTTCT	Tetracycline	Cellular
		AGCTCATGTTGATG	AAAAGCGTATTAT		protection
129	tetO	ATGTGGATACTACAA	TGCCTCCACATGATA	Tetracycline	Cellular
		CGCATGAGATT	TTTTTCCT		protection
130	tetPB-01	ACACCTGGACACGCT	ACCGTCTAGAACGCG	Tetracycline	Cellular
		GATTTT	GAATG		protection
131	tetPB-02	TGATACACCTGGACA	CGTCCAAAACGCGGA	Tetracycline	Cellular
		CGCTGAT	ATG		protection
132	tetPB-03	TGGGCGACAGTAGGC	TGACCCTACTGAAAC	Tetracycline	Cellular

		TTAGAA	ATTAGAAATATACCT		protection
133	tetQ	CGCCTCAGAAGTAAG	TCGTTCATGCGGATA	Tetracycline	Cellular
		TTCATACACTAAG	TTATCAGAAT		protection
134	tetS	TTAAGGACAAACTTT	TGTCTCCCATTGTTCT	Tetracycline	Cellular
		CTGACGACATC	GGTTCA		protection
135	tetT	CCATATAGAGGTTCC	TGACCCTATTGGTAG	Tetracycline	Cellular
		ACCAAATCC	TGGTTCTATTG		protection
136	tetW	ATGAACATTCCCACC	ATATCGGCGGAGAGC	Tetracycline	Cellular
		GTTATCTTT	TTATCC		protection
137	tet(35)	ACCCCATGACGTACC	CAACCCCACTGGCT	Tetracycline	Other
		TGTAGAGA	ACCAGTT		
138	tetX	AAATTTGTTACCGAC	CATAGCTGAAAAAAT	Tetracycline	Other
		ACGGAAGTT	CCAGGACAGTT		
139	vanB-01	TTGTCGGCGAAGTGG	AGCCTTTTTCCGGCT	Vancomycin	Cellular

		ATCA	CGTT		protection
140	vanB-02	CCGGTCGAGGAACG	TCCTCCTGCAAAAAA	Vancomycin	Cellular
		AAATC	AGATCAAC		protection
141	vanC-01	ACAGGGATTGGCTAT	TGACTGGCGATGATT	Vancomycin	Cellular
		GAACCAT	TGACTATG		protection
142	vanC-02	CCTGCCACAATCGAT	CGGCTTCATTCCGGCT	Vancomycin	Cellular
		CGTT	TGATA		protection
143	vanC2/vanC3	TTTGACTGTCGGTGC	TCAATCGTTTCAGGC	Vancomycin	Cellular
		TTGTGA	AATGG		protection
144	vanHB	GAGGTTTCCGAGGCG	CTCTCGGCGGCAGTC	Vancomycin	Cellular
		ACAA	GTAT		protection
145	vanRA-01	CCCTTACTCCCACCG	TTCGTCGCCCCATAT	Vancomycin	Cellular
		AGTTTT	CTCAT		protection
146	vanRA-02	CCACTCCGGCCTTGT	GCTAACCACATTCCC	Vancomycin	Cellular

		CATT	CTTGTTTT		protection
147	vanRB	GCCCTGTCGGATGAC	TTACATAGTCGTCTG	Vancomycin	Cellular
		GAA	CCTCTGCAT		protection
148	vanSB	GCGCGGCAAATGAC	TTTGCCATTTTATTCG	Vancomycin	Cellular
		AAC	CACTGT		protection
149	vanSC	ATCAACTGCGGGAGA	TCCGCTGTTCCGCTT	Vancomycin	Cellular
		AAAGTCT	CTT		protection
150	vanTC-01	CACACGCATTTTTTC	CAGCCAACAGATCAT	Vancomycin	Cellular
		CCATCTAG	CAAAACAA		protection
151	vanTC-02	ACAGTTGCCGCTGGT	CGTGGCTGGTCGATC	Vancomycin	Cellular
		GAAG	AAAA		protection
152	vanTE	GTGGTGCCAAGGAA	CGTAGCCACCGCAAA	Vancomycin	Cellular
		GTTGCT	AAAAT		protection
153	vanTG	CGTGTAGCCGTTCCG	CGGCATTACAGGTAT	Vancomycin	Cellular

		TTCTT	ATCTGGAAA		protection
154	vanWB	CGGACAAAGATACCC	AAATAGTAAATTGCT	Vancomycin	Cellular
		CCTATAAAG	CATCTGGCACAT		protection
155	vanWG	ACATTTTCATTTTGG	CCGCCATAAGAGCCT	Vancomycin	Cellular
		CAGCTTGTAC	ACAATCT		protection
156	vanXB	AGGCACAAAATCGA	GGGTATGGCTCATCA	Vancomycin	Cellular
		AGATGCTT	ATCAACTT		protection
157	vanYB	GGCTAAAGCGGAAG	GATATCCACAGCAAG	Vancomycin	Cellular
		CAGAAA	ACCAAGCT		protection
158	vanYD-01	AAGGCGATACCCTGA	ATTGCCGGACGGAAG	Vancomycin	Cellular
		CTGTCA	CA		protection
159	vanYD-02	CAAACGGAAGAGAG	CGGACGGTAATAGG	Vancomycin	Cellular
		GTCACCTACA	GACTGTTC		protection
160	ampC/blaDHA	TGGCCGCAGCAGAA	CCGTTTTATGCACCC	β -lactam	Antibiotic

		AGA	AGGAA		deactivation
161	ampC-01	TGGCGTATCGGGTCA	CTCCACGGGCCAGTT	β -lactam	Antibiotic
		ATGT	GAG		deactivation
162	ampC-02	GCAGCACGCCCCGTA	TGTACCCATGATGCG	β -lactam	Antibiotic
		A	CGTACT		deactivation
163	ampC-03	AACAAAAGATCCCCG	ACGCCCCGTAAATGTT	β -lactam	Antibiotic
		GTATGG	TTGCT		deactivation
164	ampC-04	TCCGGTGACGCGACA	CAGCACGCCGGTGAA	β -lactam	Antibiotic
		GA	AGT		deactivation
165	ampC-05	CTGTTCGAGCTGGGT	CAGTATCTGGTCACC	β -lactam	Antibiotic
		TCTATAAGTAAA	GGATCGT		deactivation
166	ampC-06	CCGCTCAAGCTGGAC	CCATATCCTGCACGT	β -lactam	Antibiotic
		CATAC	TGGTTT		deactivation
167	bla1	GCAAGTTGAAGCGA	TACCAGTATCAATCG	β -lactam	Antibiotic

		AAGAAAAGA	CATATACACCTAA		deactivation
168	blaCMY2-01	AAAGCCTCATGGGTG	ATAGCTTTTGTTC	β -lactam	Antibiotic
		CATAAA	CAGCATCA		deactivation
169	blaCMY2-02	GCGAGCAGCCTGAA	CGGATGGGCTTGTCC	β -lactam	Antibiotic
		GCA	TCTT		deactivation
170	blaCTX-M-01	GGAGGCGTGACGGCT	TTCAGTGCGATCCAG	β -lactam	Antibiotic
		TTT	ACGAA		deactivation
171	blaCTX-M-02	GCCGCGGTGCTGAAG	ATCGGATTATAGTTA	β -lactam	Antibiotic
		A	ACCAGGTCAGATTT		deactivation
172	blaGES	GCAATGTGCTCAACG	GTGCCTGAGTCAATT	β -lactam	Antibiotic
		TTCAAG	CTTTCAAAG		deactivation
173	bla-L1	CACCGGGTTACCAGC	GCGAAGCTGCGCTTG	β -lactam	Antibiotic
		TGAAG	TAGTC		deactivation
174	blaMOX/blaCMY	CTATGTCAATGTGCC	GGCTTGTCTCTTTC	β -lactam	Antibiotic

		GAAGCA	GAATAGC		deactivation
175	blaOXA1/blaOXA30	CGGATGGTTTGAAGG	TCTTGGCTTTTATGCT	β -lactam	Antibiotic
		GTTTATTAT	TGATGTAA		deactivation
176	blaOXA10-01	CGCAATTATCGGCCT	TTGGCTTCCGTCCC	β -lactam	Antibiotic
		AGAAACT	ATTT		deactivation
177	blaOXA10-02	TCAACAAATCGCCAG	TCCCACACCAGAAAA	β -lactam	Antibiotic
		AGA	ACCA		deactivation
178	blaOXY	CGTTCAGGCGGCAGG	GCCGCGATATAAGAT	β -lactam	Antibiotic
		TT	TTGAGAATT		deactivation
179	blaPAO	CGCCGTACAACCGGT	GAAGTAATGCGGTTC	β -lactam	Antibiotic
		GAT	TCCTTTCA		deactivation
180	blaPSE	TTGTGACCTATTCCC	TGCGAAGCACGCATC	β -lactam	Antibiotic
		CTGTAATAGAA	ATC		deactivation
181	blaROB	GCAAAGGCATGACG	CGCGCTGTTGTCGCT	β -lactam	Antibiotic

		ATTGC	AAA		deactivation
182	blaSHV	TCCCATGATGAGCAC	TTCGTCACCGGCATC	β-lactam	Antibiotic
		CTTTAAA	CA		deactivation
183	blaTEM	AGCATCTTACGGATG	TCCTCCGATCGTTGT	β-lactam	Antibiotic
		GCATGA	CAGAAGT		deactivation
184	blaTLA	ACACTTTGCCATTGC	TGCAAATTTTCGGCAA	β-lactam	Antibiotic
		TGTTTATGT	TAATCTTT		deactivation
185	blaVEB	CCCGATGCAAAGCGT	GAAAGATTCCCTTTA	β-lactam	Antibiotic
		TATG	TCTATCTCAGACAA		deactivation
186	blaZ	GGAGATAAAGTAAC	TGCTTAATTTTCCATT	β-lactam	Antibiotic
		AAATCCAGTTAGATA	TGCGATAAG		deactivation
		TGA			
187	cfxA	TCATTCTCGTTCAA	TGCAGCACCAAGAG	β-lactam	Antibiotic
		GTTTTCAGA	GAGATGT		deactivation

188	cphA	GCGAGCTGCACAAGC	CGGCCCAGTCGCTCT	β -lactam	Antibiotic
		TGAT	TC		deactivation
189	fox5	GGTTTGCCGCTGCAG	GCGGCCAGGTGACCA	β -lactam	Antibiotic
		TTC	A		deactivation
190	Pbp5	GGCGAACTTCTAATT	CGCCGATGACATTCT	β -lactam	Cellular
		AATCCTATCCA	TCTTATCTT		protection
191	penA	AGACGGTAACGTATA	GCGTGTAGCCGGCAA	β -lactam	Cellular
		ACTTTTGAAGA	TG		protection
192	int1	GGCTTCGTGATGCCT	CATTCCTGGCCGTGG	MGE/Integrase	Integrase
		GCTT	TTCT		
193	intI1	CGAACGAGTGGCGG	TACCCGAGAGCTTGG	MGE/Integrase	Integrase
		AGGGTG	CACCCA		
194	tnpA, IS21 group	CATCATCGGACGGAC	GTCGGAGATGTGGGT	MGE/Transposase	Transposase
		AGAATT	GTAGAAAGT		

195	tnpA, IS4	GGGCGGGTCGATTGA AA	GTGGGCGGGATCTGC TT	MGE/Transposase	Transposase
196	tnpA, IS6 group-01	AATTGATGCGGACGG CTTAA	TCACCAAACGTGTTTA TGGAGTCGTT	MGE/Transposase	Transposase
197	tnpA, IS6 group-02	CCGATCACGGAAAGC TCAAG	GGCTCGCATGACTTC GAATC	MGE/Transposase	Transposase
198	tnpA, IS6 group-03	GCCGCACTGTCGATT TTTATC	GCGGGATCTGCCACT TCTT	MGE/Transposase	Transposase
199	tnpA, IS6 group-04	TGCAGATGGTTTAAAC CTTGGATATTT	TCGGTTCATCAAAC GCTTCAC	MGE/Transposase	Transposase
200	tnpA, IS613 group	AGGTTCGGACTCAAT GCAACA	TTCAGCACATAACCGC CTTGAT	MGE/Transposase	Transposase
201	tnpA, ISEcp1B	GAAACCGATGCTACA ATATCCAATTT	CAGCACCGTTTGCAG TGTAAG	MGE/Transposase	Transposase

202	tp614, IS4 family	GGAAATCAACGGCAT	CATCCATGCGCTTTT	MGE/Transposase	Transposase
		CCAGTT	GTCTCT		

Table S4. Spearman's correlations between soil microbial antibiotic resistances estimated by percentage decrease of substrate induced respiration (SIR) and soil basal respiration (SBR) and the abundance and richness of antibiotic resistance genes (ARGs).

Percentage decrease	ARG	Spearman's correlation	
		<i>R</i> value	<i>P</i> value
SIR	Abundance	-0.503	*(0.047)
	Richness	-0.543	*(0.030)
SBR	Abundance	-0.729	** (0.001)
	Richness	-0.598	*(0.014)

* $P < 0.05$, and ** $P < 0.01$. n=16.

Table S5. List of antibiotic resistance genes (ARGs) which were significantly different between nanoparticle treatments (nanoparticulate La₂O₃, Nd₂O₃, and Gd₂O₃) and control tested by one-way analysis of variance (ANOVA) in combination with *post hoc* least significant difference (LSD) test.

Number	ARG	ARG classification		ANOVA		LSD		
		Antibiotic resistance	Resistant mechanism	<i>F</i> value	<i>P</i> value	La100	Nd100	Gd100
1	tetE	Tetracycline	Efflux pump	5.315	*(0.015)	**(0.006)	NS(0.356)	NS(0.833)
2	tetR-02	Tetracycline	Efflux pump	4.747	*(0.021)	*(0.018)	NS(0.305)	NS(0.416)
3	tetT	Tetracycline	Cellular protection	5.821	*(0.011)	*(0.010)	NS(0.671)	NS(0.567)
4	blaTEM	β-lactam	Antibiotic deactivation	7.076	**(0.005)	*(0.026)	NS(0.127)	NS(0.239)
5	tetB-02	Tetracycline	Efflux pump	7.399	**(0.005)	*(0.012)	*(0.024)	NS(0.362)
6	tetG-01	Tetracycline	Efflux pump	10.806	*** (0.001)	**(0.007)	*** (0.000)	NS(0.656)
7	tetG-02	Tetracycline	Efflux pump	14.581	*** (0.000)	*** (0.000)	*** (0.003)	NS(0.467)
8	vanTC-02	Vancomycin	Cellular protection	3.584	*(0.047)	*(0.048)	*(0.038)	NS(0.929)
9	acrA-04	Multidrug	Efflux pump	59.085	*** (0.000)	NS(0.495)	*** (0.000)	NS(0.422)

10	acrA-05	Multidrug	Efflux pump	4.079	*(0.033)	NS(0.595)	**(0.008)	NS(0.090)
11	yceL/mdtH-01	Multidrug	Efflux pump	3.526	*(0.049)	NS(0.505)	*(0.012)	NS(0.060)
12	tetQ	Tetracycline	Cellular protection	8.974	**(0.002)	NS(0.689)	**(0.003)	NS(0.427)
13	ampC/blaDHA	β -lactam	Antibiotic deactivation	4.680	*(0.022)	NS(0.640)	**(0.005)	NS(0.318)
14	vgb	MLSB	Antibiotic deactivation	5.137	*(0.016)	NS(0.989)	**(0.006)	NS(0.113)
15	ermB	MLSB	Cellular protection	7.764	**(0.004)	NS(1.000)	**(0.002)	NS(1.000)
16	vanRB	Vancomycin	Cellular protection	4.372	*(0.027)	NS(0.432)	*(0.011)	NS(0.818)
17	vanYD-01	Vancomycin	Cellular protection	11.363	*** (0.001)	NS(0.459)	*** (0.001)	NS(0.784)
18	mexF	Multidrug	Efflux pump	17.254	*** (0.000)	NS(0.116)	*** (0.001)	*** (0.000)
19	oprD	Multidrug	Efflux pump	4.066	*(0.033)	NS(0.833)	*(0.040)	*(0.016)
20	oprJ	Multidrug	Efflux pump	7.075	**(0.005)	NS(0.881)	*(0.021)	**(0.004)
21	tetPB-02	Tetracycline	Cellular protection	3.520	*(0.049)	NS(0.294)	*(0.017)	*(0.021)
22	blaCTX-M-01	β -lactam	Antibiotic deactivation	17.317	*** (0.000)	NS(0.997)	**(0.003)	*** (0.000)
23	bla-L1	β -lactam	Antibiotic deactivation	4.893	*(0.019)	NS(0.061)	**(0.007)	*(0.005)

24	blaROB	β -lactam	Antibiotic deactivation	6.751	**(0.006)	NS(0.972)	*(0.046)	**(0.003)
25	pikR2	MLSB	Cellular protection	6.717	**(0.007)	NS(0.644)	**(0.005)	**(0.006)
26	acrR	Multidrug	Efflux pump	4.439	*(0.026)	NS(0.950)	NS(0.533)	**(0.008)
27	emrD	Multidrug	Efflux pump	3.961	*(0.036)	NS(0.969)	NS(0.242)	*(0.011)
28	marR	Multidrug	Efflux pump	18.641	*** (0.000)	NS (1.000)	NS(0.546)	*** (0.000)
29	mepA	Multidrug	Efflux pump	5.465	*(0.013)	NS(0.843)	NS(0.411)	**(0.004)
30	qacH-01	Multidrug	Efflux pump	12.210	*** (0.001)	NS(0.782)	NS(0.223)	*** (0.000)
31	aadA1	Aminoglycoside	Antibiotic deactivation	5.837	*(0.011)	NS(0.774)	NS(0.847)	**(0.004)
32	ampC-04	β -lactam	Antibiotic deactivation	4.040	*(0.034)	NS(0.520)	NS(0.077)	**(0.007)
33	blaOXY	β -lactam	Antibiotic deactivation	4.220	*(0.030)	NS(0.960)	NS(0.061)	*(0.014)
34	penA	β -lactam	Cellular protection	5.447	*(0.013)	NS(0.962)	NS(0.153)	**(0.004)
35	ereB	MLSB	Antibiotic deactivation	5.907	*(0.010)	NS(0.867)	NS(0.943)	** (0.004)
36	mphA-01	MLSB	Antibiotic deactivation	7.276	**(0.005)	NS(0.867)	NS(0.277)	**(0.001)
37	mphB	MLSB	Antibiotic deactivation	3.942	*(0.036)	NS(1.000)	NS(0.343)	*(0.012)

38	erm(34)	MLSB	Cellular protection	4.047	*(0.033)	NS(1.000)	NS(0.114)	*(0.013)
39	erm(36)	MLSB	Cellular protection	10.145	** (0.001)	NS(0.970)	NS(0.169)	*** (0.000)
40	cmlA1-02	FCA	Efflux pump	4.104	*(0.032)	NS(0.909)	NS(0.084)	*(0.016)

La100, Nd100, and Gd100: high dose (100 mg kg⁻¹) of nano-La₂O₃, nano-Nd₂O₃, and nano-Gd₂O₃. MLSB: macrolide-lincosamide-streptogramin B resistance genes; FCA: fluoroquinolone, quinolone, florfenicol, chloramphenicol, and amphenicol resistance genes. **P* < 0.05, ***P* < 0.01, and ****P* < 0.001. n=4.

Table S6. List of antibiotic resistance genes (ARGs) groups categorized by antibiotic resistance tested by one-way analysis of variance (ANOVA) in combination with *post hoc* least significant difference (LSD) test.

Number	Antibiotic resistance	ANOVA		LSD		
		<i>F</i> value	<i>P</i> value	La100	Nd100	Gd100
1	Multidrug	17.077	*** (0.000)	NS (0.298)	*** (0.001)	*** (0.000)
2	Aminoglycoside	0.898	NS (0.471)	NS (0.130)	NS (0.379)	NS (0.502)
3	Tetracycline	13.244	*** (0.000)	*** (0.001)	** (0.002)	NS (0.718)
4	β -lactam	4.730	* (0.021)	* (0.030)	NS (0.291)	NS (0.745)
5	MLSB	5.420	* (0.014)	* (0.049)	* (0.024)	** (0.002)
6	Vancomycin	5.624	* (0.012)	NS (0.072)	* (0.012)	NS (0.550)
7	FCA	1.547	NS (0.253)	NS (0.996)	NS (0.770)	NS (0.092)
8	Sulfonamide	1.114	NS (0.382)	NS (0.825)	NS (0.244)	NS (0.290)
9	Other	2.773	NS (0.087)	NS (0.910)	* (0.032)	NS (0.927)

La100, Nd100, and Gd100: high dose (100 mg kg⁻¹) of nano-La₂O₃, nano-Nd₂O₃, and nano-Gd₂O₃. MLSB: macrolide-lincosamide-streptogramin B resistance genes; FCA: fluoroquinolone, quinolone, florfenicol, chloramphenicol, and amphenicol resistance genes; Other: ARGs with unknown mechanism or conferring resistance to special antibiotics shown in Table S3. **P* < 0.05, ***P* < 0.01, and ****P* < 0.001. n=4.

Figure legends

Fig. S1 Transmission electron microscope images of the nanoparticles used in this study. Nanoparticles were suspended in deionized H₂O.

Fig. S2 Time-course effects of nanoparticle dose on antibiotic resistance reflected by microbial biomass in fluvo-aquic soil (Inceptisol) and red soil (Ultisol). The antibiotic resistance in microbial community was determined by the percentage decrease of substrate induced respiration (SIR) after additional tetracycline exposure. a-e, Nano-La₂O₃ exposure; f-j, Nano-Nd₂O₃ exposure; k-o, Nano-Gd₂O₃ exposure. The time-course was shown as 0 d, 1 d, 7 d, 30 d, and 60 d from left to right. Error bars indicate the standard deviation of four independent replicates.

Fig. S3 Time-course effects of nanoparticle dose on antibiotic resistance reflected by microbial activity in fluvo-aquic soil (Inceptisol) and red soil (Ultisol). The antibiotic resistance in microbial community was determined by the percentage decrease of soil basal respiration (SBR) after additional tetracycline exposure. a-e, Nano-La₂O₃ exposure; f-j, Nano-Nd₂O₃ exposure; k-o, Nano-Gd₂O₃ exposure. The time-course was shown as 0 d, 1 d, 7 d, 30 d, and 60 d from left to right. Error bars indicate the standard deviation of four independent replicates.

Fig. S1

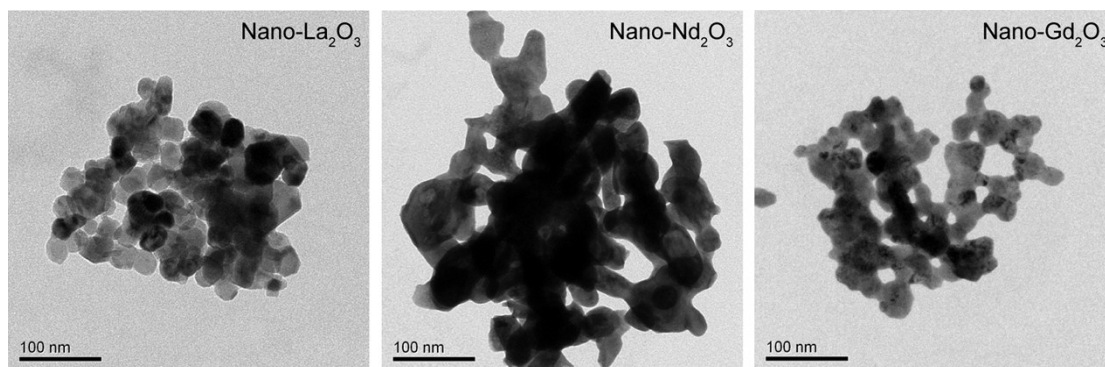
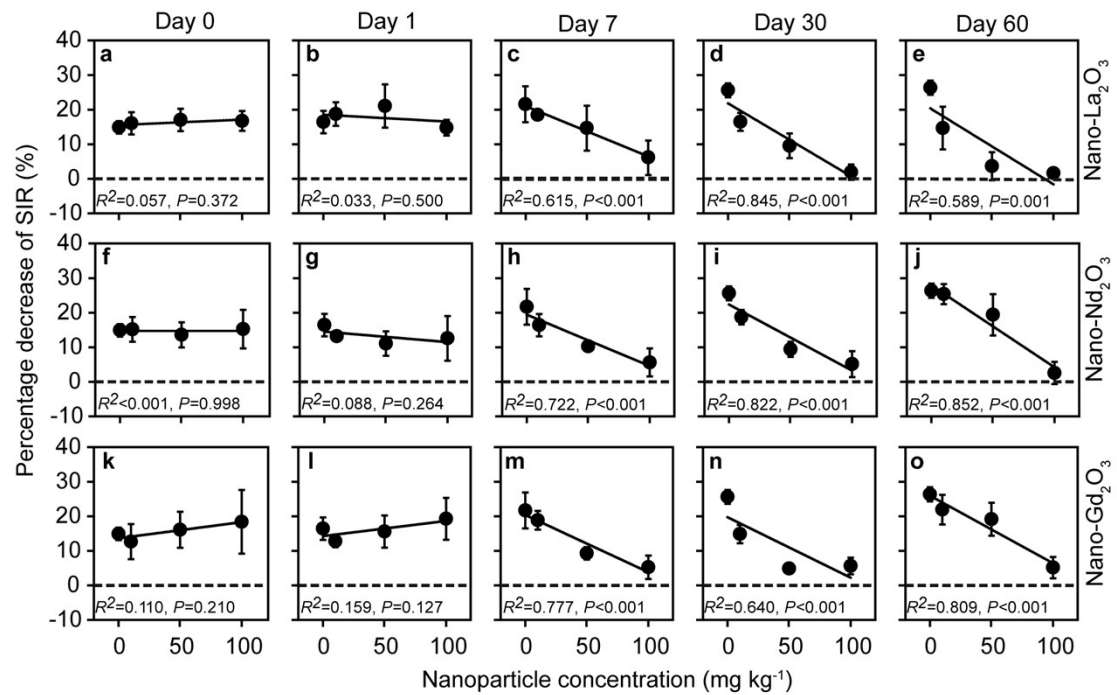


Fig. S2

Fluvo-aquic soil (Inceptisol)



Red soil (Ultisol)

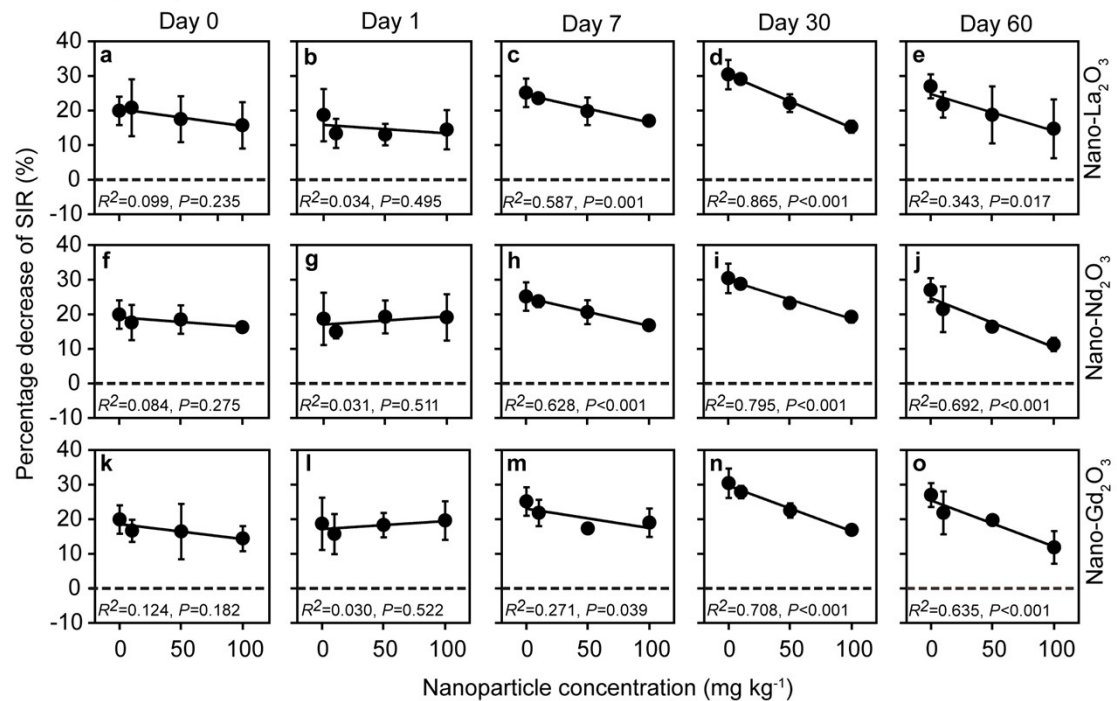
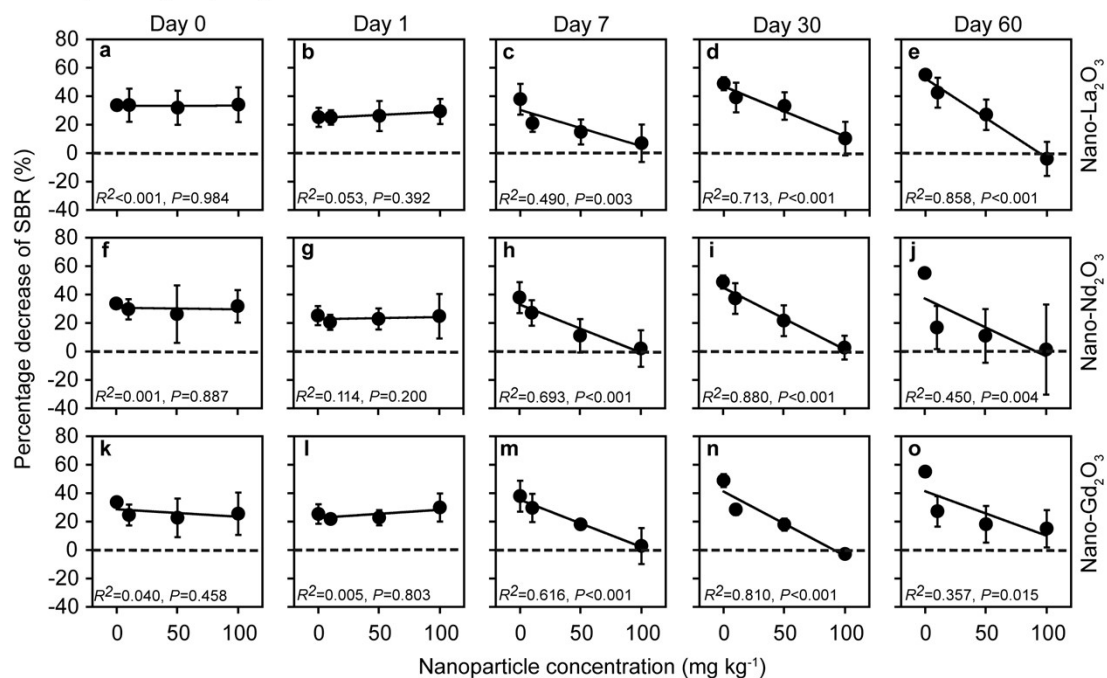


Fig. S3

Fluvo-aquic soil (Inceptisol)



Red soil (Ultisol)

