Real-time detection of the nanoparticle induced phytotoxicity in rice root tip through the visible red emissions of Eu³⁺ ions

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[†] P. Du and Y. Wu contributed equality to this work.

Accession number	Gene name	Sequence (5'-3')	Sequence (5'-3')
LOC_Os01g22490	OsUBQ5	TGAAGACCCTGACTG	CACGGTTCAACAACA
		GGAAG	TCCAG
LOC_Os05g02070	OsMT2b	CAGCTTATATGTAGG	GGGATGAAAGCAGAG
		CAGGC	GTAGA
AB012765.1	OsOVP1	CTGGTGCATCTGAGC	CGGAGGGAACTATAT
		ATGCA	GGGTC
Os11g0704500	OsMT1	ATGTCTTGCAGCTGT	AGTTGCAAGGGTTGC
		GGA	ACC
Os01g0149750	OsMT2	ATGTCGTGCTGCGGA	GCAGTTGCAGGGGTT
		GGA	GCA
LOC_Os02g51110	OsNIP2;1	ACCATGTACTACGGC	CGCGCATATCGCTCC
		GAG	GGT
LOC_Os01g71310	OsCKX4	GACCGACTACCTCCA	GGTTGACATTGCTGA
		TCTCACA	CCTGC
LOC_Os07g48560	OsWOX11	CCCTTGTCCGTTGGA	CCATGCGTACGTGCA
		TCAGA	GCATT
LOC_Os03g05510	OsCRL1	ATGACGGGATTTGGA	CTTGCTCGTGGCAGA
		TCGC	AGTAT
LOC_Os06g34180	OsFCP2	GAGGACGATGACGA	ACCACCATTATTCCCT
		TGATGATGG	CGTTCAC
Os03g0118400	OsCDK1	CTGTTCCCTGGTGAT	TCCAATGTAAAGCCA
		TCTGA	TAGCAG
Os02g0123100	OsCDK2	GCCTCATCTTTCCAT	CCCGCAATAAGGATC
		TTGT	TTTCA
AY941774	OsRB1	AGCTGACTGTGAGCG	GACCGTGGGAACAAA
		TCTAT	TACTT
AY941775	OsRB2	CTCGGCTATCTCGGT	CACTGTTTAGGCGGTT
		TTCC	GTTT

 Table S1. Primers used to study the gene expression.



Figure S1 (a)-(c) Elemental mappings and (d) EDX spectrum of $NaBiF_4$ nanoparticles. Inset shows the HR-FE-SEM image for the elemental mappings.



Figure S2 (a)-(d) Elemental mappings and (e) EDX spectrum of $NaBiF_4:Eu^{3+}$ nanoparticles. Inset shows the HR-FE-SEM image for elemental mapping.



Figure S3 (a) Images of rice seedling grown in different conditions. I: amplified root of WT-CT; II: amplified root of WT treated with 100 μ M NaBiF₄:Eu³⁺ nanoparticles. (b) Primary root length. (c) Crown root number. Error bars represent standard error of at least 5 samples. * P, < 0.01, ** P, < 0.001.



Figure S4 Rice root tip treated with 100 μ *M* NaBiF₄:Eu³⁺ nanoparticles at 4 DAG: (a) Bright channel, (b) RFP channel, and (c) Merge channel. Cross section of rice root tip treated with 100 μ M NaBiF₄:Eu³⁺ nanoparticles at 4 DAG: (d) Bright channel, (e) RFP channel, and (f) Merge channel.



Figure S5 Expression levels of crown root genes relative to *OsUBQ5*, evaluated at young seedling stage: (a) *OsCRL1*, (b) *OsWOX11*, (c) *OsCKX4*, (d) *OsFCP2*, (e) *OsCDKA;1*, (f) *OsCDKA;2*, (g) *OsRB1*, *and* (h) *OsRB2*. Error bars represent standard error of at least 3 samples. * P, < 0.01, ** P, < 0.001.