Research Paper; Submitted to "Nanoscale"

Supporting information:

Supplementary Figure 1:

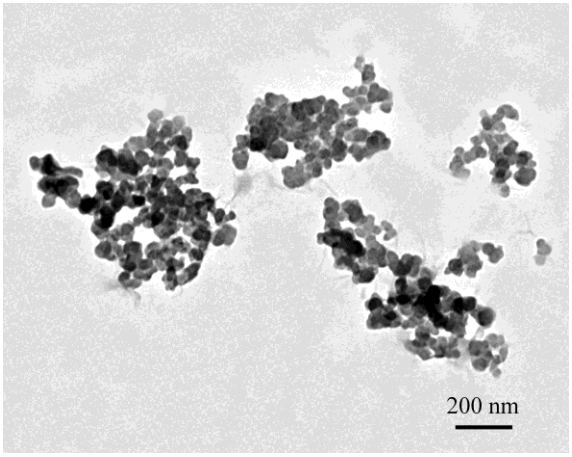

Fig. S1 TEM image of GO in K medium. Before observation, GO in K medium was sonicated.

Research Paper; Submitted to "Nanoscale"

Supplementary Figure 2:

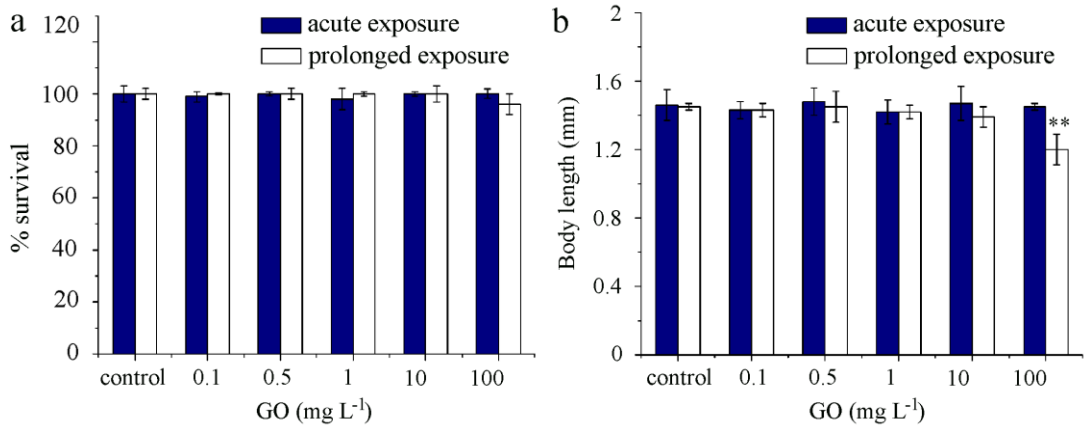

Fig. S2 Effects of GO exposure on lethality (a) and growth (b) of *C. elegans*. Exposure to GO was performed from L4-larvae for 24-hr (acute exposure) or from L1-larvae to adult (prolonged exposure). Bars represent means ± S.E.M. $^{**}p < 0.01$.

Supplementary Figure 3:

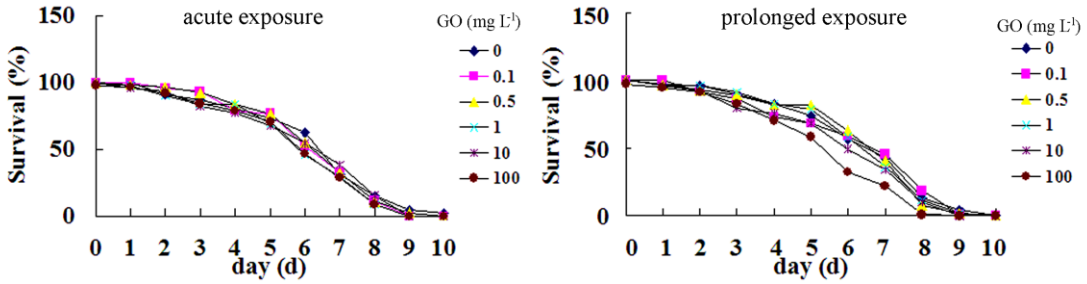

Fig. S3 Effects of GO exposure on lifespan of *C. elegans*. Exposure to GO was performed from L4-larvae for 24-hr (acute exposure) or from L1-larvae to adult (prolonged exposure).

Supplementary Figure 4:

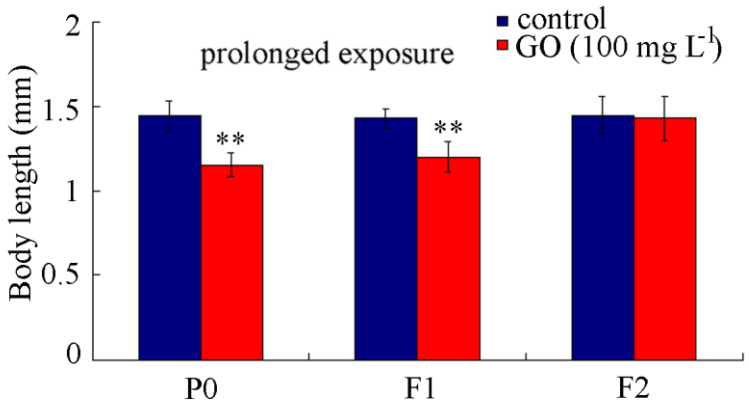

Fig. S4 Transgenerational effects of prolonged GO exposure on growth of *C. elegans*. Prolonged exposure to GO was performed from L1-larvae to adult. F1 and F2 progeny nematodes were cultured on normal NGM plates. Bars represent means ± S.E.M. $^{**}p < 0.01$.

Supplementary Table 1:

Table S1. Information on genes required for oxidative stress control in *C. elegans*

Gene	Products of the genes
sod-1	copper/zinc superoxide dismutase
sod-2	manganese - superoxide dismutase
sod-3	manganese - superoxide dismutase
sod-4	copper/zinc superoxide dismutase
sod-5	copper/zinc superoxide dismutase
isp-1	"Rieske" iron-sulfur protein
mev-1	a subunit of the enzyme succinate dehydrogenase cytochrome b
gas-1	subunit of mitochondrial complex I
clk-1	ubiquinone biosynthesis protein COQ7
ctl-1	catalase
ctl-2	catalase
ctl-3	catalase

Supplementary Table 2:

Table S2 Association of intestinal ROS production with the toxicity from prolonged exposure to GO in *C. elegans*

Dependent variable	Independent variable	
	Intestinal ROS production	
	R^2	*p* value
Body length	0.827	< 0.05
Brood size	0.839	< 0.05
Body bend	0.810	< 0.05
Head thrash	0.929	< 0.01
Intestinal autofluorescence	0.966	< 0.01

Research Paper; Submitted to "Nanoscale"

Supplementary Table 3:

Table S3. Information on genes required for intestinal development in *C. elegans*

Gene	Products of the genes
gem-4	Ca^{2+}-dependent phosphatidylserine binding protein
mtm-6	myotubularin lipid phosphatase orthologous
nhx-2	sodium/proton exchanger
opt-1	high-affinity, proton-coupled oligopeptide transporter
pkc-3	atypical protein kinase
par-3	PDZ domain-containing protein orthologous
par-6	PDZ-domain-containing protein
pgp-1	transmembrane protein
pgp-3	transmembrane protein
vha-6	membrane-bound (V0) domain of vacuolar proton-translocating ATPase (V-ATPase);
gtl-1	TRPM subfamily member of the TRP channel family
erm-1	ortholog of the ERM family of cytoskeletal linkers
eps-8	homolog of mouse epidermal growth factor receptor kinase substrate
act-5	ortholog of human cytoplasmic actin
ifb-2	nonessential intermediate filament protein
dlg-1	MAGUK protein
ajm-1	member of the apical junction molecule class
egl-8	phospholipase C beta homolog
let-413	protein with strong similarity to human ERBIN, rat DENSIN, Drosophila SCRIB and its human ortholog hSCRIB
nfm-1	homolog of human merlin/schwannomin (NF2)
inx-3	gap protein
nhx-4	sodium/proton exchanger

abts-4	anion transporter

Supplementary Table 4:

Table S4. Information on genes required for defecation in *C. elegans*

Gene	Products of the genes
unc-16	homolog of murine JIP3 (c-Jun N-terminal kinase (JNK)-interacting protein 3
unc-33	homolog of murine JIP3 (c-Jun N-terminal kinase (JNK)-interacting protein 3
unc-44	ankyrin-like protein
unc-101	adaptin orthologous to the mu1-I subunit of adaptor protein complex 1 (AP-1)
aex-1	novel, C2 calcium-binding domain protein
aex-3	guanine nucleotide exchange factor
aex-5	ortholog of calcium-dependent serine endoproteinases
cab-1	novel protein with a C-terminal motif weakly homologous
egl-36	Shaw-type voltage-gated potassium channel
unc-2	calcium channel alpha subunit
unc-36	alpha2/delta subunit of a voltage-gated calcium channel
unc-13	protein that regulates neurotransmitter release
fat-3	delta-6 fatty acid desaturase ('linoleoyl-CoA desaturase')
egl-30	ortholog of heterotrimeric G protein alpha subunit Gq (Gq/G11 class)
exp-2	member of the six-transmembrane voltage-activated (Kv-type) family of potassium channels
unc-43	type II calcium/calmodulin-dependent protein kinase (CaMKII)
egl-2	voltage-gated potassium channel
sup-9	TWK (two-P domain K^+) potassium channel subunits
sup-10	potassium channel
unc-93	transmembrane protein

unc-25	GABA neurotransmitter biosynthetic enzyme, glutamic acid decarboxylase (GAD)
lim-6	LIM class homeodomain protein
unc-47	transmembrane vesicular GABA transporter
gat-1	electrogenic, Na^+/Cl^--coupled, high-affinity GABA transporter
hlh-8	helix-loop-helix protein
exp-1	excitatory, cation-selective GABA receptor
tax-6	ortholog of calcineurin A
dsc-1	transcription factor CHX10 and related HOX domain proteins
flr-1	ion channel
flr-4	predicted Ser/Thr protein kinase
iri-1	tam3-transposase (Ac family)
smp-1	semaphorin
itr-1	putative inositol (1,4,5) trisphosphate receptor
plc-3	phospholipase C gamma homolog
vav-1	Rho/Rac-family guanine nucleotide exchange factor orthologous to the Vav proto-oncogene
ced-10	GTPase orthologous to human RAC1
mig-2	member of the Rho family of GTP-binding proteins
rho-1	Rho GTPase
crt-1	ortholog of calreticulin
shn-1	Scaffold protein Shank and related SAM domain proteins
elo-1	C-18 polyunsaturated fatty acid (PUFA) elongase
fat-2	delta-12 fatty acyl desaturase
dsc-4	subunit of the microsomal triglyceride transfer protein
tpk-1	Thiamin pyrophosphokinase
clk-1	ubiquinone biosynthesis protein COQ7
isp-1	"Rieske" iron-sulfur protein

Supplementary Table 5:

Table S5. Primers used for quantitative real-time polymerase chain reaction (PCR)

Gene	Forward primer	Reverse primer
act-1	CTGCAGATGTGTGACGACGAGGTT	CTGCAGGAAGCACTTGCGGTGAAC
clk-1	CACATACTGCTGCTTCTCGT	TGAACCAACAGATGAACCTT
ctl-1	CTCCTACACGGACACGCAT	GCATCTCCCTGGCTTTCAT
ctl-2	CGAACAGCTTCAACTATGG	GTGGCTGGGAATGTGGTAT
ctl-3	TTCTCCTACACGGACACGC	GCATCTCCCTGGCTTTCAT
gas-1	CTTGGTCTTTGGCTGTTGA	CTTGGTCTTTGGCTGTTGA
isp-1	GCAGAAAGATGAATGGTCC	CAGAAGCGTCGTAGTGAGA
mev-1	GGAATTCGCTTCTTAGGAT	GCAGTCTTGTTGCTCTTGT
sod-1	ACGCTCGTCACGCTTTAC	TCTTCTGCCTTGTCTCCG
sod-2	GGCATCAACTGTCGCTGT	ACAAGTCCAGTTGTTGCC
sod-3	TGACATCACTATTGCGGT	GGGACCATTCCTTCCAAA
sod-4	CACCAGATGACTCGAACA	AATGAGGCAAGAGAGTCG
sod-5	ATATTGCCAATGCCGTTC	CTCTTCACCTTCGGCTTT
gem-4	CACGGTGGTCAACAGTAT	TTGTATTTGGCACCTTTC
mtm-6	AAAAGGGACGCTAACAGC	ATTCTCAAACGCAAGCAG
nhx-2	GGAGCAGAATGTGAAGAA	GTGGCGGAAGTAGATAAA
opt-1	TGATGTCCGTTCCCTACT	ATGACCTGAAAGAGTGGG
pho-1	ACGGACATGATGTAGGAG	ATTAGAAGTGCGGAGAAG
pkc-3	CGTCTCCGACATCATTAG	CAACTCGGCTTCTTGACT
par-3	AAGCGTAACTGTCAACCA	CCGTCTATAACATCCTCC
par-6	ATTCTGCGTCTGGTGTCT	TTCCCTTCCATCGTTTAT
pgp-1	AATGTCCGATTCGCTTAC	CTCAGGGTTCAACGTCTT
pgp-3	GGACTTCCTGACGGTTAC	TTTGATGGGTTCCTTCTT
vha-6	ATGGAGGCAAACTTAGAG	TTCCGAGATTGACATAGC
gtl-1	CTGCTCACCACGCACAAT	AACTCCTTCATCCAACCC

erm-1	TCCACGACTCCGTATCAA	TCCTGCTCGGCAATCTTA
eps-8	ACGCAGTGACGGTAGAAG	AGCGGATACACGGATACA
act-5	GGGAGTGATGGTCGGTAT	CGGTAAGGAGAACTGGGT
ifb-2	TCAAGGCTGAATACGACA	TCCAAAGCAGAGTTACGG
dlg-1	TTGAAACGGCGTAAAGAT	CGTGATGAACTGGTGGTG
ajm-1	GTCAATCAGTTCGTCCCG	ACTCGTCCGATGGTGTCT
egl-8	GCTCGATGGCTTCAAGTA	TGAATGCTATCCCTCTGC
let-413	TTGCGTCCAACAAGTTAC	CACCAAGAAATGCTCCTC
nfm-1	ATTACGGAGGATCTGGTA	TCATCGTCGTGAACTTAT
inx-3	CAGTGGGTGCCTATTGTG	GACCGTATTCGTTCTTGG
nhx-4	GAAGATTGCTACCTGGAC	TCATAAGTGGGTGTTCCT
abts-4	CTCAGACTACAGGGATGG	GTGCCTGACTCACAAGAC
unc-16	CTCGGTGCTGATCTCACA	GCGTCTTAATCTCCTCCT
unc-33	CTCCCTGACAGACGATAA	CAGACTCCGCTAACCCTA
unc-44	TCCCAGACGGATCACTTA	ATTCCACGGTTGTTACTT
unc-101	CGGAAATTGTTGGAAGCG	CGGGCGGTATGAAGGAGA
aex-1	TGGAGCAAGAAGACCACT	GCGAATCTCCGATAACCT
aex-3	ATTACTGGGCGATGGGTG	TGGCGAACGAGTGGATTG
aex-5	AATGTGCTGGATTGGTAG	GCAATGCTCCATTCTTAA
cab-1	AATGCCGCTGTCAAGGAT	GTCTGCATCGCACTTTCG
egl-36	TGCCAGTTCCTGTTATCG	CTCCTAACCCTCCCTGTG
unc-2	CAACGCTCAGGAACTCAC	AATCAGAACTCGGAATGG
unc-36	CTCGCCACTTATGTCTCC	TCTTCAACTCGGCTCTTG
unc-13	AGTGAGCCGCTTTCTTAT	AATCCTCCACCACTTTCA
fat-3	ACTCATCACGCTGCCACA	TACCCAAGCCCAATGTCC
egl-30	AAGAGCTATGGGAGGATT	CACCAGGAACATGATTGA
exp-2	GCGGCATATTGGTGGTGT	TTGCTCGCTTTGCTGGTC
unc-43	ATTGGCAGGTGCTATTGA	TGCTGGCTGTAGATGAGT
egl-2	CCTATTTGGCTTCTGGTC	TGTAGATCCTTCGTTTCG

sup-9	GAAGATGAACGGAGGGAT	CTTTCTGTGACGGTGTCG
sup-10	TTACCGACAAGCAGTTTC	CAAGATGGCTGAGGACAC
unc-93	ACTACTTGTCGGTGTTGA	AAATACTTTGGGCTCCTC
unc-25	CGGCTCAACTGTCTACGG	TGGAGAAGTGCTCCCATG
lim-6	GTTCTGGTTGTGGGTGTC	ATAGCATTTGATGGTCGT
unc-47	TGGTCAAGGCTCTTCTAT	TTTCCAACTAATCCCATC
gat-1	AAAGTGTAGCCGAAGTAG	AACTCGTCAATGATAGCG
hlh-8	GTCAAAGGACCAAGGAAC	TGAAAGCCGACTGTAAAT
exp-1	CATCGACCAGAAATGACA	AACAACTCCAAAGCGTAA
tax-6	TGGAAAGATGGCAAGAGC	CGTTTGTCGTGACGGAAT
dsc-1	CGTATCACGGTATGGTTT	GATGCTCCTGTAGGCTTG
flr-1	TCACGGACTTGTGAGAAT	TGGTGTTCAGAGGGTTTA
flr-4	TCCACCAGTCATTCATCG	CAGAACCTCAGGAGCCAC
iri-1	AATAACGGCAGCACCTAA	GAAAGTCGTCGTGTCAAA
smp-1	CGGCAATGATGCTCTTAT	CTCCTCCTTTGTCGTTTT
itr-1	ATGGCAGGTCTTTATGTT	GAATCGGTATGCTTTGTT
plc-3	GTCATCTATCACGGGTAT	TCTATCGGCAACTTCTTA
vav-1	GTAATGGAGGATGTCTGC	TATAGCGTTGCTTAGGTT
ced-10	ATAAATCTCGGGCTCTGG	AGCACCGTACACTTGCTC
mig-2	ACAATGTGGCAAGCAAGT	TTTCGGATGAAGAATGGA
rho-1	ATTGAAGTTGACGGAAAG	TAATCGGAACATTTGGAC
crt-1	CTGTGGAGGTGGATACGT	GTCGGAGTTGAGGATGAG
shn-1	AGGAGGAAAGGTCAACGG	GTCGGAACGGCCTAGAAT
elo-1	CCGTTCTTGCTCATCTTG	TTTGGCACTGCCTTGTAC
fat-2	ACATTGCCTTTGTCCTCT	TGTCGATAGTTTGGGTTT
dsc-4	GGCTTCCCTCTACCATCA	GAATCGTCGAGTCATCCA
tpk-1	TAACGGTGAACCTACGGC	TCAGGCAGATGGACGACT
clk-1	GTGTCGGTTCAGCACTTC	GAGCCTTCATTCCATCGT
isp-1	GTACCAAGGCTGAGATTG	CAGAAGCGTCGTAGTGAG