

## Supporting information

### Physiological Effect of the Colloidal Carbon Quantum Dots on

#### *Bursaphelenchus xylophilus*

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Table S1 Primers of 24 DEGs

Wormbase ID	Type	Primer F	Primer R
BXY_0530300	down	ACTCCACCGCTGATATTGC	AATGCCGTTGATTGATGATTCCG
BXY_0581500	down	ACGGAGATACGAACTGGAGA G	TGCCTGTATAATGTTTTCGCTCTTT
BXY_0123500	down	GCTGGTGGATGTGCTGTT	GCGGCTTGAACCTGGACAA
BXY_1669000	down	ATTCTCATCAACAACGCTGGAT T	CACGCTGACGCATTATTGGA
BXY_0582900	down	GTCAACCCTCAAGAGTGCTCA	TTCCCGTCAACGATTTTCCTC
BXY_0255000	down	CTTCTGCCTCTGCTCCATTG	CGCCATAAGCCGACACATAG
BXY_0299200	down	GCCACACCATCACCAGATT	GCTTTCAGTTTCTCCTGTTTCC
BXY_0075200	down	TTGTAGTGAAGGTGAAGAGAAT TGG	ATGTCCGCTGTTGCTGTAAG
BXY_0412700	down	CGCCACAACACAGTCAGT	GTTTCAGCAGGTCTTCGTTCTT
BXY_0546100	down	ACGAAGGTTGCTATGGAGAA	GGTGGACGAAGAAGACTGTTG
BXY_0522200	down	GCACTCGGACCTGTTGAAG	GCTCTTGTCATCCACGAACTT
BXY_1236200	down	GTTGAAGGTTACAGGTGATGAC T	TAGAGACGAATGGGACGGTATT
BXY_0330200	up	GGTCCTTGTTGGCACAGTTC	CCTCTGGCAGTAATCGGTCAT
BXY_0501600	up	GGTCGTTATACCGCATCTATCT	GCTTCCTCCACCGTCTGT
BXY_0670800	up	GAGTAACGAGACAAGAGGTTG ATAC	GAGATTCCCAGGCATTTC
BXY_1755800	up	TGTATGCTCTTCTTGACGAATGC	ACGGACGATGTGAGATGGT
BXY_0586400	up	GCGGAGAGAAGCAACGAAT	GCGATGCGACACTGTGAA
BXY_0626900	up	GGAGACCTATGAGAATGATGTT GTG	GCCGATAGAAGCCAAGTTGTAAT
BXY_1025900	up	GAGAAGTTCAAGAAGAAGACG AGAG	CGAGGAGACGGTTGAGGAA
BXY_0419500	up	CGGCGTCCACAACAACAT	CCTTCTTCTCCACCTCGTTCA
BXY_1706500	up	TGATGGGATGAGTGACGAAAC	GCTGCGGAAACGGTAGATT
BXY_0116800	up	CTTCCACTCAATAATACGCAAC CA	TTCCAACGATTCCAACACTCTG
BXY_1064200	up	AATGGACGGCTTATGGAATGG	CTGCGGCTGAGAGTTGAG
BXY_0629000	up	GGCGATGTTGAGAAGTTGGA	CCGCAGTTGGCTTGAGAT

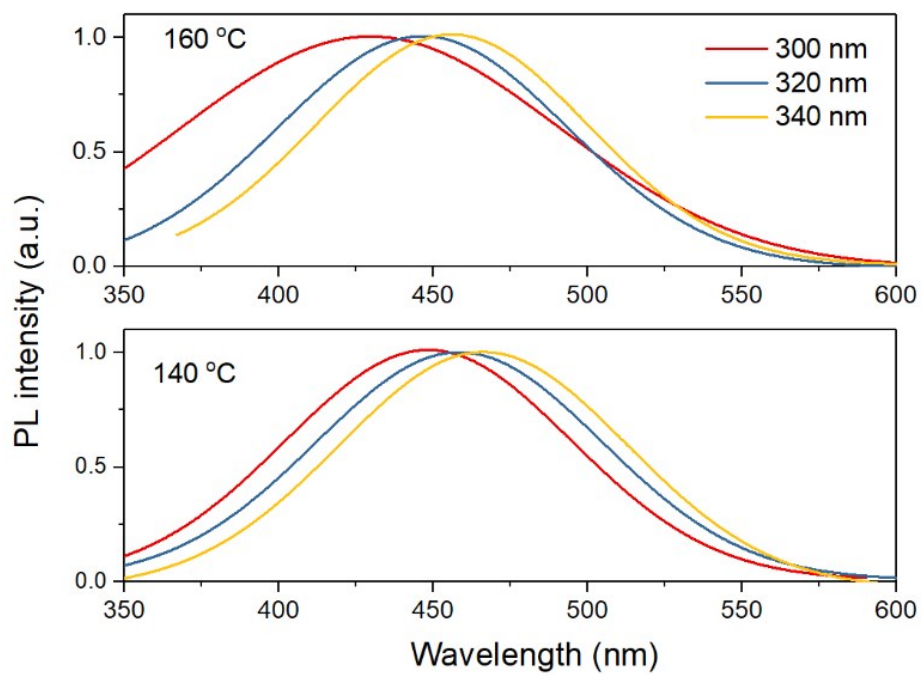


Figure S1 The excitation-dependent photoluminescence under 140°C and 160 °C

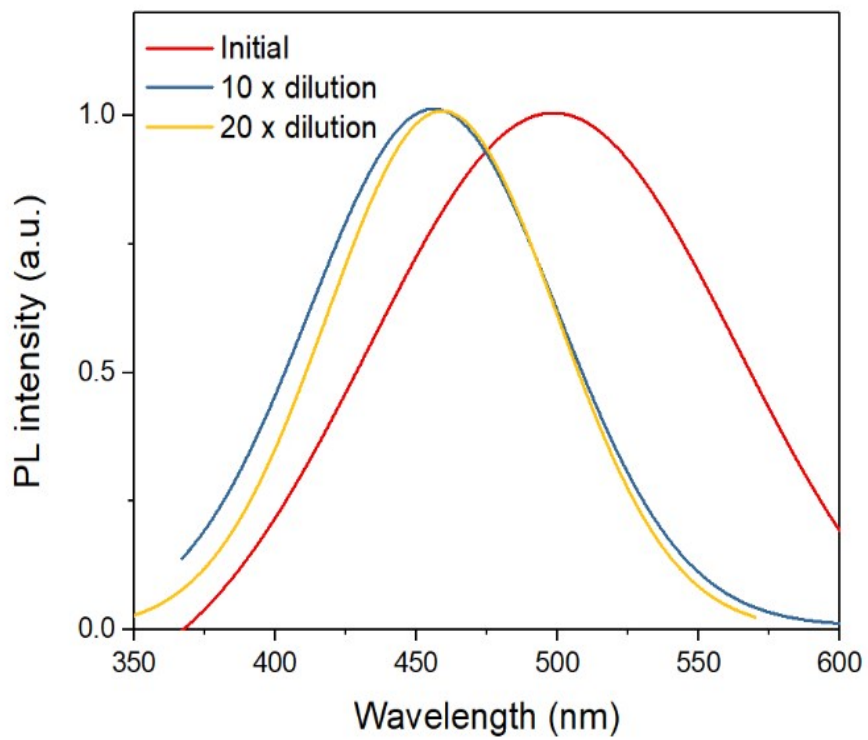
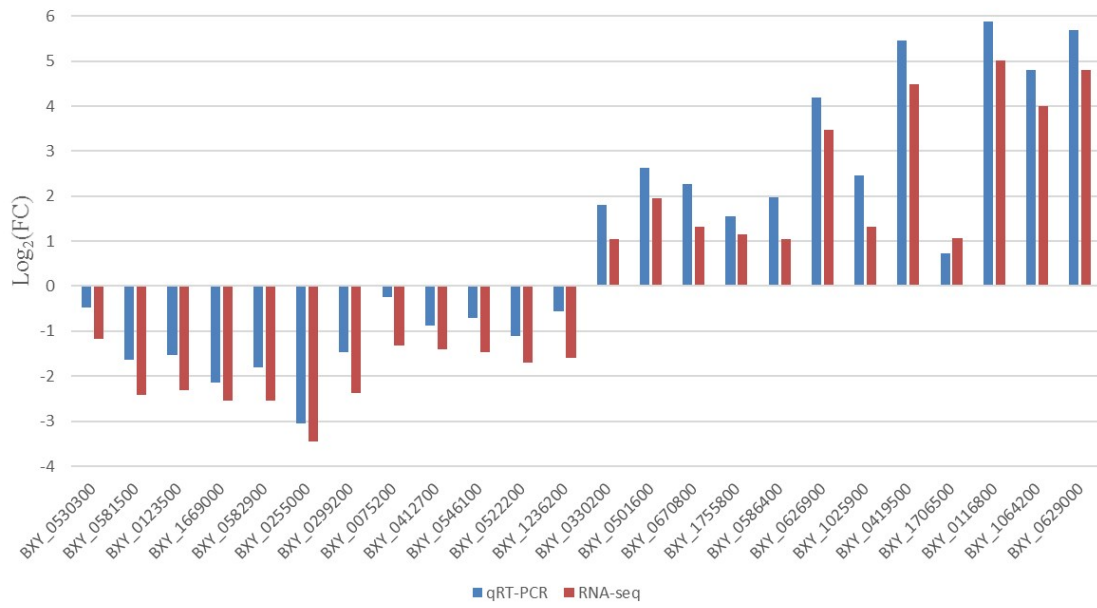


Figure S2 PL spectrum under initial concentration, 10 times dilution and 20 times dilution



**Figure S3** qRT-PCR validation of transcriptome data

**Table S2** DEGs related to the detoxification process

Wormbase ID	Log <sub>2</sub> (FC)	Type	Annotation
<i>cytochrome P450:</i>			
BXY_1188700	4.494645	up	cytochrome P450-33C2
BXY_1345300	4.435065	up	cytochrome P450-33C2
BXY_0451400	2.861694	up	cytochrome P450-33C2
BXY_0170600	2.147061	up	cytochrome P450-33C2
BXY_0799900	2.068291	up	cytochrome P450-33C9, partial
BXY_0537000	-2.10431	down	cytochrome P450-33C2
BXY_0111800	-2.29708	down	cytochrome P450-33C4
BXY_0800100	-2.30255	down	cytochrome P450-33C9, partial
BXY_0625200	-2.63122	down	cytochrome P450-33C2
BXY_0074600	-2.69735	down	cytochrome P450 33D3
<i>UDP-glucuronosyl transferase:</i>			
BXY_1673100	5.031705	up	UDP-glucuronosyl transferase 2C1
BXY_1108300	4.450396	up	Putative UDP-glucuronosyltransferase ugt-47
BXY_1073700	3.317977	up	UDP-glucosyl transferase domain containing protein
BXY_1091400	2.831768	up	Putative UDP-glucuronosyltransferase ugt-47
BXY_0112900	2.540596	up	UDP-glucuronosyltransferase 2C1
BXY_0491700	2.256199	up	Putative UDP-glucuronosyltransferase ugt-47
BXY_0497500	-2.20101	down	UDP-glucuronosyltransferase 2C1
<i>glutathione S-transferase:</i>			
BXY_1297200	6.205655	up	Probable glutathione S-transferase 8
BXY_0629000	4.802866	up	sigma class glutathione S-transferase
BXY_0629100	4.498351	up	sigma class glutathione S-transferase
BXY_1562700	3.372303	up	sigma class glutathione S-transferase
BXY_0298300	3.08482	up	Glutathione S-transferase 1
BXY_0628900	2.343462	up	sigma class glutathione S-transferase
BXY_1562600	2.271064	up	sigma class glutathione S-transferase
BXY_0175000	-2.2381	down	sigma class glutathione S-transferase
BXY_0299200	-2.38221	down	Glutathione S-transferase
BXY_0298200	-2.47133	down	Glutathione S-transferase
<i>Carboxylesterase:</i>			
BXY_0407500	-2.52669	down	Carboxylesterase, type B domain-containing protein

**Table S3** DEGs related to the Fatty acid degradation

Wormbase ID	Log <sub>2</sub> (FC)	Type	Annotation
BXY_0104400	7.314855	up	Acyl-CoA synthetase family member 2, mitochondrial
BXY_0116800	5.024139	up	Propionyl-CoA carboxylase beta chain, mitochondrial
BXY_0104500	4.990822	up	Acyl-CoA synthetase family member 2, mitochondrial
BXY_0419500	4.488005	up	Propionyl-CoA carboxylase alpha chain, mitochondrial
BXY_0670900	2.703808	up	ACetyl-CoA Acyl transferase 2 homolog
BXY_0654500	2.081778	up	Acyl-CoA oxidase/dehydrogenase

**Table S4** DEGs related to the Locomotion (GO:0040011).

Wormbase ID	Log <sub>2</sub> (FC)	Type	Annotation
BXY_0104700	10.51242	up	hypothetical protein B9Z55_020222
BXY_0104400	7.314855	up	Acyl-CoA synthetase family member 2,mitochondrial
BXY_1061400	6.448054	up	4-coumarate--CoA ligase 3
BXY_0104500	4.990822	up	Acyl-CoA synthetase family member 2,mitochondrial
BXY_0829000	4.58125	up	PREDICTED: macrophage migration inhibitory factor-like
BXY_0823300	4.320412	up	hypothetical protein Y032_0227g2821
BXY_0240300	-3.59318	down	dual specificity mitogen-activated protein kinase kinase 7-like

**Table S5** DEGs related to the Reproduction (GO:0000003).

Wormbase ID	Log <sub>2</sub> (FC)	Type	Annotation
BXY_0829000	4.58125	up	PREDICTED: macrophage migration inhibitory factor-like
BXY_1014400	3.349453	up	Phosphate-regulating neutral endopeptidase
BXY_0847600	3.152507	up	hypothetical protein B9Z55_019797
BXY_1580400	-3.66461	down	Putative transporter
BXY_0240300	-3.59318	down	dual specificity mitogen-activated protein kinase kinase 7-like
BXY_1148300	-3.51447	down	PREDICTED: uncharacterized protein K02A2.6-like
BXY_0255000	-3.45972	down	oxidoreductase, short chain dehydrogenase/reductase family protein
BXY_0499000	-3.28241	down	17beta-hydroxysteroid dehydrogenase, partial
BXY_0027200	-3.17717	down	hypothetical protein FL83_04848, partial