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1 Supporting Information

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3 Cellular response of *Chlorella pyrenoidosa* to oxidized multi-walled carbon

4 nanotubes

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- 14 Number of tables: 4

15 Composition of the OECD medium

Algal cell culture medium recommended by OECD is composed of ultrapure water and the following ingredients (mg/L): NH₄Cl 15, MgCl₂•6H₂O 12, CaCl₂•2H₂O 18, MgSO₄•7H₂O 15, KH₂PO₄ 1.6, FeCl₃•6H₂O 0.08, Na₂EDTA•2H₂O 0.1, H₃BO₃ 0.185, MnCl₂•4H₂O 0.415, ZnCl₂ 3×10^{-3} , CoCl₂•6H₂O 1.5×10⁻³, CuCl₂•2H₂O 10⁻⁵, Na₂MoO₄•2H₂O 7×10⁻³, NaHCO₃ 50.

20 Preparation of oxidized MWCNTs

The pristine MWCNTs were ultrasonically treated with a mixture of concentrated H_2SO_4 and HNO₃ (3:1, V/V) at room temperature for 1, 2, 4 and 8 h, respectively. The oxidized MWCNTs (o-MWCNTs) were then separated from the concentrated acid solution by dilution and centrifugation, and were thoroughly washed with ultrapure water to neutral. Finally, the o-MWCNTs were obtained through lyophilization, and were stored in tightly capped vials.

26 Settling experiment

Individual MWCNTs and algal cell suspensions, as well as the mixtures of MWCNTs and algal cells, were transferred to cuvettes to monitor changes in absorbance at 660 nm over time for 12 h. The settling curves, which involve the normalized absorbances versus settling time curves, were subsequently plotted.

31 Density gradient centrifugation

Sucrose solutions over a concentration range of 10% to 60% (with an increment of 10%) were prepared. Our preliminary experiment had shown that the serial sucrose concentrations with an increment of 10% were able to separate the MWCNTs from the algal cells. Beginning with the highest concentration, density gradients of sucrose were created by carefully and slowly pipetting layers of sucrose into a 22 mL glass vial inclined at an angle of 30° with decreasing concentration. The glass vials containing the density gradients were kept static for about 6 h before use. Two mL 38 aliquots of the mixtures were layered on the top of the sucrose gradients, and immediately 39 centrifuged at 1000g for 25 min, resulting in an obvious separation between algal cells and 40 MWCNTs (as shown in Fig. S2). MWCNTs distributed in the upper layer of sucrose gradient due to 41 their low density. Algal cells could be distinguished by their green color, and compact agglomerates 42 containing both algal cells and MWCNTs settled to the bottom of the vial.

43 Analysis of total lipids

The obtained cell pellets were lyophilized for 48 h. Then 9 mL of a chloroform/methanol solution 44 (1:2, V/V) were added into 22 mL glass vials containing approximately 10 mg of the cell powders. 45 After bath sonication (100 W, 40 kHz, 25 °C) for 30 min, 3 mL chloroform was added and the 46 sample was sonicated for 5 min. Three mL water was subsequently added and the sample was 47 sonicated for another 5 min. After centrifugation (1500 g, 15 min, 25 °C), the chloroform layer was 48 then pipetted and transferred to a pre-weighed test tube. The above procedures were repeated three 49 times until the chloroform layer became colorless. Finally, the extract and test tube was dried under 50 nitrogen in water bath at 45 °C, and the mass was determined. The total lipid content was calculated 51 by the difference between the two masses and was expressed as % of dry cell weight 52

53 Analysis of fatty acid composition

The cell pellets were saponifed in a 1 mL 15% NaOH-methanol solution at 100 °C for 30 min, followed by methylation in 2 mL 6 mol/L HCl-methanol solution at 85 °C for 10 min, and extraction with 1 mL methyl tertiary butyl ether/hexane solution (1:1, V/V). After being washed with 3 mL 0.03 mol/L NaOH solution and 0.5 mL saturated NaCl, the extracted organic phase was then analyzed by gas chromatography (GC, Agilent 7890A, USA) with flame ionization detection (FID). The system utilized a DB-5MS capillary column coated with 5% diphenyl cross-linked with 95% dimethylpolysiloxane (30 m×250 µm inner diameter, 0.25 µm film thickness). The samples (1 61 μ L) were injected into the GC column in splitless mode with Helium as the carrier gas at a constant 62 flow rate of 1.2 mL/min. The initial temperature was kept at 80 °C for 1 min, raised to 320 °C at a 63 rate of 12°C/min, and then kept for another 8 min. The injection and ion source temperatures were 64 275 and 230°C, respectively. The energy was -70eV in electron impact mode. The mass 65 spectrometry data were acquired in full-scan mode with the range of 50-800 m/z.

66 Analysis parameters for metabolite profiling analysis and data analysis

The system utilized a DB-5MS capillary column coated with 5% diphenyl cross-linked with 95% 67 dimethylpolysiloxane (30 m×250 μ m inner diameter, 0.25 μ m film thickness). The samples (1 μ L) 68 were injected into the GC column in splitless mode with Helium as the carrier gas at a constant flow 69 rate of 1 mL/min. The initial temperature was kept at 50 °C for 1 min, raised to 310 °C at a rate of 70 10°C/min, and then kept for another 8 min. The injection, transfer line, and ion source temperatures 71 were 280, 270, and 220 °C, respectively. The energy was -70 eV in electron impact mode. The mass 72 spectrometry data were acquired in full-scan mode with the m/z range of 50-500 at a rate of 20 73 spectra/sec after a solvent delay of 6.1 min. 74

The raw data was pre-processed using interquartile range de-noising method. The missing values 75 were then adjusted to half of the minimum value. An internal standard normalization method was 76 employed during data analysis. Principal component analysis (PCA) and orthogonal partial least 77 squares discriminant analysis (OPLS-DA) were performed by SIMCA14.1 software package 78 (Umetrics, Umea, Sweden) using the normalized data. Variable importance values (VIP) were 79 obtained from OPLS-DA, and differential metabolites with VIP>1 and p<0.05 were subsequently 80 selected. The differential metabolites were then subjected to hierarchical cluster analysis (HCA). 81 And HCA was performed using a similarity metrics of Euclidian distances and complete linkage 82 grouping. Commercial databases including KEGG (http://www.genome.jp/kegg/) and NIST 83

84 (<u>http://www.nist.gov/index.html</u>) were used to search for the metabolite pathways using the
85 MetaboAnalyst website (www.metaboanalyst.ca/).

86 Measurement of SOD activity

The obtained cells were washed with 0.01 M PBS (pH 7.0) twice, and were resuspended in 2 mL PBS. After sonication (100 W, 40 kHz, 25° C) for 20 min, 1.5 mL ethanol and 1.5 mL chloroform were added to the samples, followed by 10 minutes' vibration (150 rpm, 25° C). The aqueous layer containing crude enzymes was separated from organic layer by centrifugation (3500g, 10 min, 25° C), and was pipetted to an 8 mL vial. The samples were mixed with four reagents provided by the assay kit, and were incubated at 37° C for 40 min. Two mL chromogenic reagent was added and the absorbance at 550 nm was recorded. The result was normalized by the cell number.

Target gene	Description	Primer sequence (5'-3')	Length (bp)
accA	acetyl-CoA carboxylase	F: CGCAATACCAAGGAGAACAT	202
	- •	R: ACATCTCACGCAGGTTGAC	
accD	acetyl-CoA carboxylase	F: TAGTTTGTGCTTCGGGTGG	227
		R: CAATAAGGGCTTTCGGTTCA	
dgat7494	diacylglycerol acyltransferase	F: GCTCGCTGGGCCTGATGCTGTT	186
		R: GCGGATGAGCGGGAAGTAGA	
dgat2354	diacylglycerol acyltransferase	F: TTTGGCGAGAATGAGCAGTA	236
		R: ACCTTTGAAGGCGGGCAG	
ME	malic enzyme	F: CCCTCTCGTTCCCCTTTTATT	158
		R: AAATGCTGACGCAAGTGTGA	
PEPC	phosphoenolpyruvate carboxylase	F: AAGGAGTGGGACGAGGATAAG	238
		R: GGTGTGGGGACATTGAGATGAT	
CAH2	putative carbonic anhydrase	F: GACTCCAACATTGCGAAGAT	109
		R: GGAAGAGGTCGGTCAGGT	
<i>rbc</i> L	Rubisco large subunit	F: CTTTCCAAGGTCCTCCTCAC	208
		R: TCTCTCCAACGCATAAATGG	
HLA3	putative inorganic carbon transporter	F: TGATGTGCTTCCTCACCCT	189
		R: TCCAAAGTGTCCTGGTCCT	
psbB	photosystem II P680 chlorophyll A	F: CACCGTCTGATTGAAGAGTTGC	187
	apoprotein	R: GATGTTCCTTTCCGTCGTTCTG	
cox2	cytochrome c oxidase subunit II	F: GAAGTGGATAATCGTATGGTTG	115
	2	R: CTGCATCACATTTTGCTCCTAA	
<i>atp</i> B	ATP synthase CF1 beta subunit	F: GTTTCGTTCAAGCTGGTTCT	105
		R: GTTCTTGTAAGCCACCCATT	
<i>fts</i> H	cell division protein FtsH	F: ACAAAGTGACCGAAATCCAGAA	129
		R: TTACGAATTGGGAGACTAGAAG	
actin	reference gene	F: GCTCAACTCCTCCACGCT	187
		R: GTCCTTGCGGATGTCCAC	

94 Table S1. Sequences of primer pairs used for real-time PCR.

96 Table S2. Selected properties of the MWCNTs.

Materials	Outer diameter	Length	Elen	nental c	ontents	(%)	Specific surface	Pore volume	Electrophoretic	Hydrodynamic
	(nm)	(µm)	С	Н	Ν	0	area (m ² g ⁻¹)	(cm ³ g ⁻¹)	(μm cm/Vs)	size (nm)
p-MWCNTs	43±18	4.2 ± 0.9	97.55	0.08	ND ^a	2.82	26.4	0.050	-2.86 ± 0.13	748 ± 120
o-MWCNT1	45±18	3.5 ± 0.7	93.99	0.17	ND	5.22	53.2	0.080	-4.27 ± 0.01	284 ± 5
o-MWCNT2	45±16	2.2 ± 0.6	93.75	0.15	0.11	5.36	57.6	0.086	-4.34 ± 0.07	249 ± 6
o-MWCNT4	47±17	2.1 ± 0.5	92.44	0.20	0.12	6.25	58.9	0.100	-4.35 ± 0.01	250 ± 6
o-MWCNT8	44±18	1.7 ± 0.6	91.06	0.21	ND	7.25	76.0	0.111	-4.43 ± 0.12	228 ± 3

⁹⁷ ^a ND stands for data not detected. The data were from Ref. 1.

98 Table S3. Concentration of selected metal ions in the OECD medium with and without o-

99 MWCNT8.

Cations	Zn (µg/L)	Mn (μg/L)	Co (µg/L)	Ni (µg/L)	Cu (µg/L)	Mo (µg/L)	Mg (mg/L)	Ca (mg/L)
Without o-MWCNTs	1.45	132	0.26	<0.1	<0.1	6.67	3.64	5.73
With o-MWCNT8	< 0.1	8.57	0.15	16.0	< 0.1	5.51	2.51	2.74

Note: The presence of o-MWCNT8 decreased the concentrations of Zn, Mn, Co, Mo, Mg, and Ca
cations in the OECD medium, suggesting cation adsorption. The o-MWCNT8 released Ni into the
OECD medium, and thus increased the concentration of Ni in the presence of o-MWCNT8.

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105 Table S4. Effect of o-MWCNT8 on the fatty acid content (%) of algal cells.

Fatty acids	Control cells	5 mg/L o-MWCNTs treated cells	10 mg/L o-MWCNTs treated cells
SFA			
C12:0	0.13 ± 0.02	0.14 ± 0.01	0.14 ± 0.03
C14:0	0.66 ± 0.05	0.67 ± 0.01	0.66 ± 0.04
C15:0 iso	0.10 ± 0.01	0.12 ± 0.02	0.12 ± 0.01
C15:0 2OH	1.49 ± 0.04	1.69 ± 0.24	1.8 ± 0.01
C15:0 3OH	0.17 ± 0.15	0.31 ± 0.01	ND
C16:0	38.40 ± 1.01	33.30 ± 0.45	32.22 ± 1.12
C16:0 anteiso	9.94 ± 0.56	12.25 ± 0.89	13.16 ± 0.76
C16:0 iso 3OH	0.74 ± 0.64	ND	ND
C17:0	0.51 ± 0.02	0.33 ± 0.04	0.32 ± 0.02
C17:0 iso	0.33 ± 0.01	0.32 ± 0.01	0.27 ± 0.01
C17:0 anteiso	0.34 ± 0.13	0.60 ± 0.14	0.62 ± 0.15
C17:0 10-methyl	2.76 ± 0.31	3.46 ± 0.18	3.46 ± 0.1
C17:0 iso 3OH	0.55 ± 0.11	0.62 ± 0.07	0.82 ± 0.11
C18:0	1.32 ± 0.17	0.72 ± 0.18	0.58 ± 0.18
C18:0 iso	ND	0.76 ± 0.04	0.81 ± 0.04
Sum	57.44 ± 1.61	55.25 ± 0.63	54.95 ± 0.52
UFA			
C16:1 w7c alcohol	0.80 ± 0.10	0.82 ± 0.13	0.75 ± 0.06
C17:1 w8c	0.86 ± 0.06	0.91 ± 0.01	0.95 ± 0.01
C18:1 w5c	ND	3.53 ± 0.88	3.83 ± 0.59
C18:2 w6,9c	40.85 ± 0.65	38.78 ± 1.06	39.00 ± 1.00
Sum	42.51 ± 0.76	44.03 ± 0.04	44.53 ± 0.33
SFA/UFA ratio	1.35 ± 0.02	1.25 ± 0.01	1.23 ± 0.02
Note: NE) stands	for	not detected



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Fig. S1 Correlation between the UV800 and the TOC-based concentration of stabilized o-108 **MWCNT** suspensions.



Fig. S2 Images of vials after the density gradient centrifugation for o-MWCNT8 (A), the algal 120 cells (B), and the mixture of algal cells and o-MWCNT8 (C). 121

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123 Fig. S3 TEM images of p-MWCNTs (A), o-MWCNT1 (B), o-MWCNT2 (C), o-MWCNT4 (D)

124 and o-MWCNT8 (E). The images were from Ref. 1.

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Fig. S4 (A) Dose-response curves and (B) the correlation between calculated EC_{50} values and oxygen contents of the o-MWCNTs. Values with different letters (a–c) differ significantly (p < 0.05). Error bars represent standard deviations (n=3).



150 Fig. S6 CLSM images of untreated algal cells (A) and algal cells treated with FITC (B) and

151 FITC labeled o-MWCNT8 (C) under high magnification.



Fig. S7 TEM image of untreated algal cells untreated (A) and cells treated with 10 mg/L oMWCNT8 (B-H). Panels G and H are the magnified images of the rectangle located areas in
Figure 2 B2 and B3, respectively. Black and red arrows in the images point to o-MWCNT8
and electron-density granules in vacuoles, respectively.



Reference cited:

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189		Com	parison o	f multij	ple analy	/sis	method	ls, Sa	ci. Chine	a Chen	n., 20	16, 59 ,	, 1498-	1507.		