Silver Nanowire Exposure Results in Internalization and Toxicity to *Daphnia Magna*

Leona D. Scanlan^a, Robert B. Reed^b, Alexandre V. Loguinov^a, Philipp Antczak^c, Abderrahmane Tagmount^a, Shaul Aloni^d, Daniel Thomas Nowinski^a, Pauline Luong^a, Christine Tran^a, Nadeeka Karunaratne^a, Don Pham^a, Xin Xin Lin^a, Francesco Falciani^c, Chris P. Higgins^e, James F. Ranville^b, Chris D. Vulpe^{a*} Benjamin Gilbert^f

^aUniversity of California Berkeley, Department of Nutritional Sciences and Toxicology, 119 Morgan Hall, Berkeley, CA 94720

^b Colorado School of Mines, Department of Chemistry and Geochemistry, 1500 Illinois St., Golden, CO

^cUniversity of Birmingham School of Biosciences, Edgbaston, Birmingham, B15 2TT, UK

^dMolecular Foundry, Lawrence Berkeley National Laboratory, Materials Sciences Division, 1 Cyclotron Rd., MS 90-1116, Berkeley, CA, 94720

Colorado School of Mines, Department of Civl and Environmental Engineering, Golden, CO 80401

^fEarth Science Division, Lawrence Berkeley National Laboratory, Earth Sciences Division, 1 Cyclotron Rd., MS 74-316C, Berkeley, CA, 94720 * Address correspondence to vulpe@berkeley.edu

SUMMARY

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METHODS

Nanowire characterization. Transmission electron microscopy (TEM) and scanning transmission electron microscopy (STEM) were used to measure the morphology and dimensions of the nanowires and their surface coatings (Figures S1 & S5). The TEM (JEOL 2100F) was equipped with OXFORD INCA energy dispersive x-ray spectroscopy suite (EDS). STEM was equipped with Gatan's Digiscan II. TEM was also used to investigate the effects of aqueous medias on SiO₂ coating integrity. To do this, short SiO₂-NWs were immersed in exposure media for two hours. A droplet was placed on a lacey carbon grid, dried and imaged.

Elemental analysis. Imaging and elemental analysis of AgNW containing samples was performed with a scanning electron microscope (SEM) (Zeiss EVO) with an EDAX energy dispersive x-ray spectrometer (EDS). Individual AgNWs and aggregates were prepared on 5x5 mm silicon wafers (SPI Supplies) treated in a 5% HF solution or a 5% H₂SO₄ oxidizing solution (GODAX laboratories, Inc.) to generate, respectively, hydrophobic or hydrophilic surfaces. High-resolution imaging of NWs performed by collecting the secondary electron signal and limiting beam current to less than 100 pA. Sparse NWs in complex samples were located using the backscattered electron signal at approximately 1 nA, and their composition was established using EDAX from the Ag emission lines.

Aggregation and settling. Dynamic light scattering (DLS) (Precision Detectors) was used to measure the stability against aggregation of S-NW suspensions in *Daphnia* media and in pure water. The relative rates of AgNW settling were investigated by measuring the optical absorption spectroscopy (Ocean Optics) of unstirred 4-mL volumes of 12-mg/L suspensions

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in closed 1-cm path-length quartz cuvettes. 1-mL aliquots were extracted for DLS analysis over a 48-hour period. All solutions were modestly stirred (1x5 mm stir bar at ~200 rpm) to limit NW settling. L-NW were too large for DLS analysis, so we collected L-NW and their aggregates from solution and imaged them using SEM on silicon wafers that had been treated with HF or oxidizing solution (described above) to generate hydrophilic or hydrophobic surfaces. At 12 mg/L Ag, collection time of 1-2 hours achieved a surface coverage of AgNW suitable for SEM imaging. All abiotic AgNW stability tests were performed using glass vials and quartz cuvettes.

Zeta potential. We measured the zeta potential of PVP- and silica-coated short nanowires dispersed in ultrapure water. Long nanowires were too large for analysis. Measurements were conducted with a Malvern Zetasizer 5000 in low volume disposable cuvettes. Particle size distributions were first measured using dynamic light scattering, using at least 20 measurements recorded to calculate a mean z average size. Provided the DLS measurement showed the sample to be free from dust or aggregates, dip-type electrodes were added for zeta potential measurements. At least 20 measurements were acquired until the data quality satisfied the software automatic assessment routine. We sought to measure the zeta potential of the nanowires in the EPA and COMBO media, but in all cases recorded zero potential, indicating the NW surfaces to be completely shielded from the applied electrostatic field in due to the non-zero ionic strength of these solutions.

Shaking *versus* **still statistical significance**. Raw acute data for long and short PVP-NW were compared with statistical software (GraphPad). For the L-PVP test, a paired, two-tail t-test was performed. Intermediate values used in calculations were a t-value of 0.1465, eight degrees of freedom and a standard error of difference of 1.516. A similar t-test was

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performed on S-PVP data, with a t-value of 1.2623, 12 degrees of freedom and a standard error of difference of 0.488. Final p-values were 0.824 for S-PVP and 0.940 for L-PVP, indicating no statistical difference in daphnid lethality between still or shaken AgNW exposures.

Determination of differentially expressed gene candidates. Data were analyzed using a "Treatment vs. Control" design. Foreground intensities in each array were subtracted with local background. All negatives or flagged spots (using GenePix quality control flag system) were treated as missing values. All positive values were log (base-2)-transformed. Relative intensity ratios(treatment sample/control), or "M-values", were calculated for each gene (cDNA). Non-linear trends (if any) were corrected with loess global normalization.¹ Differential gene expression was determined with an algorithm based on α -outlier detection procedures.² Because microarray data are "noisy," a local variance estimator based on loess was used to take heteroscedasticity (if any) into consideration.² Each gene in a given "Treatment vs. Control" pair was characterized by two values: the normalized logtransformed ratio (fold change value) and the corresponding q-value (derived from pvalues, which were adjusted for multiplicity of comparisons).³ Fisher's method of metaanalysis was applied to combine p-values (this approach is scale-free and, as a result, does not require the use of between-array normalization). A multiple-slide method was used to detect candidate genes; the same technique was applied to all microarrays based on all possible combinations of a given treatment and the corresponding control biological replicates. This technique treated gene expression outcomes as Bernoulli trials (independent binary outcomes). Fisher's method-based p-values were adjusted with Bonferroni correction. A list of candidate genes was created for each treatment. All results were corrected for multiplicity of comparisons twice: 1) within a given "Experiment vs.

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Control" pair, 2) across biological replicates. Candidate genes were annotated using Blast2Go.⁴

SUPPORTING TABLES

Sample	% passed through 0.45 μm	% passed through 0.02 μm = % ionic silver	Difference = % nanorod silver
S-PVP	2.2	0.6	1.6%
L-PVP	1.0	0.2	0.8%
S-SiO2	4.4	4.4	<0.1%
L-SiO2	0.5	0.4	<0.1%

Table S1. Estimate of the proportion of silver nanorods in AgNW suspensions.

200~uL of AgNW stock solution was added to 25~mL ultrapure water and stirred for about 10 minutes. Aliquots of each solution were passed through 0.45 μm or 0.02 μm diameter filters that retained just the AgNWs, or the AgNWs and nanorods, respectively. The filtered solutions were acidified with concentrated nitric acid and measured by ICP-MS for total silver.

СОМВО		EPA			
Chemical	Concentration (mg/L)	Chemical	Concentration (mg/L)		
CaCl ₂ •2H ₂ O	55	NaHCO ₃	0.192		
MgSO ₄ •7H ₂ O	55.5	MgSO ₄ •7H ₂ O	0.246		
K ₂ HPO ₄	4.36	CaSO ₄ •2H ₂ O	0.12		
NaNO ₃	42.5	KCl	0.008		
NaHCO ₃	50.5				
Na ₂ SiO ₃ •9H ₂ O	14.2				
H ₃ BO ₃	12				

Table S2. Chemical compositions of the simulated freshwater media used in this study.

COMBO		ЕРА		
Species	Conc. in nM (µg/L)	Species	Conc. in nM (µg/L)	
AgCl ⁰	5.1 (0.55)	Ag+	7.8 (0.84)	
Ag+	3.8 (0.41)	AgCl ⁰	1.4 (0.15)	
AgCl ₂ -	0.3 (0.037)	AgSO ₄ -	0.1 (0.014)	
AgSO ₄ -	0.013 (0.0014)	AgCl ₂ -	0.013 (0.0014)	

COMBO simulated freshwater solutions.

Ranked in order of decreasing concentration. The pH was fixed at 8 and the total silver concentration was $1\mu g/L$

Media	Treatment	LC ₅₀ µg/L	95% confidence interval
СОМВО	PVP-S	421.0	322.2 - 602.6
СОМВО	PVP-L	233.9	210.1 - 257.2
СОМВО	SiO2-S	155.0	140.5 - 169.2
COMBO	SiO2-L	522.0	404.0 - 638.3
СОМВО	AgNO3	0.8	0.4 - 1.3
EPA	PVP-S	260.7	139.5 - 319.6
EPA	PVP-L	415.4	297.8 - 563.4
EPA	SiO2-S	3.6	1.7 - 5.8
EPA	SiO2-L	226.5	28.0 - 382.4
EPA	AgNO3	0.6	0.28 - 1.2

analyses.

Each LC_{50} is representative of at least 12 replicates of six AgNW exposure concentrations containing five daphnids each.

Nickname	Reason	Protein	Changes	Direction	Sequence
7657	all affected	unknown	all down	Forward	GGGGTGGCCATCGCTGTTAGTC
				Reverse	TCCATCGCGGCATCGTCCACT
7499	fold change	unknown	LP-, SP-	Forward	AACCTCTGCCAACCAGCCGTT
				Reverse	CGCCGACGGCCTCCATGATT
2267	q-value	carbonic anhydrase	LP-	Forward	AGCAGCTCGAATCTTTCCGCGA
				Reverse	TGCTCAACCGACAACGGTGGG
4057	fold change	conidiospore surface	LP+. SS-	Forward	CGGTGGCGATTACGTTCCTTCACC
		protein		Reverse	GCGCGAGGGTAATAGGGGGC
1395	mode of tox	ribosomal	LS+, SS+	Forward	TACGAGCTTCGGACGAGCCCT
				Reverse	TCCCCGTGCAGCAAAGACAAGG
18S	mode of tox	ribosonal	Ag+?	Forward	CGC TCT GAA TCA AGG GTG TT
				Reverse	AAC CCC GAA GAG GAA GAA AA
GAPDH	house	GAPDH	n/a	Forward	GGGGACAGACGTTTCCTGTA
				Reverse	AAGGGGTCATTGACAGCAAC
actin	house	actin	n/a	Forward	GGTATGTGCAAGGCTGGATT
				Reverse	GGTGTGGTGCCAGATCTTTT

Table S5. List of genes and corresponding primers used in qPCR verification of microarraydata.

Sample	GAPDH	4057/ fold	dCt	2^-dCt	Average	P-Value
con	23.720	33.740	10.020	0.001	0.001	
con	24.380	33.750	9.370	0.002		
con	24.620	33.720	9.100	0.002	Fold Change	
SS	22.740	32.560	9.820	0.001	0.772	0.097
SS	22.800	33.290	10.490	0.001	0.485	
SS	21.370	32.290	10.920	0.001	0.360	
Sample	GAPDH	7657/ all down	dCt	2^-dCt	Average	P-Value
con	23.720	25.010	1.290	0.409	0.378	
con	24.620	26.150	1.530	0.346	Fold Change	
Ag	23.270	24.700	1.430	0.371	0.983	0.588
Ag	22.780	24.340	1.560	0.339	0.898	
SS	22.740	24.700	1.960	0.257	0.681	0.072
SS	22.800	24.860	2.060	0.240	0.635	
SS	21.370	24.560	3.190	0.110	0.290	
LS	22.760	25.160	2.400	0.189	0.502	0.273
LS	22.720	24.310	1.590	0.332	0.880	
SP	22.050	28.420	6.370	0.012	0.032	0.002
SP	22.930	26.790	3.860	0.069	0.182	
SP	23.260	27.590	4.330	0.050	0.132	
Sample	actin	1395/ brix	dCt	2^-dCt	Average	P-Value
con	21.980	26.790	4.810	0.036	0.043	
con	22.540	26.830	4.290	0.051	Fold Change	
SS	21.110	25.120	4.010	0.062	1.431	0.580
SS	19.850	24.440	4.590	0.042	0.957	
LS	20.810	26.460	5.650	0.020	0.459	0.026
LS	20.420	26.280	5.860	0.017	0.397	

LS	20.890	26.540	5.650	0.020	0.459	
Sample	actin	18S ribosome	dCt	2^-dCt	Average	P-Value
con	21.980	12.730	-9.250	608.874	499.798	
con	22.540	13.930	-8.610	390.722	Fold Change	
Ag	22.060	12.070	-9.990	1016.927	2.035	0.442
Ag	21.980	12.990	-8.990	508.463	1.017	
Sample	actin	7499/ fold	dCt	2^-dCt	Average	P-Value
con	21.980	26.400	4.420	0.047	0.060	
con	22.540	26.300	3.760	0.074	Fold Change	
SP	19.430	27.690	8.260	0.003	0.054	0.068
SP	20.530	26.810	6.280	0.013	0.214	
LP	20.200	26.930	6.730	0.009	0.156	0.016
LP	20.920	27.440	6.520	0.011	0.181	
LP	21.700	28.430	6.730	0.009	0.156	
Comple		00(7/)	10	0.4 10	A	
Sample	actin	2267/q-value	act	2 ⁿ -dCt	Average	
con	21.980	2267/q-value 23.920	act 1.940	0.261	0.398	P-Value
con con	21.980 22.540	2267/q-value 23.920 23.440	act 1.940 0.900	0.261 0.536	0.398 Fold Change	P-Value
con con LP	actin 21.980 22.540 20.200	2267/q-value 23.920 23.440 23.420	act 1.940 0.900 3.220	0.261 0.536 0.107	Average0.398Fold Change0.269	P-Value 0.081
con con LP LP	actin 21.980 22.540 20.200 20.920	2267/q-value 23.920 23.440 23.420 23.640	act 1.940 0.900 3.220 2.720	0.261 0.536 0.107 0.152	Average 0.398 Fold Change 0.269 0.381	P-Value 0.081
con con LP LP LP	actin 21.980 22.540 20.200 20.920 21.700	2267/q-value 23.920 23.440 23.420 23.640 24.690	act 1.940 0.900 3.220 2.720 2.990	0.261 0.536 0.107 0.152 0.126	Average 0.398 Fold Change 0.269 0.381 0.316	P-Value 0.081
con con LP LP LP Sample	actin 21.980 22.540 20.200 20.920 21.700 actin	2267/q-value 23.920 23.440 23.420 23.640 24.690 4057/ fold	act 1.940 0.900 3.220 2.720 2.990 dct	2^-dCt 0.261 0.536 0.107 0.152 0.126 2^-dct	Average0.398Fold Change0.2690.3810.316Average	P-Value 0.081 P-Value
con con LP LP LP Sample con	actin 21.980 22.540 20.200 20.920 21.700 actin 24.320	2267/q-value 23.920 23.440 23.420 23.640 24.690 4057/ fold 35.790	act 1.940 0.900 3.220 2.720 2.990 dct 11.470	2^-dCt 0.261 0.536 0.107 0.152 0.126 2^-dct 0.000	Average 0.398 Fold Change 0.269 0.381 0.316 Average 0.001	P-Value 0.081 P-Value
con con LP LP LP Sample con con	actin 21.980 22.540 20.200 20.920 21.700 actin 24.320 25.600	2267/q-value 23.920 23.440 23.420 23.640 24.690 4057/ fold 35.790 35.870	act 1.940 0.900 3.220 2.720 2.990 dct 11.470 10.270	2^-dCt 0.261 0.536 0.107 0.152 0.126 2^-dct 0.000 0.001	Average 0.398 Fold Change 0.269 0.381 0.316 Average 0.001	P-Value 0.081 P-Value
con con LP LP LP Sample con con con	actin 21.980 22.540 20.200 20.920 21.700 actin 24.320 25.600 25.160	2267/q-value 23.920 23.440 23.420 23.640 24.690 4057/ fold 35.790 35.870 35.580	act 1.940 0.900 3.220 2.720 2.990 dct 11.470 10.270 10.420	2^-dCt 0.261 0.536 0.107 0.152 0.126 2^-dct 0.000 0.001 0.001	Average0.398Fold Change0.2690.3810.316Average0.001Fold Change	P-Value 0.081 P-Value
con LP LP LP Sample con con con LP	actin 21.980 22.540 20.200 20.920 21.700 actin 24.320 25.600 25.160 24.380	2267/q-value 23.920 23.440 23.420 23.640 24.690 4057/ fold 35.790 35.870 35.580 23.430	act 1.940 0.900 3.220 2.720 2.990 dct 11.470 10.270 10.420 -0.950	2^-dCt 0.261 0.536 0.107 0.152 0.126 2^-dct 0.000 0.001 0.001 1.932	Average 0.398 Fold Change 0.269 0.381 0.316 Average 0.001 Fold Change 3062.721	P-Value 0.081 P-Value 0.161
con LP LP LP Sample con con con LP LP	actin 21.980 22.540 20.200 20.920 21.700 actin 24.320 25.600 25.160 24.380 24.970	2267/q-value 23.920 23.440 23.420 23.640 24.690 4057/ fold 35.790 35.870 35.880 23.430 26.660	act 1.940 0.900 3.220 2.720 2.990 dct 11.470 10.270 10.420 -0.950 1.690	2^-dCt 0.261 0.536 0.107 0.152 0.126 2^-dct 0.000 0.001 1.932 0.310	Average 0.398 Fold Change 0.269 0.381 0.316 Average 0.001 Fold Change 3062.721 491.347	P-Value 0.081 P-Value 0.161

con	21.070	26.000	4.930	0.033	0.052	
con	21.950	25.770	3.820	0.071	Fold Change	
SS	20.490	24.230	3.740	0.075	1.445	0.724
SS	20.370	24.760	4.390	0.048	0.921	
LS	20.090	25.550	5.460	0.023	0.439	0.129
LS	20.140	25.510	5.370	0.024	0.467	
LS	20.180	25.880	5.700	0.019	0.371	

Table S6. Results from RT-q-PCR analysis.

Green highlights indicate agreement with microarray data, red indicates disagreement and blue indicates variation in results. All primers tested agreed with array data except for primer 1395, a protein associated with ribosomal biogenesis.

Table S7. The complete list of differentially expressed genes and BLAST analysis.

Located in a separate file (Scanlan Supplement S7) due to size of file. S7 contains foldchange and q-value information.

GeneID	Protein Function	L-PVP	L-SiO2	S-PVP	S-SiO2	Ag+
DM02485P1	Solute Carrier	-0.6				
DM05687P2	ABC related					-3.2
DM01730P3	Calcium transporting ATPase					-1.9
DM06992P4	Iron(III) dicitrate permease protein fecC		1.1			
DM06914P2	Fe Transport			-2.4	-1.4	
DM04501P3	sodium-dependent phosphate transporter			-0.2		
DM02022P2	Na/K-transporting ATPase subunit alpha			-1.1		
DM01589P2	Na/K-transporting ATPase subunit alpha				-0.7	
DM03514P2	sodium/solute symporter			-0.5		

Table S8. Probes identified by BLAST as transporter proteins that were differentiallyexpressed in response to AgNW exposure.

Red: sodium transporters; blue: other transporters.

Table S9. Detailed results for the Blast2Go functional enrichment analysis.

	Abiotic Ag+ release data						
Exposure	Ag added as NW (ug/L)	Ag+ released (ug/L)	Fraction released	NW LD ₅₀ (ug/L)	Expected Ag ⁺ release at LD ₅₀	Ag ⁺ LD ₅₀ (ug/L)	[Ag ⁺] / Ag ⁺ LD ₅₀
AgNW-S- SiO2 COMBO	12,000	8.9	0.00074	155	0.115	0.8	0.14
AgNW-S- SiO2 EPA	12,000	2.7	0.00022	3.6	0.00081	0.6	0.0014
AgNW-S- PVP EPA	12,000	1.6	0.00013	260.7	0.0347	0.6	0.058
AgNW-L- SiO2 EPA	12,000	0.3	0.00002 5	226.5	0.0056	0.6	0.0094

Data are found in a separate excel file, Scanlan Supplement S9.

Table S10. Estimation of the contribution of Ag⁺ to AgNW toxicity.

For each sample, the amount of Ag^+ released in abiotic trials at a concentration of 12 mg/L Ag (*c.f.* Figure 2) is scaled proportionally to the LD_{50} concentrations of AgNWs for the same sample and media. The last column reports the ratio between the LD_{50} for dissolved silver and the concentration of dissolved predicted released silver for each AgNW sample. Because all values are less than unity, typically much less than unity, Ag⁺ release in solution cannot be the major cause of toxicity.

SUPPORTING FIGURES



Figure S1. Transmission electron microscope images of PVP-coated silver nanorod impurities observed in the short (2 μ m long) AgNW sample.



Figure S2. Dynamic Light Scattering (DLS) observation of the stability of (a) PVP-NW and (b) SiO₂-NW in COMBO media. Initially, both samples contained a proportion of individual nanowires and small aggregates. After 24 hours, no change in aggregation state of S-PVP-NW was observed. By contrast, micron-scale aggregates of S-SiO₂-NW appeared after this time. Aggregation and settling for S-SiO₂-NW in EPA was significantly more pronounced, leading to poor quality DLS data (not shown).

Note: the algorithm used to transform DLS correlation functions to hydrodynamic radii assumed spherical particle morphology, and hence the horizontal axis is not accurate.



Figure S3. UV-vis determination of relative settling rates of AgNWs in *Daphnia* growth media. (a) Series of optical absorption spectra acquired from unstirred suspension of L-PVP-NW in COMBO media. The AgNW exhibited two characteristic surface plasmon resonance peaks. (b) Time dependent drop in absorbance (a) due to AgNW settling, monitored at 380 nm in a 1-cm pathlength cuvette with the beampath 1.5 cm beneath the solution meniscus.



Figure S4. Transmission electron microscope image of a SiO_2 -coated AgNW shows

morphological changes in the silica coating.



Figure S5. Transmission electron microscopy of (left) poly(vinylpyrrolidone)-coated (PVP) and (right) amorphous aluminum-doped silica-coated (SiO₂) AgNWs taken from the stock solutions. All SiO₂-NW exhibited enclosed voids at the tip, caused by preferential etching of silver during the removal of PVP and precipitation of the inorganic coating. The SiO₂ coatings were stable in the anaerobic stock solution.



Figures S6. Venn diagram of differentially expressed genes in each as compared to the media-only control. Gene commonly expressed in only the AgNW exposures may be useful biomarkers of exposure.





coated AgNWs in COMBO media (S-SiO₂-NW).



Figure S8. Scanning electron microscope analysis of a silver-rich precipitate located in the dried hemolymph of a daphnid exposed to ~ 2 -µm-long silica-coated AgNWs at the LC₅₀ concentration. **(a)** Precipitate imaged using the back-scattering detector (BSD) and secondary electron detector (SED). **(b)** X-ray fluorescence signal from the precipitate.



Figure S9. Nanoparticulate silver in hemolymph following Ag⁺(*aq*) **exposure. a)** Raw data from spICPMS analysis of diluted hemolymph from daphnids exposed to the LC₅₀ for silver nitrate. **b)** Corresponding distribution of particulate masses (assuming pure Ag).



Figure S10. **PVP-coated AgNWs were detectable using optical light microscopy in dark-field mode. a)** Dark-field micrograph of PVP-coated AgNW in COMBO medium. 100x objective. **b)** Dark-field micrograph of AgNW in COMBO following the addition of 4% paraformaldehyde and a 3-hour fixation period. The fixative caused all NWs to lose their luster. Following fixation, only AgNWs that adhered to the glass slide were detectable; no daphnid-associated AgNW could be identified.



Figure S11. AgNWs in the *D. magna* rostrum. Daphnid head imaged in a) bright-field and

b) dark-field mode. Arrows in **b)** indicate individual mobile AgNW.



Figure S12. **AgNW in the gut anterior.** Dark-field imaging of the anterior region of the gut of AgNW-exposed daphnids revealed freely-diffusing AgNWs. **a)** Bright-field image at low-magnification, showing region-of-interest (ROI; red box). **b)** Higher-magnification dark-field images. The sequence of images 1-5 captured over approximately 3 minutes show a number of internal AgNW to be moving.



Figure S13. **AgNW in the brood chamber. a)** Bright-field image at low-magnification showing eggs in the brood hatch behind the gut. **b)** Stationary AgNWs adhering to the daphnid exterior (top image pair), and moving AgNWs inside the brood hatch (bottom image pair) could be distinguished by adjusting the microscope focus.



Figure S14. **Dark-field imaging of daphnid gut**. Dark-field imaging of the gut of **a)** control and **b)** AgNW-exposed daphnids. Few putative AgNWs could be imaged in the gut of the exposed organisms. However, the entire gut contents of the exposed individuals gave much brighter signal in the dark-field mode than the control. The gut contents appeared to be consistent with aggregated or transformed AgNWs closely associated with food, in which individual AgNWs could not be resolved with the resolution of the optical microscope.



Figure S15. Tests of Ag⁺(*aq*) retention in the 0.2-µm filters used to remove AgNWs from suspension prior to elemental analysis of dissolved silver. We passed four 1-mL aliquots of 1, 10 or 100 nM standard silver nitrate solutions through a fresh filter and analyzed each aliquot for total silver.

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