Supplementary materials

Parameters	РН	DO(mg L ⁻¹)	Cond.(µs cm⁻¹)	Sal	NTU	OPR(mv)	Chla (µg L ⁻¹)	TDS (mg L ⁻¹)
Stream water	6.78	4.81	0.036	0.017	0.44	160	0.77	24
Parameters	TSS(mg L ⁻¹)	DOC (mg L ⁻¹)	ТР	NH₄⁺ (ppm)	т (°С)	TN	Mg ²⁺ (mg L ⁻¹)	Ca ²⁺ (mg L ⁻¹)
Stream water	3.01	1.08	0.042	0.79	20.41	1.73	4.56	68

Table S1. Hydrographical and chemical characteristics of stream waters during leaf immersion.

DO = dissolved oxygen; Cond = conductivity; Sal = Salinity; TSS = total suspended solids; DOC = dissolved organic carbon; TN = total nitrogen; TP = total phosphorus; Chl-a = chlorophyll-a; NTU

= turbidity; OPR= oxidation reduction potential; TDS =total dissolved solids oxygen; T = temperature.

Table S2. Summary of microcosm and mesocosm experiments with freshwater microbial communities to test for effects of AgNP over a period of at least 2 days and thus potentially involving

microbial community shifts.

Factoria	Orregione		Duration (day)	Referenc	
Ecosystem	Organisms	Agine concentration ($\mu g L^{-}$)	Duration (day)	e	
Stream (leaf litter)	Fungi and bacteria	100000 and 300000	7, 14 and 21	1	
Stream (water column)	Bacterioplankton	750, 7500 and 75000	12	2	
Stream/lake (water column)	Bacterioplankton	50, 100, 500, 1000, and 10000	2	3	
Lake (water column)	Bacterioplankton	10, 20, 100 and 1000	2 and 5	4	
Lake (water column)	Bacterioplankton	0. 22, 0. 89, 3.56 and 60	42	5	
Stream (leaf litter)	Fungi and bacteria	5.4 and 54	5 and 25	6	
Stroom (loof littor)	Functional hostoria	50, 250, 500, 1000, 5000, 10000,	21	7	
Stream (lear litter)	Fungi and Dacteria	25000 and 75000	21	/	

Stream (leaf litter)Fungi and bacteria250, 2500 and 5000218

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Table S3. Abundance and diversity of fungal and bacterial communities associated with the litter decomposition. N: natural light simulation group; A: artificial light at night simulation group. Different lower letters denote a significant difference between treatments (*P* < 0.05; Tukey's test).

	Samples	Base	Valid reads	Sequence	OTUs	Sobs	Shannon	Simncon	ACE	Chaol
	Samples	number		number	number		Shannon	Simpson	ACE	CliaO1
	Origin	23,411,466 ª	45,592ª	58,462ª	395ª	306 ª	3.06ª	0.16 ^b	335ª	341 ª
	N	20,089,101 ^b	41,912 ^b	49,342 ^b	401 ª	223 ^{bc}	2.05 ^b	0.37ª	247 ^{bc}	249 ^{bc}
Funci	N_AgNO₃	19,430,122°	45,309ª	48,461 ^b	282 ^b	167 ^b	2.51 ^b	0.20 ^{ab}	181 ^b	181 ^b
Fungi	N_AgNP	19,718,628°	44,175ª	50,203 ^b	287 ^b	170°	2.22 ^b	0.26 ^{ab}	193°	194°
	Α	19,775,847°	40,709 ^b	49,508 ^b	362 ^b	163°	2.12 ^b	0.29 ^{ab}	175°	183°
	A_ AgNO₃	19,337,711°	44,668ª	48,158 ^b	282 ^b	210 ^{bc}	2.61 ^b	0.22 ^{ab}	235°	236 ^{bc}

	A_AgNP	19,777,077°	43,319 ^{ab}	49,531 ^b	292 ^b	172 ^{bc}	2.39 ^b	0.17 ^b	199 ^{bc}	211 ^{bc}
	Origin	21,798,024 ^{ab}	35,967 ^b	49,693 ^{bc}	1,614ª	1,290ª	5.44ª	0.020 ^c	1,474ª	1,503ª
	Ν	23,061,790 ª	37,267 ^b	52,567 ^{ab}	1,621ª	1,292ª	5.71ª	0.009°	1,465ª	1,479ª
	N_ AgNO ₃	18,268,817 ^b	37,986 ^b	41,313 ^{cd}	1,330 ^b	931 ^d	4.12 ^{bc}	0.069ª	1,188 ^b	1,204 ^b
Bacteria	N_AgNP	21,181,498 ªb	37,087 ^b	47,786 ^{bc}	1,146°	793 ^{bc}	4.67°	0.024 ^c	989°	996°
	Α	25,665,199 ª	45,250ª	58,516ª	1,557ª	1,256ª	5.46ª	0.015°	1,450ª	1,465ª
	A_ AgNO ₃	17,075,368 ^b	35,342 ^b	38,648 ^d	1,365 ^b	995°	4.51 ^a	0.045 ^b	1,189 ^b	1,203 ^b
	A_AgNP	19,943,143 ^b	36,491 ^b	45,165 ^{bcd}	1,201 ^c	861 ^b	4.89 ^{bc}	0.017 ^c	1,062 ^{bc}	1,075 ^{bc}

Table S4. PERMANOVA showing the significant Bray-Curtis distance-based dissimilarities of fungal and bacterial community composition among initial samples, the control (N) and artificial light at night (A), N-AgNO₃ and A-AgNO₃, N-AgNP and A-AgNP treatments.

		Ν	А	$N-AgNO_3$	N-AgNP	A-AgNO ₃	A-AgNP
	Initial	0.005	0.004	0.06	0.006	0.04	0.01
	Ν		0.03	0.02	0.02	0.007	0.004
Franci	А			0.001	0.03	0.004	0.001
Fungi	$N-AgNO_3$				0.01	0.3	0.006
	N-AgNP					0.007	0.01
	A-AgNO ₃						0.001
Bacteria	Initial	0.002	0.002	0.01	0.001	0.01	0.001

Ν	0.2	0.001	0.002	0.001	0.001
А		0.001	0.001	0.002	0.004
N-AgNO ₃			0.01	0.2	0.01
N-AgNP				0.006	0.1
A-AgNO ₃					0.005

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Figure S1. Dry mass remaining of *P. stenoptera* leaf litter during the decomposition process, presented as a percentage of initial values (mean ± standard error, n = 3). N: Natural lighting simulation group; A: artificial light at night simulation group.



Figure S2. Heatmap of 50 most abundant genus of fungi (a) and bacterial (b) in samples collected from different treatments. The phylogenetic tree was calculated using the neighbor-joining method, while the relationship among samples was determined using Bray distance and the complete clustering method. The heatmap colors represent the relative percentages of the microbial genus assignments within each sample. Square colors shifted from green towards red indicate higher abundance. Note: N: natural lighting simulation group; A: artificial light at night simulation group.



Figure S3. Changes in the enzymatic activities of leaf litter during the decomposition process. Legends: (a) acid phosphatase, AP; (b) leucine-aminopeptidase, LAP; (c) β-glucosidase, β-G; (d) cellobiohydrolase, CBH; (e) polyphenol oxidase, PPO; (f) phenol oxidase, POD; N: Natural lighting simulation group; A: artificial light at night simulation group. Different letters denote a significant difference between treatments at the same sampling time (*P* < 0.05; Tukey's test).



Figure S4. Principal component analysis of the correlation patterns of enzymatic activities and litter decomposition rate in the treatments with natural light (N) (a), ALAN (A) (b), N-AgNO₃ (c), A-AgNO₃ (d), N-AgNP (e) and A-AgNP (f). Legends: acid phosphatase, AP; leucine-aminopeptidase, LAP;β-glucosidase, β-G; cellobiohydrolase, CBH; polyphenol oxidase, PPO; phenol oxidase, POD; and litter decomposition rate, k.