Rapid assessment of changes in phage bioactivity using dynamic light scattering

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This PDF file includes:

Figures S1 to S2
Tables S1 to S2

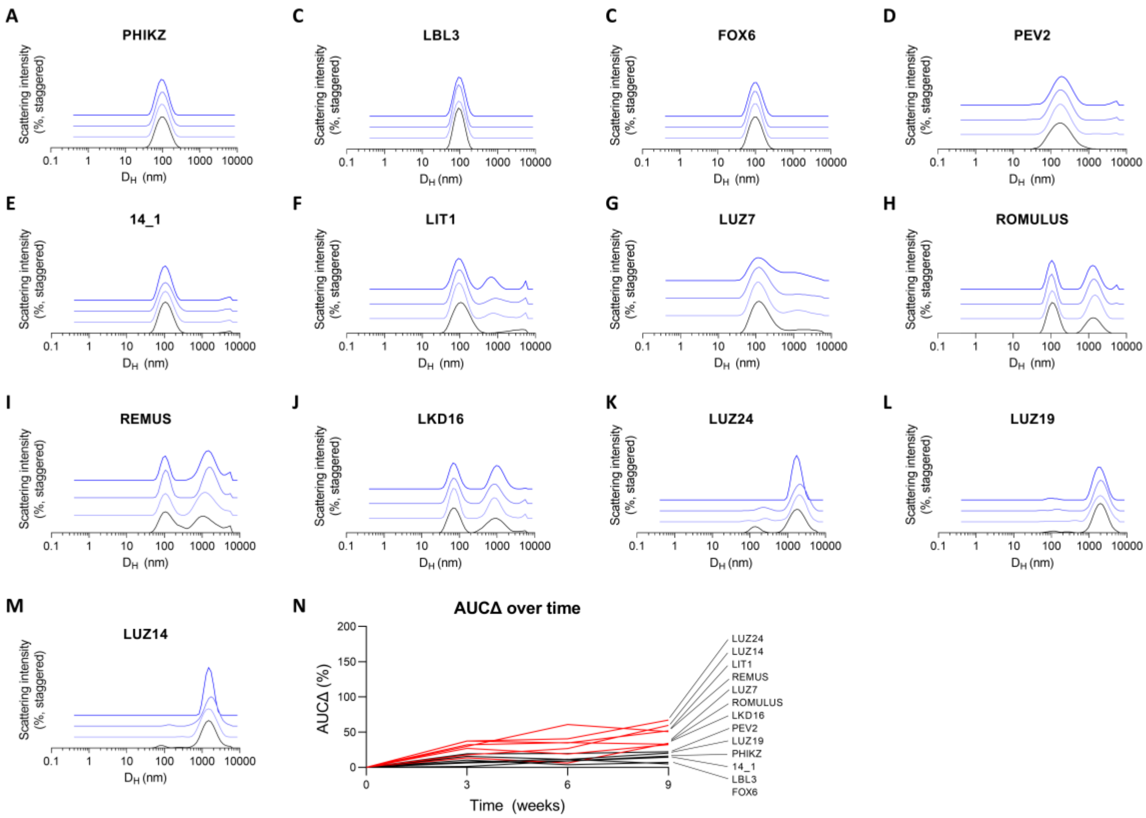

Fig. S1. Phages spontaneously fragment and aggregate in refrigerated storage over time (Belgian cohort).

(**A** through **M**) DLS spectra of phages from the Belgian cohort (BC) over a monitoring period of two months. Shown are averages of n=3 DLS measurements per phage. n=13 phages were assessed. Darker colors and vertical staggering are used to show progression in time. Few phages remained largely intact (**A** through **C**). Most phages aggregated over the monitoring period (**D** through **M**). (**N**) AUCΔ identifies the most-changed phage over the monitoring period and is consistent with our qualitative assessment of the DLS spectra.

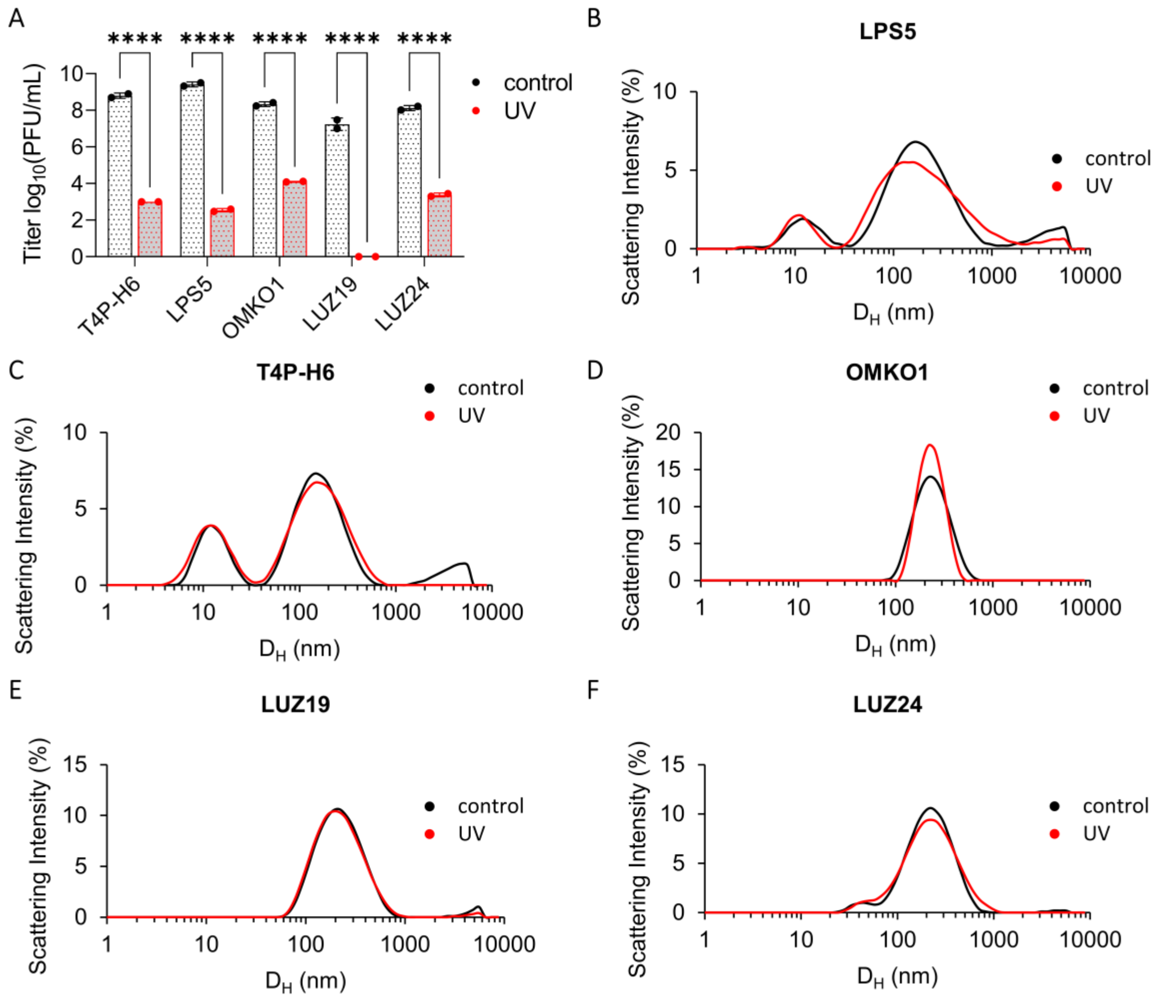

Fig. S2: DLS captures changes in phage size, but it does not capture genomic damage.
(**A**) Titer of phages after irradiation for 20 minutes with germicidal UV-C light. Results are from one experiment. Titer was measured with n=2 plaque assays per phage per condition. Two-way ANOVA with Tukey correction. **** = $p < 0.0001$. (**B** through **F**) DLS spectra of phages before and after irradiation. Shown are averages of n=3 DLS measurements per phage per condition.

Table S1. Physical and biological characteristics of CYPHY phages.

Phage	T4P-H6	LPS5	OMKO1
Plaque characteristics	Clear, well-circumscribed Size: 0.3 – 1 mm	Clear, well-circumscribed Size: 1.5 – 2.0 mm	Clear, well-circumscribed Size: 0.5 – 1.5 mm
Dimensions	Tail length: 190 ± 5 nm Tail width: 16 ± 2 nm Head length: 74 ± 2 nm Head shape: isometric	Tail length: 140 ± 2 nm Tail width: 20 ± 1 nm Head length: 70 ± 3 nm Head shape: isometric	Tail length: 212 ± 2 nm Tail width: 28 ± 1 nm Head length: 134 ± 4 nm Head shape: isometric
Morphology	*Siphoviridae*	*Myoviridae*	*Myoviridae*

Table S2. Phages used in this study.

Phage	Taxonomy	Bacterial Host	Morphology	genome size (kb)	dim. (nm) capsid / tail
LUZ14	*Autographiviridae*	*P. aeruginosa* C1	podovirus	~43	62/12
LUZ19	*Autographiviridae, Phikmvvirus*	*P. aeruginosa* PA01 K	podovirus	43.5	65/12
LUZ24	*Bruynoghevirus*	*P. aeruginosa* Li010	podovirus	45.6	63/12
LKD16	*Autographiviridae, Phikmvvirus*	*P. aeruginosa* GHB15	podovirus	43.2	65/12
LUZ7	*Schitoviridae, Luzseptimavirus*	*P. aeruginosa* Br257	podovirus	74.9	76/30
PEV2	*Schitoviridae, Litunavirus*	*P. aeruginosa* PA01 K	podovirus	72.7	70/30
LIT1	*Schitoviridae, Litunavirus*	*P. aeruginosa* US449	myovirus	72.5	74/30
LBL3	*Pbunavirus*	*P. aeruginosa* C1	myovirus	64.4	73/148
14_1	*Pbunavirus*	*P. aeruginosa* Li010	myovirus	66.2	73/148
PhiKZ	*Phikzvirus*	*P. aeruginosa* Aa245	myovirus	280.3	145/200
Romulus	*Herelleviridae, Silviavirus*	*S. aureus* (broad host range)	myovirus	131.3	90/204
Remus	*Herelleviridae, Silviavirus*	*S. aureus* (broad host range)	myovirus	134.6	90/204
Fox6	*Carmasinavirus*	*X. campestris* pv. *campestris* I11008	myovirus	61.1	78/156
OMKO1	*Phikzvirus*	*P. aeruginosa* PAO1	myovirus	281.8	134/212
LPS5	*Pakpunavirus*	*P. aeruginosa* PAO1	myovirus	93.1	70/140
T4P-H6	*Nipunavirus*	*P. aeruginosa* PA14	siphovirus	57.4	74/190
T2	*Straboviridae, Tequatrovirus*	*E. coli* B	myovirus	163.8	111/78
T3	*Autographiviridae, Teetrevirus*	*E. coli* B	podovirus	38.3	60/30
T4	*Straboviridae, Tequatrovirus*	*E. coli* B	myovirus	168.9	111/78
T6	*Straboviridae, Tequatrovirus*	*E. coli* B	myovirus	170	120/86
T7	*Autographiviridae, Tespetimavirus*	*E. coli* B	podovirus	39.9	55/29