

Algal viruses and cyanophages have distinct distributions in Lake Erie sediments

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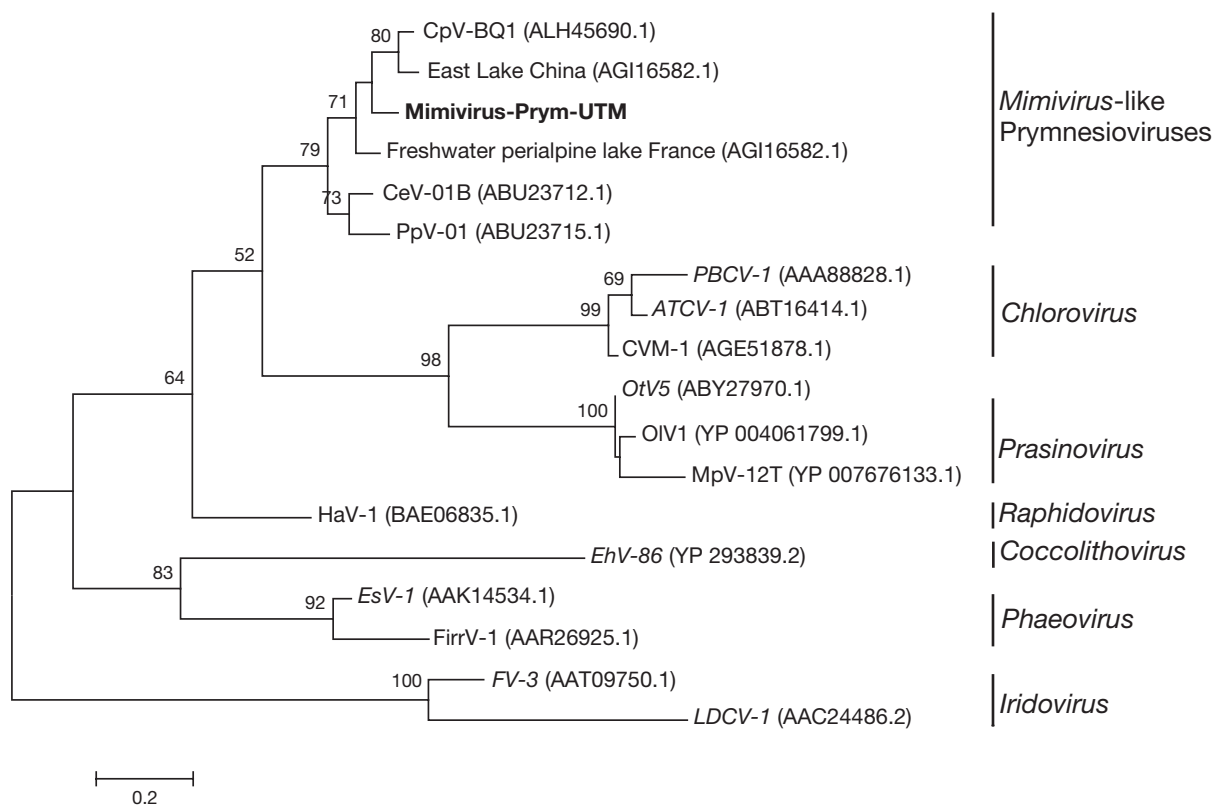


Fig. S1. Maximum likelihood phylogenetic tree of inferred putative major capsid protein amino acid sequences using the Jones-Taylor-Thornton amino acid substitution with 1000 bootstrap iterations. The bolded sequence was used to design a qPCR primer and probe set. Accession numbers for reference sequences are in parentheses.

Table S1. BLASTP search results for *po/B* OTU representative sequences.

OTU	Stations present	First Cultivated blastp match (#, name)	*Percent Identity (%)
KY082166	452	AAR05084.1 <i>Phaeocystis globosa</i> virus PgV-03T	46 - 49
KY082167	452; 882; 1326	ACP44143.1 <i>Bathycoccus</i> virus BpV178	76 - 78
KY082168	452; 1326	ACP44143.1 <i>Bathycoccus</i> virus BpV178	80 - 81
KY082169	882	YP_009174732.1 Yellowstone lake phycodnavirus 1	51 - 52
KY082170	882; 973; 1326	ACP44143.1 <i>Bathycoccus</i> virus BpV178	97 - 98
KY082171	882	ACP44143.1 <i>Bathycoccus</i> virus BpV178	79 - 80
KY082172	882	YP_009174732.1 Yellowstone lake phycodnavirus 1	51
KY082173	882	ACP44143.1 <i>Bathycoccus</i> virus BpV178	93
KY082174	882; 1326	ALH45659.1 <i>Chrysochromulina parva</i> virus BQ1	98 - 99
KY082175	882	ACP44143.1 <i>Bathycoccus</i> virus BpV178	78
KY082176	882	ADA81909.1 <i>Ostreococcus lucimarinus</i> virus OIV158	69
KY082177	452; 882; 973; 1326	AKR54192.1 <i>Micromonas</i> virus RCC:4266	77 - 78
KY082178	882; 973; 1326	FJ884779.1 <i>Ostreococcus tauri</i> virus 2 isolate OtV60	79 - 80
KY082179	882; 1326	ACP44143.1 <i>Bathycoccus</i> virus BpV178	68 - 70
KY082180	1326; 452	ACP44143.1 <i>Bathycoccus</i> virus BpV178	79 - 81
KY082181	1326	AKR54192.1 <i>Micromonas</i> virus RCC:4266	82
KY082182	1326	ACP44143.1 <i>Bathycoccus</i> virus BpV178	79
KY082183	1326	YP_009174598.1 Yellowstone lake phycodnavirus 2	86
KY082184	1326	AKR54192.1 <i>Micromonas</i> virus RCC:4266	78 - 80
KY082185	1326	ACP44120.1 <i>Micromonas</i> virus MiV130	80

*Where multiples sequence variants make up OTU, a range of identities is reported

Table S2. BLASTP search results for g20 OTU representative sequences.

OTU	Stations present	First Cultivated blastp match (#, name)	*Percent Identity (%)
KY082090	452; 1326	YP_214363.1 <i>Prochlorococcus</i> phage P-SSM2	90
KY082091	452	YP_007001618.1 <i>Synechococcus</i> phage metaG-MbCM1	63
KY082092	452	AAC23540.1 Cyanophage S-BnM1	63 - 65
KY082093	452; 1326	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	65 - 66
KY082094	452	YP_007674507.1 <i>Synechococcus</i> phage S-SKS1	88
KY082095	452	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	65
KY082096	882	YP_003097343.1 <i>Synechococcus</i> phage S-RSM4	92
KY082097	882	AAC23540.1 Cyanophage S-BnM1	65
KY082098	882	YP_007674507.1 <i>Synechococcus</i> phage S-SKS1	90 - 91
KY082099	882	YP_004323487.1 <i>Prochlorococcus</i> phage P-HM2	62
KY082100	882	YP_009133666.1 <i>Synechococcus</i> phage ACG-2014g	67
KY082101	882	YP_004322786.1 <i>Synechococcus</i> phage S-ShM2	62
KY082102	882	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	64
KY082103	882	YP_004322541.1 <i>Prochlorococcus</i> phage P-HM1	62
KY082104	882	YP_003097343.1 <i>Synechococcus</i> phage S-RSM4	94
KY082105	882	YP_004323727.1 <i>Prochlorococcus</i> phage Syn33	69
KY082106	882	YP_007673103.1 <i>Synechococcus</i> phage S-CAM1	94
KY082107	882	YP_195138.1 <i>Synechococcus</i> phage S-PM2	67
KY082108	882	YP_007673103.1 <i>Synechococcus</i> phage S-CAM1	92
KY082109	882	YP_214665.1 <i>Prochlorococcus</i> phage P-SSM4	65
KY082110	882	YP_004323487.1 <i>Prochlorococcus</i> phage P-HM2	59
KY082111	882; 1326	YP_007674507.1 <i>Synechococcus</i> phage S-SKS1	82 - 83
KY082112	882	AAK31670.1 <i>Synechococcus</i> phage S-PWM1	68
KY082113	882	YP_007001618.1 <i>Synechococcus</i> phage metaG-MbCM1	69
KY082114	882	YP_004324197.1 <i>Synechococcus</i> phage S-SSM7	85

OTU	Stations present	First Cultivated blastp match (#, name)	*Percent Identity (%)
KY082115	882	ACD93434.1 Cyanophage P-RSM5	90
KY082116	882	YP_004323727.1 <i>Prochlorococcus</i> phage Syn33	64
KY082117	882	AMO43137.1 Cyanophage S-RIM32	66
KY082118	882	YP_214363.1 <i>Prochlorococcus</i> phage P-SSM2	64
KY082119	882; 973	YP_007673103.1 <i>Synechococcus</i> phage S-CAM1	94 - 95
KY082120	882	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	64
KY082121	882	YP_009188207.1 Cyanophage P-TIM40	67
KY082122	882	YP_009213616.1 <i>Prochlorococcus</i> phage P-TIM68	67 - 68
KY082123	882	YP_717798.1 <i>Synechococcus</i> phage syn9	67
KY082124	882	AAK31670.1 <i>Synechococcus</i> phage S-PWM1	69
KY082125	882	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	52
KY082126	882	YP_009188207.1 Cyanophage P-TIM40	64
KY082127	882	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	67
KY082128	882	AAK31670.1 <i>Synechococcus</i> phage S-PWM1	72 - 74
KY082129	882	YP_214363.1 <i>Prochlorococcus</i> phage P-SSM2	91
KY082130	882	AAK31670.1 <i>Synechococcus</i> phage S-PWM1	69
KY082131	882	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	66
KY082132	882	YP_009188207.1 Cyanophage P-TIM40	60 - 61
KY082133	882	AAC23540.1 Cyanophage S-BnM1	70
KY082134	882	AIX46593.1 <i>Synechococcus</i> phage ACG-2014a	63
KY082135	882	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	66
KY082136	882	YP_003097343.1 <i>Synechococcus</i> phage S-RSM4	91
KY082137	882	AAK31670.1 <i>Synechococcus</i> phage S-PWM1	68
KY082138	882	YP_004323020.1 <i>Synechococcus</i> phage S-SM1	70
KY082139	882	YP_717798.1 <i>Synechococcus</i> phage syn9	66
KY082140	882	YP_004323727.1 <i>Prochlorococcus</i> phage Syn33	59
KY082141	882	YP_009188207.1 Cyanophage P-TIM40	65
KY082142	882	AAC23540.1 Cyanophage S-BnM1	67
KY082143	882	YP_214665.1 <i>Prochlorococcus</i> phage P-SSM4	68
KY082144	882	YP_007001618.1 <i>Synechococcus</i> phage metaG-MbCM1	68
KY082145	882	YP_007673103.1 <i>Synechococcus</i> phage S-CAM1	60
KY082146	882	YP_007001618.1 <i>Synechococcus</i> phage metaG-MbCM1	65
KY082147	882	YP_007518198.1 <i>Synechococcus</i> phage S-RIM8 A.HR1	66
KY082148	882; 973	ABB17262.1 <i>Synechococcus</i> phage S-CBM2	62 - 63
KY082149	882; 973	YP_004322270.1 <i>Synechococcus</i> phage S-SM2	66
KY082150	973	YP_009188207.1 Cyanophage P-TIM40	70
KY082151	973; 882	KU867824.1 <i>Synechococcus</i> phage S-RIMw	93 - 94
KY082152	973	YP_004322786.1 <i>Synechococcus</i> phage S-ShM2	66
KY082153	973	AAK31670.1 <i>Synechococcus</i> phage S-PWM1	68
KY082154	973	KU556819.1 Cyanophage S-RIM35	96
KY082155	1326	YP_004324197.1 <i>Synechococcus</i> phage S-SSM7	83
KY082156	1326	AAC23540.1 Cyanophage S-BnM1	67
KY082157	1326	YP_009140894.1 <i>Synechococcus</i> phage ACG-2014i	57 - 59
KY082158	1326	YP_004323264.1 <i>Prochlorococcus</i> phage P-RSM4	63
KY082159	1326	YP_004322270.1 <i>Synechococcus</i> phage S-SM2	85
KY082160	1326	YP_004322786.1 <i>Synechococcus</i> phage S-ShM2	70
KY082161	1326	YP_009213616.1 <i>Prochlorococcus</i> phage P-TIM68	82
KY082162	1326	YP_009188207.1 Cyanophage P-TIM40	67
KY082163	1326	YP_004322270.1 <i>Synechococcus</i> phage S-SM2	62
KY082164	1326	YP_004322270.1 <i>Synechococcus</i> phage S-SM2	85
KY082165	452; 1326	YP_214363.1 <i>Prochlorococcus</i> phage P-SSM2	90 - 91

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