

New lipid envelope-containing dsDNA virus isolates infecting *Micromonas pusilla* reveal a separate phylogenetic group

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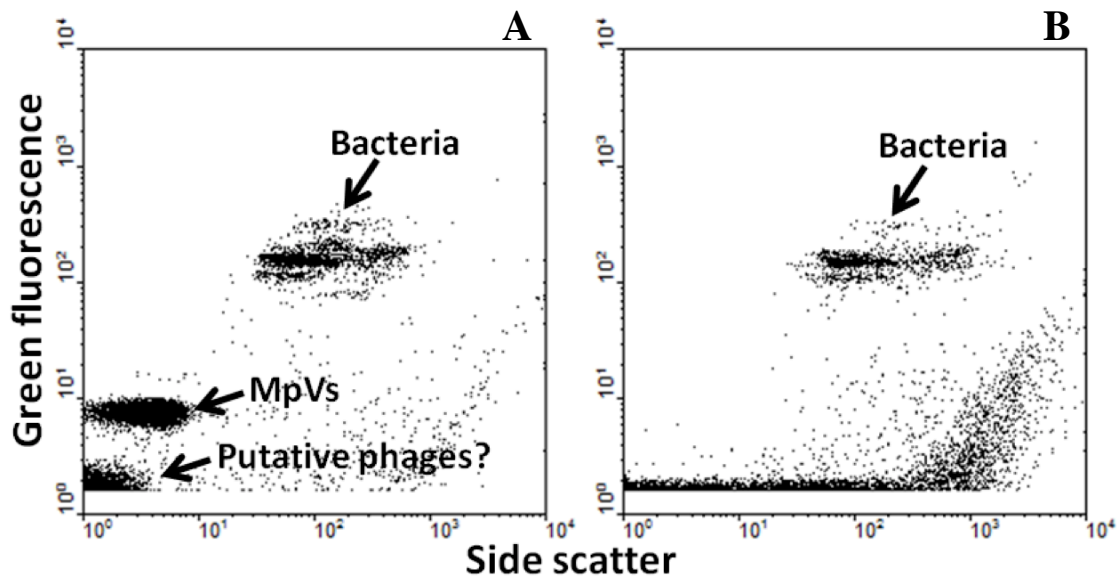
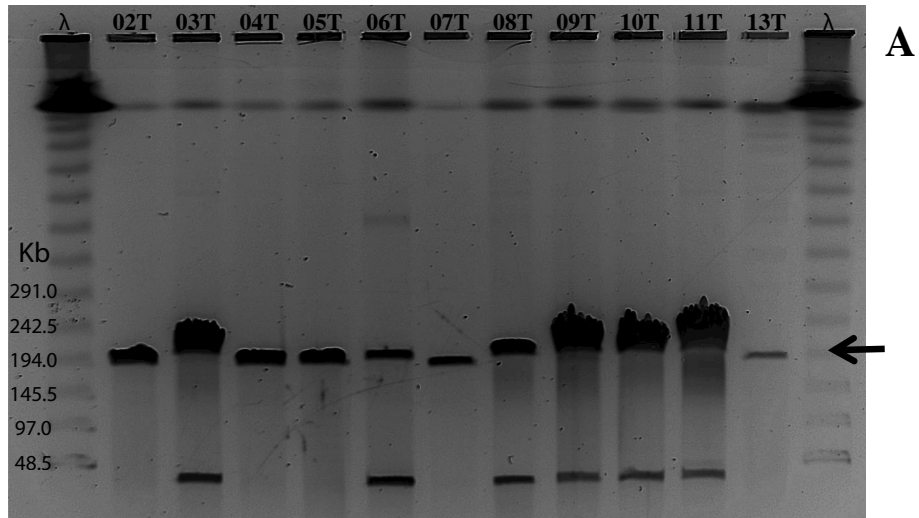
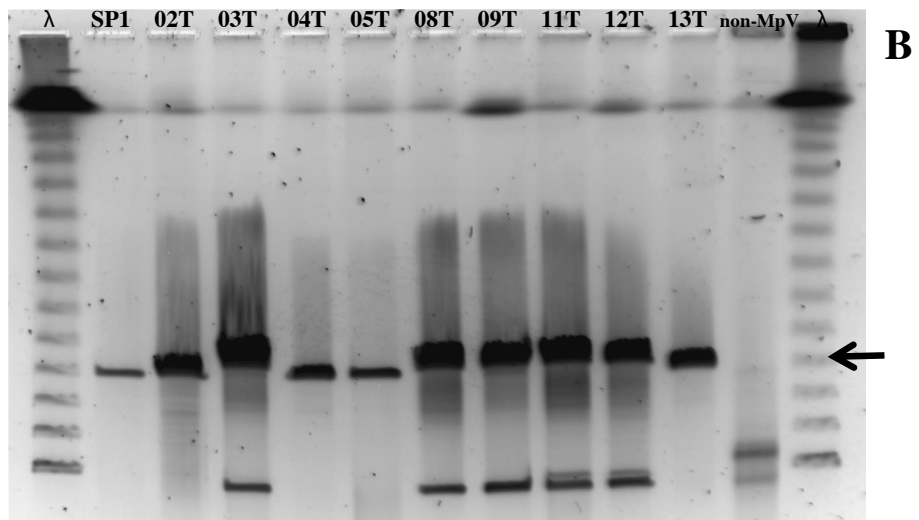


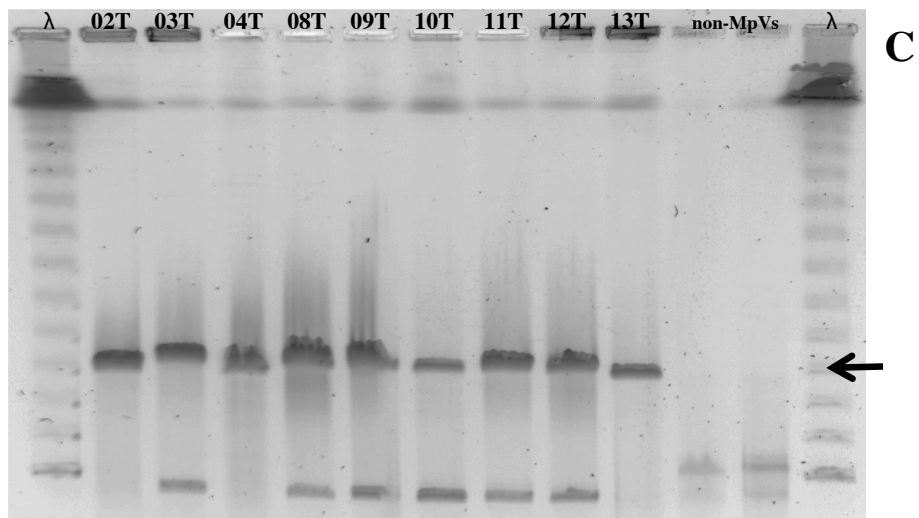
Fig. S1. Representative flow cytometry plot showing virus and bacteria populations. (A) *M. pusilla* strain CCMP1545 infected with MpV40T; (B) *M. pusilla* strain CCMP1545 uninfected. Discrimination of groups was based on green fluorescence and side scatter signatures.



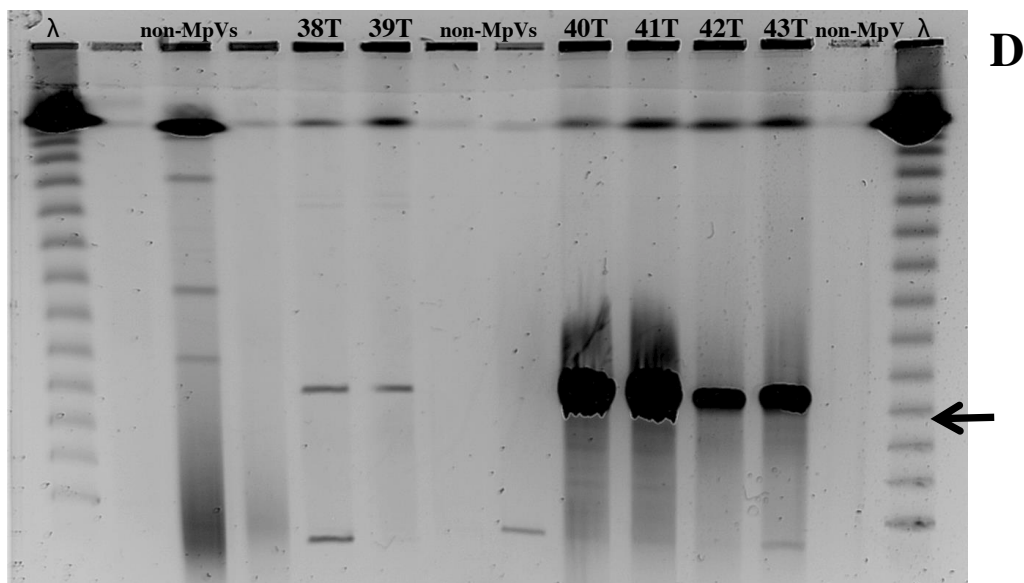
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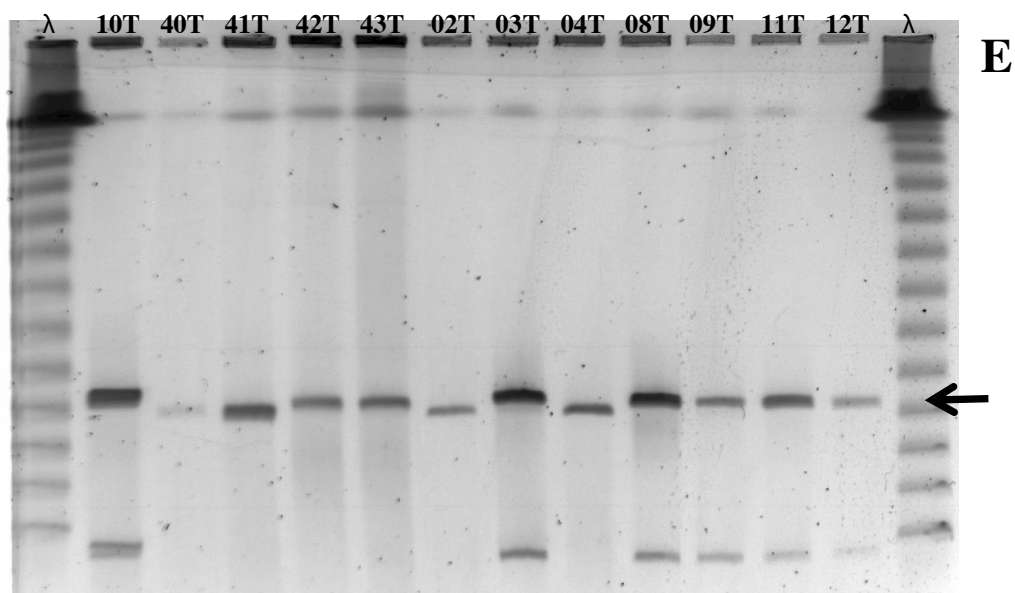
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Fig. S2. PFGE photographs. The MpV isolate loaded into each well is indicated at the top of the lane. λ symbols indicate wells loaded with DNA Lambda ladder plugs. Variable amounts of each MpV isolate were randomly loaded onto different gels to increase confidence when estimating genome size across samples that were electrophoresed separately. The arrows mark the ~200 Kb bands identified as MpV genomes. Bands < 48.5 Kb are likely from phages present in some of the cultures. **Non-MpV** denotes wells that were loaded with samples other than MpV isolates and were not relevant for this study.