

Saturation Mutagenesis Genome Engineering of Infective Φ X174 Bacteriophage via Unamplified Oligo Pools and Golden Gate Assembly

Matthew S. Faber,^{†,‡} James T. Van Leuven,^{*,‡,§,‡} Martina M. Ederer,[§] Yesol Sapozhnikov,[§] Zoë L. Wilson,[§] Holly A. Wichman,^{‡,§} Timothy A. Whitehead,^{||,⊥} and Craig R. Miller^{‡,§}

[†]Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, Michigan 48824, United States

[‡]Institute for Modeling Collaboration and Innovation, University of Idaho, Moscow, Idaho 83844, United States

[§]Department of Biological Sciences, University of Idaho, Moscow, Idaho 83844, United States

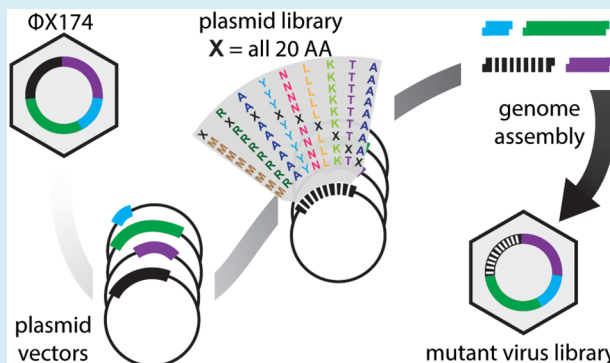
^{||}Department of Chemical & Biological Engineering, University of Colorado, Boulder, Colorado 80303, United States

[⊥]Department of Chemical Engineering & Materials Science, Michigan State University, East Lansing, Michigan 48824, United States

Supporting Information

ABSTRACT: Here we present a novel protocol for the construction of saturation single-site—and massive multisite—mutant libraries of a bacteriophage. We segmented the Φ X174 genome into 14 nontoxic and nonreplicative fragments compatible with Golden Gate assembly. We next used nicking mutagenesis with oligonucleotides prepared from unamplified oligo pools with individual segments as templates to prepare near-comprehensive single-site mutagenesis libraries of genes encoding the F capsid protein (421 amino acids scanned) and G spike protein (172 amino acids scanned). Libraries possessed greater than 99% of all 11 860 programmed mutations. Golden Gate cloning was then used to assemble the complete Φ X174 mutant genome and generate libraries of infective viruses. This protocol will enable reverse genetics experiments for studying viral evolution and, with some modifications, can be applied for engineering therapeutically relevant bacteriophages with larger genomes.

KEYWORDS: Φ X174 bacteriophage, genome engineering, nicking mutagenesis, Golden Gate cloning, oligo pool, deep mutational scanning



Predicting the tempo and trajectory of evolutionary change in the complex environments encountered by viruses and bacteria remains a challenge.^{1–3} Understanding such changes is important for fundamental evolutionary studies as well as biotechnology applications like phage therapy for multidrug resistant bacteria.⁴ Two obstacles preventing better predictions are the oversimplification of the environment in experimental evolution studies compared to wild conditions and the vast number of experimentally unexplored mutational combinations that can occur, even in short adaptive walks and small genomes. Advances in DNA sequencing and synthesis have opened new ways to study microbial evolution and overcome some of these obstacles.^{5,6} Unfortunately, suitable methods do not exist for generating comprehensive bacteriophage mutant libraries. This technology gap hinders those seeking to engineer phages for biotechnological applications and for those seeking a deeper understanding of how viruses evolve.

Methods for genetically engineering phages have recently been reviewed⁷ and commonly involve homologous recombina-

tion and recombineering. While such approaches can be improved by clever incorporation of CRISPR-Cas systems,^{8–10} the overall modest efficiencies largely limits mutagenesis to the generation and single-site mutation of chimeric genomes,^{11,12} gene deletions,¹³ and limited multisite mutagenesis.¹⁴ A recent approach combines mutagenesis by PCR with degenerate (NNK) primers with in-cell recombination to create variation at specific residues in the tail fiber of T3 phage.¹⁵ By contrast, human viruses often have reverse genetics systems in place where comprehensive mutant libraries can be prepared for single genes¹⁶ or regions within a gene^{17,18} using replicative plasmids that encode whole viruses or viral components. Similarly, deep mutational scanning can be performed on plasmid-encoded phage proteins like the MS2 capsid protein.¹⁹ As described by Hartman *et al.* 2018,¹⁹ such experiments can identify mutations that confer useful characteristics, such as MS2 capsid stability

Received: October 9, 2019

Published: December 11, 2019

Table 1. Mutant Library NGS Statistics: Summary of the of the Libraries Prior to Viral Genome Assembly

fragment	F1	F2	F3	G1	G2
residues	1–95	99–242	246–427	2–133	136–175
sequencing reads post quality filter	1 163 959	2 396 395	1 557 554	1 717 075	813 221
fold oversampling of codon combinations	441.1	792.5	412.1	619.4	821.9
percent of reads with					
no nonsynonymous mutations	23.0%	33.1%	29.7%	33.3%	25.2%
one nonsynonymous mutation	52.6%	37.4%	35.5%	38.9%	59.7%
multiple nonsynonymous mutation	24.4%	29.4%	34.7%	27.7%	15.1%
coverage of possible single nonsynonymous mutations	100%	99.9%	100%	99.8%	100%

mutations that could improve the targeted delivery of therapeutics to particular cellular compartments.

Advances in the technologies for generating mutant libraries, synthesizing DNA, and for the assembly of large DNA fragments²⁰ allow for the construction and assembly of user-defined mutagenesis of long nucleic acids. Nicking mutagenesis (NM) can be used to construct comprehensive single-site or other user-defined mutant libraries²¹ using dsDNA as a template. In NM, oligos encode the desired mutations by mismatch with the parental template. On-chip inkjet printed oligo pools have been integrated into NM,²² so one can now construct heterogeneous libraries of oligos that contain tens to hundreds of thousands of high fidelity, unique sequences^{23,22} with a low per base pair cost.

We therefore suspected that large user-defined libraries of phage could be generated by combining the advantages of replicative plasmids with advances in DNA synthesis. The bacteriophage Φ X174 is an excellent system to test this approach. High resolution X-ray crystallography structures of the capsid and spike proteins^{24,25} are available for Φ X174, making it amenable to compare empirical mutagenesis results and molecular modeling predictions, it has a very small genome²⁶ of 5386 nucleotides that is readily sequenced, and it is easily grown on a variety of lab *E. coli* strains. These attractive features of the Φ X174 experimental system have led to proof-of-principle demonstrations from other groups for synthetic genome assembly from oligonucleotides²⁷ and complete refactoring of the phage.^{28,29}

Φ X174 has also been extensively studied,^{30–33} especially as a model system for experimental evolution³⁴ since populations grow rapidly to very large size, mutation rate is high, and the fitness differences between even single mutations can be very large. One of the focal areas of work on Φ X174 and related microvirid phage has been testing models of adaptive evolution and epistasis with empirical data.^{33,35,36} The inferential power of these studies has been limited by the modest sizes of the mutational libraries.

Here we have combined Golden Gate assembly, nicking mutagenesis, and oligo pool technology to construct near comprehensive single-site and expansive multisite mutant libraries for the genes encoding the capsid F protein and spike G protein of the bacteriophage Φ X174. To our knowledge this is the first time near comprehensive single site mutant libraries of full capsid and spike proteins have been generated for an infective bacteriophage.

MATERIALS AND METHODS

Reagents. All purchased enzymes and DNA purification kits were from New England Biolabs, antibiotics were purchased from GoldBio, other chemicals were purchased from Sigma-

Aldrich. Individual primers were purchased from Integrated DNA Technologies.

Segmentation of the Φ X174 Genome. A phage assembly platform for Φ X174 was devised following.³⁷ The Φ X174 chromosome was divided into 14 genomic fragments designed to avoid host cell toxicity by separating genes from their promoters and breaking large genes into multiple segments (Supporting Information). Each segment is flanked by unique five nucleotide overlaps of WT Φ X174 sequence so that they can be amplified from the ancestral Φ X174 using PCR primers designed to incorporate terminal BsmBI restriction sites. Amplicons were cloned into pCR2.1 using the Invitrogen TOPO TA cloning system (Life Technologies, Grand Island, NY) and verified by Sanger sequencing.

Introduction of Nicking Site. The gene fragments—F1, F2, G1, G2—in the pCR2.1-TOPO plasmid (Supporting Information) had the BbvCI nicking site introduced *via* overhang PCR, type I restriction enzyme cutting, and ligation. First, PCR was performed with overhang primers (Supplemental Table S1) to introduce the BbvCI site. Standard Phusion Polymerase HF reaction conditions were used with 4 ng of template DNA, cycling conditions as follows: 98 °C, 1 min; 25X cycles of 98 °C, 10 s; 67 °C, 15 s; 72 °C, 2.5 min; followed by 72 °C for 10 min. PCR products were run on a 1% agarose gel stained with SYBR safe stain (Invitrogen) and the DNA bands at ~4600 bp were extracted using a Monarch DNA Gel Extraction Kit. Next, 1 μ g of the PCR product was digested with *KpnI* (20 U) in NEB Buffer 1.1 at 37 °C for 2 h. Digested DNA was cleaned and concentrated with a Monarch PCR and DNA Clean and Concentrate Kit and eluted into 20 μ L nuclease free H₂O. One microliter of the purified and digested DNA was ligated using T4 DNA ligase at ~25 °C for 1 h in standard conditions in a 20 μ L reaction. Five microliters of the ligation reaction were transformed into chemically competent XL1-Blue *E. coli* *via* standard protocols. Cells were plated on LB agar containing 100 μ g/mL carbenicillin and 50 μ g/mL kanamycin and grown at 37 °C for ~16 h. Cells were picked from transformation plates and grown in 50 mL TB with 100 μ g/mL carbenicillin and 50 μ g/mL kanamycin for ~12 h, cells were pelleted, and DNA purified using compact midi-preps.

Construction of Single Site Mutant Libraries. Comprehensive mutant libraries were generated using nicking mutagenesis (NM) as in Wrenbeck *et al.* 2016²¹ with modifications for using oligo pool mutagenic primers as noted in Medina-Cucurella *et al.* 2019.²² A single oligo pool encoding for all possible single missense and nonsense substitutions in F and G was designed using the custom python scripts from Medina-Cucurella *et al.* 2019²² and synthesized by Agilent (full sequences of all oligos are given in the Supporting Information). Oligo pools were designed with 20–24 bases of gene overlap flanking the mutated codon. Codons were chosen based on

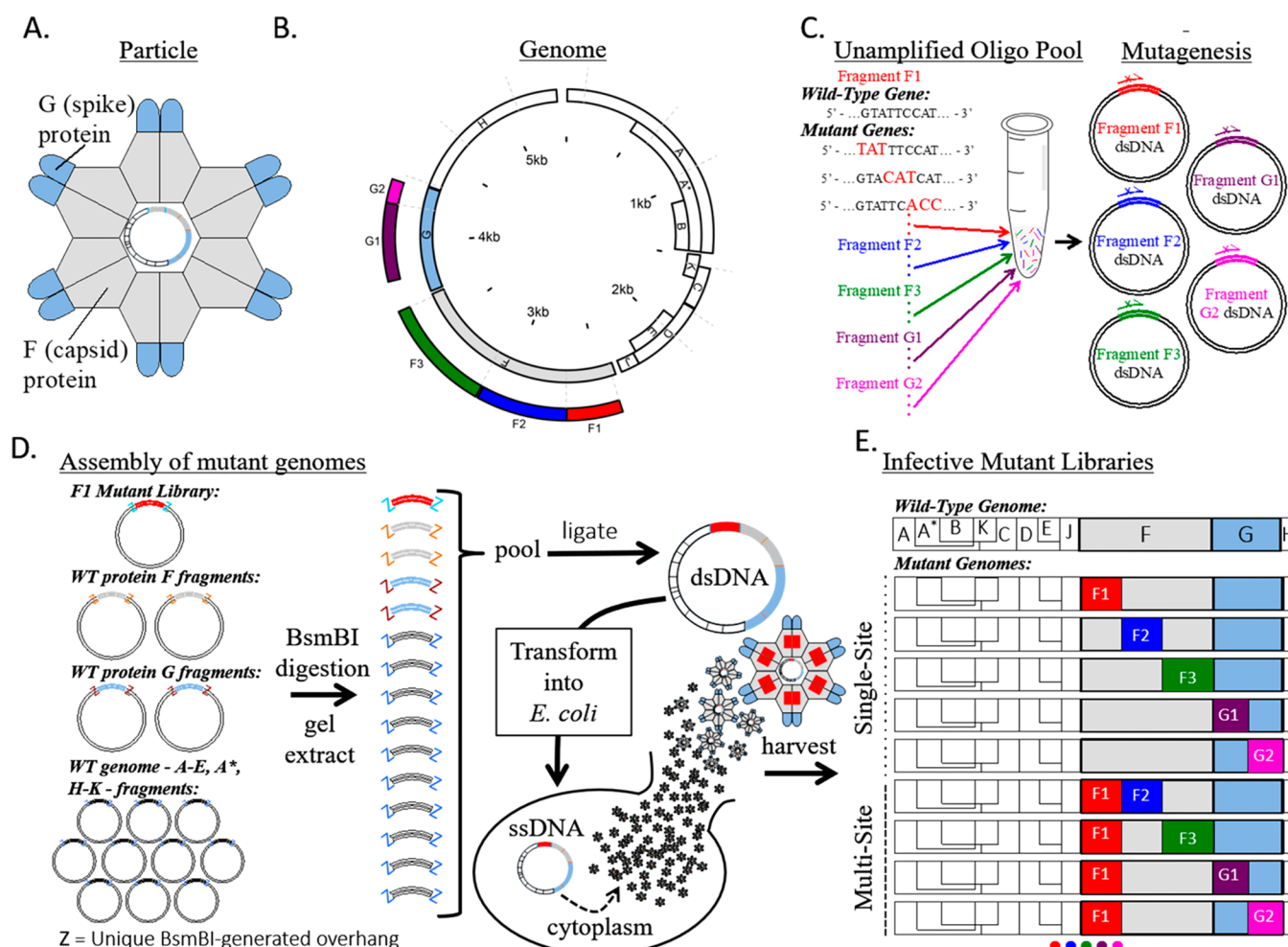


Figure 1. ΦX174 mutant library assembly. (A) Cartoon structure of the ΦX174 virion. F and G proteins are organized into pentamers and are the only exposed proteins in the mature virion. (B) A schematic of the circular ΦX174 genome showing the size and location of the synthetic genome fragments. The locations of mutated residues in genes F and G are indicated. (C) An oligo pool containing all mutagenic oligos for genes F and G was generated and used in Nicking Scanning Mutagenesis for the generation of saturation mutant libraries for genes F and G. (D) Golden Gate cloning was used to assemble the mutant genomes, which were transformed into XL1-Blue competent cells (Agilent) and plated on susceptible *E. coli* C cells. The resulting plaques were sequenced. (E) Linear schematics depicting some of the possible mutant libraries that can be generated using the workflow and existing libraries.

E. coli codon usage frequency, where the highest frequency codon that encoded the mismatch mutation was selected. 14 853 unique oligos were ordered from Agilent, where 14 853 = 12 453 ΦX174 primers – 2400 other primers. These oligos encode WT (593 primers) and all 20 possible single point mutations (including stop) (11 860 primers). This oligo pool was used directly in NM without further amplification using 2 μg of the relevant Golden Gate plasmid as a template. Libraries were electroporated into high efficiency electrocompetent XL1-Blue *E. coli* (Agilent cat #: 200228) using 1 mm electroporation cuvettes at 1200 V using a Eppendorf Eporator. Cells were plated on large bioassay plates (245 mm × 245 mm × 25 mm, Sigma-Aldrich) containing LB agar + 100 μg/mL carbenicillin and 50 μg/mL kanamycin and grown at 37 °C for ~16 h. Plates were scraped in 10 mL plain LB, broken into ~1.2 mL aliquots, pelleted, and stored –80 °C. DNA was purified from 1× aliquot using a MonarchPlasmid Mini-Prep Kit.

Illumina Sequencing Prep and Analysis. Purified library DNA was prepared for deep sequencing as in³⁸ using the primers listed in Supplemental Table S2 and gene tiling as specified in Table 1. DNA was Illumina sequenced on a Mi-Seq platform

with 250 BP paired end reads. The University of Colorado BioFrontiers Sequencing Core performed the Illumina sequencing. Data was processed using PACT³⁹ to determine the library coverage with the following changes to the default options in the configuration file: fast_filter_translate: qaverage = 20, qlimit = 0, enrichment: ref_count_threshold = 5, sel_count_threshold = 0, strict_count_threshold = True. Library coverage statistics are shown in Supplemental Table S3 and S4.

Assembly of Mutant Genomes. We pooled plasmid DNA containing all 14 of the phage DNA fragments (500 ng each) and digested them with BsmB1 (Fermentas Fast Digest, Life Technologies, Grand Island, NY) for 30 min to 1 h at 37 °C. The digested plasmids were subjected to agarose gel electrophoresis for 10 to 15 min using a 1.2% agarose gel to separate the vector from the inserts. The inserts were excised from the gel, purified using the GeneJET gel extraction kit (Fermentas), ligated overnight at 14 °C with T4 DNA ligase (Promega Corporation, Madison, WI), and 4 μL were transformed by electroporation into 50 μL of XL1-Blue electrocompetent cells (Supplemental Table S7). The transformation mix was resuspended with 950 μL of SOC and either plated immediately

Table 2. Characterization of Viable Virus Genotypes in Mutant Phage Library^a

fragment	F1	F2	F3	G1/G2	WT
possible mutants	1900	2880	3640	3440	NA
viable transformants	2300	460	5,840	19 200	6400
plaques sequenced	34	25	30	60	30
wildtype plaques	17 (50%)	11 (44%)	15 (50%)	30 (50%)	30 (100%)

^aSummary table of number of possible mutant viruses, number of viable viruses recovered from one transformation, and the number of mutant and wildtype genotypes recovered. No mutant genotypes were observed more than once.

or incubated for up to 120 min (Supplemental Table S5) at 37 °C in the presence of DNaseI (Supplemental Figure S18) to allow for cell lysis and the removal extracellular DNA, respectively. Aliquots of the cell lysates were added to 3 mL of Φ LB top agar containing 50 μ L log-phage *E. coli* C cells and plated onto a Φ LB agar plate. After four to five hours of incubation at 37 °C, recombinant phage plaques were visible and plates were removed from the incubator. To verify that the recombinant phage encoded the intended sequence, we picked about 30 plaques for each intended mutational target and Sanger sequenced the entire targeted gene. We also sequenced the F and G genes for about 30 wildtype control plaques to ensure that no mutations were naturally accumulating. Briefly, individual plaques were picked with sterile toothpicks and placed in 200 μ L Φ LB and gently swirled. One μ L of this mix was used to PCR amplify approximately 1/2 of the Φ X174 genome using Φ X-0F (5'-GAGTTTATCGCTTCCATG-3') and Φ X-2953R (5'-CCGCCAGCAATAGCACC-3') primers. Internal sequencing primers Φ X-979F (5'-CGGCCCTTACTTGAGG-3') and Φ X-1500R (5'-TTGAGATGGCAGCAACGG-3') were used to sequence gene F. Φ X-2953R was used to sequence gene G. PCR cleanups and sequencing was done at Eurofins Genomics. PCR reaction conditions were: 5 μ L 10X Taq buffer, 2.5 μ L 10 μ M Φ X-0F primer, 10 μ M Φ X-2953F primer, 0.8 μ L 12.5 μ M dNTPs, 0.5 μ L Taq polymerase (NEB #M0273), 1 μ L template, 37.7 μ L H₂O. Thermocycling conditions were 1 cycle at 95 °C for 2 min, 30 cycles at 95 °C for 15 s, 52 °C for 30 s, 68 °C for 2 min, 1 cycle at 68 °C for 5 min.

RESULTS

Our strategy for generating large user-defined mutagenesis libraries of bacteriophage Φ X174 is shown in Figure 1. The circular 5386 nucleotide genome compactly encodes 11 genes where the F and G genes encode the capsid and spike proteins, respectively (Figure 1A). The genome was segmented onto 14 separate plasmids, including 3 plasmids for the F gene and 2 for the G gene (Figure 1B). Fragment boundaries were first engineered to divide large genes, separate regulatory regions from protein coding genes, and result in fragments of similar size. Initial attempts to clone some fragments resulted in low plasmid yield, presumably due to gene toxicity. These genes were further divided and tested empirically, resulting in the final set of 14 fragments. User-defined comprehensive mutations on F and G were encoded using nicking mutagenesis with a single unamplified oligo pool containing all 11 860 mutagenic oligonucleotides (Figure 1C). Φ X174 mutant genomes were reconstituted from individual plasmids using Golden Gate cloning and transformation into a host *E. coli* strain (Figure 1D). Harvested phages contained all possible nonsynonymous mutations in the F and G genes depending on the mutagenized segments used for Golden Gate cloning (Figure 1E).

We sought a reverse genetics system for Φ X174 wherein the virus chromosome was segmented and encoded on individual

vector plasmids. Our method of construction closely followed that for the assembly of human coronavirus NL63,³⁷ where each plasmid contained unique BsmBI type IIS restriction endonuclease sites flanking unique five nucleotide overlaps of wild-type (WT) Φ X174. This architecture allows for faithful and easy assembly of the complete genome *via* Golden Gate cloning. The Φ X174 genome was separated into 14 separate nontoxic fragments by PCR and cloned into vector plasmids where genes were separated from their promoters and larger genes were segmented (full sequences for all plasmid inserts are given in Supporting Information). The segments ranged from 129 to 634 base pairs in length, with necessary additional truncations of genes D and A. Φ X174 phage could be reconstituted by digesting pooled plasmids with BsmBI, ligating inserts overnight, and transforming into electrocompetent *E. coli* C cells.

The F and G genes were targeted for saturation mutagenesis. We introduced mutations by nicking mutagenesis, which requires the presence of a BbvCI nicking site on the dsDNA plasmid. The F gene plasmid F3 encoding residues 246–427 of the F gene product contained a unique BbvCI sequence, while the remaining four plasmids (F1, F2, G1, G2) required introduction of BbvCI nicking sites in the vector backbone. The presence in each plasmid of the unique BbvCI nicking site was verified with the successful generation of circular ssDNA from the modified plasmids by BbvCI.Nt and exonuclease digestion (Supplemental Figure S1).

In nicking mutagenesis, desired mutations are introduced by libraries of mutagenic oligonucleotides, which can be sourced from unamplified oligo pools.²² We used a custom pool of 11 860 oligos that encoded nearly every missense and nonsense mutation in the F and G genes. Each missense or nonsense mutation was encoded by a single oligonucleotide. Application of nicking mutagenesis using this oligo pool for different plasmids (F1, F2, F3, G1, G2) resulted in at least 14-fold excess transformants required for 99.9% theoretical coverage of the desired library (Supplemental Table S3). The diversity of the mutant plasmid libraries was validated using deep sequencing on an Illumina MiSeq platform. All plasmid libraries have >99.7% coverage of all possible single mutations ($n = 11\,821/11\,860$, minimum counts for a mutation >5, full library statistics are given in Table 1 and Supplemental Table S4). Heatmaps showing mutation-specific frequencies for all segments are shown in Supplemental Figures S2–S17.

Mutant dsDNA libraries were transformed into nonsusceptible hosts (Agilent XL1-Blue), then plated on susceptible hosts (*E. coli* C) after a 30 min recovery in SOC. Viral titers increase rapidly after 30 min, suggesting that the XL1-Blue cells do not burst until after this time point (Supplemental Table S5). Accordingly, we reasoned that the number of plaques at 30 min represents the number of XL1-Blue cells that were transformed with viable genomes. The number of transformants varied considerably between constructs (Table 2, Supplemental Figure S19). 19 200 plaques were recovered from the cotransformed

G1/G2 libraries, where only 3440 total variants were expected in the pool. On the contrary, 460 plaques were observed for the F2 library, when 2880 total variants were in the starting plasmid pool. The under-representation of the F2 library at this scale could be remedied by transforming more competent cells. We expect that differences between fragments in the number of recovered viruses is due to in part to the tolerability of fragments to mutation, as inviable mutants would not form plaques. Estimates from deep mutational scanning of model proteins show that approximately 18–38% of all mutations are nonviable,^{40,41} and this percentage may be larger for structural proteins like F and G.

To test the validity of the mutagenesis and phage reconstitution method, we picked about 30 plaques generated from each library to Sanger sequence. Of these, 40–50% were wildtype and the remaining contained exactly one mutation (Table 2). No variants were observed more than once, supporting the deep sequencing results showing that the libraries consist of thousands of variants. Interestingly, none of the exact substitutions in these sequences have been previously observed (Supplemental Table S6), although mutations at the same residues (G106, F29, F45, F84, F185, F204, F205, and F393) have been seen in previous experiments.³⁴ In all cases the percentage of WT plaques is slightly higher than in the starting plasmid pools (*p*-values F1: 0.001, F2: 0.088, F3: 0.015, G: 0.001, 1-tailed binomial distribution), consistent with purifying selection against mutations (Table 1). In contrast, for the control where all plasmids in the Golden Gate reaction were WT, 0% (0/30) plaques contained mutations in the encoded regions.

DISCUSSION

Here we present a novel method for generating comprehensive single-site and multisite saturation mutant libraries of the spike and capsid proteins of the bacteriophage Φ X174. This method uses unamplified oligo pools, nicking scanning mutagenesis, and Golden Gate cloning of the fragmented genome.

The fragment-based system provides an ideal way to generate libraries for the study of epistasis and multimutational step regions of the neighborhood around wild type. When a gene is in multiple fragments, the number of mutational variants we expect from the assembled mutant fragments is the product of their individual variant number. Hence, since G1 contains 2640 variants and G2 contains 800 variants, they can be combined to generate 2.1 million double mutation variants. Further, nothing requires the fragments to be from the same gene. For example, since the F and G proteins bind to each other to form the capsid of Φ X174 (Figure 2), libraries combining mutations in F with mutations in G will capture mutations that can readily interact in the protein and have the potential to generate interesting instances of epistasis (Figure 2). The central challenge then becomes how to survey the vast size of these combinatorial plasmid libraries. Right now, our transformational efficiencies vary, but even at the upper end of hundreds of thousands of transformants per reaction, only a fraction of the total diversity in the library can be surveyed.

We are fortunate that our model virus has a small genome, under 6000 nts, which enabled us to assemble the 14 nontoxic fragments with sufficient transformants for near-complete coverage of the user-defined mutations. This method can be applied with little modification to other phages with small genomes like the microviridae. However, most biotech-relevant phages have larger genomes, and extension of this method to

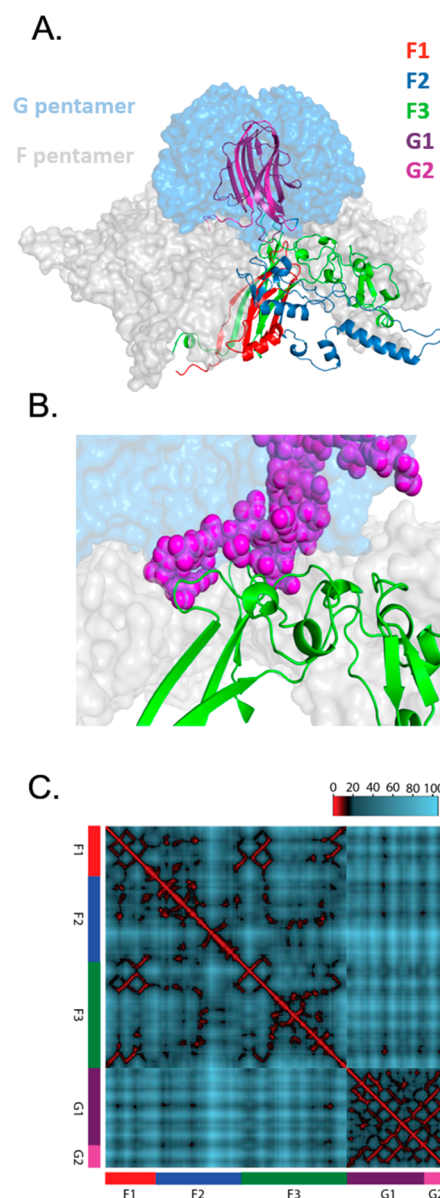


Figure 2. Structural view of potential epistatic interactions between F and G libraries. (A) Pentameric complex between F and G shown in surface view. For both F and G, one monomer is detailed as a ribbon color-coded according to the saturation mutagenesis library prepared in this work. (B) Close-up of interaction surface between the F3 sublibrary of F protein (green ribbons) and G2 sublibrary of G protein (purple spheres). (C) Distance mapping between alpha carbons in F and G crystal structure. Residues within 10 Å are colored red, 10–20 are black, and >20 are blue. Euclidian distances calculated from F–G crystal structure. Heatmap shows that many opportunities exist for close proximity (interactions) both within and between fragments.

other viruses would encounter the following technical challenges. First, increasing genome sizes decrease transformational efficiencies, and larger genomes have increased susceptibility to DNA shearing.⁴² Both size-dependent effects can disrupt the integrity and coverage of the phage libraries.⁴³ Second, our method includes restrictions on the DNA sequences that can be used. Golden Gate cloning requires a genome without unique Type IIS restriction sequences, while nicking mutagenesis requires that there be only one orientation of the BbvCI nicking site within the template DNA fragment. Third, ligating 14 fragments is close to the upper limit of Golden

Gate cloning. Additionally, increasing the size of individual fragments is difficult as the presented method depends on replicating plasmids in *E. coli*, and larger fragments are more likely to be toxic *in vivo*.

Based on the above considerations, adapting this method to larger viruses will require modifications for the genome assembly steps. There are a variety of methods available for attempting to improve genome library assembly and amplification. For improving genome assembly, we speculate that a combination of hierarchical assembly⁴⁴ with other yeast-based assembly methods⁴⁵ will allow for large viral genomes to be efficiently assembled. Yehl *et al.* 2019¹⁵ built large libraries of targeted epitope regions by combining methods; plasmid-based mutagenesis and cloning followed by recombination with wild-type phage during infection. Finally, we speculate that the TX-TL cell free expression system⁴⁶ will be able to produce the viral libraries with less bias than *in vivo* amplification in *E. coli*. In summary, we have presented a method for efficient deep mutational scanning of the bacteriophage Φ X174. We anticipate that this method will find utility in fundamental molecular evolution studies as well as translate to potential medicinal applications.

■ ASSOCIATED CONTENT

■ Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acssynbio.9b00411>.

Figures S1, S18–19, Tables S1, S2, S5, S7: Experimental details that may assist the reader in replicating the experiment or applying the method to a new system; Figures S2–S17 and Tables S3, S4, S6: Characterization of the plasmid library by deep sequencing and the mutant virus library by plaque growth and isolate sequencing (PDF)

phix174_MutOligos.fna: oligo pool sequences; phix174_primer_generation_inputs: input files for generating the oligo pool and an example of the command line input to execute the script from Medina-Cucurella *et al.* 2019;²² phix174_fragments.fna: nucleotide sequences for all inserts in carrier plasmid; phix174_fragments.gff: annotation of fragments including restriction sites and coding regions; phix174_fragments.faa: amino acid sequences of mutated genes (TXT)

■ AUTHOR INFORMATION

Corresponding Author

*E-mail: jvanleuven@uidaho.edu.

ORCID

James T. Van Leuven: 0000-0002-2730-0287

Author Contributions

#MSF and JTVL contributed equally to this work. JTVL, CRM, HAW, MSF, and TAW conceived of and designed the study. MME and HAW created the virus assembly system. MSF created the plasmid libraries. JTVL, YS, and ZLW performed the virus assembly and growth experiments. JTVL, MSF, CRM, and TAW wrote the manuscript.

Notes

The authors declare no competing financial interest.

Raw sequencing reads for the mutant libraries have been deposited in the SRA database: SAMN12660301–SAMN12660308.

■ ACKNOWLEDGMENTS

This work was supported by the National Science Foundation BEACON Centre for the Study of Evolution in Action and EPSCoR T2 under award numbers DBI-0939454 and OIA-1736253 and the National Institute of General Medical Sciences of the National Institutes of Health under award numbers P20GM104420 and R01GM076040. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

■ REFERENCES

- (1) Holmes, E. C. (2013) What can we predict about viral evolution and emergence? *Curr. Opin. Virol.* 3, 180–184.
- (2) Neher, R. A. (2013) Genetic draft, selective interference, and population genetics of rapid adaptation. *Annu. Rev. Ecol. Evol. Syst.* 44, 195–215.
- (3) Lieberman, T. D., Flett, K. B., Yelin, I., Martin, T. R., McAdam, A. J., Priebe, G. P., and Kishony, R. (2014) Genetic variation of a bacterial pathogen within individuals with cystic fibrosis provides a record of selective pressures. *Nat. Genet.* 46, 82–87.
- (4) Dedrick, R. M., Guerrero-Bustamante, C. A., Garlena, R. A., Russell, D. A., Ford, K., Harris, K., Gilmour, K. C., Soothill, J., Jacobs-Sera, D., Schooley, R. T., Hatfull, G. F., and Spencer, H. (2019) Engineered bacteriophages for treatment of a patient with a disseminated drug-resistant *Mycobacterium abscessus*. *Nat. Med.* 25, 730–733.
- (5) Barrick, J. E., and Lenski, R. E. (2013) Genome dynamics during experimental evolution. *Nat. Rev. Genet.* 14, 827–839.
- (6) Fowler, D. M., and Fields, S. (2014) Deep mutational scanning: a new stype of protein science. *Nat. Methods* 11, 801–807.
- (7) Pires, D. P., Cleto, S., Sillankorva, S., Azeredo, J., and Lu, T. K. (2016) Genetically engineered phages: a review of advances over the last decade. *Microbiol. Mol. Biol. Rev.* 80, 523–543.
- (8) Kiro, R., Shitrit, D., and Qimron, U. (2014) Efficient engineering of a bacteriophage genome using the type I-E CRISPR-Cas system. *RNA Biol.* 11, 42–44.
- (9) Lemay, M. L., Tremblay, D. M., and Moineau, S. (2017) Genome engineering of virulent lactococcal phages using CRISPR-Cas9. *ACS Synth. Biol.* 6, 1351–1358.
- (10) Schilling, T., Dietrich, S., Hoppert, M., and Hertel, R. (2018) A CRISPR-Cas9-based toolkit for fast and precise *in vivo* genetic engineering of *Bacillus subtilis* phages. *Viruses* 10, 241.
- (11) Doore, S. M., and Fane, B. A. (2015) The kinetic and thermodynamic aftermath of horizontal gene transfer governs evolutionary recovery. *Mol. Biol. Evol.* 32, 2571–2584.
- (12) Doore, S. M., Schweers, N. J., and Fane, B. A. (2017) Elevating fitness after a horizontal gene exchange in bacteriophage Φ X174. *Virology* 501, 25–34.
- (13) Uchiyama, A., Heiman, P., and Fane, B. A. (2009) N-terminal deletions of the Φ X174 external scaffolding protein affect the timing and fidelity of assembly. *Virology* 386, 303–309.
- (14) Stockdale, S. R., Collins, B., Spinelli, S., Douillard, F. P., Mahony, J., Cambillau, C., and van Sinderen, D. (2015) Structure and assembly of TP901–1 Virion unveiled by mutagenesis. *PLoS One* 10, No. e0131676.
- (15) Yehl, K., Lemire, S., Yang, A. C., Ando, H., Mimee, M., Torres, M. D. T., de la Fuente-Nunez, C., and Lu, T. K. (2019) Engineering Phage Host-Range and Suppressing Bacterial Resistance through Phage Tail Fiber Mutagenesis. *Cell* 179, 459–469.
- (16) Lee, M. E., DeLoache, W. C., Cervantes, B., and Dueber, J. E. (2015) A highly characterized yeast toolkit for modular, multipart assembly. *ACS Synth. Biol.* 4, 975–986.
- (17) Doud, M. B., Lee, J. M., and Bloom, J. D. (2018) How single mutations affect viral escape from broad and narrow antibodies to H1 influenza hemagglutinin. *Nat. Commun.* 9, 1386.
- (18) Wu, N. C., and Qi, H. (2019) Application of deep mutational scanning in hepatitis C virus. *Methods Mol. Biol.* 1911, 183–190.

- (19) Hartman, E. C., Jakobson, C. M., Favor, A. H., Lobba, M. J., Álvarez-Benedicto, E., Francis, M. B., and Tullman-Ercek, D. (2018) Quantitative characterization of all single amino acid variants of a viral capsid based drug delivery vehicle. *Nat. Commun.* 9, 1385.
- (20) van Dolleweerd, C. J., Kessans, S. A., Van de Bittner, K. C., Bustamante, L. Y., Bundela, R., Scott, B., Nicholson, M. J., and Parker, E. J. (2018) MIDAS: a modular DNA assembly system for synthetic biology. *ACS Synth. Biol.* 7, 1018–1029.
- (21) Wrenbeck, E. E., Klesmith, J. R., Stapleton, J. A., Adeniran, A., Tyo, K. E. J., and Whitehead, T. A. (2016) Plasmid-based one-pot saturation mutagenesis. *Nat. Methods* 13, 928–930.
- (22) Medina-Cucurella, A., Steiner, P. J., Faber, M. S., Beltrán, J., Borelli, A., Kirby, M. B., Cutler, S. R., and Whitehead, T. A. (2019) User-defined single pot mutagenesis using unpurified oligo pools. *Protein Eng., Des. Sel.* 32 (1), 41–45.
- (23) Kosuri, S., and Church, G. M. (2014) Large-scale *de novo* DNA synthesis: technologies and applications. *Nat. Methods* 11, 499–507.
- (24) McKenna, R., Xia, D., Willingmann, R., Ilag, L. L., Krishnaswamy, S., Rossmann, M. G., Olson, N. H., Baker, T. S., and Incardona, N. L. (1992) Atomic structure of single-stranded DNA bacteriophage Φ X174 and its functional implications. *Nature* 355, 137–143.
- (25) Dokland, T., McKenna, R., Ilag, L. L., Bowman, B. R., Incardona, N. L., Fane, B. A., and Rossmann, M. G. (1997) Structure of a viral procapsid with molecular scaffolding. *Nature* 389, 308–313.
- (26) Sanger, F., Coulson, A. R., Friedmann, T., Air, G. M., Barrell, B. G., Brown, N. L., Fiddes, J. C., Hutchinson, C. A., Slocumbe, P. M., and Smith, M. (1978) The nucleotide sequence of bacteriophage ϕ X174. *J. Mol. Biol.* 125, 225–246.
- (27) Smith, H. O., Hutchison, C. A., Pfannkuch, C., and Venter, J. C. (2003) Generating a synthetic genome by whole genome assembly: Φ X174 bacteriophage from synthetic oligonucleotides. *Proc. Natl. Acad. Sci. U. S. A.* 100, 15440–15445.
- (28) Jaschke, P. R., Lieberman, E. K., Rodriguez, J., Sierra, A., and Endy, D. (2012) A fully decompressed synthetic bacteriophage Φ X174 genome assembled and archived in yeast. *Virology* 434, 278–284.
- (29) Jaschke, P. R., Dotson, G. A., Hung, K., Liu, D., and Endy, D. (2018) Definitive demonstration by synthesis of genome annotation completeness. *bioRxiv*, 455428.
- (30) Aoyama, A., Hamatake, R. K., and Hayashi, M. (1981) Morphogenesis of Φ X174: *in vitro* synthesis of infectious phage from purified viral components. *Proc. Natl. Acad. Sci. U. S. A.* 12, 7285–7289.
- (31) Hafenstein, S., and Fane, B. A. (2002) Φ X174 genome-capsid interactions influence the biophysical properties of the virion: evidence for a scaffolding-like function for the genome during the final stages of morphogenesis. *J. of Viro.* 76, 5350–5356.
- (32) Bernal, R. A., Hafenstein, S., Esmeralda, R., Fane, B. A., and Rossmann, M. G. (2004) The Φ X174 protein J mediates DNA packaging and viral attachment to host cells. *J. Mol. Biol.* 337, 1109–1122.
- (33) Rokyta, D. R., Joyce, P., Caudle, S. B., and Wichman, H. A. (2005) An empirical test of the mutational landscape model of adaptation using a single-stranded DNA virus. *Nat. Genet.* 37, 441–444.
- (34) Wichman, H. A., and Brown, C. J. (2010) Experimental evolution of viruses: Microviridae as a model system. *Philos. Trans. R. Soc., B* 365, 2495–2501.
- (35) Caudle, S. B., Miller, C. R., and Rokyta, D. R. (2014) Environment Determines Epistatic Patterns for a ssDNA Virus. *Genetics* 196, 267–279.
- (36) Sackman, A. M., and Rokyta, D. R. (2018) Additive Phenotypes Underlie Epistasis of Fitness Effects. *Genetics* 208, 339–348.
- (37) Donaldson, E. F., Yount, B., Sims, A. C., Burkett, S., Pickles, R. J., and Baric, R. S. (2008) Systematic Assembly of a Full-Length Infectious Clone of Human Coronavirus NL63. *J. Virol.* 82, 11948–11957.
- (38) Kowalsky, C. A., Klesmith, J. R., Stapleton, J. A., Kelly, V., Reichkitzer, N., and Whitehead, T. A. (2015) High-Resolution Sequence-Function Mapping of Full-Length Proteins. *PLoS One* 10, No. e0118193.
- (39) Klesmith, J. R., and Hackel, B. J. (2019) Improved mutation function prediction via PACT: Protein Analysis and Classifier Toolkit. *Bioinformatics* 35 (6), 2707–2712.
- (40) Firnberg, E., Labonte, J. W., Gray, J. J., and Ostermeier, M. (2014) A comprehensive, high resolution map of a gene's fitness landscape. *Mol. Biol. Evol.* 31, 1581–1592.
- (41) Faber, M. S., Wrenbeck, E. W., Azouz, L. R., Steiner, P. J., and Whitehead, T. A. (2019) Impact of *in vivo* protein folding probability on local fitness landscapes. *Mol. Biol. Evol.* 36, 2764.
- (42) Rogers, S. O., and Bendich, A. J. (1988) Extraction of DNA from plant tissues. *Plant Mol. Biol. Man.* A6, 1–10.
- (43) Edwards, R. A., and Rohwer, F. (2005) Viral metagenomics. *Nat. Rev. Microbiol.* 3, 504–509.
- (44) Lee, J. M., Huddleston, J., Doud, M. B., Hooper, K. A., Wu, N. C., Bedford, T., and Bloom, J. D. (2018) Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants. *Proc. Natl. Acad. Sci. U. S. A.* 115, E8276–E8285.
- (45) Ando, H., Lemire, S., Pires, D. P., and Lu, T. K. (2015) Engineering modular viral scaffolds for targeted bacterial population editing. *Cell Systems* 1, 187–196.
- (46) Garamella, J., Marshall, R., Rustad, M., and Noireaux, V. (2016) The all *E. coli* Toolbox 2.0: a platform for cell-free synthetic biology. *ACS Synth. Biol.* 5, 344–355.