Bryan Merrill, Ph.D.

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SUMMARY

Accomplished, versatile bioinformatics scientist with a passion for discovering new biology in complex microbial communities. Creative problem-solver. Proven track record of integrating large-scale multi-omics studies from public repositories with data generated in-house. Adept at developing and optimizing analysis pipelines for deployment in the cloud. Known for nurturing successful collaborations and a positive team environment between bench and computational researchers leading to authorship on >20 publications with >2500 cumulative citations.

EDUCATION

Ph.D. Microbiology and Immunology **Stanford University** **Stanford, CA** **2015 – 2022**
- Thesis: Discovery of lifestyle-associated microbes, pathogens, and bacteriophages through deep metagenome sequencing of the gut microbiome
- Advisor: Justin Sonnenburg, Ph.D.

M.S. Microbiology and Molecular Biology **Brigham Young University** **Provo, UT** **2014 – 2015**
- Thesis: Advancing phage genomics and honeybee health through discovery and characterization of Paenibacillaceae bacteriophages
- Advisor: Sandra Hope, Ph.D.

B.S. Molecular Biology (*Magna Cum Laude*) **Brigham Young University** **Provo, UT** **2011 – 2014**

TECHNICAL SKILLS

Programming	R / RStudio, Python / Jupyter, Bash, SQL
HPC/Cloud	AWS (s3/ec2/batch), Docker, Nextflow, Linux systems administration
Bioinformatics	Workflow management: GNU Parallel, Snakemake, Github
	Read QC and alignment: FASTQC, BBTools suite, Bowtie2, SAMtools
	Metagenome assembly and binning: MEGAHIT, metaSPAdes, metaBAT2, anvi'o
	Genome ID/taxonomy/quality: QUAST, CheckM, GTDB-TK, dRep, CheckV
	Sample profiling: Kraken, BioBakery, MIDAS, IGGsearch, inStrain
	Gene function: Prodigal, Prokka, InterProScan, DIAMOND, HMMER, MMseqs2
	Databases and retrieval tools: NCBI, SRA Toolkit, EBI

EXPERIENCE

BIOINFORMATICS SCIENTIST – NUANCED HEALTH, INC. **2022 – 2023**

Software development
- Customized, optimized, deployed and was responsible for 4 Nextflow pipelines on AWS to perform the following: gathering publicly available data; (meta)genome assembly and binning; functional annotation and genome mining; read-mapping and sample profiling using public and custom reference databases.
- Deposited pipeline and analysis code for review into team-wide Github repository and reviewed team members' code, following best practices.

Data curation
- Collected and harmonized next-generation sequencing data and metadata for thousands of internal sequencing samples and publicly available metagenomes into data storage and tables for team use across several projects.

- Built large libraries of biosynthetic gene clusters from genome mining of in-house and public data, enabling exploration of effects on 'omics readouts and phenotypes.

Bioinformatics Data Science

- Collaborated on building disease & drug-response prediction models using machine learning tools to demonstrate the company's in vivo platform.
- Integrated genome mining and targeted feature extraction of LC-MS/MS metabolomics data to identify metagenome-metabolome-phenotype relationships.
- Built fixed-effects models to quantify the contribution and significance of experimental factors using *in vivo* phenotypic data from multiple time-series experiments across phenotypes and disease states.

DOCTORAL RESEARCHER – STANFORD UNIVERSITY – LAB OF JUSTIN L. SONNENBURG, PH.D.   2015 – 2022

Software development

- Developed AWS-deployed metagenomics and microbial genomics pipelines to enable QC, assembly, genome binning, compositional, and functional analysis. Processed >10k human and mouse samples from >20 lab-led and public studies to date.[1-2,5]
- Improved performance of existing tools (including programming or consulting for VirSorter, anvi'o, dRep, inStrain, cblaster) and scaling analyses for the cloud.[7,10,12]
- Developed AWS-deployed bacterial strain assembly pipeline using Illumina+Nanopore sequencing data.[1-3,10]
- Designed, built, and managed Windows and Linux-based lab servers and backups.

Leadership and community-building

- Provided documentation and onboarding for computational resources, enabling wet-lab researchers to easily learn computational tools and skills.
- Organized bi-monthly "coding club" meetups to facilitate code troubleshooting and skill building for all experience levels.

Bioinformatics Data Science

- Designed, executed, and published the largest data-per-sample human gut metagenome study to date, resulting in an unparalleled view of the gut microbiome in under-represented human populations. Discovered ~90k microbial genomes, hundreds of novel species, and prevalence patterns associated with a non-industrialized lifestyle.[1,2]
- Generated comprehensive databases of genes, syntenic gene clusters, and genomes containing ~400k human gut microbial genomes enabling global profiling and functional data analysis.[1,2,5,6,10,12,14] Identified conservation of gene clusters responsible for:
  - Aromatic amino acid reduction[14]
  - Asparagine utilization and polyamine production[6]
  - Consumption of complex baobab polysaccharides (*in preparation*)
- Characterize *B. theta* bacteriophages with capsule-dependent tropism resulting in better understanding complex host-phage dynamics in the human gut.[8,9]
- Identify alterations in the gut virome following osmotic perturbation in mice.[12]
- Assisted a Stanford core research facility that supports many academic labs to identify and trace a contagious pathogen in immunodeficient mice through strain-level analysis of gut metagenome data. Collaborated to develop a successful qPCR-based diagnostic test for isolation and quarantine of infected and exposed mice. (*in preparation*, SonnenburgLab/NSG_mouse_metagenomics)

- Contributed to the Unified Human Gut Virome catalog which includes a gold-standard reference database and analyses which reveal novel, prevalent viral clades in humans across the globe. (*in preparation*, 🌐 snayfach/UHGV)

STUDENT RESEARCHER – BRIGHAM YOUNG UNIVERSITY – LAB OF SANDRA HOPE, PH.D.　　　2012 – 2015

- Operate phage therapy research program targeting honeybee bacterial pathogen requiring:
  - Coordination with local beekeepers for sample collection
  - In-lab isolation and characterization of circulating pathogens and candidate phages
  - Safety and efficacy testing of candidate phage therapy on lab-owned beehives and healthy/infected hives in the community.
  - Publication of phages identified[16-18,22,23,25,29] and successful trial results[15,19].
- Mentor >70 undergraduate researchers enrolled in wet-lab + computational phage discovery course over 3 years, leading to student-led presentations at 5 conferences[33-45,48] and contribution in peer-reviewed publications.

IGEM TEAM – BRIGHAM YOUNG UNIVERSITY – ADVISED BY JULIANNE GROSE, PH.D.　　　2013

- Conducted research to modify capsid size of *Enterobacteria* phage T4 as part of an iGEM (International Genetically Engineered Machine) team.[46,47]

HHMI SEA-PHAGES (PHAGE HUNTERS) RESEARCHER – BRIGHAM YOUNG UNIVERSITY　　　2011 – 2012

- Isolation, sequencing, and annotation of *Mycobacterium smegmatis* bacteriophages.[28]

TEACHING EXPERIENCE

Guest Lecturer – Stanford University　　　**Winter 2021**

- MI 215: Principles of Biological Technologies with Peter Sarnow, Ph.D.

Guest Lecturer – Stanford University　　　**Winter 2020**

- MI 215: Principles of Biological Technologies with Peter Sarnow, Ph.D.

Teaching Assistant – Stanford University　　　**Spring 2017**

- MI 221: Gut Microbiota in Health and Disease with Ami Bhatt, M.D. Ph.D; Justin Sonnenburg, Ph.D.

Teaching Assistant – Brigham Young University　　　**Winter 2013 – 15**

- MMBIO 195: Phage Hunters, Comparative Genomics with Don Breakwell, Ph.D.; Julianne Grose, Ph.D.; Sandra Hope, Ph.D.

Teaching Assistant – Brigham Young University　　　**Fall 2012 – 14**

- MMBIO 194: Phage Hunters, Discovery with Don Breakwell, Ph.D.; Julianne Grose, Ph.D.; Sandra Hope, Ph.D.

HONORS, AWARDS, RESEARCH SUPPORT

National Science Foundation Graduate Research Fellowship	2015
BYU College of Life Sciences Dean's List	2014 (Fall)
BYU Office of Research and Creative Activities (ORCA) grant recipient	2014
BYU Office of Research and Creative Activities (ORCA) grant recipient	2013
Gold Medal, iGEM North American Regional Jamboree	2013
Four year full tuition Heritage Scholarship – Brigham Young University	2011-2014

PUBLICATIONS

* Authors contributed equally to this work

1. Carter MM*, Olm MR*, **Merrill BD***, Dahan D, Tripathi S, Spencer SP, Yu FB, Jain S, Neff N, Jha AR, Sonnenburg ED, Sonnenburg JL. (2023) Ultra-deep sequencing of Hadza hunter-gatherers recovers vanishing microbes. *Cell*, 186(14):3111-3124.e13. https://doi.org/10.1016/j.cell.2023.05.046

2. Olm MR*, Dahan D*, Carter MM, **Merrill BD**, Yu FB, Jain S, Meng XD, Tripathi S, Wastyk HC, Neff NF, Holmes S, Sonnenburg ED, Jha AR, Sonnenburg JL. (2022) Robust variation of the infant gut microbiome across a spectrum of lifestyles. *Science* Jun;376(6598):1220-1223. https://dx.doi.org/10.1126/science.abj2972

3. Wong EO, Brownlie EJE, Ng KM, Kathirgamanathan S, Yu FB, **Merrill BD**, Huang KC, Martin A, Tropini C, Navarre WW (2022). The CIAMIB: a Large and Metabolically Diverse Collection of Inflammation-Associated Bacteria from the Murine Gut. *mBio*, 13, 2:e0294921. https://doi.org/10.1128/mbio.02949-21

4. Lynch JB, Bennett BD, **Merrill BD**, Ruby EG, Hryckowian AJ. (2022) Independent host- and bacterium-based determinants protect a model symbiosis from phage predation. *Cell Rep* Feb;38(7):110376. https://dx.doi.org/10.1016/j.celrep.2022.110376

5. Wastyk HC, Fragiadakis GK, Perelman D, Dahan D, **Merrill BD**, Yu FB, Topf M, Gonzalez CG, Van Treuren W, Han S, Robinson JL, Elias JE, Sonnenburg ED, Gardner CD, Sonnenburg JL. (2021) Gut-microbiota-targeted diets modulate human immune status. *Cell* 184(16):4137-4153.e14. https://doi.org/10.1016/j.cell.2021.06.019

6. Han S*, Van Treuren W*, Fischer CR, **Merrill BD**, DeFelice BC, Sanchez JM, Higginbottom SK, Guthrie L, Fall LA, Dodd D, Fischbach MA, Sonnenburg JL. (2021) A metabolomics pipeline enables mechanistic interrogation of the gut microbiome. *Nature* 595, 415-420. https://doi.org/10.1038/s41586-021-03707-9

7. Eren AM, Kiefl E, Shaiber A, Veseli I, Miller SE, Schechter MS, Fink I, Pan JN, Yousef M, Fogarty EC, Trigodet F, Watson AR, Esen OC, Moore RM, Clayssen Q, Lee MD, Kivenson V, Graham ED, **Merrill BD**, Karkman A, Blankenberg D, Eppley JM, Sjödin A, Scott JJ, Vázquez-Campos X, McKay LJ, McDaniel EA, Stevens SLR, Anderson RE, Fuessel J, Fernandez-Guerra A, Maignien L, Delmont TO, Willis AD. (2020) Community-led, integrated, reproducible multi-omics with anvi'o. *Nature Microbiology* 6, 3-6. https://doi.org/10.1038/s41564-020-00834-3

8. Porter NT, Hryckowian AJ, **Merrill BD**, Fuentes JJ, Gardner JO, Glowacki RWP, Singh S, Crawford RD, Snitkin ES, Sonnenburg JL, Martens EC. (2020) Phase-variable capsular polysaccharides and lipoproteins modify bacteriophage susceptibility in *Bacteroides thetaiotaomicron*. *Nature Microbiology* 5, 1170-1181. https://doi.org/10.1038/s41564-020-0746-5

9. Hryckowian AJ*, **Merrill BD***, Porter NT, Van Treuren W, Nelson EJ, Garlena RA, Russell DA, Martens EC, Sonnenburg JL. (2020) *Bacteroides thetaiotaomicron*-infecting bacteriophage isolates inform sequence-based host range predictions. *Cell Host & Microbe* 28(3):371.379.e5. https://doi.org/10.1016/j.chom.2020.06.011

10. Ng KM, Aranda-Díaz A, Tropini C, Franklel MR, Van Treuren W, O'Loughlin CT, **Merrill BD**, Yu FB, Pruss KM, Oliveira RA, Higginbottom SK, Neff NF, Fischbach MA, Xavier KB, Sonnenburg JL, Huang KC. (2019) Recovery of the gut microbiota after antibiotics depends on host diet, community context, and environmental reservoirs. *Cell Host & Microbe* 26(5):650-665.e4. https://doi.org/10.1016/j.chom.2019.10.011

11. The Tabula Muris Consortium. (2020) A single-cell transcriptomic atlas characterizes ageing tissues in the mouse. *Nature* 583, 590-595. https://doi.org/10.1038/s41586-020-2496-1

12. Tropini C, Moss EL, **Merrill BD**, Ng KM, Higginbottom SK, Casavant EP, Gonzalez CG, Fremin B, Bouley DM, Elias JE, Bhatt AS, Huang KC, Sonnenburg JL. (2018) Transient osmotic perturbation causes long-term alteration to the gut microbiota. *Cell* 173(7):1742-1754.e17. https://dx.doi.org/10.1016/j.cell.2018.05.008

13. Lumb JH, Li Q, Popov LM, Ding S, Keith MT, **Merrill BD**, Greenberg HB, Li JB, Carette JE. (2017) DDX6 Represses Aberrant Activation of Interferon-Stimulated Genes. *Cell Rep* 20(4):819-831. https://doi.org/10.1016/j.celrep.2017.06.085

14. Dodd D, Spitzer MH, Van Treuren W, **Merrill BD**, Hryckowian AJ, Higginbottom SK, Le A, Cowan TM, Nolan GP, Fischbach MA, Sonnenburg JL. (2017) A gut bacterial pathway metabolizes aromatic amino acids into nine circulating metabolites. *Nature* 551(7682):648-652. https://doi.org/10.1038/nature24661

15. Brady TS, Fajardo CP, **Merrill BD**, Hilton JA, Graves KA, Eggett DL, Hope, S. (2018) Bystander phage therapy: Inducing host-associated bacteria to produce antimicrobial toxins against the pathogen using phages. *Antibiotics* 7(4):105. https://doi.org/10.3390/antibiotics7040105

16. **Merrill BD**, Fajardo CP, Hilton JA, Payne AM, Ward AT, Walker JK, Dhalai A, Imahara C, Mangohig J, Monk J, Pascacio C, Raj P, Salisbury A, Velez K, Bloomfield TJ, Buhler B, Duncan SG, Fuhriman DA, George J, Graves K, Heaton K, Hill HL, Kim M, Knabe BK, Ririe DB, Rogers SL, Stamereilers C, Stephenson MB, Usher BK, Ward CS, Withers JM, Wright CK, Breakwell DP, Grose JH, Hope S, Tsourkas PK. (2018) Complete genome sequences of 18 *Paenibacillus larvae* phages from the western United States. *Microbiol Resour Announc*, 7 (13) e00966-18 https://doi.org/10.1128/MRA.00966-18

17. Berg JA, **Merrill BD**, Breakwell DP, Hope S, Grose JH. (2018) A PCR-based method for distinguishing between two common beehive bacteria, *Paenibacillus larvae* and *Brevibacillus laterosporus*. *Appl Environ Microbiol* 84:e01886-18. https://doi.org/10.1128/AEM.01886-18

18. Walker JK, **Merrill BD**, Berg JA, Dhalai A, Dingman DW, Fajardo CP, Graves K, Hill HL, Hilton JA, Imahara C, Knabe BK, Mangohig J, Monk J, Mun H, Pyne AM, Salisbury A, Stamereilers C, Velez K, Ward AT, Breakwell DP, Grose JH, Hope S, Tsourkas PK. (2018) Complete genome sequences of *Paenibacillus larvae* Phages BN12, Dragolir, Kiel007, Leyra, Likha, Pagassa, PBL1c, and Tadhana. *Genome Announc* 6 (24) e01602-17. https://doi.org/10.1128/genomeA.01602-17

19. Brady TS, **Merrill BD**, Hilton JA, Payne AM, Stephenson MB, Hope. S. (2017) Bacteriophages as an alternative to conventional antibiotic use for the prevention or treatment of *Paenibacillus larvae* in honeybee hives. *J Invertebr Pathol* 150:94-100. https://doi.org/10.1016/j.jip.2017.09.010

20. Esplin IND, Berg JA, Sharma R, Allen RC, Arens DK, Ashcroft CR, Bairett SR, Beatty NJ, Bickmore M, Bloomfield TJ, Brady TS, Bybee RN, Carter JL, Choi MC, Duncan S, Fajardo CP, Foy BB, Fuhriman DA, Gibby PD, Grossarth SE, Harbaugh K, Harris N, Hilton JA, Hurst E, Hyde JR, Ingersoll K, Jacobson CM, James BD, Jarvis TM, Jaen-Anieves D, Jensen GL, Knabe BK, Kruger JL, **Merrill BD**, Pape JA, Anderson AMP, Payne DE, Peck MD, Pollock SV, Putnam MJ, Ransom EK, Ririe DB, Robinson DM, Rogers SL, Russel KA, Schoenhals JE, Shurtleff CA, Simister AR, Smith HG, Stephenson MB, Staley LA, Stettler JM, Stratton ML, Tateoka OB, Tatlow PJ, Taylor AS, Thompson SE, Townsend MH, Thurgood TL, Usher BK, Whitley KV, War AT, Ward MEH, Webb CJ, Wienclaw TM, Williamson TL, Wells MJ, Wright CK, Breakwell DP, Hope S, Grose JH. (2017) Genome sequences of 19 novel *Erwinia amylovora* bacteriophages. *Genome Announc* 5(46) e00931-17. https://doi.org/10.1128/genomeA.00931-17

21. **Merrill BD**, Ward AT, Grose JH, Burnett SH. (2016) Software-based analysis of bacteriophage genomes, physical ends, and packaging strategies. *BMC Genomics* 17:679. https://doi.org/10.1186/s12864-016-3018-2

22. Berg JA, **Merrill BD**, Crockett JT, Esplin KP, Evans MR, Heaton KE, Hilton JA, Hyde JR, McBride MS, Schouten JT, Simister AR, Thurgood TL, Ward AT, Breakwell DP, Hope S, Grose JH. (2016) Characterization of five novel *Brevibacillus* bacteriophages and genomic comparison of *Brevibacillus* phages. *PLOS One* 11(6):e0156838. https://doi.org/10.1371/journal.pone.0156838

23. **Merrill BD**, Berg JA, Graves KA, Ward AT, Hilton JA, Wake BN, Grose JH, Breakwell DP, Burnett SH. (2015) Genome sequences of five additional *Brevibacillus laterosporus* bacteriophages. *Genome Announc* 3(5):e01146-15. https://doi.org/10.1128/genomeA.01146-15

24. Asare PT, Jeong TY, Ryu S, Klumpp J, Loessner MJ, **Merrill BD**, Kim KP. (2015) Putative type 1 thymidylate synthase and dihydrofolate reductase as signature genes of a novel Bastille-like group of phages in the subfamily Spounavirinae. *BMC Genomics* 16:582. https://doi.org/10.1186/s12864-015-1757-0

25. **Merrill BD**, Grose JH, Breakwell DP, Burnett SH. (2014) Characterization of *Paenibacillus larvae* bacteriophages and their genomic relationships to Firmicute bacteriophages. *BMC Genomics* 15:745. https://doi.org/10.1186/1471-2164-15-745

26. Grose JH, Belnap DM, Jensen JD, Mathis AD, Prince JT, **Merrill BD**, Burnett SH, Breakwell DP**.** (2014) The genomes, proteomes and structure of three novel phages that infect the *Bacillus cereus* group and carry putative virulence factors. *J Virol* 88:11846-11860. https://doi.org/10.1186/1471-2164-15-745

27. Grose JH, Jensen JD, **Merrill BD**, Fisher JNB, Burnett SH, and Breakwell DP**.** (2014) Genome sequences of three novel *Bacillus cereus* bacteriophages. *Genome Announc* 2:e01118-01113. https://doi.org/10.1186/1471-2164-15-745

28. Breakwell DP, Barrus EZ, Benedict AB, Brighton AK, Fisher JNB, Gardner AV, Kartchner BJ, Ladle KC, Lunt BL, **Merrill BD**, Morrell JD, Burnett SH, and Grose JH. (2013) Genome sequences of five B1 subcluster Mycobacteriophages. *Genome Announc* 1:e00968-00913. https://journals.asm.org/doi/10.1128/genomeA.00968-13

29. Sheflo MA, Gardner AV, **Merrill BD**, Fisher JNB, Lunt BL, Breakwell DP, Grose JH, Burnett SH. (2013) Complete genome sequences of five *Paenibacillus larvae* bacteriophages. *Genome Announc* 1:e00668-00613. https://doi.org/10.1128/genomeA.00668-13

Direct involvement in isolation, sequencing, assembly, annotation, and publication of 86 bacteriophages in NCBI GenBank (as of August 2022). https://tinyurl.com/bmerrillNCBIphages

PRESENTATIONS

30. **Merrill BD**. Hunter-gatherers across geography share conserved gut bacterial species absent in industrialized societies. *Department of Microbiology and Immunology Seminar, Stanford University*. Stanford, CA. April 24, 2019. (Oral presentation)

31. **Merrill BD**, Fragiadakis GK, Smits SA, Sonnenburg ED, Sonnenburg JL. Novel bacterial genomes from the Hadza hunter-gatherer gut microbiota. *The Third Annual Stanford Microbiome Summit,* Stanford, CA. October 20, 2017. (Poster)

32. **Merrill BD**, Hryckowian AJ. Functional and genomic characterization of phages infecting a prominent member of the human gut microbiota*. The California Microbiome Initiative Meeting*. San Diego, CA. August 12-14, 2016. (Oral presentation)

33. Simister A, Heaton K, Thurgood T, Berg JA, **Merrill BD**, Ward AT, Breakwell DP, Grose JH, Hope S. The mosaic nature and evolution of three *Brevibacillus* phages and their impact on *Brevibacillus*

laterosporus and other bacteria. *American Society for Microbiology Tri-Branch Meeting*, Durango, CO. 2015. (Poster)

34. Crockett JT, Esplin KP, Hyde JR, **Merrill BD**, Berg JA, Ward AT, Breakwell DP, Grose JH, Hope S. *Brevibacillus* bacteriophages xane and jenst reveal a DNA motif indicating a gene regulatory sequence. *American Society for Microbiology Tri-Branch Meeting*, Durango, CO. 2015. (Poster)

35. Hilton JA, Schouten JT, Berg JA, **Merrill BD**, Ward AT, Breakwell DP, Grose JH, Hope S. Discovery of two novel phage clusters in *Brevibacillus laterosporus* using comparative genomics. *American Society for Microbiology Tri-Branch Meeting*, Durango, CO. 2015. (Poster)

36. McBride MS, Evans MR, Brundage BM, **Merrill BD**, Berg JA, Ward AT, Grose JH, Breakwell DP, Hope S. Comparing protein structures of a transcriptional regulator repeated in *Brevibacillus* phages. *American Society for Microbiology Tri-Branch Meeting*, Durango, CO. 2015. (Poster)

37. Wienclaw TM, Taylor AS, Bairett SR, Ashcroft CR, **Merrill BD**, Schoenhals JE, Esplin IND, Breakwell DP, Grose JH, Hope S. Phage Jenst provides a unique genome with gene products new to *Paenibacillus larvae* phages. *Sixth Annual SEA-PHAGES Symposium*, Howard Hughes Medical Institute, Ashburn, VA. 2014. (Poster)

38. Jensen GL, Berg JA, Foy BM, Grossarth SE, Harbaugh K, Ingersoll K, Kruger JL, Peck MD, Ransom EK, Smith HG, Stratton ML, Esplin IND, **Merrill BD**, Schoenhals JE, Breakwell DP, Hope S, Grose JH. Isolation and characterization of eleven phages that infect *Erwinia amylovora*. *Sixth Annual SEA-PHAGES Symposium*, Howard Hughes Medical Institute, Ashburn, VA. 2014. (Poster)

39. Miller ES, Schaff J, **Merrill BD**, Lin L, Dums J. Advancing student-accessible phage genomics at NC State University through local NGS DNA sequencing and virtual computing resources. *Sixth Annual SEA-PHAGES Symposium*, Howard Hughes Medical Institute, Ashburn, VA. 2014. (Poster)

40. Stratton ML, Harbaugh K, Foy BM, Jaen-Anieves D, Paz H, Shurtleff C, Kruger JL, Peck MD, Jensen GL, Esplin IND, **Merrill BD**, Schoenhals JE, Breakwell DP, Hope S, Grose JH. Discovery and genomic analysis of an N4-like *Erwinia amylovora* phage. *American Society for Microbiology Intermountain Branch Meeting*, Provo, UT. 2014. (Poster)

41. Ransom EK, Berg JA, Grossarth SE, Smith HG, Jaen-Anieves D, Esplin IND, **Merrill BD**, Schoenhals JE, Breakwell DP, Hope S, Grose JH. Comparative genome analysis of seven novel *Erwinia* phages reveals orthologous proteins and allows for formation of a cluster with three known Enterobacteriaceae phages. *American Society for Microbiology Intermountain Branch Meeting*, Provo, UT. 2014. (Poster)

42. Taylor AS, Bairett SR, Wienclaw TM, Ashcroft CR, Esplin IND, Schoenhals JE, **Merrill BD**, Breakwell DP, Grose JH, Hope S. Isolation and genomic analysis of *Paenibacillus larvae* bacteriophage Jenst. *American Society for Microbiology Intermountain Branch Meeting*, Provo, UT. 2014. (Poster)

43. Ingersoll K, Jensen GL, Kruger JL, Foy BM, Grossarth SE, Harbaugh K, Paz H, Esplin IND, Schoenhals JE, **Merrill BD**, Hope S, Breakwell DP, Grose JH. Isolation and characterization of Deimos-Minion, the largest *Erwinia amylovora* bacteriophage. *American Society for Microbiology Intermountain Branch Meeting*, Provo, UT. 2014. (Poster)

44. **Merrill BD**, Schoenhals JE, Graves KA, Grose JH, Hope S, Breakwell DP. DNA packaging strategies for bacteriophages identified using phylogenetic analysis of large terminase proteins. *American Society for Microbiology Intermountain Branch Meeting*, Provo, UT. 2014. (Poster)

45. **Merrill BD**, Grose JH, Breakwell DP, Hope S. Genomic analysis of six *Paenibacillus larvae* bacteriophages. *Utah Conference on Undergraduate Research*, Provo, UT. 2014. (Poster)

46. Brown A, Christopher A, Harrison C, Kiser K, Lasko D, Li X, **Merrill BD**, Peck K, Perry LJ, Sabin S, Schellhous M, Westra K, Kooyman DL, Grose JH. Phage pharming: Two approaches to expanding the use of bacteriophage in synthetic biology. *iGEM World Jamboree*, Cambridge MA. 2013. (Poster)

47. Brown A, Christopher A, Harrison C, Kiser K, Lasko D, Li X, **Merrill BD**, Peck K, Perry LJ, Sabin S, Schellhous M, Westra K, Kooyman DL, Grose JH. Phage pharming: Two approaches to expanding the use of bacteriophage in synthetic biology. *iGEM Regional Jamboree*, Toronto, Canada. 2013. (Poster)

48. **Merrill BD**, Sheflo MA, Ayer PA, Beckstead AP, Fajardo CP, Ferguson NC, Fisher JNB, Gardner AV, Graves KA, Hartmann KA, Kennedy AK, Liu JE, Lunt BL, Merrill CA, Russell RC, Wake BN, Williams KR, Zimmerman L, Grose JH, Breakwell DP, Hope S. Discovery and characterization of novel *Paenibacillus larvae* bacteriophages. *Fifth Annual SEA-PHAGES Symposium*, Howard Hughes Medical Institute, Ashburn, VA. June 7-9, 2013. (Poster, honorable mention)