Stanford

Bryan Merrill

Ph.D. Student in Microbiology and Immunology, admitted Autumn 2015

Bio

EDUCATION AND CERTIFICATIONS

- MS, Brigham Young University , Microbiology and Molecular Biology (2015)
- BS, Brigham Young University , Molecular Biology (2014)

LINKS

- ResearchGate: https://www.researchgate.net/profile/Bryan_Merrill
- Homepage: https://brymerr921.github.io/
- Sonnenburg Lab: http://sonnenburglab.stanford.edu/
- Google Scholar: https://scholar.google.com/citations?user=C__eM6YAAAAJ
- ORCiD: https://orcid.org/0000-0002-9967-5539
- Twitter: https://twitter.com/bryan_d_merrill
- Github: https://github.com/brymerr921
- LinkedIn: https://www.linkedin.com/in/bryan-merrill-713a0b5b

Publications

PUBLICATIONS

- **Robust variation in infant gut microbiome assembly across a spectrum of lifestyles.** *Science (New York, N.Y.)*
  Olm, M. R., Dahan, D., Carter, M. M., Merrill, B. D., Yu, F. B., Jain, S., Meng, X., Tripathi, S., Wastyk, H., Neff, N., Holmes, S., Sonnenburg, E. D., Jha, et al
  2022; 376 (6598): 1220-1223

- **The CIAMIB: a Large and Metabolically Diverse Collection of Inflammation-Associated Bacteria from the Murine Gut.** *mBio*
  Wong, E. O., Brownlie, E. J., Ng, K. M., Kathirgamanathan, S., Yu, F. B., Merrill, B. D., Huang, K. C., Martin, A., Tropini, C., Navarre, W. W.
  2022: e0294921

- **Molecular hallmarks of heterochronic parabiosis at single-cell resolution.** *Nature*
  Palovics, R., Keller, A., Schaum, N., Tan, W., Fehlmann, T., Borja, M., Kern, F., Bonanno, L., Calcuttawala, K., Webber, J., McGeever, A., Tabula Muris Consortium, Luo, J., et al
  2022

- **Independent host- and bacterium-based determinants protect a model symbiosis from phage predation.** *Cell reports*
  Lynch, J. B., Bennett, B. D., Merrill, B. D., Ruby, E. G., Hryckowian, A. J.
  2022; 38 (7): 110376

- **Community-led, integrated, reproducible multi-omics with anvi'o.** *Nature microbiology*
  Eren, A. M., Kiefl, E., Shaiber, A., Veseli, I., Miller, S. E., Schechter, M. S., Fink, I., Pan, J. N., Yousef, M., Fogarty, E. C., Trigodet, F., Watson, A. R., Esen, et al

2021; 6 (1): 3–6

- **A metabolomics pipeline for the mechanistic interrogation of the gut microbiome.** *Nature*
  Han, S., Van Treuren, W., Fischer, C. R., Merrill, B. D., DeFelice, B. C., Sanchez, J. M., Higginbottom, S. K., Guthrie, L., Fall, L. A., Dodd, D., Fischbach, M. A., Sonnenburg, J. L.
  2021; 595 (7867): 415-420

- **Gut-microbiota-targeted diets modulate human immune status.** *Cell*
  Wastyk, H. C., Fragiadakis, G. K., Perelman, D., Dahan, D., Merrill, B. D., Yu, F. B., Topf, M., Gonzalez, C. G., Van Treuren, W., Han, S., Robinson, J. L., Elias, J. E., Sonnenburg, et al
  2021

- **Phase-variable capsular polysaccharides and lipoproteins modify bacteriophage susceptibility in Bacteroides thetaiotaomicron.** *Nature microbiology*
  Porter, N. T., Hryckowian, A. J., Merrill, B. D., Fuentes, J. J., Gardner, J. O., Glowacki, R. W., Singh, S., Crawford, R. D., Snitkin, E. S., Sonnenburg, J. L., Martens, E. C.
  2020

- **Bacteroides thetaiotaomicron-Infecting Bacteriophage Isolates Inform Sequence-Based Host Range Predictions.** *Cell host & microbe*
  Hryckowian, A. J., Merrill, B. D., Porter, N. T., Van Treuren, W. n., Nelson, E. J., Garlena, R. A., Russell, D. A., Martens, E. C., Sonnenburg, J. L.
  2020

- **Ageing hallmarks exhibit organ-specific temporal signatures.** *Nature*
  Schaum, N. n., Lehallier, B. n., Hahn, O. n., Pálovics, R. n., Hosseinzadeh, S. n., Lee, S. E., Sit, R. n., Lee, D. P., Losada, P. M., Zardeneta, M. E., Fehlmann, T. n., Webber, J. T., McGeever, et al
  2020

- **A single-cell transcriptomic atlas characterizes ageing tissues in the mouse.** *Nature*
  2020

- **Recovery of the Gut Microbiota after Antibiotics Depends on Host Diet, Community Context, and Environmental Reservoirs.** *Cell host & microbe*
  Ng, K. M., Aranda-Díaz, A. n., Tropini, C. n., Frankel, M. R., Van Treuren, W. n., O'Laughlin, C. T., Merrill, B. D., Yu, F. B., Pruss, K. M., Oliveira, R. A., Higginbottom, S. K., Neff, N. F., Fischbach, et al
  2019; 26 (5): 650–65.e4

- **Bystander Phage Therapy: Inducing Host-Associated Bacteria to Produce Antimicrobial Toxins against the Pathogen Using Phages.** *Antibiotics (Basel, Switzerland)*
  Brady, T. S., Fajardo, C. P., Merrill, B. D., Hilton, J. A., Graves, K. A., Eggett, D. L., Hope, S.
  2018; 7 (4)

- **A PCR-Based Method for Distinguishing between Two Common Beehive Bacteria, Paenibacillus larvae and Brevibacillus laterosporus** *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*
  Berg, J. A., Merrill, B. D., Breakwell, D. P., Hope, S., Grose, J. H.
  2018; 84 (22)

- **Complete Genome Sequences of 18 Paenibacillus larvae Phages from the Western United States.** *Microbiology resource announcements*
  Merrill, B. D., Fajardo, C. P., Hilton, J. A., Payne, A. M., Ward, A. T., Walker, J. K., Dhalai, A., Imahara, C., Mangohig, J., Monk, J., Pascacio, C., Rai, P., Salisbury, et al
  2018; 7 (13)

- **A PCR-BASED METHOD FOR DISTINGUISHING BETWEEN TWO COMMON BEEHIVE BACTERIA, PAENIBACILLUS LARVAE AND BREVIBACILLUS LATEROSPORUS.** *Applied and environmental microbiology*
  Berg, J. A., Merrill, B. D., Breakwell, D. P., Hope, S., Grose, J. H.
  2018

- **Complete Genome Sequences of Paenibacillus larvae Phages BN12, Dragolir, Kiel007, Leyra, Likha, Pagassa, PBL1c, and Tadhana.** *Genome announcements*
  Walker, J. K., Merrill, B. D., Berg, J. A., Dhalai, A., Dingman, D. W., Fajardo, C. P., Graves, K., Hill, H. L., Hilton, J. A., Imahara, C., Knabe, B. K., Mangohig, J., Monk, et al
  2018; 6 (24)

- **Transient Osmotic Perturbation Causes Long-Term Alteration to the Gut Microbiota** *CELL*
  Tropini, C., Moss, E., Merrill, B., Ng, K., Higginbottom, S., Casavant, E., Gonzalez, C., Fremin, B., Bouley, D., Elias, J., Bhatt, A., Huang, K., Sonnenburg, et al

2018; 173 (7): 1742-+

- **Transient Osmotic Perturbation Causes Long-Term Alteration to the Gut Microbiota.** *Cell*
  Tropini, C., Moss, E. L., Merrill, B. D., Ng, K. M., Higginbottom, S. K., Casavant, E. P., Gonzalez, C. G., Fremin, B., Bouley, D. M., Elias, J. E., Bhatt, A. S., Huang, K. C., Sonnenburg, et al
  2018; 173 (7): 1742

- **Genome Sequences of 19 Novel Erwinia amylovora Bacteriophages.** *Genome announcements*
  Esplin, I. N., Berg, J. A., Sharma, R., Allen, R. C., Arens, D. K., Ashcroft, C. R., Bairett, S. R., Beatty, N. J., Bickmore, M., Bloomfield, T. J., Brady, T. S., Bybee, R. N., Carter, et al
  2017; 5 (46)

- **Bacteriophages as an alternative to conventional antibiotic use for the prevention or treatment of Paenibacillus larvae in honeybee hives** *JOURNAL OF INVERTEBRATE PATHOLOGY*
  Brady, T., Merrill, B. D., Hilton, J. A., Payne, A. M., Stephenson, M. B., Hope, S.
  2017; 150: 94–100

- **DDX6 Represses Aberrant Activation of Interferon-Stimulated Genes.** *Cell reports*
  Lumb, J. H., Li, Q. n., Popov, L. M., Ding, S. n., Keith, M. T., Merrill, B. D., Greenberg, H. B., Li, J. B., Carette, J. E.
  2017; 20 (4): 819–31

- **A gut bacterial pathway metabolizes aromatic amino acids into nine circulating metabolites.** *Nature*
  Dodd, D. n., Spitzer, M. H., Van Treuren, W. n., Merrill, B. D., Hryckowian, A. J., Higginbottom, S. K., Le, A. n., Cowan, T. M., Nolan, G. P., Fischbach, M. A., Sonnenburg, J. L.
  2017; 551 (7682): 648–52

- **Software-based analysis of bacteriophage genomes, physical ends, and packaging strategies** *BMC GENOMICS*
  Merrill, B. D., Ward, A. T., Grose, J. H., Hope, S.
  2016; 17

- **Characterization of Five Novel Brevibacillus Bacteriophages and Genomic Comparison of Brevibacillus Phages** *PLOS ONE*
  Berg, J. A., Merrill, B. D., Crockett, J. T., Esplin, K. P., Evans, M. R., Heaton, K. E., Hilton, J. A., Hyde, J. R., McBride, M. S., Schouten, J. T., Simister, A. R., Thurgood, T. L., Ward, et al
  2016; 11 (6)

- **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*
  Asare, P. T., Jeong, T., Ryu, S., Klumpp, J., Loessner, M. J., Merrill, B. D., Kim, K.
  2015; 16

- **Genome Sequences of Five Additional Brevibacillus laterosporus Bacteriophages.** *Genome announcements*
  Merrill, B. D., Berg, J. A., Graves, K. A., Ward, A. T., Hilton, J. A., Wake, B. N., Grose, J. H., Breakwell, D. P., Burnett, S. H.
  2015; 3 (5)

- **Correction for Sheflo et al., Complete Genome Sequences of Five Brevibacillus laterosporus Bacteriophages.** *Genome announcements*
  Sheflo, M. A., Gardner, A. V., Merrill, B. D., Fisher, J. N., Lunt, B. L., Breakwell, D. P., Grose, J. H., Burnett, S. H.
  2015; 3 (5)

- **The Genomes, Proteomes, and Structures of Three Novel Phages That Infect the Bacillus cereus Group and Carry Putative Virulence Factors** *JOURNAL OF VIROLOGY*
  Grose, J. H., Belnap, D. M., Jensen, J. D., Mathis, A. D., Prince, J. T., Merrill, B. D., Burnett, S. H., Breakwell, D. P.
  2014; 88 (20): 11846-11860

- **Characterization of Paenibacillus larvae bacteriophages and their genomic relationships to firmicute bacteriophages** *BMC GENOMICS*
  Merrill, B. D., Grose, J. H., Breakwell, D. P., Burnett, S. H.
  2014; 15

- **Genome Sequences of Three Novel Bacillus cereus Bacteriophages.** *Genome announcements*
  Grose, J. H., Jensen, J. D., Merrill, B. D., Fisher, J. N., Burnett, S. H., Breakwell, D. P.
  2014; 2 (1)

- **Genome sequences of five b1 subcluster mycobacteriophages.** *Genome announcements*
  Breakwell, D. P., Barrus, E. Z., Benedict, A. B., Brighton, A. K., Fisher, J. N., Gardner, A. V., Kartchner, B. J., Ladle, K. C., Lunt, B. L., Merrill, B. D., Morrell, J. D., Burnett, S. H., Grose, et al
  2013; 1 (6)

- **Complete Genome Sequences of Five Paenibacillus larvae Bacteriophages.** *Genome announcements*
  Sheflo, M. A., Gardner, A. V., Merrill, B. D., Fisher, J. N., Lunt, B. L., Breakwell, D. P., Grose, J. H., Burnett, S. H.
  2013; 1 (6)