

Figure 1:

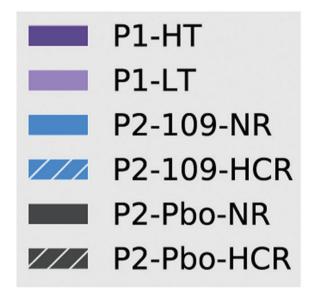
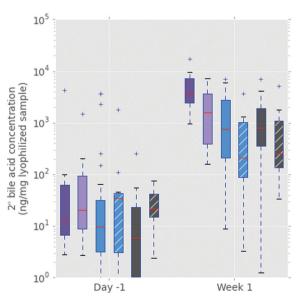


Figure 2:



Disclosures. M. Henn, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. C. Ford, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. L. D'Brien, Seres: Employee and Shareholder, Salary. L. Diao, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. L. Diao, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. L. Diao, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. K. Litcofsky, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. K. Litcofsky, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. K. Litcofsky, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. M. Wilcox, Seres Therapeutics, Inc.: Consultant, Research Contractor, Scientific Advisor and Shareholder, Salary. B. McGovern, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. J. G. Aunins, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. D. N. Cook, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. D. Seres Therapeutics, Inc.: Employee and Shareholder, Salary. D. N. Cook, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. D. N. Cook, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. M. Trucksis, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. D. N. Cook, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. M. Trucksis, Seres Therapeutics, Inc.: Employee and Shareholder, Salary. M. Seres Seres Therapeuti

622. Increased IgA Coating of Gut Microbes After Administration of Killed, Whole-Cell Oral Cholera Vaccine

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Background. Cholera vaccines are recommended for use in outbreaks to prevent infections and reduce severity of disease. Variable immune responses are observed after administration of killed, whole-cell cholera vaccines, and limited data suggest that the gut microbiome may be one factor influencing immune responses to vaccination.

Methods. We used microbial DNA sequencing of stool and serum vibriocidal titers to examine the gut microbiome and immune responses to vaccination at day 0, 7, 17 and 44 in adult vaccine recipients in Dhaka, Bangladesh. Using flow cytome-try-based bacterial cell sorting, we identified IgA-coated gut microbes in stool before and after vaccination in a subset of patients.

Results. Vibriocidal titer magnitude and kinetics were used to classify participants. Within 17 days of vaccination, 86/89 (96%) adults developed a four-fold rise in vibriocidal titer. Gut microbial diversity was not significantly changed after vaccination. Rate of seroconversion (four-fold increase in vibriocidal titer by Day 3 after vaccination) was faster in participants with increased bacteria from the genus Prevotella (multivariate analysis using linear models, *q* value 0.04). The gut microbes of participants with higher peak vibriocidal titers was characterized by increased Prevotella (3% vs. <0.1% of the total microbiome, *P* < 0.001 unpaired *t*-test, linear discriminant analysis score >3.5). Lipopolysaccharide from Prevotella species is known to increase vaccination-associated antigen-specific antibody titers in animal models. Additionally, IgA coating of gut microbes in stool increased after vaccination, sp% IgA coated at baseline to a peak level of 19% during follow-up (Wilcoxon signed rank test, *P* < 0.01).

Conclusion. Certain microbiome profiles are correlated with greater immune responses to cholera vaccination, and IgA coating of gut bacteria indicates which commensal species may be participating in the mucosal immune response. The potential for modulation of mucosal immune responses based on gut microbial species warrants further study.

Disclosures. All authors: No reported disclosures.

623. Dynamic Nature of the Gut Resistome Among Infants in Singapore Amanda Zain, MMed¹; Gaik Chin Yap, MSc²; Rikky W. Purbojati, MSc³; Daniela Isabel Moses, PhD3; Lynette P.C. Shek, FRCPCH1; Anne Goh, MMed4; Hugo P. S. Van Bever, PhD¹; Oon Hoe Teoh, MMed⁴; Jian Yi Soh, MMed¹; Biju Thomas, MD³ Mahesh Babu Ramamurthy, MD1; Daniel Y. T. Goh, MMed1; Christophe Lay, PhD5; Evelyn Loo Xiu Ling, PhD⁶; Shu-E Soh, PhD⁷; Fabian Yap, MMed⁴; Kok Hian Tan, MRCOG⁴; Yap-Seng Chong, PhD⁷; Keith M. Godfrey, PhD⁸; Peter D. Gluckman, MD⁶; Stephan Schuster, PhD³; Ritu Banerjee, MD, PhD⁹ and Bee Wah Lee, MBBS¹ ¹Department of Paediatrics, Khoo Teck Puat-National University Children's Medical Institute, National University Health System, Singapore, Singapore, ²Department of Paediatrics, Yong Loo Lin School of Medicine, National University of Singapore, Singapore, Singapore, ³Singapore Center On Environmental Life Sciences Engineering (SCELSE), Nanyang Technological University, Singapore, Singapore, ⁴Department of Paediatrics Allergy and Respiratory, KK Children's and Women's Hospital, Singapore, Singapore, ⁵Department of Paediatrics, Yong Loo Lin School of Medicine, Singapore, Singapore, 6Singapore Institute for Clinical Sciences, Agency for Science, Technology and Research Singapore, Singapore, Singapore, ⁷Department of Obstetrics & Gynaecology, National University of Singapore, Singapore, Singapore, ⁸MRC Lifecourse Epidemiology Unit and NIHR Southampton Biomedical Research Centre, University of Southampton and University Hospital Southampton NHS Foundation Trust, Southampton, United Kingdom, ⁹Division of Pediatric Infectious Diseases, Vanderbilt University, Nashville, Tennessee

Session: 64. Microbiome and Beyond Thursday, October 4, 2018: 12:30 PM

Background. The gut microbiome harbors antibiotic resistance genes (ARGs), known as the resistome, that has the potential to spread and contribute to the global