

6<sup>th</sup> Annual Conference on

## MICROBIOLOGY

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## MICROBES AND BENEFICIAL MICROBES

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**Characterizing temporal and inter-individual functional differences in pre-term human infant gut microbiome development by a metaproteomics approach**R L Hettich<sup>1</sup>, W Xiong<sup>1</sup>, A Blakeley-Ruiz<sup>1</sup>, C Brown<sup>2</sup>, M Olm<sup>2</sup>, M Rodgers<sup>3</sup>, M J Morowitz<sup>3</sup> and J F Banfield<sup>2</sup><sup>1</sup>Oak Ridge National Laboratory, USA<sup>2</sup>University of California, USA<sup>3</sup>University of Pittsburgh, USA

Details about microbial species population structure and functional dynamics during microbiome establishment are poorly understood in the human infant gut. The objective of this work is to exploit a high performance LC-MS/MS based metaproteomic approach to explore host and microbiome temporal functional shifts during microbial colonization of the pre-term infant gut. Fecal metaproteomes of nine pre-term infants were measured at discrete time-points over several months. Approximately 10,000 human and microbial protein groups were identified in each infant. In early time points, human proteins were more abundant than microbial proteins, and comprised pathways involving epithelial barrier establishment and immune response. Intriguingly, comparison of genomic and proteomic patterns identified some microbial species that were both active and in low abundance. Most functional core metabolic processes were conserved in the microbiome; however, temporal and inter-individual variations were identified. For example, lipid metabolism (specifically glycerol degradation) was dominant early in one infant, and progressed to predominantly amino acid metabolism over time, in stark contrast to other pre-term infants. These differences are likely related to microbiome or environmental factors that distinguished the infants. In response to bacterial colonization, the human hosts expressed proteins that play pivotal roles in the integrity and barrier properties of mucosal epithelial layers. The time-course metaproteomics measurements revealed core metabolic pathways in both human and microbial proteins, revealing the establishment of the mutualistic relationship between the microbiome and human host early in infancy. In total, these results reveal functional stability and inter-individual signatures of the preterm infant gut microbiome.

**Biography**

R L Hettich has completed his PhD from Purdue University and joined the Oak Ridge National Laboratory in 1986. He is a distinguished Research Scientist in the Chemical Sciences Division at ORNL and a joint Faculty Member in the Microbiology Division/ Genome Science and Technology (GST) Graduate Schools at the University of Tennessee. His research interests involve the development and demonstration of advanced mass spectrometry technology for characterizing biological samples ranging from purified proteins to environmental microbial proteomes. He has over 230 peer-reviewed publications, and is active in teaching and mentoring graduate students.

hettichrl@ornl.gov

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