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**MICROBIOLOGY & MOLECULAR GENETICS**

**Departmental Journal Club**

**MICR 6120**

**Monday**

**October 10th, 2016**

11:30am-12:20pm

RM 122 Classroom Bldg.

Presented by

Melissa Brewer  
PHD Student

Title:    Alterations of the human gut microbiome in multiple sclerosis

Authors: Sushrut Jangi, Roopali Gandhi1, Laura M. Cox, Ning Li, Felipe von Glehn, Raymond Yan, Bonny Pate1, Maria Antonietta Mazzola, Shirong Liu, Bonnie L. Glanz, Sandra Cook, Stephanie Tankou, Fiona Stuart, Kirsy Melo, Parham Nejad, Kathleen Smith, Begu¨m D. Topc¸ James Holden, Pia Kivisa¨kk, Tanuja Chitnis, Philip L. De Jager, Francisco J. Quintana, Georg K. Gerber, Lynn Bry & Howard L. Weiner

The gut microbiome plays an important role in immune function and has been implicated in several autoimmune disorders. Here we use 16S rRNA sequencing to investigate the gut microbiome in subjects with multiple sclerosis (MS, n¼60) and healthy controls (n¼43). Microbiome alterations in MS include increases in Methanobrevibacter and Akkermansia and decreases in Butyricimonas, and correlate with variations in the expression of genes involved in dendritic cell maturation, interferon signalling and NF-kB signalling pathways in circulating T cells and monocytes. Patients on disease-modifying treatment show increased abundances of Prevotella and Sutterella, and decreased Sarcina, compared with untreated patients. MS patients of a second cohort show elevated breath methane compared with controls, consistent with our observation of increased gut Methanobrevibacter in MS in the first cohort.Further study is required to assess whether the observed alterations in the gut microbiome play a role in, or are a consequence of, MS pathogenesis.