- Edison Family Center for Genome Sciences and Systems Biology, Washington University School of Medicine, Saint Louis, MO 63110, USA; Center for Gut Microbiome and Nutrition Research, Washington University School of Medicine, Saint Louis, MO 63110, USA.
- 2- Edison Family Center for Genome Sciences and Systems Biology, Washington University School of Medicine, Saint Louis, MO 63110, USA.
- 3- Chemical Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37830, USA.
- 4- A. A. Kharkevich Institute for Information Transmission Problems, Russian Academy of Sciences, Moscow, 127994, Russia; Infectious and Inflammatory Disease Center, Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA 92037, USA.
- 5- Infectious and Inflammatory Disease Center, Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA 92037, USA.
- 6- Edison Family Center for Genome Sciences and Systems Biology, Washington University School of Medicine, Saint Louis, MO 63110, USA; Center for Gut Microbiome and Nutrition Research, Washington University School of Medicine, Saint Louis, MO 63110, USA. Electronic address: jgordon@wustl.edu.

## Abstract

Dramatic increases in processed food consumption represent a global health threat. Maillard reaction products (MRPs), which are common in processed foods, form upon heat-induced reaction of amino acids with reducing sugars and include advanced glycation end products with deleterious health effects. To examine how processed foods affect the microbiota, we fed gnotobiotic mice, colonized with 54 phylogenetically diverse human gut bacterial strains, defined sugar-rich diets containing whey as the protein source or a matched amino acid mixture. Whey or  $\epsilon$ -fructoselysine, an MRP in whey and many processed foods, selectively increases Collinsella intestinalis absolute abundance and induces Collinsella expression of genomic loci directing import and metabolism of  $\epsilon$ -fructoselysine to innocuous products. This locus is repressed by glucose in C. aerofaciens, whose abundance decreases with whey, but is not repressed in C. intestinalis. Identifying gut organisms responding to and degrading potentially harmful processed food components has implications for food science, microbiome science, and public health.