

Results: Curing resulted in a greater diversity on microbial populations compared to C. In C, *Limnospira* (28%), *Enterococcus* (11%), and *Brevundimonas* (13%) are the most relatively abundant genera. In contrast, after curing, *Limnospira* (22%) decreased and *Brevundimonas* (18%) increased in SON; *Bacillus* (26%), *Staphylococcus* (23%) are major in 80W and MIC, respectively, *Enterococcus* (23%) being major in MIC; *Kosakonia* (28%) and *Komagataeibacter* (15%) were exclusively found in FREE. In α -diversity, there was a higher diversity ($p < 0.05$) in C (349) and after curing (255-302). Except for SON, cured samples showed a higher diversity index than C. In contrast, C showed a greater dominance index compared to cured treatments. For β -diversity, MIC treatments clustered together and showed significant dissimilarity with respect to C along the first principal coordinate (variance explained=83%). This was tested by similarity analysis (ANOSIM), where the model revealed a significant difference ($R^2=0.485$, $p=0.003$) in the bacterial community compositions of the killing process.

Conclusions: Killing treatments modified the composition of the microbiota of vanilla pods, which could have an influence in the pods phytochemical profile. These findings suggest that killing during curing could modulate the microbiota and provide important organoleptic characteristics.

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P27-015-24 Gut Microbiota, Diet and Health Status of Nomadic and Urban Population in Mongolia

Ganmaa Davaasambuu¹, Enkhsetseg Tserenkhuu², Bilige Menghe³

¹ Harvard T.H. Chan School of Public Health, United States

² Mongolian Health Initiative, Mongolia

³ Inner Mongolia Key Laboratory of Dairy Biotechnology and Engineering, China (People's Republic)

Objectives: The dominant culture in Mongolia has historically been pastoral nomadism. Our study aimed to evaluate the nutritional and health status of these populations, analyze the characteristics of their gut microbiota, and establish correlations between gut microbiota composition, nutrition, and health status among the Mongolian population.

Methods: Recognizing the pivotal role of dietary nutrition in maintaining health and its impact on gut microbiota, this study employed metagenome sequencing technology, questionnaire surveys, and blood index examinations to explore the intricate connections between gut microbiota, diet, and the health status of the Mongolian population across various regions.

Results: The influence of both regions and seasons on the gut microbiota of the Mongolian population was observed, with regional disparities exerting a greater impact than seasonal variations. In winter, the gut microbiota structure of pastoral populations significantly differed from that of urban populations, marked by a decrease in *Bacteroides* and an increase in *Firmicutes*, alongside notable difference of beneficial bacteria such as *Bacteroides* sp., *Bifidobacterium* sp. and *Coprococcus* sp. There was an abundance of lactic acid bacteria and *Bifidobacterium* sp. in the Mongolian population's gut, presenting favorable conditions for the development and utilization of

unique probiotic resources in Mongolia. The correlations between microbial species and blood indexes, as well as nutrients, provide novel evidence supporting the complex relationships between gut microbiota, nutrition, and the health status of the Mongolian population.

Conclusions: Our study explored the relationships between gut microbiota, nutrition, and health in Mongols, considering the variations between urban and nomadic lifestyles and dietary practices. By addressing some of the existing gaps in our understanding, our findings provide valuable insights for scientific endeavors aimed at enhancing human health.

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P27-016-24 Maternal Fortified Balanced Energy-Protein Supplementation Increases Diversity of the Maternal Gut Microbiome and the Capacity of Carbohydrate Uptake in Infant Gut

Lishi Deng¹, Steff Taelman¹, Matthew R Olm², Laécia C Toé¹, Eva Balini³, Lionel O Ouédraogo¹, Yuri Bastos-Moreira¹, Alemayehu Argaw¹, Kokeb Tesfamariam¹, Erica D Sonnenburg², Giles Hanley-Cook¹, Moctar Ouédraogo⁴, Rasmané Ganaba⁴, Wim van Criekinge¹, Lieven Huybregts¹, Michiel Stock¹, Patrick Kolsteren¹, Justin L Sonnenburg², Carl Lachat¹, Trenton Dailey-Chwalibóg¹

¹ Ghent University, Belgium

² Stanford University, United States

³ BioLizard, Belgium

⁴ AFRICSanté, Burkina Faso

Objectives: Over 20% of the global population under age 5 experienced stunted growth in 2022. Maternal balanced energy-protein (BEP) supplementation is used to support infant growth, but the response of the microbiome to such supplementation remains largely unexplored, particularly in low- and middle-income countries. The objective of this study is to evaluate the effect of maternal BEP supplementation on the composition and functionality of the gut microbiome in mother-infant dyads in rural Burkina Faso.

Methods: We conducted a randomized controlled trial in rural Burkina Faso, among pregnant women (15-40 years old) enrolled at < 21 weeks of gestation. In the intervention group women received BEP supplements throughout pregnancy and the first six months postpartum. Fecal samples were collected from women and their infants at multiple timepoints covering pregnancy and lactation, and were analyzed using deep metagenomic sequencing.

Results: A total of 731 fecal samples from 152 women and their infants were collected and sequenced, which comprised 475 maternal samples and 256 infant samples. The maternal gut microbiota exhibited a conspicuous dominance of *Prevotella* species, while *Bifidobacterium* strains were dominant in infant samples. BEP supplementation significantly increased microbiome diversity during pregnancy, with a decrease in the abundance of an *Oscillospiraceae* species in the second trimester and an increase in *Bacteroides fragilis* at 5-6 months postpartum in women. We identified concerted enriched or depleted microbial

pathways associated with BEP supplementation, including the biosynthesis of lipopolysaccharide, a factor triggering preterm labor, were depleted within the prenatal gut microbiome in women who received BEP supplements. Furthermore, the phosphotransferase system, a critical mechanism for bacterial carbohydrate uptake, exhibited enrichment in infants born to BEP-supplemented mothers.

Conclusions: Overall, our results shed light on gut microbiome dynamics in a population that is underrepresented in microbiome science. The impact of maternal BEP supplementation on the maternal and infant's gut microbiome may benefit the growth of fetuses and neonates.

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P27-017-24 Gut Microbial Pathways Associated With Proton Pump Inhibitor Use in Boston-Area Puerto Rican Adults

Deepika Dinesh¹, Xochitl Morgan², Scott Gordon³, Jong Soo Lee⁴, Kelsey M Mangano⁴, Sabrina Noel⁴, Tammy M Scott⁴, Curtis Huttenhower², Katherine L Tucker⁴, Natalia Palacios⁴

¹ University of Massachusetts Lowell, United States

² Harvard T.H. Chan School of Public Health, United States

³ UMass Lowell, Department of Public Health, United States

⁴ Center for Population Health, UMass Lowell, United States

Objectives: Proton pump inhibitors (PPIs) are used to treat gastrointestinal (GI) disorders, and are one of the most highly utilized medications worldwide; however, there are several side effects attributed to use. Change in gastric acidity by PPIs is associated with gut microbial changes. Previous work shows high PPI use in the Boston-Puerto Rican Health Study (BPRHS) participants. In addition, enrichment of stool-derived *Streptococcus anginosus*, *S. salivarius* and *S. parasanguinis* among PPI users was observed. Building on these findings, we sought to further examine microbial pathways associated with PPI use.

Methods: The BPRHS is a longitudinal cohort that enrolled Puerto Rican adults at baseline (1499) through wave 4 (~12.7y). Our analysis included 309 participants with self-collected stool samples that underwent metagenomic profiling. PPI use was self-reported and classified as any use (yes/no) in the past 30d. Cross-sectional associations between gut microbial pathways and PPI use were examined including 1) differentially abundant microbial pathways using Microbiome Multivariable Associations with Linear Models (MaAsLin2), 2) discriminative classification using random forest (RF), and 3) correlation between gut microbial taxa and pathways enriched with PPI use.

Results: Among 309 participants (68.8y $\pm$ 7.3y; female 74.6%), 112 (36.2%) self-reported PPI use. After adjusting for relevant covariates, we observed an enrichment of several pathways including fructan (β = 2.01, FDR P = 0.01), and butanediol (β = 1.81, FDR P = 0.02) biosynthesis among PPI users. Pathway-based RF classifier discriminated PPI users with mean ROC 0.67 ($\pm$ 0.07). *S. salivarius* and *S. parasanguinis* were correlated with fructan biosynthesis (ρ = 0.97 and 0.76, respectively) and butanediol biosynthesis (ρ = 0.78, and 0.75, respectively).

Conclusions: Among PPI users, there was an observed enrichment of gut microbial pathways, including fructan

biosynthesis, correlated with *S. salivarius* and *S. parasanguinis*, suggesting changes in microbial pathways associated with prebiotic fiber hydrolysis in response to gastric pH changes. Further, it is reported that *Streptococci* may synthesize butanediol and 2,3-butanediol which may harm host tissue by immune mediated and other synergistic mechanisms, thus impacting health.

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P27-018-24 Gut Microbial Taxa and Pathways Associated With Mediterranean Diet Among Boston-Area Puerto Rican Adults

Deepika Dinesh¹, Tathabhai Pakalapati², Scott Gordon², Xochitl Morgan³, Jong Soo Lee⁴, Kelsey M Mangano⁴, Sabrina Noel⁴, Tammy M Scott⁴, Curtis Huttenhower³, Katherine L Tucker⁴, Natalia Palacios⁴

¹ University of Massachusetts Lowell, United States

² Zuckerberg College of Health Sciences, UMass Lowell, United States

³ Harvard T.H. Chan School of Public Health, United States

⁴ Center for Population Health, UMass Lowell, United States

Objectives: The Mediterranean diet (MeD) is associated with positive health outcomes, which may be partly due to its impact on the gut microbiota. We sought to examine the associations between MeD and the gut microbiome among participants from the Boston Puerto Rican Health Study (BPRHS) who present with unique dietary patterns.

Methods: The BPRHS is a longitudinal cohort that enrolled Puerto Rican adults at baseline (1499) through wave 4 (~12.7y). MeD pattern summarized adherence to whole grains, vegetables, fruits (excl. fruit juice), legumes/pulses/nuts, monounsaturated and saturated fat ratio, fish/meat/poultry, dairy, and alcohol. MeD score was computed as an average of scores across four waves of collection. We examined overall microbial composition based on MeD score using alpha (Shannon) diversity and Bray-Curtis (BC) dissimilarity metrics with permutational multivariate analysis of variance (PERMANOVA). Microbiome Multivariable Associations with Linear Models (MaAsLin2) was used to identify taxa and pathways associated with MeD adherence. All analyses were adjusted for relevant covariates.

Results: Among wave 4 participants, 309 had data on metagenomic profiled stool samples (69 $\pm$ 7.3y; female 74.6%). The mean MeD score, collected by FFQ, was 4.8 $\pm$ 1.1 (range 1-8). In multivariable linear regression analysis, Shannon alpha diversity was similar across MeD scores (β = 0.06, P = 0.08). BC dissimilarities based on MeD scores explained variations in taxonomic composition (PERMANOVA R^2 = 0.01, P = 0.01). An enrichment of several taxa including *Blautia obeum* (β = 0.92, FDR P = 0.03), *Lachnospira eligens* (β = 1.01, FDR P = 0.12) and *Coprococcus comes* (β = 0.96, FDR P = 0.17), and pathways including phosphopantothenate biosynthesis (β = 0.31, FDR P = 0.08) was observed among participants with higher MeD scores.

Conclusions: In this study of Boston-area Puerto Rican adults, we identified several gut microbial taxa and pathways associated with higher MeD diet adherence. Our results are consistent with prior studies; for example, *C. comes* has been reported to be enriched in legume-rich diets, and *B. obeum* is