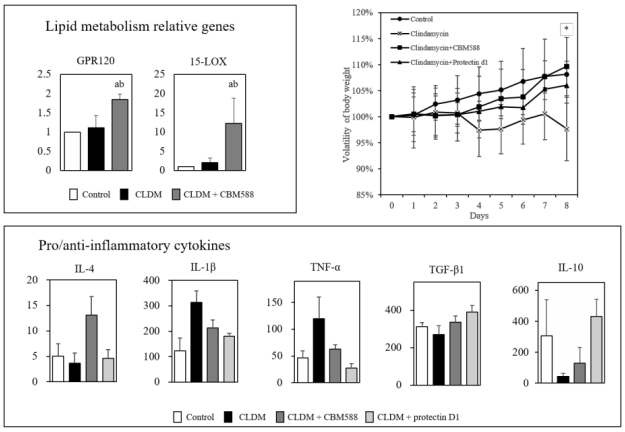
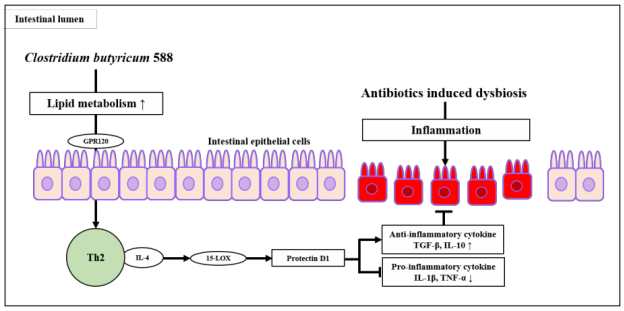
Lipid metabolism relative genes, pro/anti-inflammatory cytokines and body weight.



Conclusion. Our data suggested that CBM 588 stimulated PUFAs metabolism in the intestinal tract, and that PUFAs were signaled to Th2 cells as a ligand of GPR120. It was speculated that the stimulated Th2 cells produced IL4 and activated 15-LOX, resulting in the induction of protectin D1. Also, it became clear that protectin D1 induced anti-inflammatory cytokines in controlling antibiotic-induced gut inflammation. We provide as a new insight that lipid metabolism induction for the treatment of gut inflammatory diseases with CBM 588.

Anti-inflammatory pathway of protectin D1 induced by CBM 588.



Disclosures. **Hiroshige Mikamo, M.D, Ph.D**, **Astellas Pharma Inc.** (Grant/Research Support, Speaker's Bureau)**MSD Japan** (Grant/Research Support, Speaker's Bureau)**Pfizer Japan Inc.** (Grant/Research Support)**Sumitomo Dainippon Pharma Co., Ltd** (Grant/Research Support, Speaker's Bureau)

1206. Association of Aging, Frailty and Place of Residence with Skin, Oral and Gut Microbiome Characteristics and Pathogenicity Reservoirs

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Session: P-54. Microbiome in Health and Disease

Background. Despite their elevated risk for morbidity and mortality from infections, the microbiota of older adults remain understudied. While colonization resistance from resident microflora is a promising means to prevent infections, little is known about pathogenicity reservoirs and colonization resistance in this vulnerable population. Here we study the skin, oral, and gut microbiome dynamics of older adults in both community and Skilled Nursing Facility (SNF) settings, investigating relationships between age, frailty, environment, microbiota, and pathogenicity reservoirs.

Methods. We conducted a longitudinal metagenome survey of 47 adults age 65+ years of age; 22 residents of 3 different SNFs and 25 community dwelling individuals. We performed metagenomic whole genome shotgun sequencing on stool, oral, and skin samples from 8 sites, 1421 total. To correlate clinical and behavioral variables, we measured frailty, collected medical records, and interviewed participants on diet and lifestyle. We also draw comparisons with previous younger cohorts.

Results.
- Compared to younger adults, the skin microbiota of older adults was characterized by
  - High heterogeneity
  - Decreased stability over time, suggesting increased susceptibility to colonization and pathogenicity
  - Compositional differences including significantly lower levels of *Cutibacterium acnes,* with reciprocal increases in Staphylococci, Corynebacteria, and Malassezia
- In older adults, Frailty (Rockwood) was found to have linear correlation with relative abundance of species relevant to infection risk including *acnes,* staphylococci, streptococci, *E. coli, Akkermansia mucinophila,* and *Enterococcus faecalis*.
- The skin, oral, and gut microbiota of SNF residents had substantially elevated virulence factor and antibiotic resistance genes.

Conclusion. To the best of our knowledge, this is largest report to date of the skin metagenome in older adults. We demonstrate distinct and significant differences between cohorts with clinically relevant implications. We believe these results may inform infection control and prevention by increasing our understanding of colonization resistance and pathogenicity reservoirs, as well as advance our knowledge of the relationship between aging, the microbiome, and infections.

Disclosures. **All Authors**: No reported disclosures

1207. Combining standard bacterial vaginosis treatment with cystine uptake inhibitors to block growth of Lactobacillus iners is a potential a target for shifting the cervicovaginal microbiota towards health-associated Lactobacillus crispatus-dominant communities

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Session: P-54. Microbiome in Health and Disease

Background. Cervicovaginal microbiota domination by *Lactobacillus crispatus* is associated with beneficial health outcomes, whereas *L. iners* dominance has more adverse associations. However bacterial vaginosis (BV) treatment with metronidazole (MTZ) typically leads to domination by *L. iners* rather than *L. crispatus*. *L. iners* differs from other lactobacilli by its inability to grow in MRS media. We hypothesized that exploring this growth difference would identify targets for selective *L. iners* inhibition.

Methods. Bacteria were grown anaerobically. Nutrient uptake and metabolism were assessed using UPLC-MS/MS and isotopically labeled substrates. Bacterial genome annotation employed Prodigal, Roary, and EggNOG. Competition experiments with mock mixed communities were analyzed by 16S rRNA gene sequencing. We confirmed result generalizability using a diverse collection of South African and North American strains and genomes.

Results. Supplementing MRS broth with L-cysteine (Cys) or L-cystine permitted robust *L. iners* growth, while *L. crispatus* grew without Cys supplementation. Despite their different growth requirements, neither species could synthesize Cys via canonical pathways. Adding the cystine uptake inhibitors S-methyl-L-cysteine (SMC, Fig 1) or seleno-DL-cystine (SDLC) blocked growth of *L. iners* but not other lactobacilli, suggesting *L. iners* lacks mechanisms other lactobacilli use to exploit complex exogenous Cys sources. Notably, cydABCD, an operon with Cys/glutathione transport and redox homeostasis activities, is absent from *L. iners* but present in non-*iners Lactobacillus* species. Consistent with possible roles for cydABCD in explaining the observed phenotypes, (1) *L. iners* failed to take up exogenous glutathione and (2) supplementing MRS with reducing agents permitted *L. iners* growth, which could be blocked by SMC or SDLC. In growth competitions testing *L. iners* and *L. crispatus* within mock BV-like communities, SMC plus MTZ outperformed MTZ alone in promoting *L. crispatus* dominance (Figs 2&3).

Figure 1: S-methyl-L-cysteine (SMC) selectively blocks growth of L. iners but not other cervicovaginal Lactobacillus species in cysteine-supplemented MRS broth. Growth was measured by optical density and inhibition calculated relative to Cys-supplemented no-inhibitor control during exponential growth. Values displayed are median (+/- maximum/minimum) for 3 replicates from a single experiment. In all panels, representative data are shown from 1 of >=2 independent experiments for each bacterial strain and media condition. Results are representative of multiple strains for L. iners (n = 16), L. crispatus (n = 7), and L. jensenii (n = 2).