セミナー開催のお知らせ

UNL より講師をお招きして、セミナーを開催いたします。多数のご参加をお待ちしております。

日時　2024年 3 月 11 日(月)16 時～
場所　神戸大学 V. School
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Title: ***Clostridioides difficile*** **proline metabolism contributes to colonization human fecal communities cultured in minibioreactor arrays**

Abstract: The gastrointestinal microbiota plays an important role in limiting colonization by the clinically significant pathogen *Clostridioides difficile*. The microbiota can stimulate the immune system, alter bile acid pools, compete for nutrients, and/or produce metabolites that inhibit *C. difficile*. We previously used *in vitro* minibioreactors to investigate how different *C. difficile* strains are able to colonize human fecal microbial communities and to identify simplified communities able to inhibit *C. difficile* colonization. To better understand how microbiota composition and function influence *C. difficile* susceptibility in our model, we tested *C. difficile* susceptibility across microbial communities established from twelve different healthy people; susceptibility was tested in the absence of antibiotic or following treatment with six different antibiotics (Augmentin, azithromycin, cefaclor, ceftriaxone, clindamycin, and fidaxomicin). While all antibiotics disrupted microbiota composition, only clindamycin-treatment led to robust *C. difficile* colonization. Analysis of levels of the bile salts taurocholate, cholate, and deoxycholate in resistant and susceptible communities demonstrated no correlation between bile salt levels and susceptibility to infection. Because preliminary studies demonstrated that amino acids were partially depleted by growth of human fecal microbial communities, we hypothesized that *C. difficile* colonization in our model may be dependent upon its ability to metabolize amino acids through Stickland metabolism. To test this hypothesis, we compared the ability of a *C. difficile* mutant unable to metabolize proline (D*prdB*) to a wild-type strain. We observed that proline metabolism was important for persistence in a subset of microbial communities. Future studies will examine how microbiota composition impacts *C. difficile* occupation of different nutritional niches.