



A NOVEL ECOSYSTEM THERAPEUTIC FOR THE TREATMENT OF CLOSTRIDIUM DIFFICILE INFECTIONS

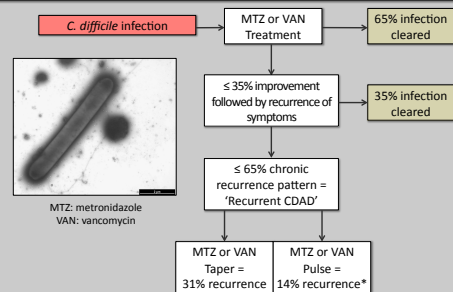
DAIGNEAULT, M.;¹ BROWN, E.;¹ SCHROETER, K.;¹ GLOOR, G.;² PETROF, E.;³ WEESE, S.;¹ ALLEN-VERCOE, E.¹

¹UNIVERSITY OF GUELPH; ²UNIVERSITY OF WESTERN ONTARIO; ³QUEEN'S UNIVERSITY; ONTARIO, CANADA

INTRODUCTION

- *Clostridium difficile* infection (CDI) is the #1 cause of hospital-acquired diarrhea¹, which in severe cases can result in death²
- Antimicrobial use is the most important risk factor for CDI³, causing an imbalance in the gut microbiota, and allowing pathogenic *C. difficile* to overgrow
- The most prevalent PCR ribotype in the US and Canada is 027 (NAP1), with 078 being identified in increasing numbers in hospitals, in the community, and in food⁴
- Standard antibiotic therapies are not always effective, often leading to recurrent CDI⁵
- Intestinal microbiota transplantation is an alternative therapy that repopulates the gut with indigenous species from healthy donor stool: it has been shown to be 92% effective⁶
- Intestinal microbiota transplantation can be problematic
 - for patient acceptance
 - in composition: preparations are undefined and despite screening protocols may still harbour pathogenic microorganisms

RECURRENT CDI



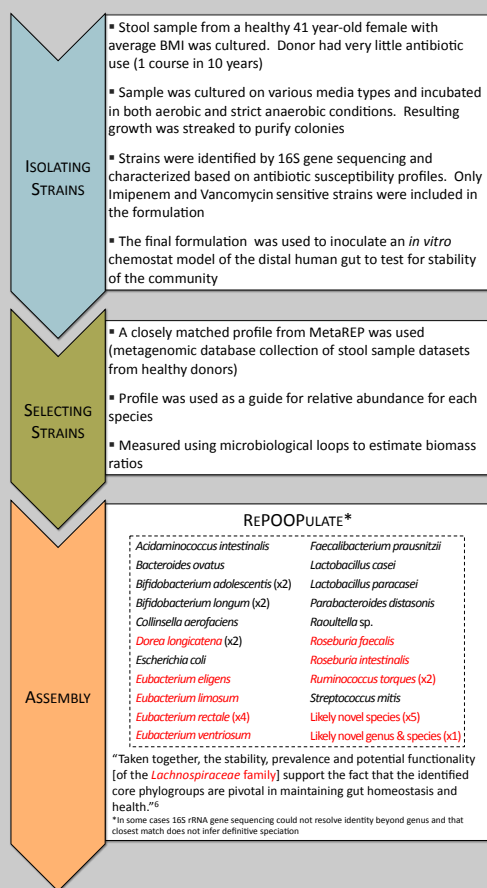
A SUITABLE ALTERNATIVE TO THESE TREATMENTS IS A NECESSITY.

*Adapted from Gough, E. et al. 2011

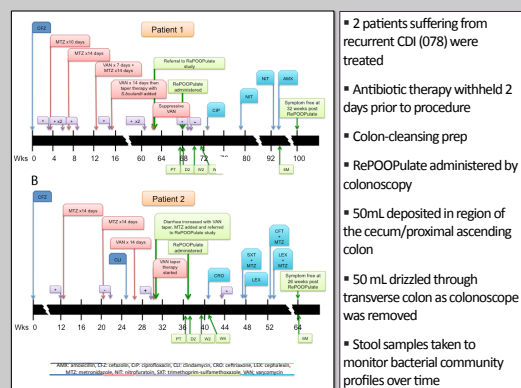
HYPOTHESIS

A DEFINED ECOSYSTEM THERAPEUTIC CAN BE USED TO EFFECTIVELY CURE RECURRENT CDI AND PERSIST IN THE HUMAN GUT

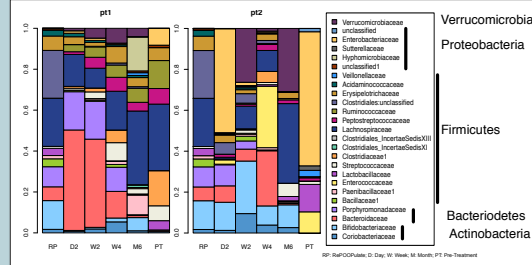
MAKING A DEFINED ECOSYSTEM THERAPEUTIC "REPOOPULATE"



PATIENT TIMELINES & OUTCOMES



STOOL COMPOSITION CHANGES OVER TIME



THE COMPOSITION OF REPOOPULATE PERSISTED IN BOTH PATIENTS OVER TIME AND SEEMED TO PROTECT AGAINST FURTHER CDI RELAPSE. BOTH PATIENTS REMAIN SYMPTOM FREE AT 32- AND 26-WEEKS POST-REPOOPULATE.

REFERENCES & ACKNOWLEDGEMENTS

This work was supported by the Southeastern Ontario Academic Medical Organization (SEAMO) and Physicians' Services Incorporated (PSI) Foundation. The authors would like to acknowledge the following people who contributed to the study: Clinical investigators (collected data, provided and cared for study patients): Lawrence Hooley¹, Cathy Lowe¹, Mark Ropoleski¹, Gerald Evans¹, Christopher A. Smith¹, Robert Bechara¹ Laboratory and technical assistance (processed samples and collected data): Curtis Noordhoff¹, Adriana Breen¹, Karen Solomon¹, Christian Ambrose¹ Bioinformatics assistance (helped with QIIME analysis and barplot production): Jean MacKinnon¹