

P0281 Asymptomatic colonisation with *Clostridioides difficile* and onwards transmission in an endemic setting

Monique Jacqueline Theresia Crobach*^{1,1}, Bastian Hornung^{1,1}, Cees Verduin^{2,3}, Margreet C. Vos^{4,4}, Joost Hopman^{5,5}, Nitin Kumar^{6,7}, Céline Harmanus^{1,1}, Mark Stares^{6,7}, Trevor Lawley^{6,7}, Ed J. Kuijper^{1,1}

¹ Leiden University Medical Centre, Leiden, Netherlands, ² Amphia Hospital Breda, current: PAMM Veldhoven, ³ Amphia Hospital Breda, current: PAMM Veldhoven, Breda, Netherlands, ⁴ Erasmus University Medical Centre, Rotterdam, Netherlands, ⁵ Radboud University Medical Centre, Nijmegen, Netherlands, ⁶ Wellcome Sanger Institute, Hinxton, United Kingdom, ⁷ Wellcome Sanger Institute, Hinxton, United Kingdom

Background: Patients asymptotically colonized by *Clostridioides difficile* on admission to the hospital can introduce the bacterium into the hospital and transmit it to the environment and other patients, who can subsequently develop *C. difficile* infection (CDI). We performed a study to (i) estimate the prevalence of *C. difficile* colonization (CDC) on admission to the hospital and (ii) investigate onward transmission in a setting with a low endemic CDI prevalence and a low proportion of 'hypervirulent' ribotypes.

Materials/methods: A multicenter study was performed in 4 hospitals located across The Netherlands (3 university-affiliated and 1 general hospital). During a 6 to 8 month period per hospital, fecal samples or rectal swabs were obtained from patients within 72hrs of hospital admission. Samples were screened for CDC by culture. In addition, samples from all hospitalized patients who were diagnosed with CDI within 1 month prior until 3 months after enrolment of asymptomatic patients were obtained and cultured. Isolates from CDC and CDI patients were whole genome sequenced on an Illumina HiSeq. Further analysis was performed with Roary and pyANI. MLST types were determined via MLSTcheck.

Results: In total, 2212 samples were obtained from patients within 72hrs of admission. The overall prevalence of CDC was 4.9% (109/2212), while the prevalence of toxigenic CDC was 3.1% (69/2212). Eight-nine isolates from CDC patients (of which 69 were obtained within 72hrs of admission) were compared to 189 isolates from incident CDI cases that were reported during the study period. The distribution of PCR ribotypes in CDI and CDC patients was similar. 272 of these strains passed QC and could be sequenced. The Roary analysis indicated a core genome of 2437 genes, so a bit more than half of the average gene content of ~4200, and a pan genome of 15477. The pyANI analysis indicates a clear separation of the RT078/ST11 genomes from all other genomes, with smaller subclusterings in the remaining genomes. Similarity analysis based on ANI identified mainly multiple strains derived from single patients.

Conclusions: In this setting, the prevalence of CDC on admission was 4.9% and onwards transmission from CDC patients was neglectable.