Genome-wide fitness analyses of the foodborne pathogen Campylobacter jejuni in vitro and in vivo models - DTU Orbit (11/03/2019)

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Campylobacter is the most common cause of foodborne bacterial illness worldwide. Faecal contamination of meat, especially chicken, during processing represents a key route of transmission to humans. There is a lack of insight into the mechanisms driving C. jejuni growth and survival within hosts and the environment. Here, we report a detailed analysis of C. jejuni fitness across models reflecting stages in its life cycle. Transposon (Tn) gene-inactivation libraries were generated in three C. jejuni strains and the impact on fitness during chicken colonisation, survival in houseflies and under nutrient-rich and -poor conditions at 4 degrees C and infection of human gut epithelial cells was assessed by Tn-insertion site sequencing (Tn-seq). A total of 331 homologous gene clusters were essential for fitness during in vitro growth in three C. jejuni strains, revealing that a large part of its genome is dedicated to growth. We report novel C. jejuni factors essential throughout its life cycle. Importantly, we identified genes that fulfil important roles across multiple conditions. Our comprehensive screens showed which flagella elements are essential for growth and which are vital to the interaction with host organisms. Future efforts should focus on how to exploit this knowledge to effectively control infections caused by C. jejuni.

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