Impact of L-fucose metabolism on growth, survival and metabolism of *Campylobacter jejuni* strain NCTC11168

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Background

Over the last years it has become clear that environmental survival and transmission, including the ability to utilise different compounds as energy source, play an important role in *Campylobacter* infections in humans.
Recently, the fucose utilisation cluster was identified [1,2] in ~65% of 3746 *C. jejuni* genomes studied [3]. This cluster is predicted to allow fuc+ *Campylobacter* to metabolize L-fucose (figure 1), which is present in many environments including the human, pig and chicken gut.
We hypothesize that possession of this cluster contributes to the repertoire of survival mechanisms exploited by *Campylobacter* during transmission to human hosts.

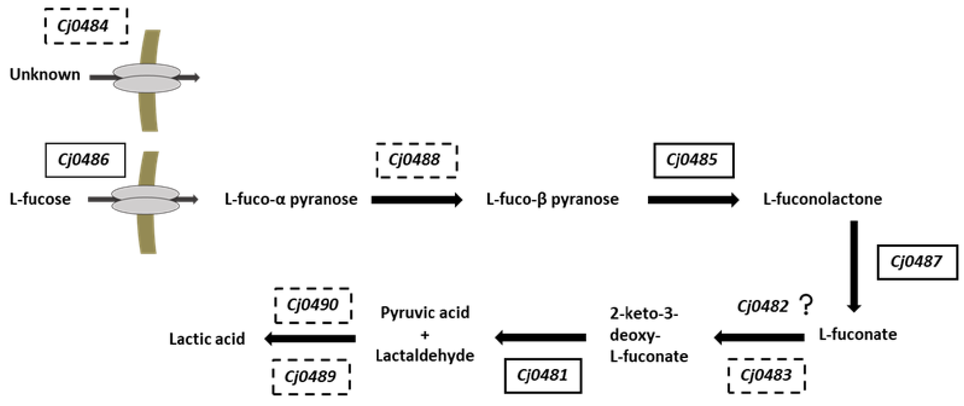


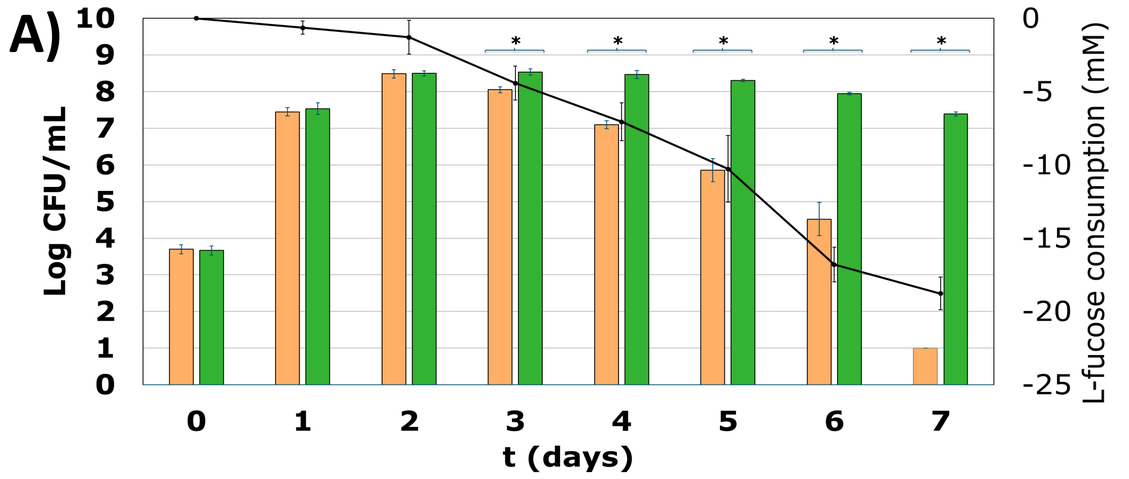
Figure 1. Fucose metabolism in *Campylobacter jejuni* strain NCTC11168. A predicted L-fucose metabolism pathway resulting in the production of pyruvate and L-lactate. Stippled square indicates non-essential gene, black square indicates essential gene and question mark indicates no experimental data is present.

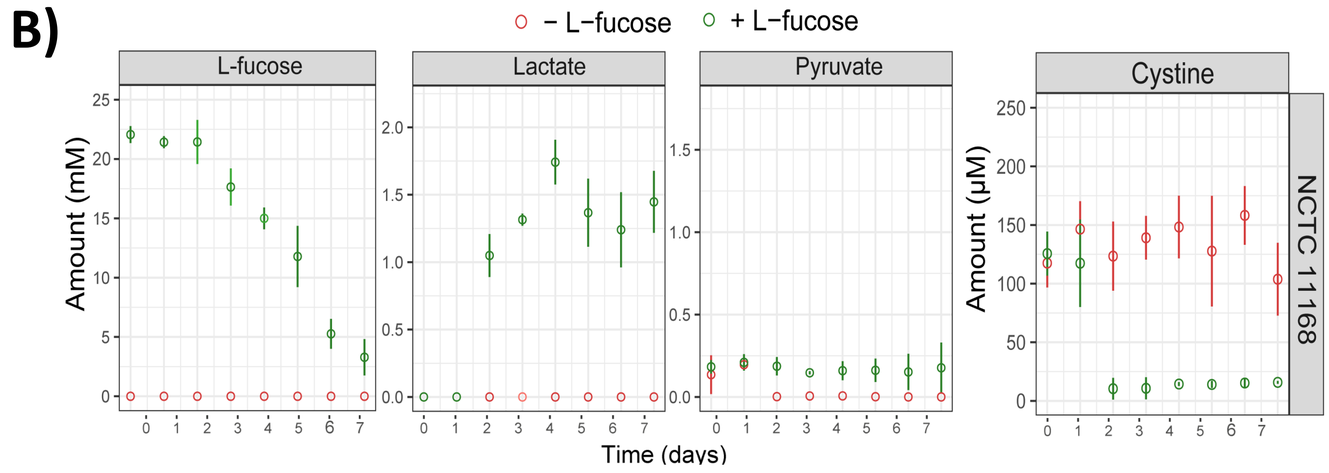
Aim

To evaluate and quantify the impact of L-fucose substrate utilisation in *C. jejuni* NCTC11168 on growth, survival, and metabolism during a 7 day growth experiment in MEMα medium at 37 °C under microaerobic conditions

Enhanced survival of *C. jejuni* NCTC11168 in MEMα + 25 mM L-fucose

Analysis of L-fucose consumption and metabolite production by *C. jejuni* NCTC11168 in MEMα medium





Prolonged spiral morphology of *C. jejuni* NCTC11168 upon addition of L-fucose to MEMα medium

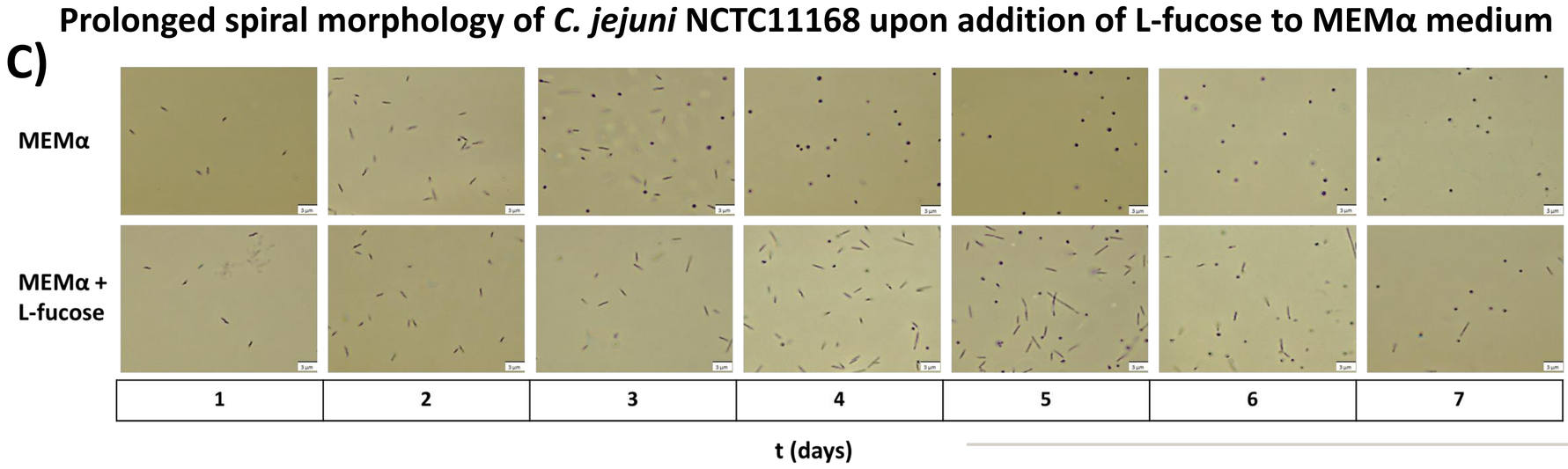


Figure 2. A) Effect of L-fucose on the growth and survival of *C. jejuni* NCTC11168. Culturable cells (logCFU/mL) of *C. jejuni* NCTC11168 in MEMα medium (orange bars) and MEMα medium + L-fucose (25 mM) (green bars) over time. Asterisks indicate P-values lower than 0.05.
B) HPLC quantification of L-fucose, lactate, pyruvate and cystine. Compound analyses of *C. jejuni* NCTC11168 grown in MEMα medium (orange circles) and MEMα medium + L-fucose (green circles) over time.
C) Microscopy images of *C. jejuni* NCTC11168 in MEMα medium -/+ L-fucose over time.

References

[1] Muraoka, W.T., and Zhang, Q. (2011) Phenotypic and genotypic evidence for L-fucose utilization by *Campylobacter jejuni*. J Bacteriol 193: 1065–1075.
[2] Stahl, M., Friis, L.M., Nothaft, H., Liu, X., Li, J., Szymanski, C.M., and Stintzi, A. (2011) L-fucose utilization provides *Campylobacter jejuni* with a competitive advantage. Proc Natl Acad Sci USA 108: 7194–7199.
[3] Dwivedi, R., Nothaft, H., Garber, J., Xin Kin, L., Stahl, M., Flint, A., van Vliet, A.H.M., Stintzi, A., & Szymanski, C. M. (2016). L-fucose influences chemotaxis and biofilm formation in *Campylobacter jejuni*. Molecular microbiology, 101(4), 575-589.

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Results

- The addition of L-fucose to MEMα medium does not result in higher CFU counts, but significantly extends culturability (survival) up to day 7 and is dependent on the consumption of L-fucose (figure 2A).
- HPLC quantification demonstrated onset of significant L-fucose consumption at day 3, with concomitant increase in lactate and pyruvate concentrations, and a decrease in cystine concentration (figure 2B).
- Microscopy analysis shows that without added L-fucose to MEMα medium, coccoid forms become dominant after day 3, whereas with added L-fucose, presumed culturable spiral shaped cells are apparent up to day 7 (figure 2C).

Key message

Metabolism of L-fucose contributes to maintenance of spiral-shaped morphology and prolonged culturability, which may contribute to environmental dispersal and transmission of fuc+ *C. jejuni* strains