The complete genome sequence and analysis of the human pathogen Campylobacter lari -
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Campylobacter lari is a member of the epsilon subdivision of the Proteobacteria and is part of the thermotolerant
Campylobacter group, a clade that includes the human pathogen C. jejuni. Here we present the complete genome
sequence of the human clinical isolate, C. lari RM2100. The genome of strain RM2100 is approximately 1.53 Mb and
includes the 46 kb megaplasmid pCL2100. Also present within the strain RM2100 genome is a 36 kb putative prophage,
termed CLIE1, which is similar to CJIE4, a putative prophage present within the C. jejuni RM1221 genome. Nearly all
(90%) of the gene content in strain RM2100 is similar to genes present in the genomes of other characterized
thermotolerant campylobacters. However, several genes involved in amino acid biosynthesis and energy metabolism,
identified previously in other Campylobacter genomes, are absent from the C. lari RM2100 genome. Therefore, C. lari
RM2100 is predicted to be multiply auxotrophic, unable to synthesize eight different amino acids, acetyl-coA, and
pantothenate. Additionally, strain RM2100 does not contain a complete TCA cycle and is missing the CydAB terminal
oxidase of the respiratory chain. Defects in the amino acid biosynthetic pathways in this organism could be potentially
compensated by the large number of encoded peptidases. Nevertheless, the apparent absence of certain key enzymatic
functions in strain RM2100 would be expected to have an impact on C. lari biology. It is also possible that the reduction in
the C. lari metabolic machinery is related to its environmental range and host preference.

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