Abstract

Long chain fatty acids (LCFAs) are used as a carbon source by several bacteria including many important pathogens. The LCFA transport and degradation pathway has been extensively studied in E. coli. In a high-throughput genetic screen performed in E. coli, a putative transcriptional regulator, DgoR, was identified as a novel component required for the successful growth of the bacterium. In the present study, we determined whether DgoR plays a role in LCFA degradation in other enteric bacteria. We chose to study the requirement of DgoR in LCFA metabolism in S. typhimurium, a bacterium very closely related to E. coli. In this direction, a dgoR deletion strain was constructed in S. typhimurium LT2 by homologous recombination. The phenotypic analysis of dgoR deletion strain on LCFAs showed that DgoR is required for the successful growth of the organism. The dgoR deletion strain could be complemented by E. coli dgoR cloned on the plasmid. However, S. typhimurium dgoR cloned on the plasmid failed to complement the deletion strain. Importantly, S. typhimurium dgoR cloned on the plasmid inhibited the growth of the wildtype strain. We are currently investigating whether a high-level expression of S. typhimurim DgoR from the plasmid is the reason for lethality. We are also cloning S. typhimurium dgoR on a low copy plasmid. In addition to our studies on S. typhimurium DgoR, in the present work we have also devised an important tool for monitoring the expression of E. coli DgoR in different carbon sources. We have tagged dgoR gene of E. coli with 3xFLAG on the chromosome. We find that the chromosomal construct expresses tagged DgoR and shows a growth pattern similar to the wildtype strain on LCFAs. These results thereby confirm that the chromosomally tagged DgoR strain can be used for physiological experiments.