Abstract

ENTEROBACTIN - LIKE SIDEROPHORE GENE CLUSTER INDUCTION IN CRONOBACTER SAKAZAKII STRAIN

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Species belonging to the recently described Cronobacter genus, include several opportunistic foodborne pathogens. These pathogens are capable of causing severe infections in neonates, such as meningitis, septicaemia and necrotizing enterocolitis.

Bacterial virulence has been previously correlated with ferric iron acquisition systems. It is known that all plasmid-harbouring Cronobacter species produce an active aerobactin-like siderophore (cronobactin) and the chromosome also contains genes encoding an enterobactin-like siderophore whose production has not been detected so far. Nevertheless it has been determined that, in vivo, enterobactin is upregulated in iron limiting conditions.

This work aims to demonstrate that the cluster encoding for the enterobactin-like siderophore synthesis is functional and responsible for the molecule synthesis. To stimulate enterobactin production, the strain used grown in an optimized medium under particular conditions. Overall, siderophore production was detected by using Chrome Azurol S (CAS) indicator solution. A bioinformatic analysis was carried out to identify and annotate the genes in the enterobactin clusters. Genes predicted to be involved in the biosynthesis were mutated by performing Campbell insertions. Enterobactin presence/absence in the wild type and mutant strains, was determined by High Performance Liquid Chromatography. Simultaneously genome analysis showed that some Cronobacter/Enterobacter strains shared iron-siderophore complex receptors, an indicator of the ability to uptake siderophores from unrelated species. This capacity was tested by cross-feeding assays in CAS agar. Results showed that the cluster encoding for the enterobactin-like siderophore is indeed functional and that this molecule might be utilized by other Cronobacter/Enterobacter species.

Assigned speakers:

Ms. Joana Carvalho, Universidade do Minho , Braga , Portugal

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