The lactic acid bacterium, Carnobacterium maltaromaticum possess a diverse range of potential virulence genes some of which are related to similar genes in Listeria monocytogenes

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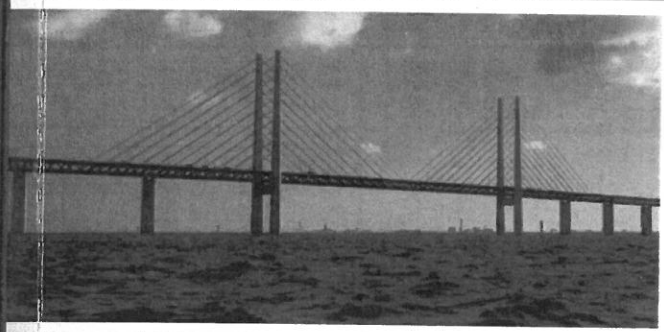

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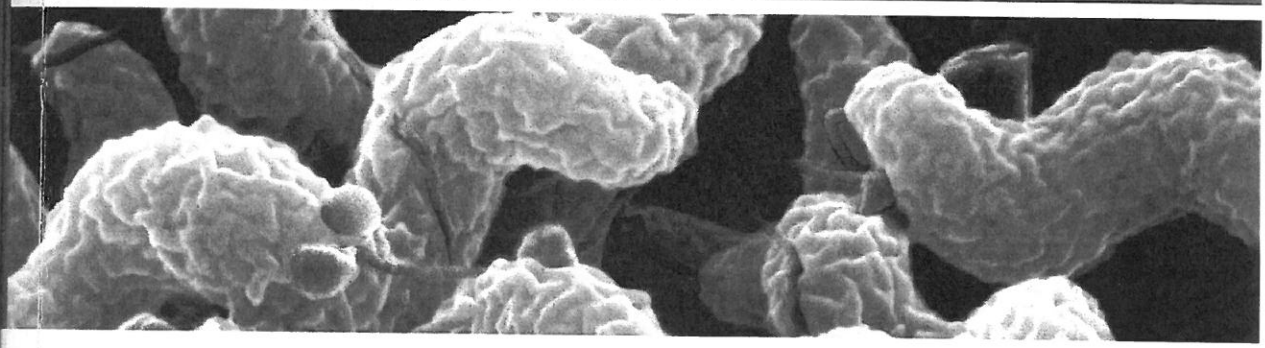

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B1.20 **Production of *Staphylococcus aureus* Enterotoxin A in cheese**

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aphylococcus aureus is the fourth most common cause of food poisoning in Europe. As it is able to grow in a wide range of mperatures, pH and NaCl concentrations a variety of food products provide a niche for this bacterium. Milk and milk prod-cts such as cheese are food products particularly associated with S. *aureus* contamination. This is partly due to that *S. aureus* the most common agent associated with mastitis in dairy cows. To produce safe food, data about enterotoxin production required to complement the existing knowledge about bacterial survival in food. We have investigated the production of *S. ureus* enterotoxin A (SEA) in semi-soft and soft cheese at various temperatures. Initially, we studied growth and SED forma-on in pasteurized milk and BHI broth at 20, 12 and 8°C. At 20 and 12°C in milk, growth is more inhibited, SED amounts are ower and it does not accumulate; at 8°C, there is no growth or SED production. The combined effect of low temperature, 2°C, and the presence of competing background microflora derived from raw milk on *S. aureus*' growth and SED production n pasteurized milk was further investigated. In the next stage, two different cheese matrices were inoculated with known oncentrations of *S. aureus* to simulate a post-contamination scenario in a cheese production process. During incubation, amples were collected regularly during 4 weeks. Critical food factors, like competing microflora and pH, which are respon-ible for down- and up-regulation of the virulence of *S. aureus*, were monitored. Bacterial growth and the amounts of SEA roduced have been measured at regular time points using viable counts and ELISA. The aim of these experiments is to iden-ify if there are situations in which: (i) no growth but enterotoxin formation is observed, and (ii) growth but no enterotoxin formation occurs. The development of more natural food preservation methods, new control strategies and risk management will benefit from knowledge about the regulation of enterotoxin production. Prevention of food-borne diseases by efficient risk identification in the food chain and a decrease in the use of chemical additives to food will increase the quality of food.

PEB1.21 **The lactic acid bacterium, *Carnobacterium maltaromaticum* possess a diverse range of potential virulence genes some of which are related to similar genes in *Listeria monocytogenes***

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Carnobacterium maltaromaticum is a lactic acid bacterial species commonly found in various fish and meat products as well as live fish. Much interest has been devoted to its application as a biopreservative agent as well as a probiotic culture. An important consideration in this regard is whether it contains any virulence genes that might compromise its use. Here, we report the results of a screening for such genes by employing whole genome sequencing of the *C. maltaromaticum* ATCC 35586 strain isolated from infected salmon. The genome contained a range of potential virulence genes including genes involved in adhesion to fibronectin and collagen, iron scavenging mechanisms, haemolysis, resistance to toxic compounds and invasion. Of particular interest was the presence of a range of internalin genes with some resemblance to *Listeria* spp. internalin genes. Finally, this strain possesses a genome segment encoding potential virulence genes including a gene similar to the central *Listeria* spp. PrfA regulator of the virulent phenotype. A total of 65 genes possessed upstream potential recognition sequences for the PrfA gene product. Among them was one of the internalin encoding genes, a gene encoding capsule synthesis as well as various genes encoding metabolic reactions.

We have also tested whether the *prfA* gene is present in other *C. maltaromaticum* strains and the induction of the potential virulent phenotype using haemolysis as the reporter phenotype under experimental conditions similar to these employed for *L. monocytogenes*. The implications of these results will be discussed.

In conclusion, *C. maltaromaticum* possess virulence genes that might explain previous observations of its ability to be an infective agent of fish and insects. The applied implications of these findings as well as the relevance for elucidating the evolution of the *L. monocytogenes* virulent phenotype are discussed.