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Draft genome sequences of *Carnobacterium maltaromaticum* and *Carnobacterium divergens*

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Carnobacteria are ubiquitous lactic acid bacteria (LAB) that frequently predominate in a range of foods, including fish, meat, and dairy products. These psychrotolerant bacteria are highly resistant to chill temperatures and freezing, and have consistently both temperate and polar aquatic environments as habitats including live fish. *C. divergens* and *C. maltaromaticum*, which are the two species most frequently isolated from natural environments and food, have been studied as protective cultures in order to inhibit growth of *Listeria monocytogenes* in food. However, the history of their application is short and the body of knowledge is rather scarce, especially regarding their content of genes encoding virulence factors and antibiotic resistances. For these reasons, carnobacteria were not considered as QPS by EFSA and therefore their voluntary introduction into food would require a thorough safety assessment. The aim of the study was to decipher the genome sequences of six *Carnobacterium* strains: Five *C. maltaromaticum* strains (including the ATCC35586[1]) and one *C. divergens* strain. The results revealed that the size of the sequences ranged between 3.3 and 3.7 Mb for *C. maltaromaticum* strains whereas the size of *C. divergens* was about 2.7 Mb suggesting that relatively large differences in terms of genome size can be observed within the *Carnobacterium* genus. Several potential antibiotic resistance genes such as potential beta-lactamases genes were identified. The genomes contain genes encoding surface components, and other functions reminiscent of a possible interaction with a host, which is a common trait for LAB and other gram positive bacteria including pathogens. These findings revealed no specific safety concern about the presence of these bacteria in food.

[1] Leisner *et al.*, 2011. Int J Food Microbiol (in press).