

# THE MICROBIOTA OF COMMON SHRIMPS (*CRANGON CRANGON*) FROM CATCH TO CONSUMER

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The common shrimp (*Crangon crangon*) is a typical product of the Belgian fishery that has recently received a regional product label, "Purus". "Purus" shrimps are exclusively caught in the North Sea by Belgian trawlers and prepared by Flemish fishermen predominantly in a traditional way; without preservatives, colorants or other additives and landed within 12h after catch.

Fresh seafood such as shrimps are very sensitive to spoilage causing off-odours and off-flavours. The main factors limiting shelf life are enzyme and microbial activities. Freshly caught shrimps are naturally contaminated with a diversity of microorganisms. The presence of these microorganisms depends among other things on the environment, water temperature, area of catch and handling and processing procedures (Jay, 1986). Most of the microorganisms on fresh seafood and during aerobic ice storage are psychrotrophic gram-negative, rod-shaped, strict aerobic or facultative anaerobic microorganisms of marine origin such as the genera *Aeromonas*, *Pseudomonas*, *Moraxella*/*Acinetobacter*, *Shewanella*, *Flavobacterium* or the family *Vibrionaceae* (Liston, 1980).

In this study the microbial population of cooked and peeled shrimps without preservatives was investigated during storage at different temperatures until spoiled.

Shrimps were caught, sorted, washed and cooked on board according to normal fishery procedures. At these different stages of processing, shrimps were collected and put on ice for transport. Microbiological analyses started one day after catch. In order to study the effect of the shell, some cooked shrimps were peeled manually as sterile as possible in the laboratory. From all different stages of processing, shrimps were stored on ice (0 ±0.5°C) and at 7.5±0.5°C (extreme refrigerator conditions) for several days. Microbiological analysis was performed at regular time intervals during storage. The study of the microbiota was done on several general and group-specific growth media. Molecular techniques [rep-PCR (GTG)<sub>5</sub> analysis, 16S rRNA and *gyrB* gene sequencing] were used for clustering and identification.

DGGE analysis based on the V3 region of the 16S rRNA gene was performed from plateswabs of the different media and direct from the shrimp matrix to visualise shifts in the total microbial community on shrimps under different conditions.

The results showed that the boiling process leads to a two <sup>10</sup>log decrease in microbial count. In addition, a steep decrease in bacterial count was noticed after peeling. Results of total counts during storage showed that cooked and peeled shrimps stored at the highest temperature were microbiologically spoiled (>10<sup>8</sup> cfu/g) after 7 days, while iced shrimps had a shelf life of 12 days.

DGGE analysis showed clear shifts in the total microbial community under different conditions. Analysis of the microbiota using 16S rRNA gene sequencing limited the identification of the microorganisms to genus level. Further identification to species level was performed by sequencing analysis of the household gyrase B subunit (*gyrB*) gene and phylogenetic tree analysis. Using *gyrB* sequence analysis, several species of especially two marine genera (*Pseudoalteromonas* and *Psychrobacter*) were identified. These genera were dominant under practically all conditions tested (cooked, peeled, ice stored, temperature abuse) and were specific for seafood without preservatives.

## References

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