

Changes in microbial diversity of ESL-milk over the production process

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In recent years microfiltrated and pasteurized ESL-milk has gained more and more importance on the dairy market. For the production of this type of milk, raw skim milk is microfiltrated by ceramic membranes with pore sizes of 0.8-1.4 µm and then pasteurized.

In this study flora analyses of three different batches of milk, produced by one manufacturer, were conducted using FT-IR spectroscopy. As raw milk is subjected to various contamination sources during the milking process and storage, the raw milk samples comprised a high degree of microbial biodiversity. Among 100 quantitatively chosen isolates, 14-30 different species and 10-23 genera were detected and assigned to the following taxonomic groups: facultative anaerobic Gram-negative bacteria, obligate aerobic Gram-negative bacteria, High GC Gram-positives, spore-formers, lactic acid bacteria, other Gram-positives (mainly Staphylococci) and yeasts. The highest shares were obligate aerobic Gram-negative bacteria with *Pseudomonas* spp., *Acinetobacter junii* / *johnsonii* and *Stenotrophomonas maltophilia* as main representatives. High GC Gram-positives (0-30%) mainly comprised *Microbacterium lacticum*, *Corynebacterium* spp. and *Brachybacterium conglomeratum*. Lactic acid bacteria (mainly *Lactococcus lactis*) had shares of 4-23%. Microfiltration lead to a reduction of cfu of 4-5 log units, and the microbial diversity also decreased to 13-16 different species and 10-11 genera. Highest shares (53-80%) were High GC-Grampositives, mainly *Microbacterium* spp.. Obligate aerobic Gram-negatives (*Stenotrophomonas maltophilia*, *Rhizobium radiobacter* / *Agrobacterium tumefaciens*, *Chryseobacterium* sp.) obtained 11-43%. All Gram-negative bacteria were eliminated by pasteurization, because of their relatively low heat tolerance. Accordingly, the three different floras of microfiltrated and pasteurized milk comprised 82-99% High GC Gram-positives, i.e. mainly *Microbacterium lacticum* and the spore-forming bacteria *Paenibacillus amylolyticus* / *glucanolyticus*, *Brevibacillus agri*, *Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus subtilis* and *Bacillus cereus*.

Isolates, which could not be identified by FT-IR- spectroscopy were identified by gene sequence analysis. Spectra of these strains were then used to upgrade the FT-IR databases.