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Reaction kinetics of heat-induced aggregation in skim milk concentrates: Comparison of lab-scale indirect heating and direct steam injection

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Heat stability of concentrated milk, i.e. the ability of milk protein to withstand severe heat treatments has been an issue since the beginning of industrial milk processing. Methods measuring heat coagulation time (HCT) as the usual parameter have limited relevance for industrial UHT processes with very short holding times at high temperature. However, there is a strong interest in long-term preservation of milk concentrates of high total solids content by heat treatment. This would give the opportunity to be able to avoid high energy consumption for spray drying of milk concentrates. In this study, a new lab-scale indirect heating method was established to describe heat stability of milk concentrates by measuring time and temperature within the sample until visual flocculation occurred. It appeard that visually detectable flocculation of concentrated milk samples of various total solids is strongly dependent on heating time and temperature in combination as well as total solids. Thus, the underlying mechanism of flocculation can be kinetically described. Another lab-scale technique was used to follow coagulation of the concentrated skim milk samples by particle sizing and separation techniques of the aggregates of casein micelles formed during heat treatment for a reaction kinetic approach towards heat-induced coagulation of preheated and non-preheated milk. We also found that a kinetic description of heat-induced aggregation of caseins also applies for direct steam injection heat treatment with some limitations. It was proven that direct heat-treatment is likely to be the method of choice for milk concentrate heat treatment for a long shelf life.

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Identification of *Bifidobacterium spp*. and *Bifidobacterium animalis subsp*. lactis from Egyptian women breast milk and feces of breast fed infant based on16S rRNA gene

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Bifidobacterium represent one of the major genera of the intestinal tract of human and animals and are used, in probiotics, in dairy and non-dairy foods to restore the intestinal microflora which confer a health benefit. The identification of *Bifidobacterium* by phenotypic features is commonly unreliable and also time, money and effort consuming. In order to improve identification methods decreasing time, money and effort consuming and precise based on molecular level to identify of probiotic bacteria in complex microbial communities, the application of 16S-23S rRNA oligonucleotide probes is the best and most reliable approach in rapid and precise identification of species. The 16S rRNA gene was used for the systematic identification of bifidobacteria. In this study, we used seven primer pairs on complex communities to facilitate the examination of complex micro ecosystems. The 2 primers Bif162-Bif662 and Bflac2-Bflac5 showed positive results with *Bifidobacterium spp*. and B.animalis subsp lactis, these strains were isolated from breast milk of human and feces of breast fed infants. The 2 DNA fragments were sequenced and submitted in GenBank "NCBI" under accessions number "KT758845"and "KT758846". The long term goal of this research is to obtain patent protection for *Bifidobacterium* sp which isolated from Egyptian resources and use it in food and dairy products.

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