

The challenge of replicable cheese

The MetaCheese project investigates the microbial composition during cheese making and ripening to understand the contribution to quality and flavor.

Denmark dairies have a long tradition of high-quality cheese production. As the number of dairies has been reduced, production is increasingly being centralized at large modernized production facilities. One major challenge that the cheese makers face is in maintaining constant quality and flavor characteristics when the production environment is changed. Further challenges include understanding the consequences of utilizing milk from different sources, the effect of pre-treatment technologies such as micro filtration and protein fortification, and storage temperature variation on the resulting cheeses. We are exploring such questions in light of the cheeses' microbiomes.

The cheese microbiome

Cheese production is critically dependent on a complex society of microorganisms that drive both acidification during the initial steps, and later the flavor development. This complex society of microorganisms, known as the 'microbiome', originates both from starter and adjunct cultures deliberately introduced by the cheesemaker, but also from organisms already present in the milk itself, or present as the dairy's 'house flora' – e.g. associated with production equipment or the brine.

Understanding structure and function

Generating a detailed understanding of cheese microbiome structure and function will ultimately be key to optimizing final cheese quality. Traditional microbial analyses like plate counts can only provide limited information, as many microorganisms are extremely challenging (if not impossible) to cultivate under laboratory conditions. Today, state-of-the-art molecular biology methodologies enable researchers to characterize the DNA of full microbial

communities in any sample (known as a metagenome), thus rendering it possible to reveal the cheese microbiome composition even for the rarest microorganisms present. It is therefore possible to obtain information on the composition of the cheese microbiome at the different stages of cheese making and ripening activities. However, this just provides a glimpse into what is there, and not what they are doing. Thus, a second set of analyses, based on two other techniques can be employed. Firstly, characterizing the RNA produced by the microbe using metatranscriptomics, can tell us what genes are expressed. And secondly, biochemical tools such as metabolomics can profile important chemical components like aroma compounds. Then, to build the bridge between these complex datasets, advanced computer 'multi-omics' modeling can be applied (**Fig. 1**). The application of this analytical strategy to cheese production is still in its infancy, but we believe, it will have significant impact in the near



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Project info

Title: Fra oste-mikrobiom til robuste osteprocesser (MetaCheese)

Objective: To use a multi-omics approach to map the microbial composition during cheese making and ripening to understand the functional role in relation to cheese quality and flavor.

Project manager: Professor Tom Gilbert, Research Director, Section for Evolutionary Genomics, GLOBE Institute, University of Copenhagen (UCPH).

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Project period: January 2019 – December 2020.

Financed by the Milk Levy Fund



Abstract:

Cheese production is dependent on a complex society of microorganisms – the cheese microbiome. The MetaCheese project is using advanced molecular biology methodologies to map the cheese microbiome and understand its functional role during cheese making and flavor formation. Analyzing microbial DNA (metagenomics) will make it possible to decode the cheese microbiome composition. Understanding the interactions between species and their functional role in cheese quality and flavor is being analyzed using RNA (metatranscriptomics) – based characterization and bio-chemical (metabolic) profiling. Overall, this will provide insights into the flexibility of modern industrial cheese production and the influences on final cheese quality and flavor.

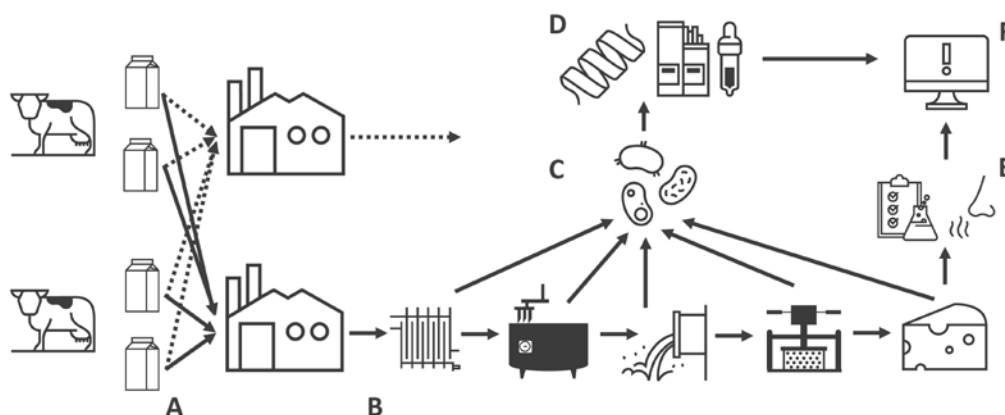


Figure 1: The MetaCheese Project. We are exploring (A) the roles of different milk sources, dairy locations and ripening temperatures on shaping the microbial activity and final quality of cheese. To do this we (B) take sample at different steps of the cheese making process, (C) purify the microbes present and (D) generate from each DNA, RNA and other biochemical data, as well as (E) other measures of quality on the final cheese. This data is integrated into a powerful computational pipeline (F), in order to deconstruct the role of the different variables on the outcome.

future as the strategy will provide direct insight into the functional role that microorganisms play at different stages of cheese making and flavor formation processes. Therefore, it becomes possible to identify not only what microorganisms are in the cheese, but also how they are interacting with each other during the production as well as the subsequent ripening processes. It will also be possible to build up a detailed picture of how key flavor compounds vary alongside the changes in the cheese microbiome at different stages in the cheese making and ripening process.

Project contribution

The MetaCheese project provides insights into the flexibility of modern industrial cheese production and the influences on final cheese quality

by applying the above described multi-omics approach to explore the structure and functional role of the cheese microbiome. This knowledge will help the Danish dairy industry ensure robust production of premium quality cheeses, even when they need to move production to different locations or apply different milk bases. This in turn will serve to increase not only the cost-efficiency of cheese production in general throughout Denmark, but also the overall cheese quality and in the end also benefitting the consumer. Furthermore, the biological insights obtained from the systematic multi-omics approach will provide new insights into the role of different microorganisms during fermentation in general, which will serve to have a wider impact across areas interested in fermentation but also development of culture-based solutions for the food industry. ●