

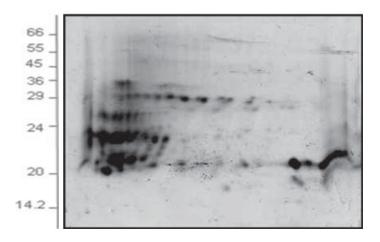
Project number: 5550

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The milk proteome: a tool for understanding milk quality and functionality



Kev external stakeholders:

Cheese manufacturers

Practical implications for stakeholders:

This study has a very high relevance for the Irish cheese industry, and its need to supply high quality products over the whole year. As milk composition changes over the lactation cycle, milk at late lactation stage is less suitable for cheese manufacturing due to the changing plasmin levels.

Main results:

- We clearly demonstrated differences in proteolysis in cheeses made from milk taken over different stages of the lactation cycle.
- From this study, it could be seen that there are significant changes in the profile over the lactation cycle and, while similar studies have been done on this topic, the application of proteomic tools gives another a deeper insight into the specific changes occurring due to proteolysis.
- Proteomics is a very helpful tool to characterize the differences between cheese samples during ripening and also over lactation.

Opportunity / Benefit:

This project has developed significant additional research capacity in a very new field (proteomic analysis of food systems) which offers new advanced analytical capability of interest in the context of a range of new research project areas, including analysis by food companies. In addition, the project involved applying these tools to applied research questions of direct scientific and industrially-relevant interest (e.g., impact of seasonality and somatic cell count on dairy product quality). Additional knowledge on milk quality issues is of indirect economic impact by providing additional knowledge for dairy companies in Ireland.

Collaborating Institutions:

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External collaborators: Prof. Alan Kelly

1. Project background:

The objective of this project was to use proteomic tools to explore aspects of the milk protein and enzyme system of scientific and industrial significance. The term 'proteomics' refers to a family or toolkit of techniques relatively recently developed, to separate and identify complex mixtures of proteins. While this approach has been adopted in many fields of biological research, it has not been extensively used for analysis of dairy proteins (which can be very complex in composition and interactions in dairy products), and this project was designed to exploit its advantages for this purpose.

Throughout the project, the proteomic tools developed have been shown to be an excellent and precise approach for analysing milk quality, in terms of proteins and enzymes present. Milk contains a complex protein and enzyme system, and the huge increase in resolving power, and potential for characterisation, offered by proteomic tools presents a much more vivid and rounded picture of the milk protein system, and in particular, changes induced either on the farm or due to processing.

2. Questions addressed by the project:

- o Can we use proteomic tools to explore compositional changes in milk over a complete lactation?
- o Can we use proteomic tools to investigate changes in cheese protein/peptides during ripening?

3. The experimental studies:

During this project, milk over a whole lactation cycle was obtained from the experimental herd in Moorepark at approximately monthly intervals, and Cheddar cheese was manufactured on a one liter scale. The composition was analysed after one day and the cheese was ripened for 6 months; the ripening process was studied by Urea-PAGE and 2-DE, as well as plasmin activity. It could clearly be seen that there are differences in proteolysis of the different cheeses made over the lactation cycle which, despite the small scale of the study, was the first such demonstration. This study thus has a very high relevance for the Irish cheese industry, and its need to supply high quality products over the whole year. The milk composition changes over the lactation cycle, and milk at late lactation stage is less suitable for cheese manufacturing. From this study, it could be seen that there are significant changes in the profile over the lactation cycle and, while similar studies have been done on this topic, the application of proteomic tools gives another insight into this topic. 2-DE is a very helpful tool to characterise the differences between cheese samples during ripening and also over lactation.

4. Main results:

- There were clearly differences in the protein/peptide composition of milk samples obtained over lactation stage.
- o The major compositional difference between cheeses manufactured at different stages of lactation was moisture, which correlated positively with advancing lactation.
- One- and 2-D gel electrophoresis showed proteolysis during 6 months ripening was more developed in later lactation stages.
- The proteomic patterns of Cheddar cheeses produced at different lactation stages suggests that the variability in hydrolysis of caseins and derived low molecular mass products in cheese is mainly due to plasmin.

5. Opportunity/Benefit:

This project has developed significant additional research capacity in a very new field (proteomic analysis of food systems) which offers new advanced analytical capability of interest in the context of a range of new research project areas, including analysis by food companies. The findings of this research may be of interest to the cheese manufacturers, as the seasonality of milk supply in some countries cannot guarantee the production of high quality products in certain months.

7



6. Dissemination: Main publications:

- o Hinz K, O'Connor PM, O'Brien B, Huppertz T, Ross RP, Kelly AL. (2012). Proteomic study of proteolysis during ripening of Cheddar cheese made from milk over a lactation cycle. J Dairy Res. 2012 May;79(2):176-84.
- o Hinz K, O'Connor PM, Huppertz T, Ross RP, Kelly AL. (2012) Comparison of the principal proteins in bovine, caprine, buffalo, equine and camel milk. J Dairy Res. 2012 May;79(2):185-91.
- 7. Compiled by: Sheila Morgan