Determination of cheese origin by using 26S rRNA gene fingerprinting of yeast communities by PCR DGGE: an application on Fried Cheese from Wielkopolska region

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1. INTRODUCTION

Fried cheese from Wielkopolska is one of the few traditional fermented products in Poland endowed with a Protected Geographical Indication (PGI) label. Its traditional manufacturing process, maintained through the ages in the Wielkopolska region, gives the product an original and specific character. The sensory properties of the fried cheese are closely related to the particular cheese technology, but also to its associated microbiota which plays a key role in creating its typical aroma and taste.

To eliminate unfair competition and the misleading of consumers by promoting non-genuine products, it is necessary to create an effective traceability system of food articles.

THE MAIN AIM of this study was to propose an analytical tool that will permit to link microbial ecology to the geographical origin of the food with protected status.

2. MATERIALS and METHODS

Samples of curd ripened fried cheese manufactured in six dairy factories – five from Wielkopolska region and one from Silesia were purchased at the market.

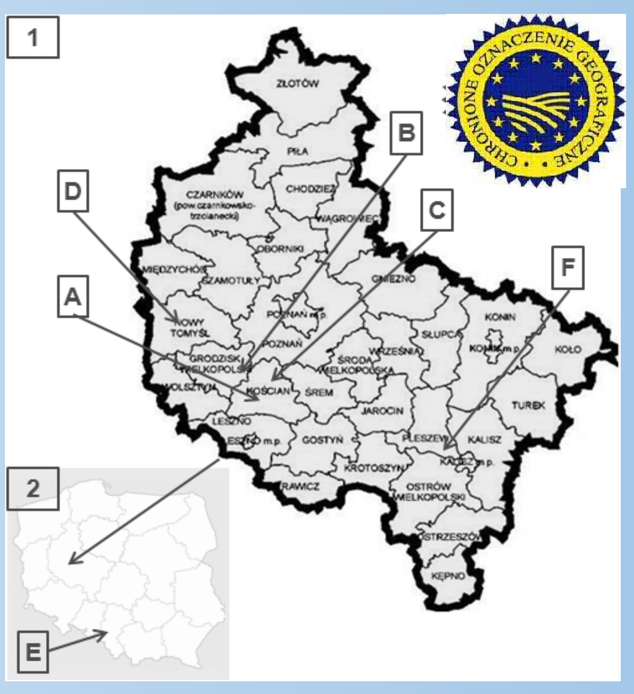
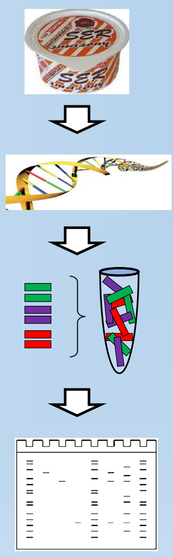


Fig. 1 Origins of fried cheese samples, 1 – Wielkopolska region, 2- Poland, (A,B,C,D,E – samples from Wielkopolska, E – sample from Silesia)

The yeast community of curd ripened fried cheeses from two different regions of Poland were evaluated by PCR-DGGE analysis of the D1/D2 region of the 26S rRNA gene. Total microbial DNA were directly extracted from cheese samples and amplified using eucaryotic universal primers.



Extraction of global DNA from cheese samples

PCR amplification of 26S rDNA region by universal primer

Separation PCR product using a denaturing gradient

Fig . 2 Flowchart of experiment

3. RESULTS

Sufficient intensities of the bands let on farther examination of the gel. The band profiles of cheeses from different sources were specific for almost each district, and the product from Silesia in particular (fig. 2, line D). Band 3 which correspond to *Kluyveromyces marxianus* was present in each analyzed samples. Sequence of band no. 1 showed the homology to *Galactomyces geotrichum*. This microorganism appeared in all samples except for E sample.

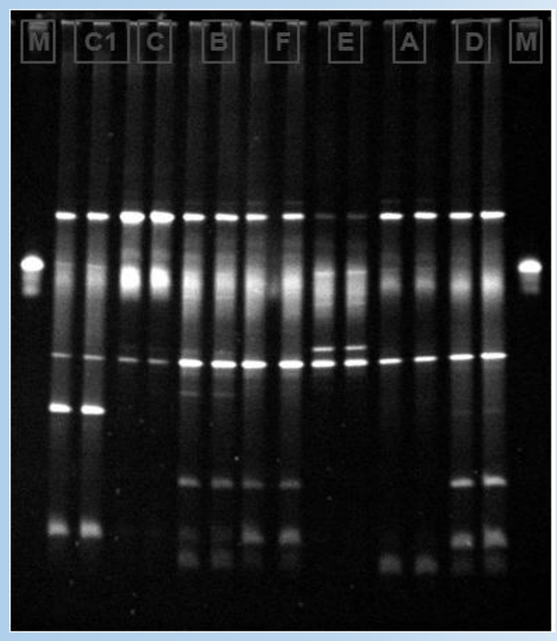


Fig. 3 PCR-DGGE 26S rRNA gene band profile of fried cheeses , A-F – manufacturers, M - marker

Cluster analysis and Factorial Variance Analysis of the DGGE gel patterns for five fried cheeses from Wielkopolska region and one from Silesia, showed the fungal composition similarity among the different geographical region. Two main clusters were observed: the first cluster including cheeses from Wielkopolska region; the second cluster encompassed cheese samples from Silesia.

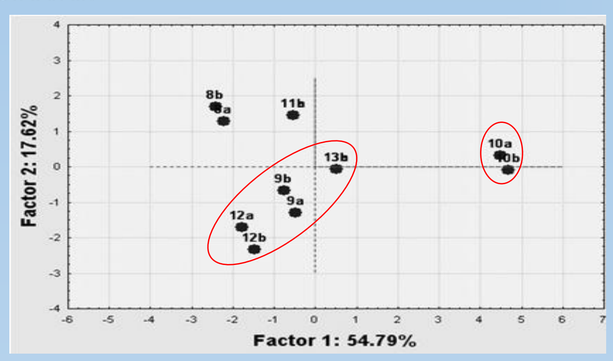


Fig. 4 Factorial variance analysis of 26S rDNA band profile of Fried cheeses from five districts of Wielkopolska and one from Silesia

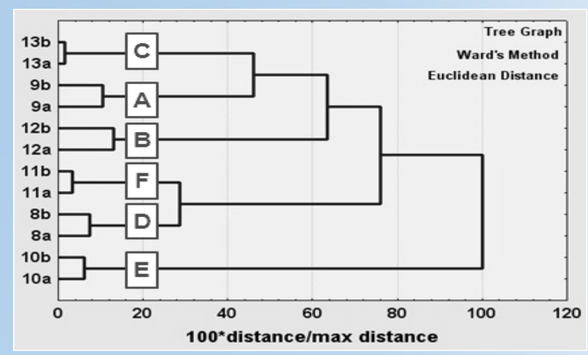


Fig. 5 Cluster analysis of 26S rDNA band profiles of Fried cheeses from five districts of Wielkopolska and one from Silesia

4. CONCLUSION

The PCR-DGGE profile of microbiota communities in analysed cheeses showed that DGGE profiles could provide unique biological bar codes which allow tracking back the food to its authentic location.

This method seems to be an effective, simple and rapid traceability tool for some fermented dairy food products denominated with protected status.

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