

Influence of *Lactobacillus delbrueckii* on the ripening of Swiss Raclette cheese

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Introduction

A large variety of lactic acid bacteria are used as starter or adjunct cultures in the production of fermented products such as cheese.

Amongst others fast acidification and high proteolytic and peptidolytic activities are important traits for strain selection for cheesemaking. In this study 46 strains of *Lactobacillus delbrueckii* were screened for their proteolytic and peptidolytic activities *in vitro*. Additionally, their genomes were sequenced, assembled and annotated. The analysis of phenotypic and genotypic data revealed significant diversity in these strains. Based on these data, strains of *L. delbrueckii* were added as adjunct cultures for the manufacture of Swiss Raclette cheeses.

Peptidolytic Diversity

Various peptidolytic activities were studied in cell free extract and in cell slurry using different substrates. A principle component analysis of the data is shown in figure 1. For cheese trials mixtures of strains with complementary activities were chosen to cover a preferably high activity of peptidases during ripening.

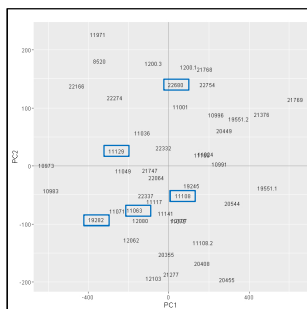
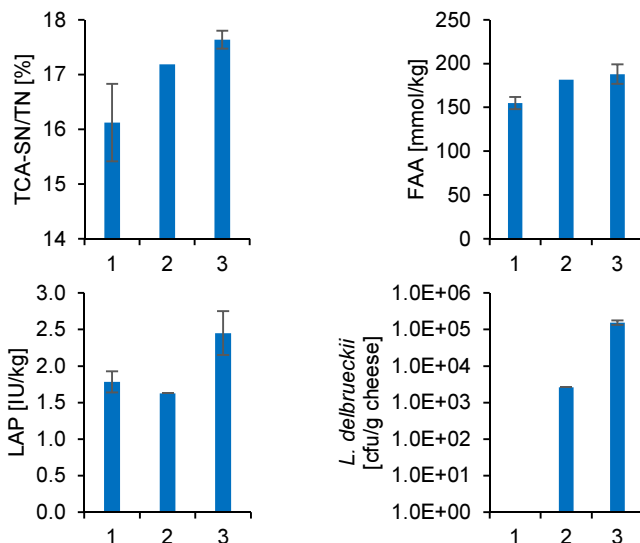


Figure 1 Principle component analysis performed on the phenotypic screening data. Numbers mark the *L. delbrueckii* strains of the Agroscope strain collection (FAM) used in this study. Boxes show the strains used in the cheese trials (figure 3).

Cheese Trials



Conclusion

The phenotypic screening revealed different peptidolytic activities on various substrates amongst the tested *L. delbrueckii*. This diversity can also be shown with the phylogenetic analysis of the core genome. Various mixtures of *L. delbrueckii* were tested in cheese trials and compared to control cheese without adjunct cultures. A sensory panel stated cheese with a mixture of FAM19282, FAM22680 and FAM11063 as more aromatic than the control. These data indicate an influence of *L. delbrueckii* strains on the ripening of Swiss Raclette cheese. The obtained data will be verified in future cheese trials and further mixtures will be tested. Furthermore it is planned to match the wet lab data to the genome data in a genome wide association study.

Genotypic Diversity

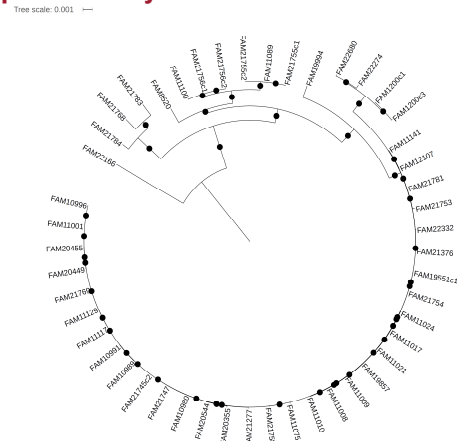


Figure 2 Phylogenetic tree of *L. delbrueckii* strains. Based on the core genome of the studied strains, we constructed a maximum likelihood tree with 1000 bootstraps replicates using RAxML.

Figure 3

Results of TCA-SN/TN (TCA-SN: 12% trichloroacetic acid soluble nitrogen, TN: total nitrogen), FAA (total free amino acids), L-leucine aminopeptidase (LAP) and colony forming units (cfu) of *L. delbrueckii* after 120d of ripening in cheese produced without (1) and with (2+3) *L. delbrueckii*.

(1) Control, n=3; (2) FAM11108, FAM11129, FAM11063, n=1; (3) FAM19282, FAM22680, FAM11063, n=2

The results show differences of cheese produced with *L. delbrueckii* in comparison to the control cheese. TCA-SN/TN, FAA and LAP are higher for mixture (3) in comparison to the control cheese. This cheese was also stated as more aromatic than the control by a trained sensory panel (three independent sessions, n=55).

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