Proteome analysis of *Lactobacillus plantarum* strain under cheese-like conditions

Sydney Isaacks

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Relevance

- Not many scientists have considered a proteomic approach to investigate this topic
- *L. plantarum* specifically is known to be prominent during cheese-ripening
- Understanding the proteome of *L. plantarum* under cheese-like conditions provides insight into how these bacteria adapt to the cheese-making environment potential stress and also how they impact the flavor and texture of cheese
- Cheese production is a multi-billion dollar industry worldwide and so understanding the production could help improve efficiency, profitability, and overall quality of cheese production
- Understanding more about how microorganisms adapt to different environments can have implications in many different areas like microbiology and food science

Aims and Hypothesis

- Analyze the proteome of a certain strain of *Lactobacillus plantarum,* a bacteria commonly found in fermented foods, under cheese-like conditions using a 2D gel electrophoresis technique

- Identify and record changes in protein expression under conditions that mimic the cheese-making environment, **specifically regarding salt tolerance**

- Determine biological functions of the differentially expressed proteins and understand their roles in the adaptations of *L. plantarum* to a cheese-like environment

- They hypothesized that *L. plantarum* would exhibit changes in its proteome when in this specific environment and that there would be upregulation of stress proteins

General Techniques

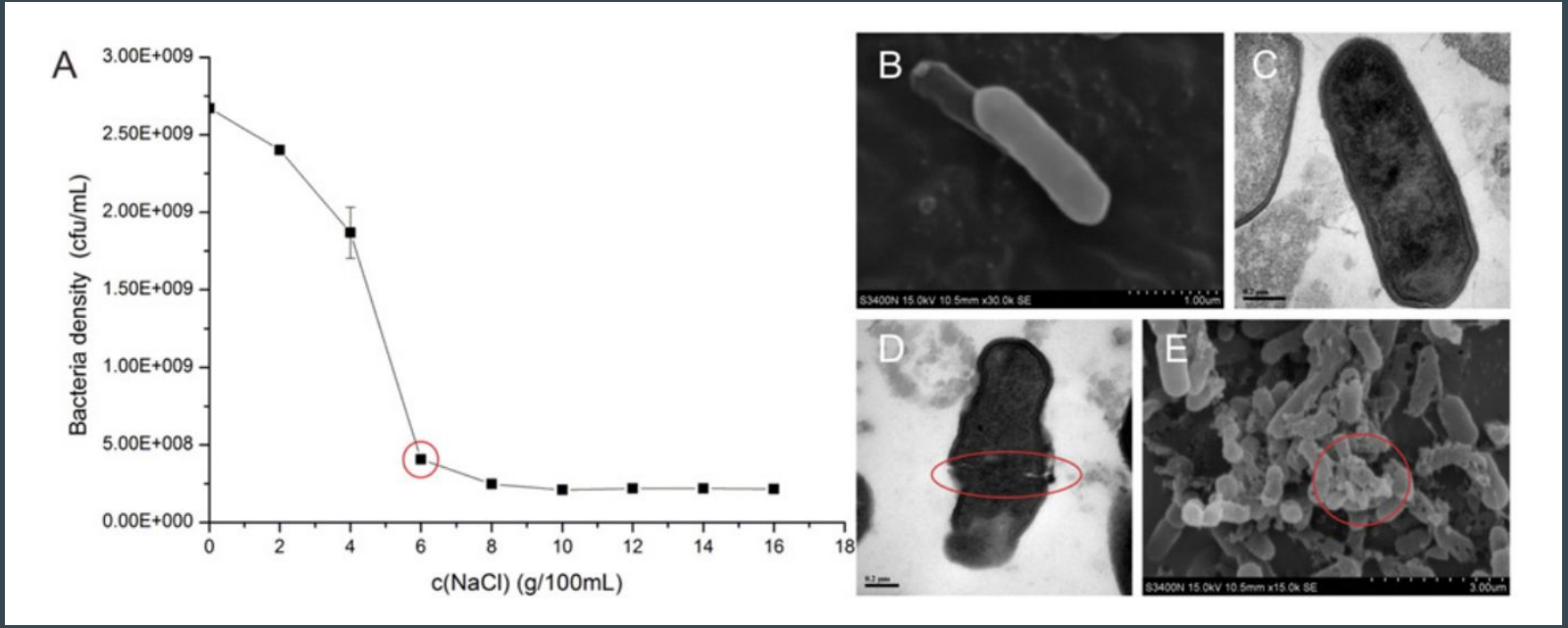
- ‘Cheese-like conditions’ entailed using a nutrient rich medium that included components such as cheese whey, casein, and sodium chloride which helped to simulate the conditions found in cheese during the production process, including the availability of complex carbohydrates and proteins, high salt concentrations, and changes in pH and oxygen levels

- The strain of *L. plantarum* was grown in MRS broth for 8 hours then transferred into MRS broth with differing sodium concentrations

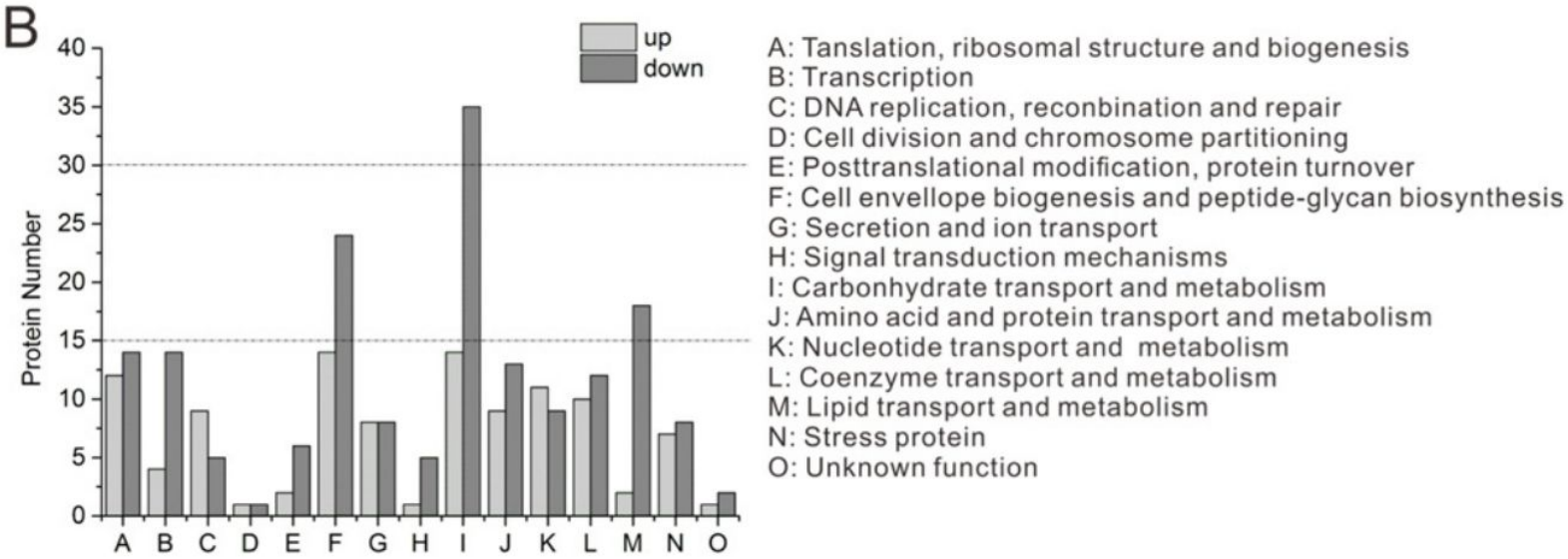
- Proteins were extracted from the bacterial cells using a modified trichloroacetic acid precipitation method, and two-dimensional gel electrophoresis was used to separate and analyze the proteins.

- Protein spots that showed significant changes in intensity under cheese-like conditions compared to MRS broth were selected for identification by mass spectrometry and were then analyzed

Results



- There was a decrease of growth rate in high salinity
- There was morphological damage to the cells in high salinity
- 6% NaCl was used for proteomic analysis based on this



- They wanted to look at which proteins were altered the most based on up or down regulation
- Proteins involved in carbohydrate transport and metabolism, cell envelope and peptide-glycan biosynthesis, and lipid transport and metabolism had the most significant changes in expression
- It also is of note that there were changes in expression of the stress protein

Conclusions

- A comprehensive proteome profile of *L. plantarum* strain under cheese-like conditions was revealed

- *L. plantarum* increased the levels of enzymes responsible for flavor development

- The upregulation of proteins involved in stress response suggests that *L. plantarum* can be under stress in the cheese-making environment in comparison to the lab environment, likely from the high levels of salinity which is what they hypothesized

- *L. plantarum* adapts to the high salinity cheese-making environment by upregulating enzymes involved in areas like carbohydrate metabolism especially, indicating that the bacterium has developed the ability to utilize complex carbohydrates and proteins present in the cheese-making environment

Comments

- Limitations

- Future research

- The authors used very confident language
  - “dramatic change”

- The authors declared at the end that “no conflict of interest exists”

References

Wu Z, Wang P, He J, Pan D, Zeng X, Cao J. 2019. Proteome Analysis of *Lactobacillus plantarum* strain under cheese-like conditions. Journal of Proteomics 146:165–171. doi: 10.1021/acs.jproteome.9b00244.