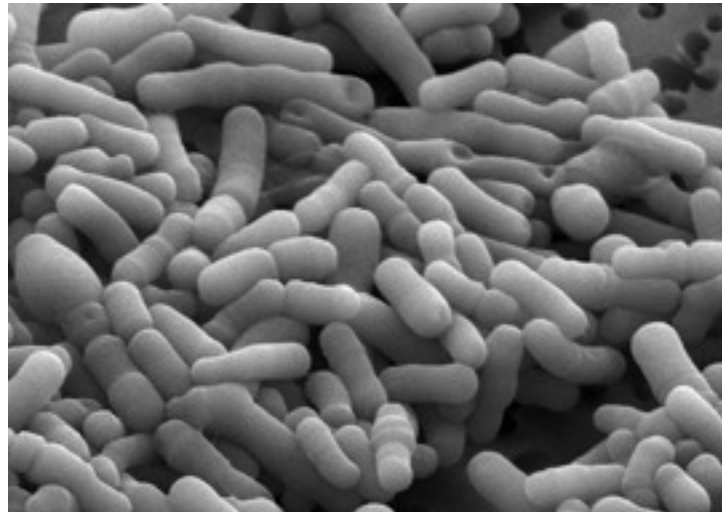


Group-specific comparison of four lactobacilli isolated from human sources using differential blast analysis



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Abstract

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RESEARCH PAPER

Group-specific comparison of four lactobacilli isolated from human sources using differential blast analysis

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Lactic acid bacteria (LAB) have been used in fermentation processes for centuries. More recent applications including the use of LAB as probiotics have significantly increased industrial interest. Here we present a **comparative genomic analysis of four completely sequenced *Lactobacillus* strains**, isolated from the human gastrointestinal tract, versus 25 lactic acid bacterial genomes present in the public database at the time of analysis. *Lactobacillus acidophilus* NCFM, *Lactobacillus johnsonii* NCC533, *Lactobacillus gasseri* ATCC33323, and *Lactobacillus plantarum* WCFS1 are all considered probiotic and widely used in industrial applications. Using Differential Blast Analysis (DBA), each genome was compared to the respective remaining three other *Lactobacillus* and 25 other LAB genomes. DBA highlighted strain-specific genes that were not represented in any other LAB used in this analysis and also identified group-specific genes shared within lactobacilli. Initial comparative analyses highlighted a significant number of genes involved in cell adhesion, stress responses, DNA repair and modification, and metabolic capabilities. Furthermore, the range of the recently identified potential autonomous units (PAUs) was broadened significantly, indicating the possibility of distinct families within this genetic element. Based on in silico results obtained for the model organism *L. acidophilus* NCFM, DBA proved to be a valuable tool to identify new key genetic regions for functional genomics and also suggested re-classification of previously annotated genes.

Outline

- Introduction
 - *Lactobacillus*
 - The role of *Lactobacillus* in the industry
- Methods
 - Differential Blast Analysis (DBA)
 - Protein Artemis Comparison Tool (pACT)
- Results
 - Genome Atlases
 - Alignment of genomes by pACT
 - 16S rRNA tree
- Conclusion

Introduction

Lactobacilli
database

Genomes	Accession Number
<i>Lactobacillus acidophilus</i> NCFM	CP000033
<i>Lactobacillus gasseri</i> ATCC33323	CP000413
<i>Lactobacillus johnsonii</i> NCC533	AE017198
<i>Lactobacillus plantarum</i> WCFS1	NC_004567

Lactic acid
bacteria
database

Table 1 Firmicutes and Actinobacteria used to generate the custom LAB database

Organisms	Genomes	Plasmids
Bacilli	1	5
Bifidobacteriae	2	11
Brevibacteriae	1	0
Enterococci	1	9
Lactobacilli	3	31
Lactococci	2	23
Leuconostoc sp	1	5
Oenococci	1	0
Pediococci	1	2
Streptococci	12	18

Introduction

- *Lactobacillus*
 - Found in the gastrointestinal tract of humans and animals
 - 28 completed *Lactobacillus* genomes are available in the NCBI Genome database today

- The role of *Lactobacillus* in the industry
 - Fermentation of dairy products
 - Probiotics



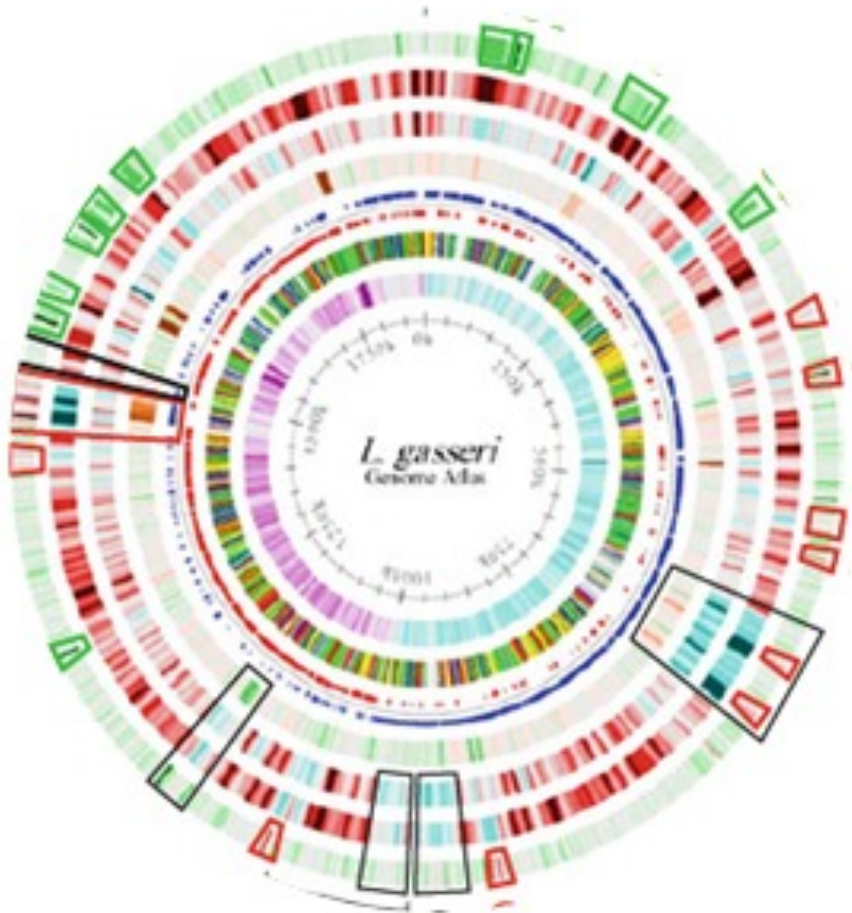
Methods

- Differential Blast Analysis (DBA)
 - Comparison of genomes
 - Identification of group-specific or unique regions
 - Not dependent on gene annotation

- Protein Artemis Comparison Tool (pACT)
 - Comparison of genomes on amino acid level
 - Identification of similarities and differences
 - Gene localization on the chromosome

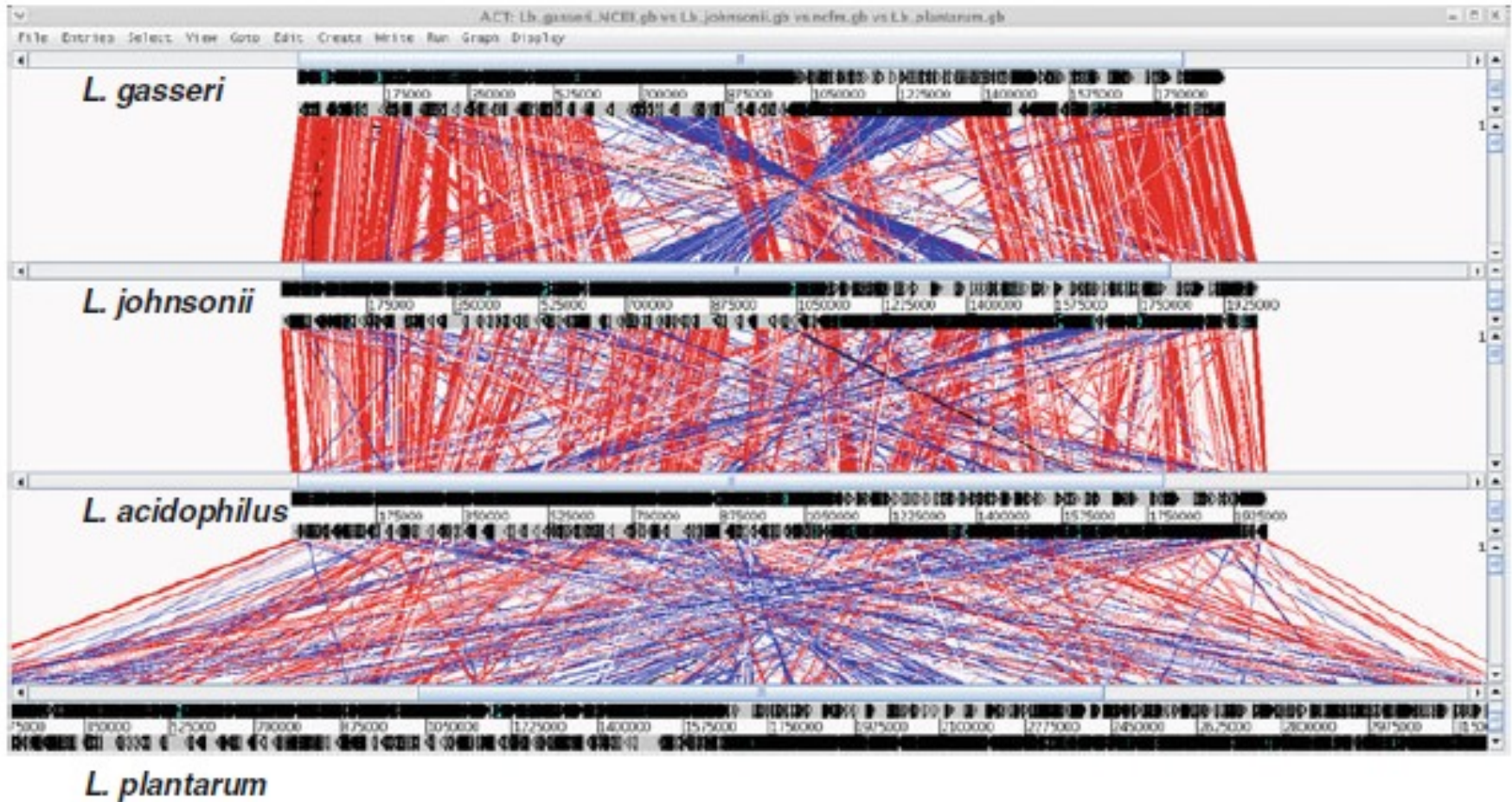
Results

Genome Atlases



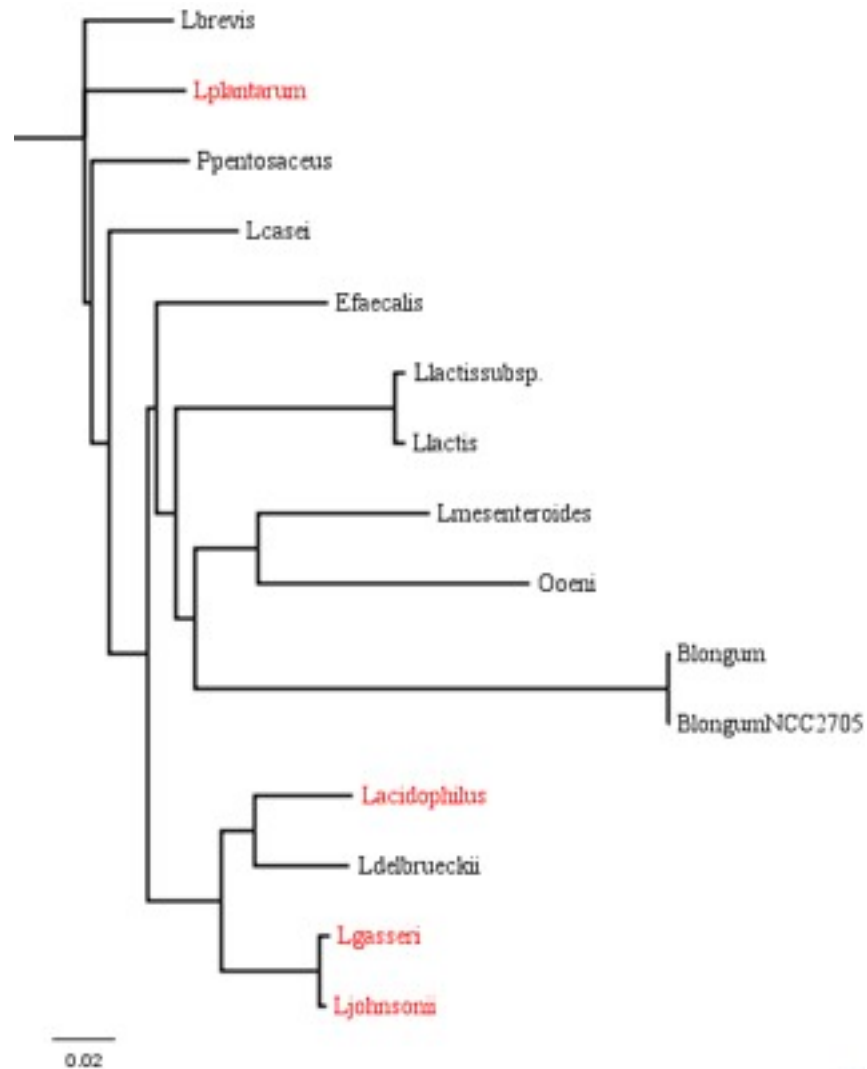
Results

Alignment of genomes by pACT



Results

16S rRNA tree



Conclusion

- Differential Blast Analysis (DBA) was used to identify genetic regions shared by the four Lactobacilli.
- Examples of these genetic regions are surface-binding proteins, drug resistance systems, bile salt hydrolases and carbohydrate and transport metabolism systems.
- Due to the bigger genome, *L. plantarum* has more species-specific genes when compared to the other three Lactobacilli.
- *L. gasseri* and *L. johnsonii* showed high similarity but still represent two different species.

Thank you for listening