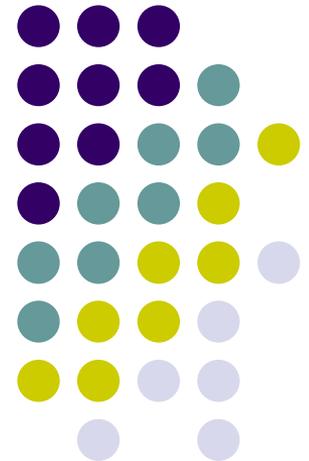
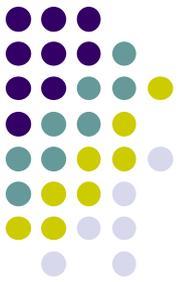


# The industrial potential of Lactic Acid Bacteria

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# Lactic Acid bacteria

- Gram +
  - Sequencing of genomes flourishes (25 published)
  - They have the ability to ferment sugars to lactic acid
  - Low percentage G+C
  - In industry used in the production of many foods and fermentative beverages; bacteriocins, pharmaceuticals (vitamin B)
  - In 2001, the full genome of *Lactococcus lactis* is sequenced
  - At present the genomes of:
    - 15 *Lactobacillus*
    - 3 *Lactococcus*
    - 3 *Streptococcus*
    - 2 *Leuconostoc*
    - 1 *Pediococcus*
    - 1 *Oenococcus*
- are sequenced



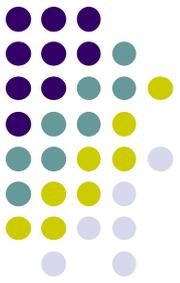
# Lactic Acid bacteria

- Genomics provides unprecedented opportunities to inspect the physiology and metabolic processes of the LAB.
- Most LAB genomes are relatively small in size.
- In some genes in the process of evolution, horizontal transfer and gene duplication took place.
- In *Streptococcus thermophilus*, *Lactobacillus bulgaricus*, *Lactobacillus helveticus*, more than 10% of the coding genes have lost their functions and are represented by pseudogenes.
- *S. thermophilus* generates a virulence associated gene related to antibiotic resistance and adhesion functions, which distinguishes it from the pathogenic *S. neighbors*.
- The LAB genome can be easily regulated, controlled, and engineered to "domesticate" under industrial conditions.

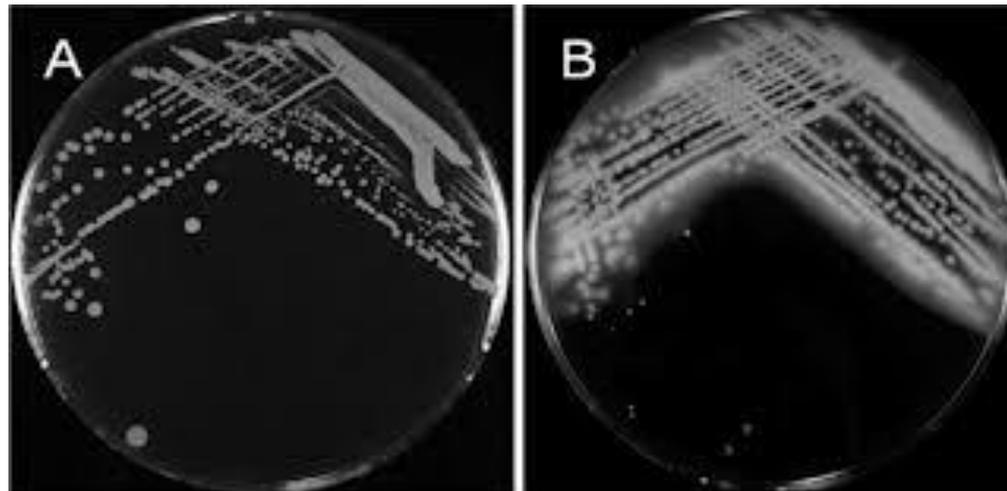
**Table 2** General features of the sequenced LAB genomes (data were collected from genome database of the National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov/sites/entrez?db=genome>)

Strain names	Origin/usage	NCBI access no.	GC content (%)	Length (Kb)	Genome size (Mb)	No. of genes	No. of proteins	No. of pseudogenes	References
<i>Lactobacillus acidophilus</i> NCFM <sup>a</sup>	Probiotics	NC_006814	34.7	1,993	1.99	1,936	1,862	0	Altermann et al. (2005)
<i>Lactobacillus brevis</i> ATCC 367 <sup>b</sup>	Beer fermentation, sourdough starter culture	NC_008497	46.2	2,291	2.34	2,314	2,218	52	Makarova et al. (2006)
		NC_008498 (pLVIS1)	38.6	13		12	11	1	
		NC_008499 (pLVIS2)	38.5	36		25	22	3	
<i>Lactobacillus casei</i> ATCC 334 <sup>a</sup>	Swiss cheese, probiotics	NC_008526	46.6	2,895	2.92	2,909	2,751	82	Makarova et al. (2006)
		NC_008502 (pLSEII)	42.2	29		20	20	0	
<i>Lactobacillus casei</i> BL23 <sup>b</sup>	Starter culture, probiotics	NC_010999	46.3	3,079	3.08	3,044	3,044	0	
<i>Lactobacillus delbrueckii</i> ssp. <i>bulgaricus</i> ATCC 11842 <sup>c</sup>	Yogurt fermentation	NC_008529	49.7	1,864	1.86	2,217	1,562	533	van de Guchte et al. (2006)
<i>Lactobacillus delbrueckii</i> ssp. <i>bulgaricus</i> ATCC BAA-365 <sup>c</sup>	Yogurt fermentation	NC_008529	49.7	1,857	1.86	2,040	1,721	192	Makarova et al. (2006)
<i>Lactobacillus fermentum</i> IFO 3956 <sup>b</sup>	Probiotics, animal & plant material	NC_010610	51.5	2,098	2.10	1,912	1,843	0	Morita et al. (2008)
<i>Lactobacillus gasseri</i> ATCC 33323 <sup>c</sup>	Probiotics	NC_008530	35.3	1,894	1.89	1,898	1,755	43	Azcarate-Peril et al. (2008); Makarova et al. (2006)
<i>Lactobacillus helveticus</i> DPC 4571 <sup>c</sup>	Cheese flavor development	NC_010080	37.1	2,080	2.08	1,838	1,610	155	Callanan et al. (2008)
<i>Lactobacillus johnsonii</i> NCC 533 <sup>c</sup>	Probiotics	NC_005362	34.6	1,992	1.99	1,918	1,821	0	Pridmore et al. (2004)
<i>Lactobacillus plantarum</i> WCFS1 <sup>b</sup>	Vegetable fermentation, probiotics	NC_004567	44.5	3,308	3.35	3,135	3,007	42	Kleerebezem et al. (2003); van Kranenburg et al. (2005)
		NC_006375 (pWCFS101)	39.5	2		3	3	0	
		NC_006376 (pWCFS102)	34.3	2		4	4	0	
		NC_006377 (pWCFS103)	40.8	36		43	43	0	
<i>Lactobacillus reuteri</i> F275 <sup>b</sup>	Probiotics	NC_009513	38.9	2,000	2.00	2,027	1,900	39	
<i>Lactobacillus reuteri</i> JCM 1112 <sup>b</sup>	Probiotics	NC_010609	38.9	2,039	2.04	1,901	1,820	0	Morita et al. (2008)
<i>Lactobacillus sakei</i> ssp. <i>sakei</i> 23K <sup>b</sup>	Meat fermentation	NC_007576	41.3	1,884	1.88	1,963	1,879	0	Chaillou et al. (2005)
<i>Lactobacillus salivarius</i> ssp. <i>salivarius</i> UCC118 <sup>b</sup>	Probiotics	NC_007929	32.9	1,827	2.13	1,864	1,717	49	Claesson et al. (2006)
		NC_006529 (pSF118-20)	39.1	20		27	27	0	
		NC_006530 (pSF118-44)	39.6	44		49	47	2	

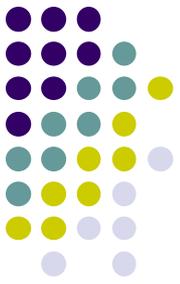
# MGEs



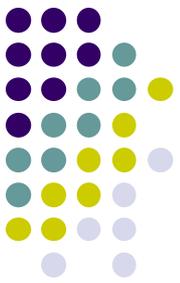
- LAB genomes include so-called variable mobile genomic elements, including plasmids and prophage insertion elements.
- The presence of MGEs contributes to the plasticity of the genome and to the adaptation to the environment.
- One of the most recently discovered MGEs in LAB is the 242 kb plasmid pMP118 in *Lactobacillus salivarius*.
- pMP118 encodes two enzymes for the pentose phosphate pathway: transketolase and transaldolase.



# MGEs



- LABs are widely used in industry due to their physiological characteristics - probiotic properties, interactions in the population, specific response under stress conditions.
- Genomics and functional genomic approaches are characterized by highly throughput, large scale combinations of experimental and computational methods that are used to detect genes, signaling pathways, metabolic stages, regulatory chains.



- Genomics revealed that the improvement in substrate absorption is mainly based on duplication of genes or horizontal transfer.
- In *Lactobacillales*, gene duplication occurs even in the phosphotransferase system, the amino acid transport, which increases their adaptation to the nutrient-rich environment.

