



Sequence and comparative analysis of *Leuconostoc* dairy bacteriophages

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FOOD

MICROBIOLOGY

NETWORK

9th Symposium on Food Microbiology

May 12-13 2011

Konventium (LO skolen), Helsingør

The LMC Food Microbiology Network was established in 2003 in order to initiate new and intensify existing collaborations between researchers working on food microbiology within LMC. One of the means by which to achieve this is through a yearly meeting in May/June. The primary activities within the LMC Food Microbiology Network include collaborations between:

- Division of Microbiology and Risk Assessment, National Food Institute, DTU (Coordinator)
- Division of Food Production Engineering, National Food Institute, DTU
- Center for Systems Microbiology, Institute for Systems Biology, DTU
- Department of Veterinary Disease Biology, Faculty of Life Sciences, KU
- Food Microbiology, Department of Food Science, Faculty of Life Sciences, KU
- Molecular Microbial Ecology Group, Department of Biology, KU.
- Department of Biochemistry and Molecular Biology, University of Southern Denmark.
- Department of Food Science, University of Aarhus.



Food

Microbiology

Network

Program

Thursday May 12th

09 30 - 10 00	Registration (coffee)		
10 00	Welcome by organizer (Lars B. Jensen)		
	<u>Session I: Phages</u> Chair Mogens Kilstrup and Lars B. Jensen		
10 05	Karin Hammer	DTU	Overview lecture on phages
10 35	Lone Brønsted	KU-Life	Identification of a novel receptor of phages infecting <i>Campylobacter jejuni</i>
11 00	Witold Kot	KU-Life	Sequence and comparative analysis of <i>Leuconostoc</i> dairy bacteriophages
11 20	Peter Kjelgaard	KU-Life	Mutations interfering with mobilization of prophages and pathogenicity islands
11 40- 12 00	Break		
	<u>Session II Antimicrobial compounds</u> Chair: Lars B. Jensen and Nete Bernbom		
12 00	Gitte Knudsen	DTU	Sub-lethal concentrations of antibiotics affect gene expression and physiology of <i>Listeria monocytogenes</i>
12 20	Line E. Thomsen	KU-Life	Peptoid inhibits essential cellular functions through unspecific binding to DNA in <i>S. aureus</i>
12 40	Ellen G. Christensen	DTU	Triclosan exposure induce aminoglycoside resistance in <i>Listeria monocytogenes</i>
13 00 - 14 00	Lunch		
	<u>Session II: Production and processing</u> Chair : Søren Aabo and Marianne Halberg Larsen		
14 00	Krist Gernaey	DTU	Linking population heterogeneity to fermentator mechanistic modeling approach
	Jan Martinussen	DTU	Lactic Acid Bacteria as a new platform for sustain: biochemicals – challenges and opportunities
14 30			
15 00	Jakob Vang Rytter	DTU	Redirecting carbon fluxes in <i>Corynebacterium glutamicum</i>
15 20	Cleide O.A. Møller	DTU	Modelling transfer of <i>Salmonella</i> DT104 during the grinding of pork
15 40	Thomas Janzen	Chr. Hansen	Use of urease negative mutants from <i>S. thermophilus</i> to avoid floating curd during cottage cheese production

16 00 - 16 15	Break		
	Poster flashes		
16 15	Katrine Joensen	SSI	Detection of a New bacteriophage among <i>Salmonella</i> outbreak isolates
16 20	Finn K. Vogensen	KU-Life	Analysis of lactococcal 936 phage population at a dairy by quantitative PCR and PCR-DGGE.
16 25	Cecilie Marvig Nielsen	KU-Life	Heat tolerance of dairy lactococcal c2 phages
16 30	Cisse Hedegaard Porsby	DTU	Effect of tropodithietic acid on gene expression in <i>Salmonella Typhimurium</i>
16 35	Marianne Kirstine Kjeldsen	SSI	Development of a multiple-locus variable number tandem repeat analysis for subtyping of <i>Salmonella Dublin</i>
16 40	Paw Dalgaard	DTU	Pasta Salad Predictor – development of a new tool to support shelf-life and safety management
16 45	Per Sand Røshaug	KU-Life	Predictive model of <i>Listeria monocytogenes</i>
16 50	Sidsel Henriksen	DTU	The impact of commercially available starter cultures on virulence properties of <i>Salmonella Typhimurium</i> in in-vitro cell culture assays and gene expression studies
16 55	Tine Rask Licht	DTU	Effects of putatively prebiotic carbohydrates on pathogenic infections

17 00 - 18 30 Poster session and drinks

19 00 Dinner

Friday May 13th

8 00 - 9 00 Breakfast

Session VI: Intestinal microbiology

Chair: Tine R Licht+ Dennis Sandris Nielsen

9 00	Lars Engstrand	Karolinska	Abstract missing
9 40	Anders Bergström	DTU	Gut Low Density Array (GULDA), a novel approach to the study of the intestinal

microbial system

10 00	Tine Ebersbach	DTU	Metagenomic sequencing of the faecal microbiota of guinea pigs fed with probiotics
10 20	Mathilde B. Kristensen	DTU	The complexity of the murine microbiota influences recruitment of immune cells in early life
10 40	Anne Holch	DTU	<i>Listeria monocytogenes</i> strains encoding <i>inlA</i> with premature stop codons are able to infect pregnant mice
11 00 - 11 15	Break		
	<u>Session V: Biofilm and adhesion</u>		
	Chair: Paw Dalgaard and Susanne Knøchel		
11 15	Tim Tolker-Nielsen	Panum	Mechanisms involved in the formation of <i>Pseudomonas aeruginosa</i> biofilms
11 45	Nete Bernbom	DTU	The effect of marine bacterial biofilms on attachment of common microbial biofoulers
12 05	Julie Szavik	KU-Life	Initial adhesion of <i>Listeria monocytogenes</i> to solid surfaces under liquid flow
12 25	Closing of the symposium		
12 30	Lunch		

12. Sequence and comparative analysis of *Leuconostoc* dairy bacteriophages.

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Phages cause large problems in the dairy industry, resulting in significant losses during production. Till date, most work regarding dairy bacteriophages has been focused on bacteriophages of *Lactococcus lactis*. However, the dairy industry is experiencing increasing problems with *Leuconostoc* phages. This group of phages has only been described very limitedly in the literature. Here we present the genomic sequence and the comparative sequence analysis of 10 *Leuconostoc* bacteriophages lytic to *Ln. mesenteroides* or *Ln. pseudomesenteroides*. The sequences were obtained using the 454 Roche Next Generation Sequencing technology. The full genomic sequence was determined with 44-876 average coverage. Bacteriophages had dsDNA genome with the size in range from 25.8 kb till 28.4 kb. The genome G+C content was around 36% in all cases. The putative ORFs were predicted and putative function was assigned based on local similarities between sequences found in various databases. The genomes seem to be modularly organized. The comparative analysis showed that the phages belonged to two distinct phage species, correlating to the species of the host. Electron microscopy pictures showed that the phages could be classified into two major groups based on the baseplate structure, which correlated with the comparative genome analysis.