Analysis of lactococcal 936 phage population at a dairy by quantitative PCR and PCR-DGGE

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Publication date:
2011

Document version
Early version, also known as pre-print

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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.

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Program

Thursday May 12th

09 30 - 10 00	Registration (coffee)		
10 00	Welcome by organizer (Lars B. Jensen)		
	Session I: Phages		
	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 *Campylobacter jejuni*
11 00	Witold Kot	KU-Life	Sequence and comparative analysis of *Leuconostoc* dairy bacteriophages
11 20	Peter Kjelgaard	KU-Life	Mutations interfering with mobilization of prophages and pathogenicity islands
11 40- 12 00	Break		
	Session II Antimicrobial compounds		
	Chair: Lars B. Jensen and Nete Bernbom		
12 00	Gitte Knudsen	DTU	Sub-lethal concentrations of antibiotics affect gene expression and physiology of *Listeria monocytogenes*
12 20	Line E. Thomsen	KU-Life	Peptoid inhibits essential cellular functions through unspecific binding to DNA in *S. aureus*
12 40	Ellen G. Christensen	DTU	Triclosan exposure induce aminoglycoside resistance in *Listeria monocytogenes*
13 00 - 14 00	Lunch		
	Session II: Production and processing		
	Chair : Søren Aabo and Marianne Halberg Larsen		
14 00	Krist Gernaey	DTU	Linking population heterogeneity to fermentatior mechanistic modeling approach
14 30	Jan Martinussen	DTU	Lactic Acid Bacteria as a new platform for sustain biochemicals – challenges and opportunities
15 00	Jakob Vang Rytter	DTU	Redirecting carbon fluxes in *Corynebacterium glutamicum*
15 20	Cleide O.A. Møller	DTU	Modelling transfer of *Salmonella* DT104 during the grinding of pork
15 40	Thomas Janzen	Chr. Hansen	Use of urease negative mutants from *S. thermophilus* 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 *Salmonella* 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 *Salmonella Typhimurium*
16 35	Marianne Kirstine Kjeldsen	SSI	Development of a multiple-locus variable number tandem repeat analysis for subtyping of *Salmonella Dublin*
16 40	Paw Dalgaard	DTU	Pasta Salad Predictor – development of a new tool to support shelf-life and safety management
16 45	Per Sand Roshaug	KU-Life	Predictive model of *Listeria monocytogenes*
16 50	Sidsel Henriksen	DTU	The impact of commercially available starter cultures on virulence properties of *Salmonella Typhimurium* 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 instestinal

			microbial system
10 00	Tine Ebersbach	DTU	Metagenomic sequencing of the faecal microbiota of gunea 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	*Listeria monocytogenes* strains encoding *inlA* with premature stop codons are able to infect pregnant mice
11 00 - 11 15	Break		
	Session V: Biofilm and adhesion		
	Chair: Paw Dalgaard and Susanne Knøchel		
11 15	Tim Tolker-Nielsen	Panum	Mechanisms involved in the formation of Pseudomonas aeruginosa 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 *Listeria monocytogenes* to solid surfaces under liquid flow
12 25	Closing of the symposium		
12 30	Lunch		

22. Analysis of lactococcal 936 phage population at a dairy by quantitative PCR and PCR-DGGE.

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Most Danish cheeses are made with undefined mesophilic DL-starter cultures. Due to their complexity it is difficult to quantify phages attacking the starter culture as traditional plaque assays does not work for mixed strains. We developed a quantitative PCR assay for detection of the most common lactococcal phages from the 936 phage species, using the small terminase gene *terS* as PCR target. To evaluate the number of 936 phage strains, we developed a PCR-DGGE assay, where the receptor binding protein (or anti-receptor) gene *rbp* was the PCR target. We analysed for the presence of 936 phages in whey samples obtained from a Danish dairy over 5 weeks. The dairy used bulk starter production, and changed between two starters A and B at a weekly basis. The analysis showed that after change of starter the level of phage declined to 10^7 - 10^8 936 phage genomes per mL for 1-2 days and then increased over the next days to levels between $10^8 - 10^9$ 936 phage genomes per mL. When PCR-DGGE profiles were analysed they clearly clustered according to the starter used indicating that e.g. the phages present in the whey from earlier use of starter A was still present in the dairy environment after one week using starter B, and vice versa.