

GUEST COMMENTARY

9th International Symposium on Lactic Acid Bacteria

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and Jeroen Hugenholtz

4589

MEETING PRESENTATIONS

Comparative Genomics of Enzymes in Flavor-Forming
Pathways from Amino Acids in Lactic Acid Bacteria

Mengjin Liu, Arjen Nauta, Christof
Francke, and Roland J. Siezen

4590-4600

Genome Sequence and Characteristics of Lrm1, a Prophage
from Industrial *Lactobacillus rhamnosus* Strain M1

Evelyn Durmaz, Michael J. Miller,
M. Andrea Azcarate-Peril, Stephen
P. Toon, and Todd R.
Klaenhammer

4601-4609

Analysis of the Genome Sequence of *Lactobacillus gasseri*
ATCC 33323 Reveals the Molecular Basis of an
Autochthonous Intestinal Organism

M. Andrea Azcarate-Peril, Eric
Altermann, Yong Jun Goh, Richard
Tallon, Rosemary B. Sanosky-
Dawes, Erika A. Pfeiler, Sarah
O'Flaherty, B. Logan Buck, Alleson
Dobson, Tri Duong, Michael J.
Miller, Rodolphe Barrangou, and
Todd R. Klaenhammer

4610-4625

Engineering of a Human Vaginal *Lactobacillus* Strain for
Surface Expression of Two-Domain CD4 Molecules

Xiaowen Liu, Laurel A. Lagenaur,
Peter P. Lee, and Qiang Xu

4626-4635

Morphology, Genome Sequence, and Structural Proteome
of Type Phage P335 from *Lactococcus lactis*

Simon J. Labrie, Jytte Josephsen,
Horst Neve, Finn K. Vogensen, and
Sylvain Moineau

4636-4644

Evaluation of Reuterin Production in Urogenital Probiotic
Lactobacillus reuteri RC-14

Peter Cadieux, Anette Wind, Philip
Sommer, Laura Schaefer, Kate
Crowley, Robert A. Britton, and
Gregor Reid

4645-4649

Oral Administration of *Lactobacillus* Strains Isolated from
Breast Milk as an Alternative for the Treatment of
Infectious Mastitis during Lactation

E. Jiménez, L. Fernández, A.
Maldonado, R. Martín, M. Olivares,
J. Xaus, and J. M. Rodríguez

4650-4655

Improved Cloning Vectors for Bifidobacteria, Based on the
Bifidobacterium catenulatum pBC1 Replicon

Pablo Álvarez-Martín, Ana Belén
Flórez, Abelardo Margolles, Gloria
del Solar, and Baltasar Mayo

4656-4665

Specific Interaction of the Unmodified Bacteriocin
Lactococcin 972 with the Cell Wall Precursor Lipid II

Beatriz Martínez, Tim Böttiger,
Tanja Schneider, Ana Rodríguez,
Hans-Georg Sahl, and Imke
Wiedemann

4666-4670

Reduced Lysis upon Growth of *Lactococcus lactis* on
Galactose Is a Consequence of Decreased Binding of the
Autolysin AcmA

Anton Steen, Girbe Buist, Naomi
E. Kramer, Ruud Jalving, Germaine
F. J. D. Benus, Gerard Venema,
Oscar P. Kuipers, and Jan Kok

4671-4679

Influence of Shifting Positions of Ser, Thr, and Cys
Residues in Prenisin on the Efficiency of Modification
Reactions and on the Antimicrobial Activities of the
Modified Prepeptides

Jacek Lubelski, Wout Overkamp,
Leon D. Kluskens, Gert N. Moll,
and Oscar P. Kuipers

4680-4685

Differential Transcriptional Response of *Bifidobacterium*
longum to Human Milk, Formula Milk, and
Galactooligosaccharide

Rina González, Eline S. Klaassens,
Erja Malinen, Willem M. de Vos,
and Elaine E. Vaughan

4686-4694

Implication of an Outer Surface Lipoprotein in Adhesion of *Bifidobacterium bifidum* to Caco-2 Cells

***Streptococcus thermophilus* Core Genome: Comparative Genome Hybridization Study of 47 Strains**

Impact of *luxS* and Suppressor Mutations on the Gastrointestinal Transit of *Lactobacillus rhamnosus* GG

Functional Analysis of Four Bile Salt Hydrolase and Penicillin Acylase Family Members in *Lactobacillus plantarum* WCFS1

High-Throughput Identification and Validation of In Situ-Expressed Genes of *Lactococcus lactis*

Exopolysaccharides Produced by Intestinal *Bifidobacterium* Strains Act as Fermentable Substrates for Human Intestinal Bacteria

Suppressive Effect on Activation of Macrophages by *Lactobacillus casei* Strain Shirota Genes Determining the Synthesis of Cell Wall-Associated Polysaccharides

Isolation and Characterization of Carnocyclin A, a Novel Circular Bacteriocin Produced by *Carnobacterium maltaromaticum* UAL307

Variations in the Degree of D-Alanylation of Teichoic Acids in *Lactococcus lactis* Alter Resistance to Cationic Antimicrobials but Have No Effect on Bacterial Surface Hydrophobicity and Charge

Transcriptome Analysis of the *Lactococcus lactis* ArgR and AhrC Regulons

Plasmid pCS1966, a New Selection/Counterselection Tool for Lactic Acid Bacterium Strain Construction Based on the *oroP* Gene, Encoding an Orotate Transporter from *Lactococcus lactis*

Improvement of *Lactobacillus plantarum* Aerobic Growth as Directed by Comprehensive Transcriptome Analysis

Multiplex Fast Real-Time PCR for Quantitative Detection and Identification of *cos*- and *pac*-Type *Streptococcus thermophilus* Bacteriophages

GENETICS AND MOLECULAR BIOLOGY

Protein Kinase A Regulates Growth, Sporulation, and Pigment Formation in *Aspergillus fumigatus*

Simone Guglielmetti, Isabella Tamagnini, Diego Mora, Mario Minuzzo, Alessio Scarafoni, Stefania Arioli, Jukka Hellman, Matti Karp, and Carlo Parini 4695–4702

Thomas Bovbjerg Rasmussen, Morten Danielsen, Ondrej Valina, Christel Garrigues, Eric Johansen, and Martin Bastian Pedersen 4703–4710

Sarah Lebeer, Ingmar J. J. Claes, Tine L. A. Verhoeven, Chong Shen, Ivo Lambrichts, Jan L. Ceuppens, Jos Vanderleyden, and Sigrid C. J. De Keersmaecker 4711–4718

Jolanda M. Lambert, Roger S. Bongers, Willem M. de Vos, and Michiel Kleerebezem 4719–4726

Herwig Bachmann, Michiel Kleerebezem, and Johan E. T. van Hylckama Vlieg 4727–4736

Nuria Salazar, Miguel Gueimonde, Ana María Hernández-Barranco, Patricia Ruas-Madiedo, and Clara G. de los Reyes-Gavilán 4737–4745

Emi Yasuda, Masaki Serata, and Tomoyuki Sako 4746–4755

Leah A. Martin-Visscher, Marco J. van Belkum, Sylvie Garneau-Tsodikova, Randy M. Whittall, Jing Zheng, Lynn M. McMullen, and John C. Vederas 4756–4763

Efstathios Giaouris, Romain Briandet, Mickael Meyrand, Pascal Courtin, and Marie-Pierre Chapot-Chartier 4764–4767

Rasmus Larsen, Sacha A. F. T. van Hijum, Jan Martinussen, Oscar P. Kuipers, and Jan Kok 4768–4771

Christian Solem, Els Defoor, Peter Ruhdal Jensen, and Jan Martinussen 4772–4775

Marc J. A. Stevens, Anne Wiersma, Willem M. de Vos, Oscar P. Kuipers, Eddy J. Smid, Douwe Molenaar, and Michiel Kleerebezem 4776–4778

Beatriz del Rio, María Cruz Martín, Noelia Martínez, Alfonso H. Magadán, and Miguel A. Alvarez 4779–4781

Christina Grosse, Thorsten Heinekamp, Olaf Kniemeyer, Alexander Gehrke, and Axel A. Brakhage 4923–4933

ENZYMOMOLOGY AND PROTEIN ENGINEERING

Esterase Autodisplay: Enzyme Engineering and Whole-Cell Activity Determination in Microplates with pH Sensors

Eva Schultheiss, Svenja Weiss, Elisa Winterer, Ruth Maas, Elmar Heinzle, and Joachim Jose 4782-4791

PHYSIOLOGY AND BIOTECHNOLOGY

Emulsifying and Metal Ion Binding Activity of a Glycoprotein Exopolymer Produced by *Pseudoalteromonas* sp. Strain TG12

Tony Gutierrez, Tracy Shimmield, Cheryl Haidon, Kenny Black, and David H. Green 4867-4876

Expression of Green Fluorescent Protein Fused to Magnetosome Proteins in Microaerophilic Magnetotactic Bacteria

Claus Lang and Dirk Schöler 4944-4953

MYCOLOGY

Intracellular pH Homeostasis Plays a Role in the Tolerance of *Debaryomyces hansenii* and *Candida zeylanoides* to Acidified Nitrite

Henrik Dam Mortensen, Tomas Jacobsen, Anette Granly Koch, and Nils Arneborg 4835-4840

PUBLIC HEALTH MICROBIOLOGY

Microencapsulation of Bacteriophage Felix O1 into Chitosan-Alginate Microspheres for Oral Delivery

Yongsheng Ma, Jennifer C. Pacan, Qi Wang, Yongping Xu, Xiaoqing Huang, Anton Korenevsky, and Parviz M. Sabour 4799-4805

Evaluation of Major Types of Shiga Toxin 2e-Producing *Escherichia coli* Bacteria Present in Food, Pigs, and the Environment as Potential Pathogens for Humans

Lothar Beutin, Ulrike Krüger, Gladys Krause, Angelika Miko, Annett Martin, and Eckhard Strauch 4806-4816

In Vitro Study of the Effect of Cationic Biocides on Bacterial Population Dynamics and Susceptibility

Louise E. Moore, Ruth G. Ledger, Peter Gilbert, and Andrew J. McBain 4825-4834

Diversity of Human Vaginal Bacterial Communities and Associations with Clinically Defined Bacterial Vaginosis

Brian B. Oakley, Tina L. Fiedler, Jeanne M. Marrazzo, and David N. Fredricks 4898-4909

Molecular Comparison of *Mycobacterium avium* Isolates from Clinical and Environmental Sources

Elizabeth D. Hilborn, Mitchell A. Yakus, Terry C. Covert, Stephanie I. Harris, Sandra F. Donnelly, Michael T. Schmitt, Sean Toney, Stephanie A. Bailey, and Gerard N. Stelma, Jr. 4966-4968

Fibrinogen Induces Biofilm Formation by *Streptococcus suis* and Enhances Its Antibiotic Resistance

Laetitia Bonifait, Louis Grignon, and Daniel Grenier 4969-4972

ENVIRONMENTAL MICROBIOLOGY

A PCR-Based Method for Monitoring *Legionella pneumophila* in Water Samples Detects Viable but Noncultivable Legionellae That Can Recover Their Cultivability

Eric Dusserre, Christophe Ginevra, Sylvie Hallier-Soulier, François Vandenesch, Gabriel Festoc, Jerome Etienne, Sophie Jarraud, and Maëlle Molmeret 4817-4824

Magnetic Resonance Imaging of Structure, Diffusivity, and Copper Immobilization in a Phototrophic Biofilm

V. R. Phoenix and W. M. Holmes 4934-4943

MICROBIAL ECOLOGY

Spatial and Temporal Patterns in the Microbial Diversity of a Meromictic Soda Lake in Washington State

Pedro A. Dimitriu, Holly C. Pinkart, Brent M. Peyton, and Melanie R. Mormile 4877-4888

Short Peptide Induces an "Uncultivable" Microorganism To Grow In Vitro

D. Nichols, K. Lewis, J. Orjala, S. Mo, R. Ortenberg, P. O'Connor, C. Zhao, P. Vourros, T. Kaeberlein, and S. S. Epstein 4889-4897

Molecular Characterization of the Diversity and Distribution of a Thermal Spring Microbial Community by Using rRNA and Metabolic Genes

Justine R. Hall, Kendra R. Mitchell, Olan Jackson-Weaver, Ara S. Kooser, Brandi R. Cron, Laura J. Crossey, and Cristina D. Takacs-Vesbach 4910-4922

Isolation of Microbes from Lake Vostok Accretion Ice

Tom D'Elia, Ram Veerapaneni, and Scott O. Rogers 4962-4965

Diversity of Uncultured *Epsilonproteobacteria* from Terrestrial Sulfidic Caves and Springs

Megan L. Porter and Annette Summers Engel 4973-4977

FOOD MICROBIOLOGY

SEL, a Selective Enrichment Broth for Simultaneous Growth of *Salmonella enterica*, *Escherichia coli* O157:H7, and *Listeria monocytogenes*

Hyochin Kim and Arun K. Bhunia 4853-4866

Retail Survey of Brazilian Milk and Minas Frescal Cheese and a Contaminated Dairy Plant To Establish Prevalence, Relatedness, and Sources of *Listeria monocytogenes* Isolates

J. Renaldi F. Brito, Emilia M. P. Santos, Edna F. Arcuri, Carla C. Lange, Maria A. V. P. Brito, Guilherme N. Souza, Mônica M. P. O. Cerqueira, J. Marcela Soto Beltran, Jeffrey E. Call, Yanhong Liu, Anna C. S. Porto-Fett, and John B. Luchansky 4954-4961

INVERTEBRATE MICROBIOLOGY

***Babesia* Species Occurring in Austrian *Ixodes ricinus* Ticks**

Marion Blaschitz, Melanie Narodoslavsky-Gföller, Michaela Kanzler, Gerold Stanek, and Julia Walochnik 4841-4846

METHODS

Rapid Ultrafiltration Concentration and Biosensor Detection of Enterococci from Large Volumes of Florida Recreational Water

Stephaney D. Leskinen and Daniel V. Lim 4792-4798

Detection of a Lysozyme Inhibitor in *Proteus mirabilis* by a New Reverse Zymogram Method

Lien Callewaert, Lise Vanderkelen, Daphne Deckers, Abram Aertsen, Johan Robben, and Chris W. Michiels 4978-4981

BIODEGRADATION

Conversion of Daidzein and Genistein by an Anaerobic Bacterium Newly Isolated from the Mouse Intestine

Anastasia Matthies, Thomas Clavel, Michael Gütschow, Wolfram Engst, Dirk Haller, Michael Blaut, and Annett Braune 4847-4852

ERRATUM

Gnotobiotic Mouse Immune Response Induced by *Bifidobacterium* sp. Strains Isolated from Infants

Odile Ménard, Marie-José Butel, Valérie Gaboriau-Routhiau, and Anne-Judith Waligora-Dupriet 4982

AUTHOR'S CORRECTION

**Improvement of the Glutaryl-7-Aminocephalosporanic Acid
Acylase Activity of a Bacterial γ -Glutamyltranspeptidase**

Chiaki Yamada, Kyoko Kijima,
Sayaka Ishihara, Chinatsu Miwa,
Kei Wada, Toshihiro Okada, Keiichi
Fukuyama, Hidehiko Kumagai, and
Hideyuki Suzuki

4983

Cover photograph (Copyright © 2008, American Society for Microbiology. All Rights Reserved.): The J. C. C. van Speyk lighthouse towers high (37 m above sea level—quite an altitude by Dutch standards) above the town of Egmond aan Zee, The Netherlands, where for the third time running the triannual International Symposium on Lactic Acid Bacteria will be taking place. This event, which is being held for the ninth time, will host approximately 600 participants from all parts of the world and will cover all current ongoing research relating to lactic acid bacteria. (See related commentary on page 4589 and related articles on pages 4590–4781.)