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# Bacteriophage Ecology Group (BEG) News

Dedicated to the *ecology* and *evolutionary biology* of the parasites of unicellular organisms (UOPs)

© Stephen T. Abedon (editor)

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January 1, 2004 issue (volume 19)

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## Editorial



### ASM Conference on the New Phage Biology

This Summer (2004) from August 1 to August 5 there will be an ASM brouhaha devoted entirely to phage biology. To quote the blurb from the ASM site

The meeting will bring together scientists interested in phage biology, both its vibrant basic science and its exciting new applications in biotechnology and anti-bacterial therapeutics. Bacteriophages were discovered at the beginning of the 20th century, enjoyed decades of promise as anti-bacterial agents before being eclipsed by the antibiotic era. Phage biology was the first model system in the DNA era and dominated life science into the 70s before being largely abandoned in favor of the study of other model organisms. Recently, phages have come back into the spotlight as major factors in pathogenesis, bacterial evolution, and ecology. Moreover, new structural, genomic and single-molecule technologies have, in combination with classical phage molecular genetics, given rise to an explosion in our knowledge of phage, their compelling elegance of function and their almost inconceivable diversity. Scientists from all these areas are encouraged to come together to establish new interactions in celebration of the phage renaissance.

Responsible for the meeting are Ry Young (organizer) and Sankar Adyha (chair). Topics are tentatively to include:

- Phage Gene Regulation And Development
- Phage Genomics, Evolution, Taxonomy
- Phage DNA/RNA Replication & Repair
- Phage Structural Biology And Morphogenesis
- Phage Ecology Phage-Host Interactions
- Phage In Pathogenesis
- Phage In Biotechnology
- Phage Therapeutics

The abstract deadline is May 7. More details (and dates) can be found at: <http://www.asm.org/Meetings/>. Follow the link titled ASM Conferences.

This is a **description** of Key Biscayne, Florida, the meeting s location:

The Village of Key Biscayne was incorporated on June 18, 1991. The Village is located on a barrier island approximately seven miles south of the City of Miami on Biscayne Bay. The secluded island of Key Biscayne can be reached via the scenic Rickenbacker Causeway, which spans beautiful Biscayne Bay. Located just south of Downtown Miami and north of Coconut Grove. This island is home to miles of golden sand beaches and features a quiet neighborhood atmosphere with many parks. The residents and visitors of this small island enjoy sailing, biking, hiking, swimming with dolphins and climbing to the top of the 1825 lighthouse on the southern tip of the island.



Yes, southern Florida in August, but I m sure that the beaches, at night, are wonderful.



Please consider coming to this conference if you have any substantial interest in some aspect of phage biology. It is designed to be a venue where the many people with disparate research interests from pathogenesis to nanostructure who now find themselves concerned with bacteriophage can meet and mingle with the traditional phage biology community.

## Editorial Archive

- **BEG: What we are, Where we are, Where we're going** by Stephen T. Abedon
- **When Grown *In Vitro*, do Parasites of Multicellular Organisms (MOPs) become Unicellular Organism Parasites (UOPs)?** by Stephen T. Abedon
- **Bacteriophages as Model Systems** by Stephen T. Abedon
- **2000 and Sun: A Phage Odyssey** by Stephen T. Abedon
- **Lytic, Lysogenic, Temperate, Chronic, Virulent, Quoi?** by Stephen T. Abedon
- **Which Ecology are You?** by Stephen T. Abedon
- **Science NetWatch October 13, 2000**
- **The Best of Times, the Worst of Times** by Ry Young
- **Naming Bacteriophages** by Hans-Wolfgang Ackermann and Stephen T. Abedon
- **The Bacteriophage Rise** by Stephen T. Abedon
- **Mathematics for Microbiologists** by Stephen T. Abedon
- **Shipping Phages** by Hans-Wolfgang Ackermann
- **Calling a Phage a "Phage"** by Stephen T. Abedon
- **Phage or Phages** by Hans-Wolfgang Ackermann
- **The Phage Manifesto** by Ry Young
- **The Félix d'Hérelle Phage Center Changes Hands** by Hans-Wolfgang Ackermann
- **Phage T4 Meets Microbial Diversity** by Jim D. Karam
- **Phage T1: A lambdoid phage with attitude?** by Andrew Kropinski
- **ASM Conference on the New Phage Biology**

Editorials should be written on subjects relevant to The Bacteriophage Ecology Group as an organization, to *BEG News* (either the concept or a given issue of *BEG News*), or the science of Bacteriophage Ecology. While my assumption is that I will be writing the bulk of these editorials, I wish to encourage as many people as possible to seek to relieve me of this duty, as often as possible. Additionally, I welcome suggestions of topics that may be addressed. Please address all correspondences to [microdude+@osu.edu](mailto:microdude+@osu.edu) or to "Editorials," *Bacteriophage Ecology Group News*, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. Please send all submissions as Microsoft Word documents, if possible (I'll let you know if I have trouble converting other document

## New BEG Members

Please welcome our newest members

name (home page links)	status	e-mail	address
Robert Armon	PI	<a href="mailto:brodsky@xtra.co.nz">brodsky@xtra.co.nz</a> or <a href="mailto:cvrrobi@tx.technion.ac.il">cvrrobi@tx.technion.ac.il</a>	Environmental Microbiology, Division of Environmental, Water and Agricultural Engineering, Faculty of Civil and Environmental Engineering, Technion-Israel Institute of Technology, Technion, Haifa 32000 Israel
	interests:	Bacteriophages in environmental engineering, interaction of lytic phages with biofilms, and rapid methods of phage detection and isolation. ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
John Dennehy	---	<a href="mailto:john.dennehy@yale.edu">john.dennehy@yale.edu</a>	Department of Ecology and Evolutionary Biology, Yale University, Osborn Memorial Laboratories, 165 Prospect Street, PO Box 208106, New Haven, CT 06520-8106
	interests:	Using phage $\phi 6$ to study cooperation, cheating, life history, evolution of sex. ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
Donald (Don) Hall	PI	<a href="mailto:dinodoc@charter.net">dinodoc@charter.net</a>	Paleo Research Lab, 309 Williams Street, Narrows, VA. 24124
	interests:	Microorganisms and how they represent past/present environments with emphasis on research for antibiotic/antitoxin substances within isolated bacteria. ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
Paul Hyman	---	<a href="mailto:hyman.16@osu.edu">hyman.16@osu.edu</a>	Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906
	interests:	Molecular biology of phage adaptation and phage structural biology. ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
Kara J. O'Keefe	---	<a href="mailto:kara.okeefe@yale.edu">kara.okeefe@yale.edu</a>	Department of Ecology and Evolutionary Biology, Yale University, Osborn Memorial Laboratories, 165 Prospect Street, PO Box 208106, New Haven, CT 06520-8106
	interests:	Population biology of cystoviruses ( $\phi 6$ and relatives); the role of geography in natural phage populations--geographic population size, dispersal distance, gene flow ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
Bernhard Rupp	PI	<a href="mailto:br@llnl.gov">br@llnl.gov</a>	Macromolecular Crystallography and Structural Genomics, LLNL-BBRP L448, University of California, Livermore, CA 94551
	interests:	Macromolecular crystallography; <i>Mycobacterium tuberculosis</i> genomics. ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
Lidia Semchuk	PI	<a href="mailto:Vir509@biocc.univ.kiev.ua">Vir509@biocc.univ.kiev.ua</a>	Department of Virology of the Biological Faculty of Taras Shevchenko Kiev National University, 02033 Volodimirska 64., Kiev, Ukraine
	interests:	Phytopathogenic bacteria bacteriophages: isolation from environment, identification, their ecology, host range, and characterization. ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
Roy Stevens	PI	<a href="mailto:rstevens@dental.temple.edu">rstevens@dental.temple.edu</a>	Department of Endodontics, Director, Oral Infectious Diseases Research Laboratory, Temple University School of Dentistry, 3223 N. Broad Street, Philadelphia, PA 19140
	interests:	Bacteriophages that infect strains of <i>Actinobacillus actinomycetemcomitans</i> ; relationship between these phages and disease (periodontal disease) in patients infected with <i>A. actinomycetemcomitans</i> . ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	
Marjolijn Tijdens	---	<a href="mailto:M.Tijdens@nioo.knaw.nl">M.Tijdens@nioo.knaw.nl</a>	NIOO-KNAW-Centre for Limnology, Microbial Ecology department, Postbus 1299, 3600 BG Maarssen
	interests:	Ecology of freshwater bacteriophages infecting cyanobacteria. ( <a href="#">contents</a>   <a href="#">BEG members</a>   <a href="#">top of page</a> )	

The [BEG members page](#) can be found at [www.phage.org/beg\\_members.htm](http://www.phage.org/beg_members.htm). There are two ways of "joining" BEG. One, the "traditional" way, is to have your name listed on the web page and on the list server. The second, the "non-traditional" way, is to have your name only listed on the list server. The latter I refer to as "non-members" on that list. Members, e.g., individuals listed on the [BEG members list page](#), should be limited to individuals who are actively involved in science (research, instruction, outreach, industry) and who can serve as a phage ecology resource to interested individuals. If you have an interest in phage ecology but no real expertise in the area, then you should join as a non-member. To join as a member, please contact BEG using the following link: [microdude+@osu.edu](mailto:microdude+@osu.edu). Include:

- your name
- your e-mail address
- your snail-mail address
- the URL of your home page (if you have one)
- a statement of whether or not you are the principal investigator
- a statement of your research interests (or phage ecology interests)
- a list of your phage ecology references, if any

Note that it is preferable that you include the full reference, including the abstract, if the reference is not already present in the **BEG bibliography**. Responsibility of members includes keeping the information listed on the **BEG members page** up to date including supplying on a reasonably timely basis the full references of your new phage ecology publications. Reprints can also be sent to *The Bacteriophage Ecology Group*, care of Stephen Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. To join BEG as a non-member, please contact BEG using the following link: <http://mansfield.ohio-state.edu/mailman/listinfo/beg>.

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## Meetings

**Please send photos, etc. from meetings, etc. for inclusion in this section.**

### ASM Conference on the New Phage Biology

See this quarter's [editorial](#) and [phage image](#) for links and details.

The BEG [Meetings link](#) will continue. Reminders of upcoming meetings will be placed in this section of *BEG News*. [If you know of any meetings that might be of interest to BEG members, or would like to recap a meeting that you've attended, then please send this information for posting to microdude+@osu.edu or to "BEG Meetings," Bacteriophage Ecology Group News, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906.](#)

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## Submissions

### Early (pre-1950) Phage References

as collected (mostly) by [Hansjürgen Raettig](#)

& as entered by Laurenda Slusher and Jocelyn Witter under the direction of [S.T. Abedon](#)

please note that the following list has not been error checked against either Raettig's list nor against original documents

this list was updated on June 8, 2004, to reflect the inadvertent absence of late-alphabet authors (i.e., X, Y, and Z), with 158 references added

1. Über das Verhalten des Typhusbacillus und des *Bacillus coli communis* im Trinkwasser. Frankland, P. (1895). *Zschr. f. Hyg.* 19:393
2. L'action bactéricide des eaux de la Jumna et du Gange sur le microbe du choléra. Hankin, M. E. (1896). *Ann. Inst. Pasteur* 10:511
3. Les microbes des rivières de l'Inde. Hankin, M. E. (1896). *Ann. Inst. Pasteur* 10:175
4. Bakteriolytische Enzyme als Ursache der erworbenen Immunität und die Heilung von Infektionskrankheiten durch dieselben. Emmerich, R., Löw, O. (1899). *Zschr. f. Hyg.* 31:1
5. Bakteriolytine. Gamaleja (1899). *Zbl. f. Bakt. I. Orig.* 26:661
6. Kie physiologische Bakteriologie des Darmkanals. Klein, A. (1902). *Arch. Hyg.* 45:117
7. Über Baktericide von Bakterienfiltraten. Krencker, E. (1903). *Inaug. -Diss., Straßburg* 1903
8. Experimentelle Untersuchungen über Bakterienatagonismus. I. Lode, A. (1903). *Zbl. f. Bakt. I. Orig* 33:196
9. Über thermolabile Stoffwechselprodukte als Ursache der natürlichen Wachstumshemmung der Mikroorganismen. Eijkman, C. (1904). *Zbl. f. Bakt. I. Orig.* 37:436
10. Über die Bedeutung der bakteriellen Hemmungsstoffe für die Physiologie und Pathologie des Darms. Conradi, H., Kurpjuweit, O. (1905). *Münch. med. Wschr.* 1905?:2164 und 2228
11. Über spontane Wachstumshemmung der Bakterien infolge Selbstvergiftung. Conradi, H., Kurpjuweit, O. (1905). *Münch. med. Wschr.* 1905?:1761
12. Über die Ursache der Wachstumshemmung in Bakterienkulturen. Eijkman, C. (1906). *Berl. klin. Wschr.* 1906?:499
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14. Untersuchungen über die Autotoxine (Conradi) und ihre Bedeutung als Ursache der Wachstumshemmung in Bakterienkulturen. Manteufel (1906). *Berl. klin. Wschr.* 43:313

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16. Die bakteriellen hemmungsstoffe Conradis und ihr Einfluß auf das Wachstum der Anaerobier des Darmes. Passini, F. (1906). *Wien. klin. Wschr.* 1906:627
17. Über den Einfluß der Stoffwechselprodukte auf das Wachstum der Bakterien. Rahn, O. (1906). *Zbl. f. Bakt. II. Abtg* 16:417-609.
18. Experimentelle Untersuchungen über das biologische Verhalten der Bakterien im Dickdarm. Rolly (1906). *Dtsch. med. Wschr* 1906:1733
19. Über die Wachstumshemmung in Bakterienkulturen. Eijkman, C. (1907). *Dtsch. med. Wschr.* 1907?:265
20. Das Problem der Entwicklungshemmung in Bakterienkulturen und seine Beziehungen zu den Absterbeerscheinungen der Bakterien im Darmkanal. Manteufel (1907). *Zschr. f. Hyg* 57:337
21. Studien über Hetero- und Isantagonismus, mit besonderer Berücksichtigung der Verhältnisse bei infektiösen Erkrankungen der Harnwege. Faltin, R. (1908). *Zbl. f. Bakt. I. Orig.* 46:"6 109 und 222"
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23. Bakterien-Antifermente und Bakteriolyse. Kantorowicz, A. (1909). *Münch. med. Wschr* 1909:897
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25. An investigation on the nature of the ultramicroscopic viruses. Twort, F. W. (1915). *Lancet* 1915:1241
26. Über Variabilitätserscheinungen des Typhus-bacillus, die bereits bei seiner Isolierung aus dem infizierten Organismus auftreten. Gildemeister, E. (1916). *Zbl. f. Bakt. I. Orig.* 78:209
27. Sur un microbe invisible antagoniste des bacilles dysentériques. D'Hérelle, F. (1917). *Compt. rend. Acad. Sci.* 165:373
28. Weitere Mitteilungen über Variabilitätsschwankungen bei Bakterien, die bereits bei ihrer Isolierung aus dem Organismus zu beobachten sind. Gildemeister, E. (1917). *Zbl. f. Bakt. I. Orig.* 79:49
29. Sur le rôle du microbe filtrant bactériophage dans la dysenterie bacillaire. D'Hérelle, F. (1918). *Compt. rend. Acad. Sci.* 167:970
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36. Sur le principe bactériophage de D'HÉRELLE. Bablet, J. (1920). *Compt. rend. Soc. Biol.* 83:1322
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51. *B. dysentérique* et bactériophage de d'Hérelle chez les chenilles de *Galleria mellonella*. Metalnikow, S. B. (1920). *Compt. rend. Soc. Biol.* 83:667
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67. Hemolytic exudates and transmissible bacterial autolysis. Bordet, J. (1921). *Johns Hopkins Hosp.* 32:302
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- [Pioneering genetic researcher Gisela Mosig dies](#)
- [Updated Eiserling T4 Virion](#)
- [Some Recent Phage and Phage-Related U.S. Patents \(1976-present\)](#)
- [Some Images of BEG Members](#)
- [Early Phage References, pre-1950](#)

Submissions are non-editorial items describing or highlighting some aspect of bacteriophage ecology including news pieces, historical pieces, reviews, and write-ups of research. Peer review of submissions is possible and a desire for peer review should be indicated. Send all submissions to [microdude+@osu.edu](mailto:microdude+@osu.edu) or to "Submissions", Bacteriophage Ecology Group News, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. Please send all submissions as Microsoft Word documents, if possible (I'll let you know if I have trouble converting any other document formats), and in English.

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## Phage Images

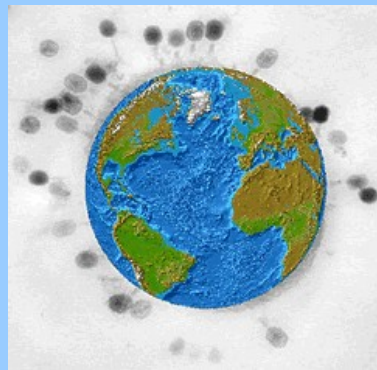


Image is from the [ASM Conference on the New Phage Biology](#), a.k.a., [Ry Young's Phage Summit](#), Aug. 1-5 at the Biscayne Sonesta Resort, in Key Biscayne, Florida (near Miami). Click [here](#) for more information.

## Phage Image Archive

- [BEG Phage Images Page](#)
- [The Face of the Phage](#)
- [Bacteriophage T2](#)
- [SSV1-Type Phage](#)
- [Saline Lake Bacteriophage](#)
- [Coliphage LG1](#)
- [Bacteriophage HK97](#)
- [Phage T4 \(art\)](#)
- [Phage T4 on the pedestal outside of Barker Hall at Berkeley](#)
- [Electron micrograph of phage P22](#)
- [Thin section of T4 phages hitting a microcolony of \*E. coli\* K-12](#)
- [T4 phage v1](#)
- [T4 Tail Model](#)
- [Gingerbread phage](#)
- [T4 adsorbing en mass](#)
- [Lysis of \*E. coli\* O157](#)
- [Homologous Recombination - 2000 by Jake McKinlay](#)



- [X-Ray Structure of Bacteriophage HK97](#) by William R. Wikoff
- [Balloon Phage T4](#) by Celeste O'Neil and Larry Goodridge
- [Image from the 2004 ASM Conference on the New Phage Biology](#)

Please send any phage images that you would like to present in this section to "Phage Images," *The Bacteriophage Ecology Group*, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. Alternatively, you may scan the images yourself and send them as an attachment to [microdude+@osu.edu](mailto:microdude+@osu.edu). Please save all scans in gif or jpg formats and preferably with an image size (in terms of width, height, and kbytes) that will readily fit on a standard web page. No copyrighted material without permission, please!

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## New Publications

New bacteriophage publications are listed below. Each quarter not-yet-listed publications from the previous two years will be presented along with their abstracts. The indicator "???" denotes, of course, that specific information is not yet in the [BEG Bibliography](#). Please help in the compilation of the [BEG Bibliography](#) by supplying any updated information, correcting any mistakes, and, of course, e-mailing with the references to your bacteriophage ecology publications, as well as the references to any bacteriophage ecology publications that you know of but which are not yet in the bibliography or to point out references that are not appropriate for the bibliography (send to [microdude+@osu.edu](mailto:microdude+@osu.edu) or to "BEG Bibliography," *Bacteriophage Ecology Group News*, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906). This list is also present with available abstracts at the [end](#) of *BEG News*.

1. Genetic details, optimization, and phage life histories. Bull, J. J., Pfening, D. W., Wang, I.-W. (2004). *Trends in Ecology and Evolution* 19:76-82. [\[PRESS FOR ABSTRACT\]](#)
2. Complete sequence and evolutionary genomic analysis of the *Pseudomonas aeruginosa* transposable bacteriophage D3112. Wang, P. W., Chu, L., Guttman, D. S. (2004). *Journal of Bacteriology* 186:400-410. [\[PRESS FOR ABSTRACT\]](#)
3. Experimental examination of bacteriophage latent-period evolution as a response to bacterial availability. Abedon, S. T., Hyman, P., Thomas, C. (2003). *Applied and Environmental Microbiology* 69:7499-7506. [\[PRESS FOR ABSTRACT\]](#)
4. Survival of F-specific RNA coliphage, feline calicivirus, and *Escherichia coli* in water: a comparative study. Allwood, P. B., Malik, Y. S., Hedberg, C. W., Goyal, S. M. (2003). *Applied and Environmental Microbiology* 69:5707-5710. [\[PRESS FOR ABSTRACT\]](#)
5. Application of host-specific bacteriophages to the surface of chicken skin leads to a reduction in recovery of *Campylobacter jejuni*. Atterbury, R. J., Connerton, P. L., Dodd, C. E. R., Rees, C. E. D., Connerton, I. F. (2003). *Applied and Environmental Microbiology* 69:6302-6306. [\[PRESS FOR ABSTRACT\]](#)
6. Prophage induction and expression of prophage-encoded virulence factors in group A *Streptococcus* serotype M3 strain MGAS315. Banks, D. J., Lei, B., Musser, J. M. (2003). *Infection and Immunity* 71:7079-7086. [\[PRESS FOR ABSTRACT\]](#)
7. Incidence of enteric viruses in groundwater from household wells in Wisconsin. Borchardt, M. A., Bertz, P. D., Spencer, S. K., Battigelli, D. A. (2003). *Applied and Environmental Microbiology* 69:1172-1180. [\[PRESS FOR ABSTRACT\]](#)
8. Specific identification of certain probiotic *Lactobacillus rhamnosus* strains with PCR primers based on phage-related sequences. Brandt, K., Alatosava, T. (2003). *International Journal of Food Microbiology* 84:189-196. [\[PRESS FOR ABSTRACT\]](#)
9. Phage as agents of lateral gene transfer. Canchaya, C., Fournous, G., Chibani-Chennoufi, S., Dillmann, M. L., Brussow, H. (2003). *Current Opinion in Microbiology* 6:417-424. [\[PRESS FOR ABSTRACT\]](#)
10. Effect of soil properties on saturated and unsaturated virus transport through columns. Chu, Y., Jin, Y., Baumann, T., Yates, M. V. (2003). *Journal of Environmental Quality* 32:2017-2025. [\[PRESS FOR ABSTRACT\]](#)
11. Viruses and marine pollution. Danovaro, R., Armeni, M., Corinaldesi, C., Mei, M. L. (2003). *Marine Pollution Bulletin* 46:301-304. [\[PRESS FOR ABSTRACT\]](#)
12. Sunscreen products increase virus production through prophage induction in marine bacterioplankton. Danovaro, R., Corinaldesi, C. (2003). *Microbial Ecology* 45:109-118. [\[PRESS FOR ABSTRACT\]](#)
13. The source of laterally transferred genes in bacterial genomes. Daubin, V., Lerat, E., Perriere, G. (2003). *Genome biology* 4:R57. [\[PRESS FOR ABSTRACT\]](#)
14. Occurrence of coliphages in urban stormwater and their fate in stormwater management systems. Davies, C. M., Yousefi, Z., Bavor, H. J. (2003). *Letters in Applied Microbiology* 37:299-303. [\[PRESS FOR ABSTRACT\]](#)
15. Filamentous phages linked to virulence of *Vibrio cholerae*. Davis, B. M., Waldor, M. K. (2003). *Current Opinion in*

16. Identification of new phages to type *Staphylococcus aureus* strains and comparison with a genotypic method. de Gialluly, C., Loulergue, J., Bruant, G., Mereghetti, L., Massuard, S., van der Mee, N., Audurier, A., Quentin, R. (2003). *The Journal of hospital infection* 55:61-67. [PRESS FOR ABSTRACT]
17. The diversity and evolution of the T4-type bacteriophages. Desplats, C., Krisch, H. M. (2003). *Research in Microbiology* 154:259-267. [PRESS FOR ABSTRACT]
18. Usefulness of different groups of bacteriophages as model micro-organisms for evaluating chlorination. Duran, A. E., Muniesa, M., Moce-Llivina, L., Campos, C., Jofre, J., Lucena, F. (2003). *Journal of Applied Microbiology* 95:29-37. [PRESS FOR ABSTRACT]
19. Phage conversion of exfoliative toxin A in *Staphylococcus aureus* isolated from cows with mastitis. Endo, Y., Yamada, T., Matsunaga, K., Hayakawa, Y., Kaidoh, T., Takeuchi, S. (2003). *Veterinary Microbiology* 96:81-90. [PRESS FOR ABSTRACT]
20. Direct estimates of the contribution of viral lysis and microzooplankton grazing to the decline of a *Micromonas* spp. population. Evans, C., Archer, S. D., Jacquet, S., Wilson, W. H. (2003). *Aquatic Microbial Ecology* 30:207-219. [PRESS FOR ABSTRACT]
21. Host range of chlamydiaphages  $\phi$ CPAR39 and Chp3. Everson, J. S., Garner, S. A., Lambden, P. R., Fane, B. A., Clarke, I. N. (2003). *Journal of Bacteriology* 185:6490-6492. [PRESS FOR ABSTRACT]
22. Viral influence on aquatic bacterial communities. Fuhrman, J. A., Schwalbach, M. (2003). *The Biological Bulletin* 204:192-195. [PRESS FOR ABSTRACT]
23. Removal of *Encephalitozoon intestinalis*, calicivirus, and coliphages by conventional drinking water treatment. Gerba, C. P., Riley, K. R., Nwachuku, N., Ryu, H., Abbaszadegan, M. (2003). *Journal of Environmental Science and Health Part A Toxic-Hazardous Substances & Environmental Engineering* 38:1259-1268. [PRESS FOR ABSTRACT]
24. Bacteriophage biocontrol and bioprocessing: application of phage therapy to industry. Goodridge, L., Abedon, S. T. (2003). *SIM News* 53:254-262. [PRESS FOR ABSTRACT]
25. Study on interaction between T4 phage and *Escherichia coli* B by microcalorimetric method. Guosheng, L., Yi, L., Xiangdong, C., Peng, L., Ping, S., Songsheng, Q. (2003). *Journal of Virological Methods* 112:137-143. [PRESS FOR ABSTRACT]
26. Genetically modified filamentous phage as bactericidal agents: a pilot study. Hagens, S., Blasi, U. (2003). *Letters in Applied Microbiology* 37:318-323. [PRESS FOR ABSTRACT]
27. Identification of an inducible bacteriophage in a virulent strain of *Streptococcus suis* serotype 2. Harel, J., Martinez, G., Nassar, A., Dezfulian, H., Labrie, S. J., Brousseau, R., Moineau, S., Gottschalk, M. (2003). *Infection and Immunity* 71:6104-6108. [PRESS FOR ABSTRACT]
28. Validation of phage T7 biological dosimeter by quantitative polymerase chain reaction using short and long segments of phage T7 DNA. Hegedus, M., Modos, K., Ronto, Gy, Fekete, A. (2003). *Photochemistry and photobiology* 78:213-219. [PRESS FOR ABSTRACT]
29. Fate of physical, chemical, and microbial contaminants in domestic wastewater following treatment by small constructed wetlands. Hench, K. R., Bissonnette, G. K., Sexstone, A. J., Coleman, J. G., Garbutt, K., Skousen, J. G. (2003). *Water Research* 37:921-927. [PRESS FOR ABSTRACT]
30. Bacteriophages with tails: chasing their origins and evolution. Hendrix, R. W., Hatfull, G. F., Smith, M. C. M. (2003). *Research in Microbiology* 154:253-257. [PRESS FOR ABSTRACT]
31. Phage therapy: a reappraisal of bacteriophages as antibiotics. Inal, J. M. (2003). *Archivum Immunologiae et Therapiae Experimentalis* 51:237-244. [PRESS FOR ABSTRACT]
32. A fluoroquinolone induces a novel mitogen-encoding bacteriophage in *Streptococcus canis*. Ingre, K. T., Ren, J., Prescott, J. F. (2003). *Infection and Immunity* 71:3028-3033. [PRESS FOR ABSTRACT]
33. Maintenance of species identity and controlling speciation of bacteria: a new function for restriction/modification systems? Jeltsch, A. (2003). *Gene* 317:13-16. [PRESS FOR ABSTRACT]
34. Microbiological indicators of water quality in the Xochimilco canals, Mexico City. Juarez-Figueroa, L. A., Silva-Sanchez, J., Uribe-Salas, F. J., Cifuentes-Garcia, E. (2003). *Salud publica de Mexico* 45:389-395. [PRESS FOR ABSTRACT]
35. [Bacteriophage therapy: Stalin's forgotten medicine]. Kaulen, H. (2003). *Deutsche medizinische Wochenschrift* 128:307. [NO ABSTRACT]
36. Myoviridae bacteriophages of *Pseudomonas aeruginosa*: a long and complex evolutionary pathway. Krylov, V., Pleteneva, E., Bourkaltseva, M., Shaburova, O., Volckaert, G., Sykilinda, N., Kurochkina, L., Mesyanzhinov, V. (2003). *Research in Microbiology* 154:269-275. [PRESS FOR ABSTRACT]

37. The genome of bacteriophage  $\phi$ KMV, a T7-like virus infecting *Pseudomonas aeruginosa*. Lavigne, R., Burkal'tseva, M. V., Robben, J., Sykilinda, N. N., Kurochkina, L. P., Grymonprez, B., Jonckx, B., Krylov, V. N., Mesyanzhinov, V. V., Volckaert, G. (2003). *Virology* 312:49-59. [\[PRESS FOR ABSTRACT\]](#)
38. Population dynamics and gene transfer in genetically modified bacteria in a model microcosm. Lilley, A. K., Bailey, M. J., Barr, M., Kilshaw, K., Timms-Wilson, T. M., Day, M. J., Norris, S. J., Jones, T. H., Godfray, H. C. J. (2003). *Molecular Ecology* 12:3097-3107. [\[PRESS FOR ABSTRACT\]](#)
39. Characterisation of technologically proficient wild *Lactococcus lactis* strains resistant to phage infection. Madera, C., Garcia, P., Janzen, T., Rodriguez, A., Suarez, J. E. (2003). *International Journal of Food Microbiology* 86:213-222. [\[PRESS FOR ABSTRACT\]](#)
40. Detection of *Escherichia coli* using immunomagnetic separation and bacteriophage amplification coupled with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Madonna, A. J., Van Cuyk, S., Voorhees, K. J. (2003). *Rapid Communications in Mass Spectrometry* 17:257-263. [\[PRESS FOR ABSTRACT\]](#)
41. Genetic diversity and temporal variation in the cyanophage community infecting marine *Synechococcus* species in Rhode Island's coastal waters. Marston, M. F., Sallee, J. L. (2003). *Applied and Environmental Microbiology* 69:4639-4647. [\[PRESS FOR ABSTRACT\]](#)
42. Experimental protection of mice against lethal *Staphylococcus aureus* infection by novel bacteriophage  $\phi$ MR11. Matsuzaki, S., Yasuda, M., Nishikawa, H., Kuroda, M., Ujihara, T., Shuin, T., Shen, Y., Jin, Z., Fujimoto, S., Nasimuzzaman, M. D., Wakiguchi, H., Sugihara, S., Sugiura, T., Koda, S., Muraoka, A., Imai, S. (2003). *The Journal of infectious diseases* 187:613-624. [\[PRESS FOR ABSTRACT\]](#)
43. [Development of cyanobacterial phages at the Institute of Microbiology and Virology of the National Academy of Sciences of Ukraine (History and perspectives)]. Mendzhul, M. I., Lysenko, T. G., Syrchin, S. A. (2003). *Mikrobiolohichnyi zhurnal* 65:133-140. [\[PRESS FOR ABSTRACT\]](#)
44. Bacteriophage and the evolution of epidemic cholera. Miller, J. F. (2003). *Infection and Immunity* 71:2981-2982. [\[NO ABSTRACT\]](#)
45. Bacteriophage ST64B, a genetic mosaic of genes from diverse sources isolated from *Salmonella enterica* serovar Typhimurium DT 64. Mmolawa, P. T., Schmieger, H., Heuzenroeder, M. W. (2003). *Journal of Bacteriology* 185:6481-6485. [\[PRESS FOR ABSTRACT\]](#)
46. Shiga toxin 2-converting bacteriophages associated with clonal variability in *Escherichia coli* O157:H7 strains of human origin isolated from a single outbreak. Muniesa, M., de Simon, M., Prats, G., Ferrer, D., Panella, H., Jofre, J. (2003). *Infection and Immunity* 71:4554-4562. [\[PRESS FOR ABSTRACT\]](#)
47. Experimental bacteriophage-mediated virulence in strains of *Vibrio harveyi*. Munro, J., Oakey, J., Bromage, E., Owens, L. (2003). *Diseases of Aquatic Organisms* 54:187-194. [\[PRESS FOR ABSTRACT\]](#)
48. Concentrations and inactivation of *Ascaris* eggs and pathogen indicator organisms in wastewater stabilization pond sludge. Nelson, K. L. (2003). *Water Science and Technology* 48:89-95. [\[PRESS FOR ABSTRACT\]](#)
49. [Bacteriophage therapy and colleague Martin Arrowsmith]. Nevasaari, K. (2003). *Duodecim; laaketieteellinen aikakauskirja* 119:1367. [\[NO ABSTRACT\]](#)
50. Biology of the temperate *Streptococcus thermophilus* bacteriophage TP-J34 and physical characterization of the phage genome. Neve, H., Freudenberg, W., Diestel-Feddersen, F., Ehlert, R., Heller, K. J. (2003). *Virology* 315:184-194. [\[PRESS FOR ABSTRACT\]](#)
51. Microbial water quality improvement by small scale on-site subsurface wetland treatment. Nokes, R. L., Gerba, C. P., Karpiscak, M. M. (2003). *Journal of Environmental Science and Health Part A Toxic-Hazardous Substances & Environmental Engineering* 38:1849-1855. [\[PRESS FOR ABSTRACT\]](#)
52. Scope of potential bacterial agents of diarrhoea and microbial assessment of quality of river water sources in rural Venda communities in South Africa. Obi, C. L., Potgieter, N., Bessong, P. O., Matsaung, G. (2003). *Water Science and Technology* 47:59-64. [\[PRESS FOR ABSTRACT\]](#)
53. Suppression of leaf feeding and oviposition of phytophagous ladybird beetles (Coleoptera: Coccinellidae) by chitinase gene-transformed phylloplane bacteria and their specific bacteriophages entrapped in alginate gel beads. Otsu, Y., Mori, H., Komuta, K., Shimizu, H., Nogawa, S., Matsuda, Y., Nonomura, T., Sakuratani, Y., Tosa, Y., Mayama, S., Toyoda, H. (2003). *Journal of Economic Entomology* 96:555-563. [\[PRESS FOR ABSTRACT\]](#)
54. Faecal contamination of greywater and associated microbial risks. Ottoson, J., Stenstrom, T. A. (2003). *Water Research* 37:645-655. [\[PRESS FOR ABSTRACT\]](#)
55. Phage evolution: new worlds of genomic diversity. Papke, R. T., Doolittle, W. F. (2003). *Current Biology* 13:R606-R607. [\[PRESS FOR ABSTRACT\]](#)
56. Bacteriophage control of *Pseudomonas plecoglossicida* infection in ayu *Plecoglossus altivelis*. Park, S. C., Nakai, T. (2003). *Diseases of Aquatic Organisms* 53:33-39. [\[PRESS FOR ABSTRACT\]](#)
57. Development of a novel method of lytic phage delivery by use of a bacteriophage P22 site-specific recombination system. Platt, R., Reynolds, D. L., Phillips, G. J. (2003). *FEMS Microbiology Letters* 223:259-265. [\[PRESS FOR](#)

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58. Bacterial debris—an ecological mechanism for coexistence of bacteria and their viruses. Rabinovitch, A., Aviram, I., Zaritsky, A. (2003). *Journal of Theoretical Biology* 224:377-383. [\[PRESS FOR ABSTRACT\]](#)
59. Virus succession observed during an *Emiliania huxleyi* bloom. Schroeder, D., Oke, J., Malin, G., Wilson, W. H. (2003). *Applied and Environmental Microbiology* 69:2484-2490. [\[PRESS FOR ABSTRACT\]](#)
60. Survival of indicator organisms during enrichment on tetrachloroethene. Skramstad, J. D., Hurst, C. J., Novak, P. J. (2003). *Water Environment Research* 75:368-376. [\[PRESS FOR ABSTRACT\]](#)
61. Development of a microplate assay for the detection of single plaque-forming units of bacteriophage  $\Phi$ X174 in crude lysates. Slattery, S. D., Valentine, C. R. (2003). *Environmental and Molecular Mutagenesis* 41:121-125. [\[PRESS FOR ABSTRACT\]](#)
62. Viruses of hyperthermophilic Archaea. Snyder, J. C., Stedman, K., Rice, G., Wiedenheft, B., Spuhler, J., Young, M. J. (2003). *Research in Microbiology* 154:474-482. [\[PRESS FOR ABSTRACT\]](#)
63. Enteric virions and microbial biofilms—a secondary source of public health concern? Storey, M. V., Ashbolt, N. J. (2003). *Water Science and Technology* 48:97-104. [\[PRESS FOR ABSTRACT\]](#)
64. Characterization of a *Vibrio cholerae* phage isolated from the coastal water of Peru. Talledo, M., Rivera, I. N. G., Lipp, E. K., Neale, A., Karaolis, D., Huq, A., Colwell, R. R. (2003). *Environmental microbiology* 5:350-354. [\[PRESS FOR ABSTRACT\]](#)
65. [Transduction of plasmid antibiotic resistance determinants with pseudo-T-even bacteriophages]. Taniashin, V. I., Zimin, A. A., Shliapnikov, M. G., Boronin, A. M. (2003). *Genetika* 39:914-926. [\[PRESS FOR ABSTRACT\]](#)
66. Set a microbe to kill a microbe: drug resistance renews interest in phage therapy. Thacker, P. D. (2003). *Journal of the American Medical Association* 290:3183-3185. [\[PRESS FOR ABSTRACT\]](#)
67. Survival of indicators of bacterial and viral contamination in wastewater subjected to low temperatures and freezing: application to cold climate waste stabilisation ponds. Torrella, F., Lopez, J. P., Banks, C. J. (2003). *Water Science and Technology* 48:105-112. [\[PRESS FOR ABSTRACT\]](#)
68. Calcium hypochlorite as a disinfecting additive for dental stone. Twomey, J. O., Abdelaziz, K. M., Combe, E. C., Anderson, D. L. (2003). *The Journal of prosthetic dentistry* 90:282-288. [\[PRESS FOR ABSTRACT\]](#)
69. The prophage sequences of *Lactobacillus plantarum* strain WCFS1. Ventura, M., Canchaya, C., Kleerebezem, M., de Vos, W. M., Siezen, R. J., Brussow, H. (2003). *Virology* 316:245-255. [\[PRESS FOR ABSTRACT\]](#)
70. pGIL01, a linear tectiviral plasmid prophage originating from *Bacillus thuringiensis* serovar *israelensis*. Verheust, C., Jensen, G., Mahillon, J. (2003). *Microbiology (Reading England)* 149:2083-2092. [\[PRESS FOR ABSTRACT\]](#)
71. Selection of bacteriophage-resistant mutants of *Streptococcus thermophilus*. Viscardi, M., Capparelli, R., Di Matteo, R., Carminati, D., Giraffa, G., Iannelli, D. (2003). *Journal of Microbiological Methods* 55:109-119. [\[PRESS FOR ABSTRACT\]](#)
72. Risk management in biological evolution. Wagner, A. (2003). *Journal of Theoretical Biology* 225:45-57. [\[PRESS FOR ABSTRACT\]](#)
73. Efficacy and durability of *Bacillus anthracis* bacteriophages used against spores. Walter, M. H. (2003). *Journal of Environmental Health* 66:9-15, 24. [\[PRESS FOR ABSTRACT\]](#)
74. Suppression of *Salmonella* growth by wild-type and large-plaque variants of bacteriophage Felix O1 in liquid culture and on chicken frankfurters. Whichard, J. M., Sriranganathan, N., Pierson, F. W. (2003). *Journal of Food Protection* 66:220-225. [\[PRESS FOR ABSTRACT\]](#)
75. Wide geographic distribution of bacteriophages that lyse the same indigenous freshwater isolate (*Sphingomonas* sp. strain B18). Wolf, A., Wiese, J., Jost, G., Witzel, K. P. (2003). *Applied and Environmental Microbiology* 69:2395-2398. [\[PRESS FOR ABSTRACT\]](#)
76. Sorption of MS2 bacteriophage to layered double hydroxides: effects of reaction time, pH, and competing anions. You, Y., Vance, G. F., Sparks, D. L., Zhuang, J., Jin, Y. (2003). *Journal of Environmental Quality* 32:2046-2053. [\[PRESS FOR ABSTRACT\]](#)
77. Genome of *Xanthomonas oryzae* bacteriophage Xp10: an odd T-odd phage. Yuzenkova, J., Nechaev, S., Berlin, J., Rogulja, D., Kuznedelov, K., Inman, R., Mushegian, A., Severinov, K. (2003). *Journal of Molecular Biology* 330:735-748. [\[PRESS FOR ABSTRACT\]](#)
78. Virus retention and transport as influenced by different forms of soil organic matter. Zhuang, J., Jin, Y. (2003). *Journal of Environmental Quality* 32:816-823. [\[PRESS FOR ABSTRACT\]](#)
79. Autolysis and autoaggregation in *Pseudomonas aeruginosa* colony morphology mutants. D'Argenio, D. A., Calfee, M. W., Rainey, P. B., Pesci, E. C. (2002). *Journal of Bacteriology* 184:6481-6489. [\[PRESS FOR ABSTRACT\]](#)
80. Uneven growth and different susceptibility to viruses among bacteria increase estimates of virus production in the

81. Flow cytometric analysis of an *Emiliania huxleyi* bloom terminated by viral infection. Jacquet, S., Heldal, M., Iglesias-Rodriguez, D., Larsen, A., Wilson, W. H. (2002). *Aquatic Microbial Ecology* 27:111-124. [\[PRESS FOR ABSTRACT\]](#)
82. Bacteriophages isolated from activated sludge process and their polyvalency. Kahn, M. A., Satoh, H., Katayama, H., Kurisu, F., Mino, T. (2002). *Water Research* 36:3364-3370. [\[PRESS FOR ABSTRACT\]](#)
83. [The resistance conferred by the R/M system LlaBIII against bacteriophages]. Kong, J., Josephsen, J., Ma, G. R. (2002). *Acta Microbiologica Sinica* 42:246-250. [\[PRESS FOR ABSTRACT\]](#)
84. Marine phage genomics. Paul, J. H., Sullivan, M. B., Segall, A. M., Rohwer, F. (2002). *Comparative Biochemistry and Physiology part B Biochemistry & Molecular Biology* 133:463-476. [\[PRESS FOR ABSTRACT\]](#)
85. Coccolithovirus (*Phycodnaviridae*): characterisation of a new large dsDNA algal virus that infects *Emiliania huxleyi*. Schroeder, D., Oke, J., Malin, G., Wilson, W. H. (2002). *Archives of Virology* 147:1685-1698. [\[PRESS FOR ABSTRACT\]](#)
86. Estimation of biologically damaging UV levels in marine surface waters with DNA and viral dosimeters. Wilhelm, S. W., Jeffrey, W. H., Suttle, C. A., Mitchell, D. L. (2002). *Photochemistry and photobiology* 76:268-273. [\[PRESS FOR ABSTRACT\]](#)
87. Virus dynamics in a coccolithophore-dominated bloom in the North Sea. Wilson, W. H., Tarran, G., Zubkoy, M. V. (2002). *Deep Sea Research Part II: Tropical Studies in Oceanography* 49:2951-2963. [\[PRESS FOR ABSTRACT\]](#)
88. Inhibition of spontaneous induction of lambdoid prophages in *Escherichia coli* cultures: simple procedures with possible biotechnological applications. Czyz, A., Los, M., Wrobel, B., Wegrzyn, G. (2001). *BMC biotechnology [electronic resource]* 1:1. [\[PRESS FOR ABSTRACT\]](#)

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## New Publications with Abstracts

For your convenience, a list of new publications without associated abstracts (but with links to abstracts) is found [above](#). The list presented below is identical to the [above list](#) except that abstracts are included.

1. **Genetic details, optimization, and phage life histories.** Bull, J. J., Pfening, D. W., Wang, I.-W. (2004). *Trends in Ecology and Evolution* 19:76-82. Optimality models assume that phenotypes evolve by natural selection largely independently of underlying genetic mechanisms. This neglect of genetic mechanisms is considered an advantage by some evolutionary biologists but a fatal flaw by others. The controversy has gone unresolved, in part, from a lack of complex phenotypes that meet optimality criteria and for which the underlying genetic mechanisms are known. Here, we look at both perspectives for lysis time in bacteriophages. We find that the basic assumptions of the optimality model are compatible with the genetic details, but the optimality model is limited in its ability to accommodate lysis time plasticity because the mechanistic underpinnings of plasticity are poorly known.
2. **Complete sequence and evolutionary genomic analysis of the *Pseudomonas aeruginosa* transposable bacteriophage D3112.** Wang, P. W., Chu, L., Guttman, D. S. (2004). *Journal of Bacteriology* 186:400-410. Bacteriophage D3112 represents one of two distinct groups of transposable phage found in the clinically relevant, opportunistic pathogen *Pseudomonas aeruginosa*. To further our understanding of transposable phage in *P. aeruginosa*, we have sequenced the complete genome of D3112. The genome is 37,611 bp, with an overall G+C content of 65%. We have identified 53 potential open reading frames, including three genes (the c repressor gene and early genes A and B) that have been previously characterized and sequenced. The organization of the putative coding regions corresponds to published genetic and transcriptional maps and is very similar to that of enterobacteriophage Mu. In contrast, the International Committee on Taxonomy of Viruses has classified D3112 as a  $\lambda$ -like phage on the basis of its morphology. Similarity-based analyses identified 27 open reading frames with significant matches to proteins in the NCBI databases. Forty-eight percent of these were similar to Mu-like phage and prophage sequences, including proteins responsible for transposition, transcriptional regulation, virion morphogenesis, and capsid formation. The tail proteins were highly similar to prophage sequences in *Escherichia coli* and phage Phi12 from *Staphylococcus aureus*, while proteins at the right end were highly similar to proteins in *Xylella fastidiosa*. We performed phylogenetic analyses to understand the evolutionary relationships of D3112 with respect to Mu-like versus  $\lambda$ -like bacteriophages. Different results were obtained from similarity-based versus phylogenetic analyses in some instances. Overall, our findings reveal a highly mosaic structure and suggest that extensive horizontal exchange of genetic material played an important role in the evolution of D3112.
3. **Experimental examination of bacteriophage latent-period evolution as a response to bacterial availability.** Abedon, S. T., Hyman, P., Thomas, C. (2003). *Applied and Environmental Microbiology* 69:7499-7506. For obligately lytic bacteriophage (phage) a trade-off exists between fecundity (burst size) and latent period (a component of generation time). This trade-off occurs because release of phage progeny from infected bacteria coincides with destruction of the machinery necessary to produce more phage progeny. Here we employ phage mutants to explore issues of phage latent-period evolution as a function of the density of phage-susceptible bacteria.

Theory suggests that higher bacterial densities should select for shorter phase latent periods. Consistently, we have found that higher host densities ( $\geq 10^7$  bacteria/ml) can enrich stocks of phage RB69 for variants that display shorter latent periods than the wild type. One such variant, dubbed *sta5*, displays a latent period that is ~70 to 80% of that of the wild type—which is nearly as short as the RB69 eclipse period—and which has a corresponding burst size that is ~30% of that of the wild type. We show that at higher host densities ( $\geq 10^7$  bacteria/ml) the *sta5* phage can outcompete the RB69 wild type, though only under conditions of direct (same-culture) competition. We interpret this advantage as corresponding to slightly faster *sta5* population growth, resulting in multifold increases in mutant frequency during same-culture growth. The *sta5* advantage is lost, however, given indirect (different-culture) competition between the wild type and mutant or given same-culture competition but at lower densities of phage-susceptible bacteria ( $< 10^6$  bacteria/ml). From these observations we suggest that phage displaying very short latent periods may be viewed as specialists for propagation when bacteria within cultures are highly prevalent and transmission between cultures is easily accomplished.

4. **Survival of F-specific RNA coliphage, feline calicivirus, and *Escherichia coli* in water: a comparative study.** Allwood, P. B., Malik, Y. S., Hedberg, C. W., Goyal, S. M. (2003). *Applied and Environmental Microbiology* 69:5707-5710. The relationship between the survival of enteric viral pathogens and their indicators (coliform bacteria and coliphages) is not well understood. We compared the survival rates of feline calicivirus (FCV), *Escherichia coli*, and a male-specific RNA coliphage MS2 at 4, 25, and 37°C for up to 28 days in dechlorinated water. The survival rates of *E. coli* and FCV, a surrogate of noroviruses (NV), had a high degree of correlation at 4 and 25°C, while MS2 phage survived significantly longer ( $P < 0.05$ ) at these two temperatures. At 37°C, the survival rates for all three organisms were highly correlated. Decimal reduction values indicating the number of days needed for 90% reduction in titer (D values) decreased for all three organisms as storage temperatures increased. FCV had the shortest D value among all three organisms at all temperatures investigated. These findings indicate that F-specific RNA phages may be useful indicators of NV in the environment.
5. **Application of host-specific bacteriophages to the surface of chicken skin leads to a reduction in recovery of *Campylobacter jejuni*.** Atterbury, R. J., Connerton, P. L., Dodd, C. E. R., Rees, C. E. D., Connerton, I. F. (2003). *Applied and Environmental Microbiology* 69:6302-6306. Retail poultry products are widely purported as the major infection vehicle for human campylobacteriosis. Numerous intervention strategies have sought to reduce *Campylobacter* contamination on broiler carcasses in the abattoir. This study reports the efficacy of bacteriophage in reducing the number of recoverable *Campylobacter jejuni* cells on artificially contaminated chicken skin.
6. **Prophage induction and expression of prophage-encoded virulence factors in group A *Streptococcus* serotype M3 strain MGAS315.** Banks, D. J., Lei, B., Musser, J. M. (2003). *Infection and Immunity* 71:7079-7086. The genome of the highly virulent group A *Streptococcus* (GAS) serotype M3 strain MGAS315 has six prophages that encode six proven or putative virulence factors. We examined prophage induction and expression of prophage-encoded virulence factors by this strain under in vitro conditions inferred to approximate in vivo conditions. Coculture of strain MGAS315 with Detroit 562 (D562) human epithelial pharyngeal cells induced the prophage encoding streptococcal pyrogenic exotoxin K (SpeK) and extracellular phospholipase A(2) (Sla) and the prophage encoding streptodornase (Sdn). Increased gene copy numbers after induction correlated with increased *speK*, *sla*, and *sdn* transcript levels. Although *speK* and *sla* are located contiguously in prophage Phi315.4, these genes were transcribed independently. Whereas production of immunoreactive SpeK was either absent or minimal during coculture of GAS with D562 cells, production of immunoreactive Sla increased substantially. In contrast, despite a lack of induction of the prophage encoding *speA* during coculture of GAS with D562 cells, the *speA* transcript level and production of immunoreactive streptococcal pyrogenic exotoxin A (SpeA) increased. Exposure of strain MGAS315 to hydrogen peroxide, an oxidative stressor, induced the prophage encoding mitogenic factor 4 (MF4), and there was a concomitant increase in the *mf4* transcript. All prophages of strain MGAS315 that encode virulence factors were induced during culture with mitomycin C, a DNA-damaging agent. However, the virulence factor gene transcript levels and production of the encoded proteins decreased after mitomycin C treatment. Taken together, the results indicate that a complex relationship exists among environmental culture conditions, prophage induction, and production of prophage-encoded virulence factors.
7. **Incidence of enteric viruses in groundwater from household wells in Wisconsin.** Borchardt, M. A., Bertz, P. D., Spencer, S. K., Battigelli, D. A. (2003). *Applied and Environmental Microbiology* 69:1172-1180. Recent studies on the contamination of groundwater with human enteric viruses have focused on public water systems, whereas little is known about the occurrence of viruses in private household wells. The objective of the present study was to estimate the incidence of viruses in Wisconsin household wells located near seepage land application sites or in rural subdivisions served by septic systems. Fifty wells in seven hydrogeologic districts were sampled four times over a year, once each season. Reverse transcriptase PCR (RT-PCR), followed by Southern hybridization, was used to detect enteroviruses, rotavirus, hepatitis A virus (HAV), and Norwalk-like viruses (NLVs). In addition, cell culture was used to detect culturable enteroviruses. Companion water samples were collected for total coliforms, *Escherichia coli*, fecal enterococci, F-specific RNA coliphages, nitrate, and chloride analyses. Among the 50 wells, four (8%) were positive for viruses by RT-PCR. Three wells were positive for HAV, and the fourth well was positive for both rotavirus and NLV in one sample and an enterovirus in another sample. Contamination was transient, since none of the wells was virus positive for two sequential samples. Culturable enteroviruses were not detected in any of the wells. Water quality indicators were not statistically associated with virus occurrence, although some concordance was noted for chloride. The present study is the first in the United States to systematically monitor private household wells for virus contamination and, combined with data for public wells, provides further insight on the extent of groundwater contamination with human enteric viruses.
8. **Specific identification of certain probiotic *Lactobacillus rhamnosus* strains with PCR primers based on phage-related sequences.** Brandt, K., Alatossava, T. (2003). *International Journal of Food Microbiology* 84:189-196. PCR primers derived from *Lactobacillus rhamnosus* phage Lc-Nu genome were used to screen the presence of phage-related sequences in *Lb. rhamnosus* strains. Several primer pairs derived from structural and replication gene regions of phage Lc-Nu amplified PCR products of expected sizes from bacterial strains revealing phage-related sequences in 10 of 11 *Lb. rhamnosus* strains. Strain-specific PCR primers for three probiotic *Lb. rhamnosus* strains were derived from these phage-related sequences for identification and detection purposes. Specificity of these primers was tested against 11 *Lb. rhamnosus* strains and over 40 other bacterial strains.

9. **Phage as agents of lateral gene transfer. Canchaya, C., Fournous, G., Chibani-Chennoufi, S., Dillmann, M. L., Brusow, H. (2003). *Current Opinion in Microbiology* 6:417-424.** When establishing lysogeny, temperate phages integrate their genome as a prophage into the bacterial chromosome. Prophages thus constitute in many bacteria a substantial part of laterally acquired DNA. Some prophages contribute lysogenic conversion genes that are of selective advantage to the bacterial host. Occasionally, phages are also involved in the lateral transfer of other mobile DNA elements or bacterial DNA. Recent advances in the field of genomics have revealed a major impact by phages on bacterial chromosome evolution.
10. **Effect of soil properties on saturated and unsaturated virus transport through columns. Chu, Y., Jin, Y., Baumann, T., Yates, M. V. (2003). *Journal of Environmental Quality* 32:2017-2025.** Viruses from contaminant sources can be transported through porous media to drinking water wells. The objective of this study was to investigate inactivation and sorption of viruses during saturated and unsaturated transport in different soils. Bacteriophages  $\phi$ X174 and MS-2, and Br- tracer in a phosphate-buffered saline solution were introduced into saturated and unsaturated soil columns as a step function under constant flow rate and hydraulic conditions. Results showed that significantly greater virus removal occurred in the unsaturated columns than in the saturated columns in the two soils containing high metal oxides content. However, the increase in virus retention under unsaturated conditions was not significant in two other soils having high phosphorus and calcium contents and high pH, and in another soil with high organic matter content. The results imply that the extent of water content effect on inactivation and sorption of viruses can range from significant to minimal depending on the properties of the transport medium. We found that the presence of in situ metal oxides was a significant factor responsible for virus sorption and inactivation. Therefore, soils with high metal oxides content may have the potential to be used as hydrological barriers in preventing microbial contamination in the subsurface environments. We also found that the water content effect on virus removal and inactivation strongly depended on solid properties of the testing medium.
11. **Viruses and marine pollution. Danovaro, R., Armeni, M., Corinaldesi, C., Mei, M. L. (2003). *Marine Pollution Bulletin* 46:301-304.** This short review summarises the present knowledge on pollutant impacts on marine viruses, virus-host systems and their potential ecological implications. Excess nutrients from sewage and river effluents are a primary cause of marine eutrophication and mucilage formation, often related to the development of large viral assemblages. At the same time, hydrocarbons, polychlorinated biphenyl and pesticides alter ecosystem functioning and can determinate changes in the virus-host interactions, thus increasing the potential of viral infection. All these pollutants might have synergistic effects on the virus-host system and are able to induce prophage, thus increasing the impact of viruses on marine ecosystems.
12. **Sunscreen products increase virus production through prophage induction in marine bacterioplankton. Danovaro, R., Corinaldesi, C. (2003). *Microbial Ecology* 45:109-118.** Classical pollutants (e.g., hydrocarbon, pesticides) have been recently recognized to induce lytic cycle in lysogenic bacteria, but information on micro-pollutants is almost completely lacking. We investigated the effects of cosmetic sun products (sunscreen and solar oil) on viral abundance and bacterial activity. We found that both sunscreen and solar oil acted as pollutants, inducing viral development and controlling bacterial abundance and production, thus leading to an increase of the virus to bacterium ratio. Short-term experiments revealed that sunscreen supplementation induced the lytic cycle in a large fraction of total bacterial abundance (13-24% of bacteria, at low and high concentrations, respectively), whereas solar oil had a lower impact (6-9%). A synchronized development of the phage-host system was observed only after sunscreen addition. The addition of sunscreen, even at low concentrations, had a significant impact on all enzymatic activities (aminopeptidase, glucosidase, and phosphatase), which increased significantly. However, when enzymatic activities were normalized per cell, a selective enhancement was observed for certain enzymes (e.g., aminopeptidase) and inhibition for others (e.g., glucosidase). These results indicate that sunscreen products can modify C, N, and P biogeochemical cycling in seawater and increase virus abundance through prophage induction in marine bacterioplankton.
13. **The source of laterally transferred genes in bacterial genomes. Daubin, V., Lerat, E., Perriere, G. (2003). *Genome biology* 4:R57.** BACKGROUND: Laterally transferred genes have often been identified on the basis of compositional features that distinguish them from ancestral genes in the genome. These genes are usually A+T-rich, arguing either that there is a bias towards acquiring genes from donor organisms having low G+C contents or that genes acquired from organisms of similar genomic base compositions go undetected in these analyses. RESULTS: By examining the genome contents of closely related, fully sequenced bacteria, we uncovered genes confined to a single genome and examined the sequence features of these acquired genes. The analysis shows that few transfer events are overlooked by compositional analyses. Most observed lateral gene transfers do not correspond to free exchange of regular genes among bacterial genomes, but more probably represent the constituents of phages or other selfish elements. CONCLUSIONS: Although bacteria tend to acquire large amounts of DNA, the origin of these genes remains obscure. We have shown that contrary to what is often supposed, their composition cannot be explained by a previous genomic context. In contrast, these genes fit the description of recently described genes in lambdoid phages, named 'morons'. Therefore, results from genome content and compositional approaches to detect lateral transfers should not be cited as evidence for genetic exchange between distantly related bacteria.
14. **Occurrence of coliphages in urban stormwater and their fate in stormwater management systems. Davies, C. M., Yousefi, Z., Bavor, H. J. (2003). *Letters in Applied Microbiology* 37:299-303.** AIMS: To investigate the occurrence of coliphages in, and their removal from, urban stormwater. METHODS AND RESULTS: Inflow and outflow concentrations of somatic and f-specific RNA coliphages to two stormwater treatment systems were determined on 21 occasions over a period of 5 months. Somatic coliphages were detected in 19 (90%) of the constructed wetland inlet samples, 13 (62%) of the pond inlet samples, and less frequently at the outlets of the two systems. F-specific RNA coliphages were detected at the inlets but only occasionally at the pond outlet. Somatic coliphages were found to attach preferentially to particles <5 microm in size and persisted in the sediments of the two systems. CONCLUSIONS: Treatment systems providing conditions that are conducive to the settlement of fine particles may effectively remove sediment-bound coliphages and, therefore, possibly enteric viruses from stormwater. SIGNIFICANCE AND IMPACT OF THE STUDY: The results will aid the design of systems for effective removal of viral contaminants from urban stormwater.
15. **Filamentous phages linked to virulence of *Vibrio cholerae*. Davis, B. M., Waldor, M. K. (2003). *Current***

*Opinion Microbiology 6:35-42.* The pathogenicity of *Vibrio cholerae* depends on its production of two key virulence factors: the toxin co-regulated pilus (TCP), a colonization factor, and cholera toxin, an exotoxin. Genes encoding both virulence factors were introduced into *V. cholerae* by horizontal gene transfer. The toxin genes are contained within the genome of CTX $\phi$ , an integrated filamentous phage identified in 1996. In the past few years, it has been shown that CTX $\phi$  relies on novel processes for phage DNA integration, replication and secretion. In addition, expression of CTX $\phi$  genes—including the toxin genes—and transmission of CTX $\phi$  were recently found to be promoted by the antirepressor RstC, which is encoded within RS1, a newly described satellite phage of CTX $\phi$ . The genetic island that encodes TCP has also been described as a filamentous phage; however, these sequences are unlike the genome of any previously characterized filamentous phage.

16. **Identification of new phages to type *Staphylococcus aureus* strains and comparison with a genotypic method.** de Gialluly, C., Loulergue, J., Bruant, G., Mereghetti, L., Massuard, S., van der Mee, N., Audurier, A., Quentin, R. (2003). *The Journal of hospital infection* 55:61-67. The aim of this study was to optimize the epidemiological monitoring of strains of *Staphylococcus aureus*, a major cause of hospital-acquired infections. From September to December 1998 47 *S. aureus* strains isolated from swabs taken from orthopaedic and trauma patients were studied. Thirty-five isolates were sensitive to methicillin (MSSA) and 12 were methicillin-resistant (MRSA). Ten of the 47 isolates could not be phage-typed using the international set of typing phages: five of these isolates were MSSA and five were MRSA. These MRSA isolates, which were also not typeable by the phages currently recommended for phage-typing MRSA, were lysed by locally isolated experimental phages 584 and 1814. Phage 1814 lysed the gentamicin-resistant MRSA and phage 584 acted on the gentamicin-sensitive MRSA. Both new phages were inactive against the methicillin-sensitive isolates. Cloning of certain isolates was confirmed by macrorestriction genomic profiles obtained by pulsed-field gel electrophoresis analysis (PFGE). The results showed good discriminatory ability of antibiotic-resistance pattern phenotyping and phage-typing when the phages used were adapted to epidemic-associated MRSA strains
17. **The diversity and evolution of the T4-type bacteriophages.** Desplats, C., Krisch, H. M. (2003). *Research in Microbiology* 154:259-267. Recent studies suggest that viruses are the most numerous entities in the biosphere; bacteriophages, the viruses that infect Eubacteria and Archaea, constitute a substantial fraction of this population. In spite of their ubiquity, the vast majority of phages in the environment have never been studied and nothing is known about them. For the last 10 years our research has focused on an extremely widespread group of phages, the T4-type. It has now become evident that phage T4 has a myriad of relatives in nature that differ significantly in their host range. The genomes of all these phages have homology to the T4 genes that determine virion morphology. Although phylogenetically related, these T4-type phages can be subdivided into four groups that are increasingly distant from T4: the T-evens, the pseudo T-evens, the schizo T-evens and the exo T-evens. Genomic comparisons between the various T4-type phages and T4 indicate that these genomes share homology not only for virion structural components but also for most of the essential genes involved in the T4 life cycle. This suggests that horizontal transmission of the genetic information may have played a less general role in the evolution of these phages than has been supposed. Nevertheless, we have identified several regions of the T4-type genome, such as the segment containing the tail fiber genes that exhibit evidence of extensive modular shuffling during evolution. The T4-type genomes appear to be a mosaic containing a large and fixed group of essential genes as well as highly variable set of non-essential genes. These non-essential genes are probably important for the adaptation of these phages to their particular life-style. Furthermore, swapping autonomous domains within the essential proteins may slightly modify their function(s) and contribute to the adaptive ability of the T4-type phage family. Regulatory sequences also display considerable evolutionary plasticity and this too may facilitate the adaptation of phage gene expression to new environments and stresses.
18. **Usefulness of different groups of bacteriophages as model micro-organisms for evaluating chlorination.** Duran, A. E., Muniesa, M., Moce-Llivina, L., Campos, C., Jofre, J., Lucena, F. (2003). *Journal of Applied Microbiology* 95:29-37. **AIMS:** To assess the usefulness of bacterial and viral indicators in chlorination processes and to collect quantitative information necessary for risk assessment analysis in water disinfection processes based on chlorination. **METHODS AND RESULTS:** Naturally occurring bacterial indicators, bacteriophages and enteroviruses were determined to evaluate the effect of chlorination in groundwater and secondary sewage effluents. Additionally, the effect of chlorinating on selected bacteriophages, enteroviruses and *Escherichia coli* was also tested in spiked samples of bottled water and sewage effluents. Results indicate that chlorination inactivates more efficiently bacteria than phages and enteroviruses. Among the human viruses, phages infecting *Bacteroides fragilis* and selected somatic coliphages belonging to the Siphoviridae family were the most persistent to chlorination. **CONCLUSIONS:** The three groups of bacteriophages studied were all more resistant to chlorination than bacteria and some of the phages were more resistant than enteroviruses. Results presented here indicate that it is very risky to generalize from information obtained with inactivation experiments done with single isolates of any phage or virus. If possible, inactivation studies should be done with naturally occurring populations. Phages offer a good opportunity for studying naturally occurring populations. Thus, the bacteriophages offer a range of resistance to chlorination that may represent most of the viruses that can be found in water. **SIGNIFICANCE AND IMPACT OF THE STUDY:** Data reported in this study support the inclusion of bacteriophages as additional indicators of the efficiency of water chlorination processes and water quality.
19. **Phage conversion of exfoliative toxin A in *Staphylococcus aureus* isolated from cows with mastitis.** Endo, Y., Yamada, T., Matsunaga, K., Hayakawa, Y., Kaidoh, T., Takeuchi, S. (2003). *Veterinary Microbiology* 96:81-90. An exfoliative toxin produced by *Staphylococcus aureus* is the causative agent of staphylococcal scalded-skin syndrome (SSSS) in young children. Recently, we reported that only few isolates of *S. aureus* from bovine mastitis contained the eta gene encoding exfoliative toxin A (ETA) and produced ETA in vitro. In this study, we isolated temperate phages from two ETA-positive bovine isolates of *S. aureus* by treatment with mitomycin C. Polymerase chain reaction (PCR) assay of the phage genomes suggested that the temperate phages carried the structural gene for ETA. Moreover, the nucleotide sequence analysis of the PCR products revealed that the eta gene was located very close to an amidase gene on the phage genomes. The nucleotide sequence for the amidase gene of the bovine phage (bovine phi ETA) differed at nine positions from that of the amidase gene of phi ETA from a human isolate reported by Yamaguchi et al. [Mol. Microbiol. 38 (2000) 694], suggesting that eta-converting phages are heterogeneous. Bovine phi ETA had a head with a hexagonal outline and a non-contractile and flexible tail. Bovine phi ETA was able to lysogenize ETA-negative bovine isolates of *S. aureus*, and the lysogenized *S. aureus*



isolates had the ability to produce ETA. These results suggest the possibility of horizontal transmission of the eta gene by temperate bacteriophages among bovine isolates of *S. aureus*.

20. **Direct estimates of the contribution of viral lysis and microzooplankton grazing to the decline of a *Micromonas* spp. population.** Evans, C., Archer, S. D., Jacquet, S., Wilson, W. H. (2003). *Aquatic Microbial Ecology* **30:207-219**. During a mesocosm study in Raunefjorden, Norway, a *Micromonas* spp. population, initially showing exponential net growth, dramatically declined after Day 4 of the experiment. Using a modification of the dilution approach originally developed to quantify grazing by microzooplankton on phytoplankton, it was possible to partition the mortality of *Micromonas* spp. between grazing and viral lysis on Days 5, 6 and 7 during the population decline. Parallel dilution experiments were carried out in which 0.2  $\mu\text{m}$ - and 10 kDa-filtered water was used as the diluents. In this way, gradients of grazing pressure (0.2  $\mu\text{m}$  series) and grazing pressure + viral concentration (10 kDa series) were produced. Model 1 linear regression of the fraction of whole water versus the apparent growth rate of chlorophyll *a* and *Micromonas* spp. provided an estimate of mortality in the 0.2  $\mu\text{m}$  and 10 kDa dilution series. On Days 5, 6 and 7, the slopes of the linear regressions of 0.2  $\mu\text{m}$  and 10 kDa dilution series were significantly different at  $p = 0.083, 0.001$  and  $0.093$  respectively. From the differences in slope between the series, estimates of viral mortality amounted to a turnover rate of the *Micromonas* spp. standing stocks of 10, 25 and 9%  $\text{d}^{-1}$ . This compares to a turnover rate by the microzooplankton of 48, 26 and 23%  $\text{d}^{-1}$ . On all 3 d the combined viral lysis and grazing mortality exceeded estimates of the potential production of *Micromonas* spp., in part accounting for the population decline. This study demonstrates that the dilution approach can be adapted to directly determine virus-induced mortality rates of specific phytoplankton. However, further work is required to determine how the specificity of viral infection and variety of viral infection cycles affect the results of this modified dilution approach when applied to other phytoplankton taxa and communities.
21. **Host range of chlamydiaphages  $\phi$ CPAR39 and Chp3.** Everson, J. S., Garner, S. A., Lambden, P. R., Fane, B. A., Clarke, I. N. (2003). *Journal of Bacteriology* **185:6490-6492**. The host range of  $\phi$ CPAR39 is limited to four Chlamydomonada species: *C. abortus*, *C. caviae*, *C. pecorum*, and *C. pneumoniae*. Chp3 (a newly discovered bacteriophage isolated from *C. pecorum*) shares three of these hosts (*C. abortus*, *C. caviae*, and *C. pecorum*) but can additionally infect *Chlamydomonada felis*. The ability to support replication was directly correlated with the binding properties of the respective bacteriophages with their host species. Binding studies also show that  $\phi$ CPAR39 and Chp3 use different host receptors to infect the same host cells: cell binding is sensitive to proteinase K treatment, confirming that the chlamydiaphage receptors are proteinaceous in nature.
22. **Viral influence on aquatic bacterial communities.** Fuhrman, J. A., Schwalbach, M. (2003). *The Biological Bulletin* **204:192-195**. Bacterial viruses, or bacteriophages, have numerous roles in marine systems. Although they are now considered important agents of mortality of bacteria, a second possible role of regulating bacterial community composition is less well known. The effect on community composition derives from the presumed species-specificity and density-dependence of infection. Although models have described the "kill the winner" hypothesis of such control, there are few observational or experimental demonstrations of this effect in complex natural communities. We report here on some experiments that demonstrate that viruses can influence community composition in natural marine communities. Although the effect is subtle over the time frame suitable for field experiments (days), the cumulative effect over months or years would be substantial. Other virus roles, such as in genetic exchange or microbial evolution, have the potential to be extremely important, but we know very little about them.
23. **Removal of *Encephalitozoon intestinalis*, calicivirus, and coliphages by conventional drinking water treatment.** Gerba, C. P., Riley, K. R., Nwachuku, N., Ryu, H., Abbaszadegan, M. (2003). *Journal of Environmental Science and Health Part A Toxic-Hazardous Substances & Environmental Engineering* **38:1259-1268**. The removal of the Microsporidia, *Encephalitozoon intestinalis*, feline calicivirus and coliphages MS-2, PRD-1, and Fr were evaluated during conventional drinking water treatment in a pilot plant. The treatment consisted of coagulation, sedimentation, and mixed media filtration. Fr coliphage was removed the most (3.21 log), followed by feline calicivirus (3.05 log), *E. coli* (2.67 log), *E. intestinalis* (2.47 log), MS-2 (2.51 log), and PRD-1 (1.85 log). With the exception of PRD-1 the greatest removal of the viruses occurred during the flocculation step of the water treatment process.
24. **Bacteriophage biocontrol and bioprocessing: application of phage therapy to industry.** Goodridge, L., Abedon, S. T. (2003). *SIM News* **53:254-262**. Here we take a slightly different tack from the mostly clinical considerations of phage therapy, emphasizing instead the role of phages as a means of selectively reducing bacterial loads in nonclinical settings. Since the phrase phage *therapy* carries a connotation of medical doctors administering phages as living drugs to suffering patients, we instead employ the alliterations *bacteriophage biocontrol* and *bacteriophage bioprocessing* to describe, as we review here, the more generalized application of phages as everything from biocontrol agents on the farm to the bioprocessing of certain foods. We also provide a primer on phage-based methods of bacterial diagnosis.
25. **Study on interaction between T4 phage and *Escherichia coli* B by microcalorimetric method.** Guosheng, L., Yi, L., Xiangdong, C., Peng, L., Ping, S., Songsheng, Q. (2003). *Journal of Virological Methods* **112:137-143**. The process that T4 phages multiply in host cells of *Escherichia coli* B was determined using LKB-2277 Bioactivity Monitor by means of stopped-flow method, and the growth was measured turbidometrically at the same time at 37°C. By analyzing thermo-curves, quantitative parameters could be obtained to characterize the interactions of host cells and phages. The parameters such as  $k(a)$ ,  $P(\text{max})$ ,  $G$  etc. change regularly with the decrease of multiplicity of infection (MOI) value. Infection-lysis equations were fitted and the lytic rate constant  $k(L)$  was obtained. The results show that the metabolic activity of infected cells is more intensive than that of normal cells. The phenomenon of lysis inhibition (LIN) was first detected with the microcalorimetric method, and the mechanism is discussed.
26. **Genetically modified filamentous phage as bactericidal agents: a pilot study.** Hagens, S., Blasi, U. (2003). *Letters in Applied Microbiology* **37:318-323**. AIMS: To evaluate the ability of a filamentous phage encoding lethal proteins to kill bacteria without host-cell lysis. METHODS AND RESULTS: Bacterial survival was determined after

infection of a growing *Escherichia coli* culture with phage M13 encoding either the restriction endonuclease BglII gene or modified phage  $\lambda$  S holin genes. The genetically engineered phage exerted a high killing efficiency while leaving the cells structurally intact. When compared with a lytic phage, the release of endotoxin was minimized after infection with the genetically modified phages. **CONCLUSIONS:** Genetically engineered phage can be used for efficient killing, concomitantly minimizing endotoxin release. **SIGNIFICANCE AND IMPACT OF THE STUDY:** This feasibility study provides a possible strategy for the use of genetically engineered phage as bactericidal agents by optimizing the advantages and minimizing potential risks such as release of pyrogenic cell wall components.

27. **Identification of an inducible bacteriophage in a virulent strain of *Streptococcus suis* serotype 2.** Harel, J., Martinez, G., Nassar, A., Dezfulian, H., Labrie, S. J., Brousseau, R., Moineau, S., Gottschalk, M. (2003). *Infection and Immunity* 71:6104-6108. *Streptococcus suis* infection is considered to be a major problem in the swine industry worldwide. Most virulent Canadian isolates of *S. suis* serotype 2 do not produce the known virulence markers for this pathogen. PCR-based subtraction hybridization was adapted to isolate unique DNA sequences which were specific to virulent strains of *S. suis* isolated in Canada. Analysis of some subtracted DNA clones revealed significant homology with bacteriophages of gram-positive bacteria. An inducible phage (named Ss1) was observed in *S. suis* following the incubation of the virulent strain 89-999 with mitomycin C. Phage Ss1 has a long noncontractile tail and a small isometric nucleocapsid and is a member of the Siphoviridae family. Ss1 phage DNA appears to be present in most Canadian *S. suis* strains tested in this study, which were isolated from diseased pigs or had proven virulence in mouse or pig models. To our knowledge, this is the first report of the isolation of a phage in *S. suis*.
28. **Validation of phage T7 biological dosimeter by quantitative polymerase chain reaction using short and long segments of phage T7 DNA.** Hegedus, M., Modos, K., Ronto, Gy, Fekete, A. (2003). *Photochemistry and photobiology* 78:213-219. Phage T7 can be used as a biological dosimeter; its reading, the biologically effective dose (BED), is proportional to the inactivation rate  $|\ln(n/n_0)|$ . For the measurement of DNA damage in phage T7 dosimeter, a quantitative polymerase chain reaction (QPCR) methodology has been developed using 555 and 3826 bp fragments of phage T7 DNA. Both optimized reactions are so robust that an equally good amplification was obtained when intact phage T7 was used in the reaction mixture. In the biologically relevant dose range a good correlation was obtained between the BED of the phage T7 dosimeter and the amount of ultraviolet (UV) photoproducts determined by QPCR with both fragments under the effect of five various UV sources. A significant decrease in the yield of photoproducts was detected by QPCR in isolated T7 DNA and in heated phage compared with intraphage DNA with all irradiation sources. Because the yield of photoproducts was the same in B, C and A conformational states of T7 DNA, a possible explanation for modulation of photoproduct frequency in intraphage T7 DNA is that the presence of bound phage proteins induces an alteration in DNA structure that can result in increased induction of photoproducts
29. **Fate of physical, chemical, and microbial contaminants in domestic wastewater following treatment by small constructed wetlands.** Hench, K. R., Bissonnette, G. K., Sexstone, A. J., Coleman, J. G., Garbutt, K., Skousen, J. G. (2003). *Water Research* 37:921-927. In order to evaluate the efficacy of constructed wetlands for treatment of domestic wastewater for small communities located in rural areas, small-scale wetland mesocosms (400 L each) containing two treatment designs (a mixture of *Typha*, *Scirpus*, and *Juncus* species; control without vegetation) were planted into two depths (45 or 60 cm) with pea gravel. Each mesocosm received 19 L/day of primary-treated domestic sewage. Mesocosms were monitored (inflow and outflow samples) on a monthly basis over a 2-year period for pH, total suspended solids (TSS), 5-day biochemical oxygen demand (BOD(5)), total Kjeldahl nitrogen (TKN), dissolved oxygen (DO), and conductivity. Microbiological analyses included enumeration of fecal coliforms, enterococci, *Salmonella*, *Shigella*, *Yersinia*, and coliphage. Significant differences between influent and effluent water quality for the vegetated wetlands ( $p < 0.05$ ) were observed in TSS, BOD(5), and TKN. Increased DO and reduction in fecal coliform, enterococcus, *Salmonella*, *Shigella*, *Yersinia*, and coliphage populations also were observed in vegetated wetlands. Greatest microbial reductions were observed in the planted mesocosms compared to those lacking vegetation. Despite marked reduction of several contaminants, wetland-treated effluents did not consistently meet final discharge limits for receiving bodies of water. Removal efficiencies for bacteria and several chemical parameters were more apparent during the initial year compared to the second year of operation, suggesting concern for long-term efficiency and stability of such wetlands.
30. **Bacteriophages with tails: chasing their origins and evolution.** Hendrix, R. W., Hatfull, G. F., Smith, M. C. M. (2003). *Research in Microbiology* 154:253-257. Comparative genomic analysis of the tailed bacteriophages shows that they are genetically mosaic with respect to each other, implying that horizontal exchange of sequences is an important component of their evolution. Horizontal exchange occurs intensively among closely related phages but also at reduced frequency across the entire population of tailed phages. It results in exchange of homologous functions, exchange of analogous but non-homologous functions as with the prophage integrases, and introduction of novel functions into the genome as with the morons. Extrapolation of these processes back in evolutionary time leads to a speculative model for the origins and early evolution of phages.
31. **Phage therapy: a reappraisal of bacteriophages as antibiotics.** Inal, J. M. (2003). *Archivum Immunologiae et Therapiae Experimentalis* 51:237-244. The concept of phage therapy to treat bacterial infections was born with the discovery of the bacteriophage almost a century ago. After a chequered history, its current renaissance is fueled by the dangerous appearance of antibiotic-resistant bacteria on a global scale. As a mark of this renewed interest, the unanswered problems of phage therapy are now being addressed, especially for human use. Phage therapy in the agricultural, food-processing and fishery industries is already being successfully applied, and this review, whilst being aware of the potential drawbacks, emphasizes the need for further carefully controlled empirical data on its efficacy and safety in treating human and animal disease, especially in view of its numerous advantages over antibiotics. Finally the potential of phage therapy against bioterrorism and the emergence of second generation phage antibacterials based on phage-derived single-protein lysis systems are addressed.
32. **A fluoroquinolone induces a novel mitogen-encoding bacteriophage in *Streptococcus canis*.** Ingrey, K. T., Ren, J., Prescott, J. F. (2003). *Infection and Immunity* 71:3028-3033. This study investigated whether the recently recognized emergence of canine streptococcal toxic shock syndrome (STSS) and necrotizing fasciitis (NF) might be partly attributed to the use of fluoroquinolones to treat *Streptococcus canis* infections in dogs. Both

mitomycin and the fluoroquinolone enrofloxacin caused bacteriophage-induced lysis of *S. canis* strain 34, an isolate from a case of canine STSS and NF. Fluoroquinolone-evoked, bacteriophage-induced lysis occurred over a range of concentrations similar to those that would occur after treatment of dogs with these agents. To search for a possible bacteriophage-encoded streptococcal superantigen gene(s), a library of the 36.5 (□1.1)-kb bacteriophage, designated phisc1, was made by ligating 3- to 7-kb Tsp5091-digested phisc1 fragments into an EcoRI-digested  $\lambda$ ZapII vector. Recombinants were screened for mitogenic activity by using canine peripheral blood lymphocytes. Of 800 recombinants screened, 11 recombinants with mitogenic effects were identified, and their inserts were sequenced. The highest homology of 11.6 kb of sequenced phisc1 DNA was to the completely sequenced *Streptococcus pneumoniae* bacteriophage MM1. Seven of the 11 phisc1 sequenced inserts contained a 552-bp open reading frame, scm, with 27% amino acid similarity to pokeweed (*Phytolacca americana*) mitogen. PCR showed this gene to be present in 22 of 23 *S. canis* isolates tested. Quantitative reverse transcription-PCR showed that bacteriophage induction was associated with a 58-fold enhancement of expression of this gene relative to that in a noninduced culture of a similar age. The presence of this gene on a fluoroquinolone-induced bacteriophage may explain the association observed between fluoroquinolone use in dogs and the development of canine STSS and NF

33. **Maintenance of species identity and controlling speciation of bacteria: a new function for restriction/modification systems? Jeltsch, A. (2003). *Gene* 317:13-16.** Bacteria frequently exchange DNA among each other by horizontal gene transfer. However, maintenance of species identity and in particular speciation requires a certain barrier against an unregulated uptake of foreign DNA. Here it is suggested that formation of such a barrier is one important biological function of restriction/modification systems, in addition to the classical function of protection of bacteria against bacteriophage infection. This model explains the extreme variability and wide distribution of restriction/modification systems among prokaryotes, the prevalence of RM-systems in pathogenic bacteria and the existence of several RM-systems in single bacterial strains.
34. **Microbiological indicators of water quality in the Xochimilco canals, Mexico City. Juarez-Figueroa, L. A., Silva-Sanchez, J., Uribe-Salas, F. J., Cifuentes-Garcia, E. (2003). *Salud publica de Mexico* 45:389-395.**  
OBJECTIVE: To quantify microbiology indicators of fecal contamination in the effluents of two waste water treatment plants and in samples collected in several canals in Xochimilco. MATERIAL AND METHODS: A cross sectional study was performed. Ten sites, 5 from plant effluents and 5 from canals, were selected for sampling during November and December 2001. Fecal coliforms and enterococci were quantified by membrane filtration, male specific ( $F^+$ ) and somatic coliphages by double agar layer technique, and *Cryptosporidium* oocysts and *Giardia* cysts by concentration with Envirocheck filter followed by immunofluorescence microscopy quantification. The average of organisms counts from effluents and canal water were compared with t Student test. RESULTS: Treated water discharge in canals showed a low count of Fecal Coliforms (average 40.4/100 ml), enterococci (average 58.8/100 ml) and *Cryptosporidium* oocysts (average 13.2/100 l), while coliphages and *Giardia* cyst rendered higher counts (average 1467.5/100 ml and 1199.8/100 l, respectively) suggesting the water treatment methods could fail to remove these agents. A significant lower count of *Giardia* cysts (average 45/100 l) and no *Cryptosporidium* oocysts were found in irrigation canals, which suggests a natural clearance of these pathogens. Strains of *Escherichia coli* isolated in one of the canals contaminated with sewage had antimicrobial multi-resistance that was transferred by conjugation suggesting that resistance is encoded in a plasmid potentially transferable to other pathogenic bacteria. CONCLUSIONS: Cost effective and culturally acceptable waste treatment methods will require careful planning and consultation if they are to be adopted and maintained by local populations.
35. **[Bacteriophage therapy: Stalin's forgotten medicine]. Kaulen, H. (2003). *Deutsche medizinische Wochenschrift* 128:307.**
36. **Myoviridae bacteriophages of *Pseudomonas aeruginosa*: a long and complex evolutionary pathway. Krylov, V., Pleteneva, E., Bourkaltseva, M., Shaburova, O., Volckaert, G., Sykilinda, N., Kurochkina, L., Mesyanzhinov, V. (2003). *Research in Microbiology* 154:269-275.** Recently we have accomplished the entire DNA sequence of bacteriophage  $\phi$ KZ, a giant virus infecting *Pseudomonas aeruginosa*. The 280334-bp of  $\phi$ KZ genome is a linear, circularly permuted and terminally redundant, AT-rich dsDNA molecule that contains no sites for NotI, PstI, SacI, SmaI, XhoI and XmaII endonucleases. Limited homology to other bacteriophages on the DNA and protein levels indicated that  $\phi$ KZ represents a distinct branch of the Myoviridae family. In this work, we analyzed a group of six *P. aeruginosa* phages (Lin68, Lin21, PTB80, NN, EL, and RU), which are morphologically similar to  $\phi$ KZ, have similar genome size and low G+C content. All phages have a broad host range among *P. aeruginosa* strains, and they are resistant to the inhibitory action of many *P. aeruginosa* plasmids. The analysis of the genomic DNA by restriction enzymes and DNA-DNA hybridization shows that phages are representative of three  $\phi$ KZ-like species:  $\phi$ KZ-type ( $\phi$ KZ, Lin21, NN and PTB80), EL-type (EL and RU) and Lin68 which has a shorter tail than other phages. Except for related phages EL and RU, all  $\phi$ KZ-like phages have identical N-terminal amino acid sequences of the major capsid protein. Random genome sequencing shows that the EL and RU phages have no homology to the  $\phi$ KZ-like phages on DNA level. We propose that the  $\phi$ KZ, Lin21, NN, PTB80 and Lin68 phages can be included in a new  $\phi$ KZ genus, and that the EL and RU phages belong to a separate genus within the Myoviridae family. Based on the resistance to many restriction enzymes and the transduction ability, there are indications that over the long pathway of evolution, the  $\phi$ KZ-like phages probably inherited the capacity to infect different bacterial species.
37. **The genome of bacteriophage  $\phi$ KMV, a T7-like virus infecting *Pseudomonas aeruginosa*. Lavigne, R., Burkal'tseva, M. V., Robben, J., Sykilinda, N. N., Kurochkina, L. P., Grymonprez, B., Jonckx, B., Krylov, V. N., Mesyanzhinov, V. V., Volckaert, G. (2003). *Virology* 312:49-59.** The complete DNA sequence of a new lytic T7-like bacteriophage  $\phi$ KMV is presented. It is the first genome sequence of a member of the Podoviridae that infects *Pseudomonas aeruginosa*. The linear G + C-rich (62.3%) double-stranded DNA genome of 42,519 bp has direct terminal repeats of 414 bp and contains 48 open reading frames that are all transcribed from the same strand. Despite absence of homology at the DNA level, 11 of the 48  $\phi$ KMV-encoded putative proteins show sequence similarity to known T7-type phage proteins. Eighteen open reading frame products have been assigned, including an RNA polymerase, proteins involved in DNA replication, as well as structural, phage maturation, and lysis proteins. Surprisingly, the major capsid protein completely lacks sequence homology to any known protein. Also, the strong virulence toward many clinical *P. aeruginosa* isolates and a short replication time make  $\phi$ KMV attractive for phage therapy or a potential source for antimicrobial proteins.

38. **Population dynamics and gene transfer in genetically modified bacteria in a model microcosm.** Lilley, A. K., Bailey, M. J., Barr, M., Kilshaw, K., Timms-Wilson, T. M., Day, M. J., Norris, S. J., Jones, T. H., Godfray, H. C. J. (2003). *Molecular Ecology* 12:3097-3107. The horizontal transfer and effects on host fitness of a neutral gene cassette inserted into three different genomic loci of a plant-colonizing pseudomonad was assessed in a model ecosystem. The KX reporter cassette (kanamycin resistance, aph, and catechol 2, 3, dioxygenase, xylE) was introduced on the disarmed transposon mini-Tn5 into: (I) the chromosome of a spontaneous rifampicin resistant mutant *Pseudomonas fluorescens* SBW25R; (II) the chromosome of SBW25R in the presence of a naturally occurring lysogenic-phage (phage Phi101); and (III) a naturally occurring plasmid pQBR11 (330 kbp, tra+, Hgr) introduced into SBW25R. These bacteria were applied to *Stellaria media* (chickweed) plants as seed dressings [c.  $5 \times 10^4$  colony-forming units (cfu)/seed] and the seedlings planted in 16 microcosm chambers containing model plant and animal communities. Gene transfer to pseudomonads in the phyllosphere and rhizosphere was found only in the plasmid treatment (III). Bacteria in the phage treatment (II) initially declined in density and free phage was detected, but populations partly recovered as the plants matured. Surprisingly, bacteria in the chromosome insertion treatment (I) consistently achieved higher population densities than the unmanipulated control and other treatments. Plasmids were acquired from indigenous bacterial populations in the control and chromosome insertion treatments. Plasmid acquisition, plasmid transfer from inocula and selection for plasmid carrying inocula coincided with plant maturation.
39. **Characterisation of technologically proficient wild *Lactococcus lactis* strains resistant to phage infection.** Madera, C., Garcia, P., Janzen, T., Rodriguez, A., Suarez, J. E. (2003). *International Journal of Food Microbiology* 86:213-222. The aim of this work was to establish whether *Lactococcus lactis* strains isolated from spontaneous dairy fermentations exhibited useful milk-processing capabilities and resistance to bacteriophage infection in order to be used as components in starter formulations. The 33 out of 100 isolates of *L. lactis*, originated from farmhouse cheeses, were found to be resistant to a collection of 34 phages belonging to the c2 and 936 groups. Six of the isolates were discarded as potential starters because they were lysogenic and other five because they produced tyramine. Plasmid and chromosomal profiles of the 22 remaining isolates allowed their classification into 16 different strains. All of these were good lactic acid producers from lactose, moderately proteolytic and, in eight cases, diacetyl production from citrate was observed. The mechanism(s) leading to the phenotype of phage resistance was identified for all the strains used in this study. Inhibition of adsorption was the most frequent one, although genetic determinants for some abortive infection systems were also detected (abiB, abiG and abil). Frequently, more than one mechanism was present in the same strain. One of the strains, *L. lactis* IPLA542, was selected as a model starter for pilot fermentations. It clotted milk normally both in the absence and in the presence of phage at concentrations that completely abolished the process when promoted by a phage-susceptible strain.
40. **Detection of *Escherichia coli* using immunomagnetic separation and bacteriophage amplification coupled with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry.** Madonna, A. J., Van Cuyk, S., Voorhees, K. J. (2003). *Rapid Communications in Mass Spectrometry* 17:257-263. The application of whole cell analysis by matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) has emerged as a valuable tool for rapidly identifying/detecting bacteria. This technique requires minimal sample preparation and is simple to perform, but is generally limited to purified samples of bacteria at concentrations greater than  $1.0 \times 10^6$  cells/mL. In this paper, we describe a bacterial detection method that integrates immunomagnetic separation with bacteriophage amplification prior to MALDI-MS analysis. The developed method consists of three main stages: (1) isolation of a target bacterium by immunomagnetic separation; (2) infection of the immuno-captured bacterium with a lytic bacteriophage; and (3) assay of infected medium for bacteriophage progeny using MALDI-MS to produce a molecular weight signal for the virus capsid protein. With this technique, the presence of *Escherichia coli* in broth was determined in less than 2 h total analysis time at a concentration of approximately  $5.0 \times 10^4$  cells/mL.
41. **Genetic diversity and temporal variation in the cyanophage community infecting marine *Synechococcus* species in Rhode Island's coastal waters.** Marston, M. F., Sallee, J. L. (2003). *Applied and Environmental Microbiology* 69:4639-4647. The cyanophage community in Rhode Island's coastal waters is genetically diverse and dynamic. Cyanophage abundance ranged from over  $10^4$  phage ml<sup>-1</sup> in the summer months to less than  $10^2$  phage ml<sup>-1</sup> during the winter months. Thirty-six distinct cyanomyovirus g20 genotypes were identified over a 3-year sampling period; however, only one to nine g20 genotypes were detected at any one sampling date. Phylogenetic analyses of g20 sequences revealed that the Rhode Island cyanomyoviral isolates fall into three main clades and are closely related to other known viral isolates of *Synechococcus* spp. Extinction dilution enrichment followed by host range tests and PCR restriction fragment length polymorphism analysis was used to detect changes in the relative abundance of cyanophage types in June, July, and August 2002. Temporal changes in both the overall composition of the cyanophage community and the relative abundance of specific cyanophage g20 genotypes were observed. In some seawater samples, the g20 gene from over 50% of isolated cyanophages could not be amplified by using the PCR primer pairs specific for cyanomyoviruses, which suggested that cyanophages in other viral families (e.g., Podoviridae or Siphoviridae) may be important components of the Rhode Island cyanophage community.
42. **Experimental protection of mice against lethal *Staphylococcus aureus* infection by novel bacteriophage  $\phi$ MR11.** Matsuzaki, S., Yasuda, M., Nishikawa, H., Kuroda, M., Ujihara, T., Shuin, T., Shen, Y., Jin, Z., Fujimoto, S., Nasimuzzaman, M. D., Wakiguchi, H., Sugihara, S., Sugiura, T., Koda, S., Muraoka, A., Imai, S. (2003). *The Journal of infectious diseases* 187:613-624. The protective effects of bacteriophages were assessed against experimental *Staphylococcus aureus* infection in mice. Of the *S. aureus* phages isolated in the study,  $\phi$ MR11 was representatively used for all testing, because its host range was the most broad and it carries no genes for known toxins or antibiotic resistance. Intraperitoneal injections ( $8 \times 10^8$  cells) of *S. aureus*, including methicillin-resistant bacteria, caused bacteremia and eventual death in mice. In contrast, subsequent intraperitoneal administration of purified  $\phi$ MR11 (MOI > or = 0.1) suppressed *S. aureus*-induced lethality. This lifesaving effect coincided with the rapid appearance of  $\phi$ MR11 in the circulation, which remained at substantial levels until the bacteria were eradicated. Inoculation with high-dose  $\phi$ MR11 alone produced no adverse effects attributable to the phage. These results uphold the efficacy of phage therapy against pernicious *S. aureus* infections in humans and suggest that  $\phi$ MR11 may be a potential prototype for gene-modified, advanced therapeutic *S. aureus* phages.
43. **[Development of cyanobacterial phages at the Institute of Microbiology and Virology of the National**

Academy of Sciences of Ukraine (History and perspectives)]. Mendzhul, M. I., Lysenko, T. G., Syrchin, S. A. (2003). *Mikrobiolohichnyi zhurnal* 65:133-140. The paper deals with the basic trends of fundamental investigations of the Department of Algae Viruses in the field of cyanophagia-ecology, biological and physico-chemical properties of cyanophages as well as interrelation with the host cells. Such problems as a possibility to use the system cyanophage-cyanobacteria as the experimental model for development of the unified functional model of productive infection, efficient methods of prophylaxis and therapy of virus infections as well as the solution of various biotechnological problems are discussed.

44. **Bacteriophage and the evolution of epidemic cholera.** Miller, J. F. (2003). *Infection and Immunity* 71:2981-2982.
45. **Bacteriophage ST64B, a genetic mosaic of genes from diverse sources isolated from *Salmonella enterica* serovar Typhimurium DT 64.** Mmolawa, P. T., Schmieger, H., Heuzenroeder, M. W. (2003). *Journal of Bacteriology* 185:6481-6485. The complete sequence of the double-stranded DNA (dsDNA) genome of the *Salmonella enterica* serovar Typhimurium ST64B bacteriophage was determined. The 40,149-bp genomic sequence of ST64B has an overall G+C content of 51.3% and is distinct from that of P22. The genome architecture is similar to that of the lambdoid phages, particularly that of coliphage  $\lambda$ . Most of the putative tail genes showed sequence similarity to tail genes of Mu, a nonlambdoid phage. In addition, it is likely that these tail genes are not expressed due to insertions of fragments of genes related to virulence within some of the open reading frames. This, together with the inability of ST64B to produce plaques on a wide range of isolates, suggests that ST64B is a defective phage. In contrast to the tail genes, most of the head genes showed similarity to those of the lambdoid phages HK97 and HK022, but these head genes also have significant sequence similarities to those of several other dsDNA phages infecting diverse bacterial hosts, including *Escherichia*, *Pseudomonas*, *Agrobacterium*, *Caulobacter*, *Mesorhizobium*, and *Streptomyces*: This suggests that ST64B is a genetic mosaic that has acquired significant portions of its genome from sources outside the genus *Salmonella*.
46. **Shiga toxin 2-converting bacteriophages associated with clonal variability in *Escherichia coli* O157:H7 strains of human origin isolated from a single outbreak.** Muniesa, M., de Simon, M., Prats, G., Ferrer, D., Panella, H., Jofre, J. (2003). *Infection and Immunity* 71:4554-4562. Shiga toxin 2 ( $Stx_2$ )-converting bacteriophages induced from 49 strains of *Escherichia coli* O157:H7 isolated during a recent outbreak of enterocolitis in Spain were examined in an attempt to identify the variability due to the  $stx_2$ -converting phages. The bacterial isolates were divided into low-, medium-, and high-phage-production groups on the basis of the number of phages released after mitomycin C induction. Low- and medium-phage-production isolates harbored two kinds of phages but released only one of them, whereas high-phage-production isolates harbored only one of the two phages. One of the phages,  $\phi$ SC370, which was detected only in the isolates with two phages, showed similarities with phage 933W. The second phage,  $\phi$ LC159, differed from  $\phi$ SC370 in morphology and DNA structure. When both phages were present in the same bacterial chromosome, as occurred in most of the isolates, only SC370 was detected in the supernatants of the induced cultures. If  $\phi$ LC159 was released, its presence was masked by  $\phi$ SC370. When  $\phi$ SC370 was absent, large amounts of  $\phi$ LC159 were released, suggesting that there was some regulation of phage expression between the two phages. To our knowledge, this is the first description of clonal variability due to phage loss. The higher level of phage production was reflected in the larger amounts of  $Stx_2$  toxin produced by the cultures. Some relationship between phage production and the severity of symptoms was observed, and consequently these observations suggest that the virulence of the isolates studied could be related to the variability of the induced  $stx_2$ -converting phages.
47. **Experimental bacteriophage-mediated virulence in strains of *Vibrio harveyi*.** Munro, J., Oakey, J., Bromage, E., Owens, L. (2003). *Diseases of Aquatic Organisms* 54:187-194. Vibriosis is a major disease problem in prawn aquaculture. Until now there has been no clear explanation why some strains of *Vibrio* are pathogenic, while others are not. This study demonstrated that the presence of the bacteriophage *V. harveyi* myovirus like (VHML) may confer virulence to *V. harveyi* Strain 642. This was demonstrated by infecting naive avirulent *V. harveyi* Strains 12, 20, 45 and 645 with the bacteriophage and converting them into virulent strains. The previously naive strains of *Vibrio* infected with Bacteriophage VHML from *V. harveyi* Strain 642 demonstrated up-regulation of haemolysin, up-regulation of protein excretion, additional proteins which were recognised as toxic proteins from Strain 642 by monoclonal antibodies specific to the exotoxin sub-units, and a significant increase in mortality of larval *Penaeus monodon*. It was concluded that Bacteriophage VHML conferred virulence to *V. harveyi* Strains 12, 20, 45 and 645 and that Bacteriophage VHML either fully or partly confers virulence in *V. harveyi* Strain 642.
48. **Concentrations and inactivation of *Ascaris* eggs and pathogen indicator organisms in wastewater stabilization pond sludge.** Nelson, K. L. (2003). *Water Science and Technology* 48:89-95. During treatment in wastewater stabilization ponds (WSPs) many pathogens, in particular helminth eggs, are concentrated in the sludge layer. Because periodic removal of the sludge is often required, information is needed on the concentrations and inactivation of pathogens in the sludge layer to evaluate the public health risk they pose upon removal of the sludge. In this paper, previous reports on the sludge concentrations of various pathogen indicator organisms and helminth eggs are reviewed and results from our own recent experiments are reported. The advantages and disadvantages of several methods for studying inactivation in the sludge layer are discussed, as well as implications for the management of WSP sludge. In our recent experiments, which were conducted at three WSPs in central Mexico, sludge cores, dialysis chambers, and batch experiments were used to measure the inactivation rates of fecal coliform bacteria, fecal enterococci,  $F^+$  coliphage, somatic coliphage, and *Ascaris* eggs. The first-order inactivation rate constants were found to be approximately 0.1, 0.1, 0.01, 0.001, and 0.001  $d^{-1}$ , respectively. The concentrations of all the organisms were found to vary both vertically and horizontally in the sludge layer; therefore, to determine the maximum and average concentration of organisms in the sludge layer of a WSP, complete sludge cores must be collected from representative locations throughout the pond.
49. **[Bacteriophage therapy and colleague Martin Arrowsmith].** Nevasaari, K. (2003). *Duodecim; laaketieteellinen aikakauskirja* 119:1367.

50. **Biological characterization of the temperate *Streptococcus thermophilus* bacteriophage TP-J34 and physical characterization of the phage genome.** Neve, H., Freudenberg, W., Diestel-Feddersen, F., Ehlert, R., Heller, K. J. (2003). *Virology* 315:184-194. The temperate *Streptococcus thermophilus* bacteriophage TP-J34 was identified in the lysogenic host strain J34. The majority of phage particles produced upon induction was defective and noninfectious, consisting of DNA-filled heads lacking tails. A physical map (45.6 kb) was established. Analysis of minor restriction bands of the DNA isolated from phage particles as well as the analysis of the protein pattern indicated that phage TP-J34 is a pac-type phage. This was confirmed by immunoelectron microscopy using antisera raised against virulent cos- and pac-type *S. thermophilus* phages. The lysogenic host J34 but not its noninducible derivative J34-12 contained phage DNA in the nonintegrated state and exhibited autolysis at elevated temperatures. Prophage-carrying strains grew homogeneously while 16 of 20 prophage-cured derivatives aggregated and sedimented rapidly. When phage TP-J34 was propagated lytically on a prophage-cured host strain, a 2.7-kb site-specific deletion occurred in the phage genome. This deletion was also identified in the prophage DNAs of relysogenized strains.
51. **Microbial water quality improvement by small scale on-site subsurface wetland treatment.** Nokes, R. L., Gerba, C. P., Karpiscak, M. M. (2003). *Journal of Environmental Science and Health Part A Toxic-Hazardous Substances & Environmental Engineering* 38:1849-1855. It has been demonstrated that large constructed wetlands used for domestic wastewater treatment are useful in the reduction of enteric microorganisms. This study evaluated the ability of three small-scale, on-site subsurface wetlands with different vegetation densities to remove total coliforms, fecal coliforms, coliphage, *Giardia* and *Cryptosporidium*. These wetlands were found to be equally efficient in the removal of enteric bacteria and coliphage as larger constructed wetlands. *Giardia* and *Cryptosporidium* were usually undetectable after passage of the wastewater through the subsurface wetlands. Coliphage removal increased with increasing vegetation density.
52. **Scope of potential bacterial agents of diarrhoea and microbial assessment of quality of river water sources in rural Venda communities in South Africa.** Obi, C. L., Potgieter, N., Bessong, P. O., Matsaung, G. (2003). *Water Science and Technology* 47:59-64. The microbial quality of several, usually untreated, surface domestic water sources, used by rural communities in the Venda Region of South Africa, was assessed to gauge their fitness for human consumption and to highlight the possible impact of waterborne diseases. The water sources studied were six points on the Levubu River and the rivers Mutale, Ngwedi, Tshinane, Makonde, Mutshindudi and Mudaswali. Total and faecal coliform, heterotrophic bacteria, enterococci and coliphage counts were used as indicators/surrogates to estimate the degree of bacterial and viral contamination respectively by standard methods. The presence of potential bacterial agents of diarrhoea such as *Salmonella*, *Shigella*, *Campylobacter*, *Plesiomonas*, *Aeromonas* and *Vibrio* was also determined. Results showed that the ranges of counts with regard to all the water sources investigated were  $2.9 \times 10^2$  -  $6.3 \times 10^4$  CFU/100 mL for faecal coliforms,  $6.0 \times 10^2$  -  $3.7 \times 10^4$  CFU/100 mL for total coliforms,  $1.8 \times 10^2$  -  $1.3 \times 10^6$  CFU/mL for heterotrophic plate count,  $1.0 \times 10(1)$  -  $3.7 \times 10^4$  CFU/100 mL for enterococci and 0-13 PFU/100 mL for coliphages. These values are far higher than the acceptable maximum limits prescribed for South Africa by the Dept of Water & Forestry and the Water Research Commission - 0 CFU/100 mL, 5 CFU/100 mL,  $1.0 \times 10^2$  CFU/mL, 0 CFU/100 mL and 1 PFU/100 mL for faecal coliforms, total coliforms, heterotrophic bacteria, enterococci and coliphages respectively. *Salmonella*, *Shigella*, *Vibrio cholerae*, *Campylobacter*, *Aeromonas* and *Plesiomonas* were isolated from several of the water sources investigated. The use of these water sources for drinking and domestic purposes poses a serious threat to the health and well being of the users and calls for urgent government intervention.
53. **Suppression of leaf feeding and oviposition of phytophagous ladybird beetles (Coleoptera: Coccinellidae) by chitinase gene-transformed phylloplane bacteria and their specific bacteriophages entrapped in alginate gel beads.** Otsu, Y., Mori, H., Komuta, K., Shimizu, H., Nogawa, S., Matsuda, Y., Nonomura, T., Sakuratani, Y., Tosa, Y., Mayama, S., Toyoda, H. (2003). *Journal of Economic Entomology* 96:555-563. The chitinase gene-transformed strain KPM-007E/chi of *Enterobacter cloacae* was vitally entrapped in sodium alginate gel beads with its specific virulent bacteriophage EcP-01 to provide a new method for microbially digesting chitinous peritrophic membranes of phytophagous ladybird beetles *Epilachna vigintioctopunctata*. First, chitinase SH1 from a gram-positive bacterium *Kurthia zopfii* was overproduced by *Escherichia coli* cells and purified by affinity column chromatography. The purified enzyme effectively digested peritrophic membranes dissected from the ladybird beetles to expose epithelial tissues beneath the peritrophic membrane, and the beetles that had ingested chitinase after submergence in chitinase solution had considerably reduced their feeding on tomato leaves. KPM-007E/chi, entrapped in the alginate beads, released the chitinase. More chitinase was released when KPM-007E/chi was present with their specific virulent bacteriophage EcP-01 in the beads because of lysis of bacterial cells infected with the bacteriophages. This chitinase release from the microbial beads (containing KPM-007E/chi and EcP-01) was sufficient to digest the peritrophic membrane as well as to suppress feeding of bead-sprayed tomato leaves by the ladybird beetles. A daily supply of tomato leaves treated with the microbial beads considerably suppressed leaf feeding and oviposition by the ladybird beetles, suggesting a possible application of chitinase-secreting bacteria for suppressing herbivorous insect pests.
54. **Faecal contamination of greywater and associated microbial risks.** Ottoson, J., Stenstrom, T. A. (2003). *Water Research* 37:645-655. The faecal contamination of greywater in a local treatment system at Vibyasen, north of Stockholm, Sweden was quantified using faecal indicator bacteria and chemical biomarkers. Bacterial indicator densities overestimated the faecal load by 100-1000-fold when compared to chemical biomarkers. Based on measured levels of coprostanol, the faecal load was estimated to be  $0.04 \text{ g person}^{-1} \text{ day}^{-1}$ . Prevalence of pathogens in the population and the faecal load were used to form the basis of a screening-level quantitative microbial risk assessment (QMRA) that was undertaken for rotavirus, *Salmonella typhimurium*, *Campylobacter jejuni*, *Giardia lamblia* and *Cryptosporidium parvum*. The different exposure scenarios simulated—direct contact, irrigation of sport fields and groundwater recharge—gave unacceptably high rotavirus risks ( $0.04 < \text{Pinf} < 0.60$ ) despite a low faecal load. The poor reduction of somatic coliphages, which were used as a virus model, in the treatment was one main reason and additional treatment of the greywater is suggested. Somatic coliphages can under extreme circumstances replicate in the wastewater treatment system and thereby underestimate the virus reduction. An alternative QMRA method based on faecal enterococci densities estimated similar risks as for rotavirus. Growth conditions for *Salmonella* in greywater sediments were also investigated and risk modelling based on replication in the system increased the probability of infection from *Salmonella* 1000-fold, but it was still lower than the risk of a

55. **Phage evolution: new worlds of genomic diversity.** Papke, R. T., Doolittle, W. F. (2003). *Current Biology* **13**:R606-R607. A recent comparative survey of genomes of phages infecting mycobacteria reveals a vast combinatorial network of gene rearrangements and may provide general models for pattern and process in genome evolution.
56. **Bacteriophage control of *Pseudomonas plecoglossicida* infection in ayu *Plecoglossus altivelis*.** Park, S. C., Nakai, T. (2003). *Diseases of Aquatic Organisms* **53**:33-39. Two previously isolated phages were used to examine the therapeutic effects against *Pseudomonas plecoglossicida* infection in ayu *Plecoglossus altivelis*. Phage PPp-W4 (Podoviridae) inhibited the in vitro growth of *P. plecoglossicida* more effectively than Phage PPpW-3 (Myoviridae), and a mixture (PPpW-3/W-4) of the 2 phages exhibited the highest inhibitory activity. In phage therapy experiments, ayu were fed *P. plecoglossicida*-impregnated feed ( $10^7$  CFU fish<sup>-1</sup>) and then fed phage-impregnated feed ( $10^7$  PFU fish<sup>-1</sup>). Mortalities of fish receiving PPpW-3, PPpW-4, PPpW-3/W-4, and a control fish receiving no phages were 53.3, 40.0, 20.0 and 93.3%, respectively. Phage (PPpW-3/W-4)-receiving fish also showed high protection against water-borne infection with *P. plecoglossicida*. In a field trial, when phage (PPpW-3/W-4)-impregnated feed was administered to ayu in a pond where the disease occurred naturally, daily mortality of fish decreased at a constant level (5% d<sup>-1</sup>) to one-third after a 2 wk period. The causal relationship of phages in this phenomenon was verified by the long-lasting appearance of administered phages in the kidneys of the fish, and a disappearance of *P. plecoglossicida* from apparently healthy fish. Neither phage-resistant organisms nor phage-neutralizing antibodies were detected in diseased fish or apparently healthy fish, respectively. These results indicate the potential for phage control of the disease.
57. **Development of a novel method of lytic phage delivery by use of a bacteriophage P22 site-specific recombination system.** Platt, R., Reynolds, D. L., Phillips, G. J. (2003). *FEMS Microbiology Letters* **223**:259-265. Bacteriophage therapy represents a potential alternative to the use of antibiotics to control proliferation of pathogenic bacteria. As an alternative to the strategy where a limited number of doses of large numbers of lytic bacteriophages are administered, a novel method delivery system was developed so that phages are continually released into the culture. Specifically, a non-pathogenic *Escherichia coli* strain was constructed that was lysogenic for a lytic mutant of bacteriophage  $\lambda$ . This lysogen was shown to be effective at decreasing the number of  $\lambda$ -sensitive *E. coli* in vitro. Construction of this *E. coli* strain was accomplished by development of a plasmid-based system utilizing the site-specific recombination machinery of bacteriophage P22 to integrate DNA constructs into the host chromosome. This recombination system is useful for strain construction and other genetic manipulations in both *E. coli* and *Salmonella enterica* serovars.
58. **Bacterial debris—an ecological mechanism for coexistence of bacteria and their viruses.** Rabinovitch, A., Aviram, I., Zaritsky, A. (2003). *Journal of Theoretical Biology* **224**:377-383. A model of bacteria and phage survival is developed based on the idea of shielding by bacterial debris in the system. This model is mathematically formulated by a set of four nonlinear difference equations for susceptible bacteria, contaminated bacteria, bacterial debris and phages. Simulation results show the possibility of survival, and domains of existence of stable and unstable solutions.
59. **Virus succession observed during an *Emiliania huxleyi* bloom.** Schroeder, D., Oke, J., Malin, G., Wilson, W. H. (2003). *Applied and Environmental Microbiology* **69**:2484-2490. Denaturing gradient gel electrophoresis was used as a molecular tool to determine the diversity and to monitor population dynamics of viruses that infect the globally important coccolithophorid *Emiliania huxleyi*. We exploited variations in the major capsid protein gene from *E. huxleyi*-specific viruses to monitor their genetic diversity during an *E. huxleyi* bloom in a mesocosm experiment off western Norway. We reveal that, despite the presence of several virus genotypes at the start of an *E. huxleyi* bloom, only a few virus genotypes eventually go on to kill the bloom.
60. **Survival of indicator organisms during enrichment on tetrachloroethene.** Skramstad, J. D., Hurst, C. J., Novak, P. J. (2003). *Water Environment Research* **75**:368-376. A laboratory study was performed as the basis for a full-scale bioaugmentation project at a site contaminated with chlorinated ethenes. The objectives of this study were to 1) develop a protocol to enrich for a tetrachloroethene (PCE)-dechlorinating culture from waste activated sludge and anaerobic digester biosolids and 2) monitor the survival of fecal coliform bacteria and bacteriophage, which model enteric viruses, during the enrichment process. A culture was enriched in 8 days with the ability to degrade 6-microM PCE to cis-dichloroethene. Using the enrichment protocol in two identical experiments, significant inactivation of fecal coliform bacteria (2 log) and somatic coliphage (0.33 log) was observed in one of the experiments; no inactivation occurred in the second experiment. The number of F-specific coliphage decreased in both experiments (0.87 and 1.26 log inactivation). Despite the decrease in some of the coliform and bacteriophage numbers, the quantity of organisms and phage particles present after enrichment was still high (approximately  $7.5 \times 10^5$  most probable number/L,  $6.9 \times 10^6$  plaque-forming units (PFU)/L, and  $3.3 \times 10^5$  PFU/L, for fecal coliform bacteria, somatic coliphage, and F-specific coliphage, respectively). This may be cause for concern, depending on the current and future groundwater use at or near a site undergoing bioaugmentation with cultures derived from waste activated sludge and anaerobic digester biosolids.
61. **Development of a microplate assay for the detection of single plaque-forming units of bacteriophage  $\phi$ X174 in crude lysates.** Slattery, S. D., Valentine, C. R. (2003). *Environmental and Molecular Mutagenesis* **41**:121-125. Mice containing the  $\phi$ X174 am3 transgene can be used for measuring in vivo mutation; however, the single burst analysis method used for distinguishing in vivo mutations from mutations generated during sample processing is labor-intensive. A liquid microplate assay was developed that detects a single mutant plaque-forming unit (PFU) of  $\phi$ X174 bacterial virus in the presence of excess nonmutant virus. The assay is based on inhibiting reduction of the tetrazolium dye, MTS, by bacterial cells selective for mutant virus. The assay is performed with crude lysates of infected bacteria and is as accurate as scoring viral plaques on a bacterial lawn. This microplate assay may have application in increasing throughput of the single burst analysis of  $\phi$ X174 in transgenic mouse mutation assays.

62. **Viruses of hyperthermophilic Archaea.** Snyder, J. C., Stedman, K., Rice, G., Wiedenheft, B., Spuhler, J., Young, M. J. (2003). *Research in Microbiology* 154:474-482. The viruses of Archaea are likely to be useful tools for studying host evolution, host biochemical pathways, and as tools for the biotechnology industry. Many of the viruses isolated from Archaea show distinct morphologies and genes. The euryarchaeal viruses show morphologies similar to the head-and-tail phage isolated from Bacteria; however, sequence analysis of viral genomes from Crenarchaea shows little or no similarity to previously isolated viruses. Because viruses adapt to host organism characteristics, viruses may lead to important discoveries in archaeal biochemistry, genetics, and evolution.
63. **Enteric virions and microbial biofilms—a secondary source of public health concern?** Storey, M. V., Ashbolt, N. J. (2003). *Water Science and Technology* 48:97-104. Through their many sorption sites, microbial biofilms can accumulate both organic and inorganic particulate and colloidal material from bulk water environments. An application of such first principles to the ecology of "biocolloidal" enteric virions would suggest that they too may be concentrated by biofilms in a similar way. Though previous studies have isolated human gastrointestinal (enteric) virions from microbial biofilms, the exact human health significance of this has been neither fully investigated nor completely understood. Through an assessment of the location, accumulation and persistence of model enteric virion ( $\phi$ X174, MS2 and B40-8 bacteriophages as well as 20 nm fluorescent latex microspheres) within biofilms, the aim of the current study was to investigate whether the interaction of enteric virions with distribution pipe biofilms could provide a secondary source of public health concern to consumers. Model enteric virions were found to be incorporated into biofilms at concentrations representing 1% of those present in the adjacent bulk water environment. A sub-population (0.01%) of these persisted throughout an experimental period of 30 days, inferring their potential to accumulate over time. Furthermore, model enteric virions were partitioned into bacterial microcolonies, environments where biofilm bacteria can persist and re-grow, even in the presence of "acceptable" levels of disinfection. A risk model for enteric virion accumulation and release from distribution pipe biofilms suggested that associated risks may exceed USEPA benchmark values. These findings could have wide-reaching implications in water treatment and distribution strategies, and necessitate a re-appraisal of current water guideline values.
64. **Characterization of a *Vibrio cholerae* phage isolated from the coastal water of Peru.** Talledo, M., Rivera, I. N. G., Lipp, E. K., Neale, A., Karaolis, D., Huq, A., Colwell, R. R. (2003). *Environmental microbiology* 5:350-354. A *Vibrio cholerae* bacteriophage, family Myoviridae, was isolated from seawater collected from the coastal water of Lima, Peru. Genome size was estimated to be 29 kbp. The temperate phage was specific to *V. cholerae* and infected 12/13 *V. cholerae* O1 strains and half of the four non-O1/non-O139 strains tested in this study. *Vibrio cholerae* O139 strains were resistant to infection and highest infection rates were obtained in low nutrient media amended with NaCl or prepared using seawater as diluent.
65. **[Transduction of plasmid antibiotic resistance determinants with pseudo-T-even bacteriophages].** Taniashin, V. I., Zimin, A. A., Shliapnikov, M. G., Boronin, A. M. (2003). *Genetika* 39:914-926. Transduction of antibiotic resistance determinants of the plasmid pBR322 with pseudoT-even bacteriophages RB42, RB43, and RB49 was studied. It is established that antibiotic resistance determinants of plasmid pBR322 from *Escherichia coli* recA<sup>+</sup>- and recA<sup>-</sup>-donor strains do not differ significantly in respect to the efficiency of transduction. Amber mutants RB43-21, RB43-33, and a double amber mutant RB43am21am33 were obtained. These mutants facilitated transduction experiments in some cases. Transduction of antibiotic resistance markers of the vector plasmid pBR325 and recombinant plasmid pVT123, containing a DNA fragment with hoc segE uvsW genes of phage T4, was studied. The frequency of appearance of transductants resistant to pseudoT-even bacteriophages used in transduction was determined, and the sensitivity of resistant transductants to 32 RB bacteriophages and also to phages  $\lambda$ , T2, T4, T5, T6, T7, and BF23 was estimated. The efficiency of plating pseudoT-even bacteriophages RB42 and RB43 on strain *E. coli* 802 himA hip carrying mutations in genes that encode subunits of the Integration Host Factor (IHF) was shown to be higher than on isogenic strain *E. coli* 802. The growth of pseudoT-even bacteriophages limited in vivo by modification-restriction systems of chromosomal (EcoKI, EcoBI), phage (EcoP11), and plasmid (EcoRI, EcoR124I, and EcoR124II) localization was analyzed. It was shown that these phages were only slightly restricted by the type I modification-restriction systems EcoBI, EcoR124I, and EcoR124II. Phage RB42 was restricted by systems EcoKI, EcoP11, and EcoRI; phage RB43, by systems EcoKI and EcoRI; and phage RB49, by the EcoRI modification-restriction system.
66. **Set a microbe to kill a microbe: drug resistance renews interest in phage therapy.** Thacker, P. D. (2003). *Journal of the American Medical Association* 290:3183-3185. Phage therapy predated antibiotics by decades, but was largely supplanted when these drugs became available. Now, however, the emerging threat posed by antibiotic-resistant pathogens is spurring a resurgence of interest in phage, as a potential therapy to cure or prevent infections and as a tool to kill food-borne pathogens.
67. **Survival of indicators of bacterial and viral contamination in wastewater subjected to low temperatures and freezing: application to cold climate waste stabilisation ponds.** Torrella, F., Lopez, J. P., Banks, C. J. (2003). *Water Science and Technology* 48:105-112. The survival of bacterial and viral pollution indicators and *Salmonella* in urban wastewaters under freezing conditions (-14°C for up to 60 days) is reported. Presumptive, total and faecal coliforms (PC, TC, FC), salmonellae and coliphages were tested. The dynamics of somatic coliphage (*E. coli* C) and F-pili specific coliphage inactivation were compared at 4°C and 25°C over various run times. On freezing of the wastewater, it was found that PC, TC and FC showed a first rapid phase (days) of inactivation followed by a slower second phase (up to 4 weeks) and then stabilisation at between 1-10% of the initial population size, depending on the wastewater sample used. *Salmonella* spp. were detectable in 0.1 ml of raw wastewater and were still detected up to 2 days after freezing but none were detected in 100 ml samples after 4, 42 and 60 days, although microbiologically similar but antigenically different forms were found. Viral indicators of pollution showed a slow but constant decrease in viability during the first month but then stabilised at between 10-20% survivors (10% in somatic *E. coli* C phages, 15.8% in somatic *Salmonella* phages and 17.9% in F-pili specific coliphages). Using electron microscopy, no difference in susceptibility to freezing could be detected with respect to morphological phage types, which were either small icosahedral particles or complex tailed phages. The study of viral indicators at 4°C versus 25°C showed a higher survival of the various coliphages over time at 4°C. F-pili specific leviviridae were particularly susceptible to the antiviral factors at 25°C and no viable units per ml were detected after one month at that temperature, whereas somatic coliphages were detected in higher numbers after this period, especially at 4°C.



68. **Calcium hypochlorite as a disinfecting additive for dental stone.** Twomey, J. O., Abdelaziz, K. M., Combe, E. C., Anderson, D. L. (2003). *The Journal of prosthetic dentistry* 90:282-288. STATEMENT OF PROBLEM: Dental casts come into direct contact with impression materials and other items that are contaminated by saliva and blood from a patient's mouth, leaving the casts susceptible to cross-contamination. Topical methods of disinfecting casts are difficult to control, while immersion methods are potentially destructive. Thus, an additional method to control cross-contamination between patients and laboratory personnel is needed. PURPOSE: This study was undertaken in an attempt to develop a dental stone with disinfecting properties and adequate compressive and tensile strengths. MATERIAL AND METHODS: Calcium hypochlorite [Ca(OCl)<sub>2</sub>] in aqueous solution in concentrations from 0 to 1.5% was tested as a disinfecting additive to type V dental stone. The compressive and tensile strength properties of the modified stone were measured (MPa) using a universal testing machine at a consistency similar to unmodified stone. Strength data were analyzed by 1-way ANOVA and post hoc Tukey-Kramer procedure ( $\alpha < \text{or} = .05$ ). To measure the disinfecting ability, the effect on *Bacillus subtilis* bacteriophage phi29 was tested in triplicate to find the minimum concentration at which no phage was detected. Additionally, 3 impressions were disinfected with CaviCide, and 3 impressions rinsed in water served as controls. RESULTS: In general, the effect of adding the disinfectant to the stone was a decrease in strength. Exceptions were the dry compressive strength, for which there was a significant increase in strength ( $P=.048$ ) at 0.5%, and the wet compressive and wet tensile strength, which showed no significant difference between the 1.5% and the control. When Ca(OCl)<sub>2</sub> was added at the concentration 0.5% (2765 ppm available chlorine), the gypsum had acceptable mechanical properties; dry compressive strength was  $78.86 \pm 4.12$  MPa, and dry tensile strength was  $10.64 \pm 1.27$  MPa, compared to control values of  $67.85 \pm 6.28$  and  $13.41 \pm 1.24$  MPa, respectively. At concentrations of 0.3% and higher (36 1650 ppm of available chlorine), calcium hypochlorite was able to completely inactivate phi29. CONCLUSION: It is possible to prepare a type V dental stone that contains a disinfectant, has adequate mechanical properties, and will reduce numbers of residual microorganisms. For example, stone mixed with water containing 0.5% Ca(OCl)<sub>2</sub> meets these criteria
69. **The prophage sequences of *Lactobacillus plantarum* strain WCFS1.** Ventura, M., Canchaya, C., Kleerebezem, M., de Vos, W. M., Siezen, R. J., Brussow, H. (2003). *Virology* 316:245-255. The *Lactobacillus plantarum* commensal WCFS1 contains four prophage elements in its genome. Lp1 and Lp2 are two about 40-kb-long uninducible prophages that share closely related DNA packaging, head and tail genes defining a second lineage of pac-site Siphoviridae in *L. plantarum*, distinct from *L. plantarum* phage phiG1e, but related to Bacillus phage SPP1 and Lactococcus phage TP901-1. Northern analysis revealed transcribed prophage genes exclusively near both attachment sites. Comparative genomics identified candidate lysogenic conversion genes (LCG) downstream of the lysis cassette and within the lysogeny module. Notable are genes with sequence similarities to putative LCG from *Streptococcus pyogenes* prophages and to a *Bacillus* plasmid. Both prophages harbored tRNA genes. R-Lp3 and R-Lp4 represent short prophage remnants; R-Lp3 abuts Lp2 and displays sequence links to cos-site Siphoviridae.
70. **pGIL01, a linear tectiviral plasmid prophage originating from *Bacillus thuringiensis* serovar *israelensis*.** Verheust, C., Jensen, G., Mahillon, J. (2003). *Microbiology (Reading England)* 149:2083-2092. *Bacillus thuringiensis* serovar *israelensis* harbours, in addition to several circular plasmids, a small linear molecule of about 15 kb. Sequence analysis of this molecule, named pGIL01, showed the presence of at least 30 ORFs, five of which displayed similarity with proteins involved in phage systems: a B-type family DNA polymerase, a LexA-like repressor, two potential muramidases and a DNA-packaging protein (distantly related to the P9 protein of the tectiviral phage PRD1). Experimental evidence confirmed that pGIL01 indeed corresponds to the linear prophage of a temperate phage. This bacteriophage, named GIL01, produces small turbid plaques and is sensitive to organic solvents, which suggests the presence of lipid components in its capsid. Experiments using proteases and exonucleases also revealed that proteins are linked to the genomes of both pGIL01 prophage and GIL01 phage at their 5' extremities. Altogether, these features are reminiscent of those of phages found in the Tectiviridae family, and more specifically of those of PRD1, a broad-host-range phage of Gram-negative bacteria. Dot-blot hybridization, PFGE, PCR and RFLP analyses also showed the presence of pGIL01 variants in the *Bacillus cereus* group.
71. **Selection of bacteriophage-resistant mutants of *Streptococcus thermophilus*.** Viscardi, M., Capparelli, R., Di Matteo, R., Carminati, D., Giraffa, G., Iannelli, D. (2003). *Journal of Microbiological Methods* 55:109-119. Phage-resistant mutants have been isolated from *Streptococcus thermophilus*. Selection was carried out using anti-phage antibodies or Hoechst 33258-labelled phages. Two mutants out of eight tested displayed reduced acidifying capacity. Selection of the bacteria that extruded more rapidly the fluorochrome 5-6-carboxyfluorescein diacetate (CFDA) restored the acidifying capacity of these two mutants to the level of the parental strains. Mutants displaying phage resistance and good acidifying capacity were obtained in 4-5 days. New phages that are able to overcome the protection mechanisms of the existing bacteria arise continually in the dairy environment. The procedures described here permit to replace promptly the starter culture susceptible to newly emerged phages with a resistant one.
72. **Risk management in biological evolution.** Wagner, A. (2003). *Journal of Theoretical Biology* 225:45-57. I present a framework to study the evolution of traits that allow an organism to survive life-threatening but rare risks. Specifically, I am concerned with risks so rare that any one individual in a population may not experience the risk-causing event in its lifetime. A theory of rare risk management is virtually absent in evolutionary biology, although it is well developed in economics. This is surprising because of the great influence economics had on evolutionary biology, and because biology is full of examples for evolved risk management traits. They include the ability of bacteria to sporulate, of pathogens to survive antibiotic treatment, of temperate bacteriophages to enter a lytic life cycle, as well as traits that allow higher organisms to survive rare environmental disasters, such as sporadic wildfires and irregular flooding. I make predictions about the sustenance of risk management traits under two scenarios, one where the catastrophic events cause individual deaths, and another one where catastrophic events cause population extinction. A well-developed theory of risk management will not only predict the distribution of risk management traits, but may also serve other purposes, such as to reconstruct the spectrum of environments that an organism encountered in its evolutionary history from the record stored in its genome's memory
73. **Efficacy and durability of *Bacillus anthracis* bacteriophages used against spores.** Walter, M. H. (2003). *Journal of Environmental Health* 66:9-15, 24. Antibiotics and vaccines help fight anthrax disease, but there are

no anthrax spore control methods suitable for use in environments where humans are present. The work reported in this article indicates that bacteriophages may help reduce risk from anthrax spores. Dose-response studies demonstrated that higher concentrations of mixed *Bacillus anthracis* bacteriophages ( $3.5 \times 10^8$  plaque-forming units per milliliter) inhibited subsequent growth of bacteria when sprayed on *B. anthracis* spores. Phages also were tested for durability under conditions designed to simulate environments possibly encountered during mass phage production, storage, and use against anthrax spores. They remained infectious at temperatures from  $-20^\circ\text{C}$  to  $37^\circ\text{C}$ , under filtration, aerosolization, and treatments with perspiration and blood. Phages were sensitive to temperatures over  $55^\circ\text{C}$  and to desiccation. Ultraviolet light reduced spore viability more than phage infectivity under similar conditions. The potential for personal or environmental decontamination of anthrax spores with phages is discussed.

74. **Suppression of *Salmonella* growth by wild-type and large-plaque variants of bacteriophage Felix O1 in liquid culture and on chicken frankfurters.** Whichard, J. M., Sriranganathan, N., Pierson, F. W. (2003). *Journal of Food Protection* 66:220-225. The bacteriophage Felix O1, a member of Myoviridae, is specific for, and possesses a broad host range within, the genus *Salmonella*. This work explores a Felix O1 phage-based intervention for *Salmonella enterica* serotype Typhimurium DT104 that is potentially applicable at several stages of animal production and processing. A variant of Felix O1 was obtained that produces a larger, clearer plaque phenotype (LP) on *Salmonella* Typhi than wild-type Felix O1 (WT) does, not unlike r mutants of phage T4. LP exhibited slightly more extensive overall suppression of *Salmonella* Typhi in brain heart infusion (BHI) broth, as ascertained on the basis of culture turbidity (optical density at 600 nm). Both phage variants suppressed log phase BHI broth cultures containing  $8.2 \times 10^6$  CFU of *Salmonella* Typhimurium DT104 per ml. A PFU/CFU ratio of 1.0 was effective for WT and LP, whereas increasing the PFU/CFU ratio to 5.0 did not increase suppression. Untreated *Salmonella*-contaminated frankfurters were compared with treated samples (PFU/CFU ratio,  $1.9 \times 10^4$ ) to test WT and LP for their ability to suppress *Salmonella* growth on chicken frankfurters contaminated with 300 CFU of *Salmonella* Typhimurium DT104. Suppression levels of 1.8 and 2.1 log units were achieved with WT and LP, respectively ( $P = 0.0001$ ), but no difference was found between the performances of the two variants ( $P = 0.5088$ ).
75. **Wide geographic distribution of bacteriophages that lyse the same indigenous freshwater isolate (*Sphingomonas* sp. strain B18).** Wolf, A., Wiese, J., Jost, G., Witzel, K. P. (2003). *Applied and Environmental Microbiology* 69:2395-2398. An indigenous freshwater bacterium (*Sphingomonas* sp. strain B18) from Lake Plubetasee (Schleswig-Holstein, Germany) was used to isolate 44 phages from 13 very different freshwater and brackish habitats in distant geographic areas. This bacterial strain was very sensitive to a broad spectrum of phages from different aquatic environments. Phages isolated from geographically distant aquatic habitats, but also those from the same sample, were diverse with respect to morphology and restriction pattern. Some phages were widely distributed, while different types coexisted in the same sample. It was concluded that phages could be a major factor in shaping the structure of bacterial communities and maintaining a high bacterial diversity.
76. **Sorption of MS2 bacteriophage to layered double hydroxides: effects of reaction time, pH, and competing anions.** You, Y., Vance, G. F., Sparks, D. L., Zhuang, J., Jin, Y. (2003). *Journal of Environmental Quality* 32:2046-2053. Batch sorption and column breakthrough studies were conducted to investigate the potential of layered double hydroxides (LDHs) to remove bacteriophage MS2 from contaminated waters. All four of the LDHs evaluated in this study had very high retention capacities for MS2. Sorption results showed that MS2 could be completely removed from  $5.2 \times 10^2$  plaque-forming units (pfu)/mL solution by Mg-Al LDH 2 (i.e., 2:1 Mg to Al ratio LDH), with the highest sorption capacity observed in this study of  $1.51 \times 10^{10}$  pfu/g. Attachment of MS2 to LDHs was a rapid process and reached quasi-equilibrium after a 1-h reaction time. Within the pH range studied (pH 4-9), Mg-Al LDH 2 showed high sorption potential for MS2 at all pH values but sorption decreased slightly with increasing solution pH. Background solution anions influenced virus sorption, with  $\text{SO}_4^{2-}$  and  $\text{HPO}_4^{2-}$  decreasing sorption significantly whereas the presence of  $\text{NO}_3^-$  had little effect on the attachment of MS2 to Mg-Al LDH 2. The addition of another virus ( $\phi\text{X174}$ ) only caused a slight decrease in the retention of MS2 by Mg-Al LDH 2, suggesting that there was insignificant competitive sorption between MS2 and  $\phi\text{X174}$  on LDH surfaces. Results from column experiments indicate that there was no MS2 breakthrough from columns packed with Mg-Al LDH 2-coated sand, suggesting complete MS2 retention at the virus concentration tested. The high mass recovery by beef extract solution revealed that the removal of viruses by the LDH was due to sorption of MS2 to LDH surfaces, rather than inactivation.
77. **Genome of *Xanthomonas oryzae* bacteriophage Xp10: an odd T-odd phage.** Yuzenkova, J., Nechaev, S., Berlin, J., Rogulja, D., Kuznedelov, K., Inman, R., Mushegian, A., Severinov, K. (2003). *Journal of Molecular Biology* 330:735-748. Xp10 is a lytic bacteriophage of the phytopathogenic bacterium *Xanthomonas oryzae*. Though morphologically Xp10 belongs to the Syphoviridae family, it encodes its own single-subunit RNA polymerase characteristic of T7-like phages of the Podoviridae family. Here, we report the determination and analysis of the 44,373 bp sequence of the Xp10 genome. The genome is a linear, double-stranded DNA molecule with 3' cohesive overhangs and no terminal repeats or redundancies. Half of the Xp10 genome contains genes coding for structural proteins and host lysis functions in an arrangement typical for temperate dairy phages that are related to the *Escherichia coli*  $\lambda$  phage. The other half of the Xp10 genome contains genes coding for factors of host gene expression shut-off, enzymes of viral genome replication and expression. The two groups of genes are transcribed divergently and separated by a regulatory region, which contains divergent promoters recognized by the host RNA polymerase. Xp10 has apparently arisen through a recombination between genomes of widely different phages. Further evidence of extensive gene flux in the evolution of Xp10 includes a high fraction (10%) of genes derived from an HNH-family endonuclease, and a DNA-dependent DNA polymerase that is closer to a homolog from *Leishmania* than to DNA polymerases from other phages or bacteria.
78. **Virus retention and transport as influenced by different forms of soil organic matter.** Zhuang, J., Jin, Y. (2003). *Journal of Environmental Quality* 32:816-823. Organic materials are widespread in natural soil and aquatic environments. Their effect on virus transport is very important in assessing the risk for contamination of ground water by viruses. This study aimed to determine how different forms (mineral-associated and dissolved) of natural organic matter influence the retention and transport of two bacteriophages (MS-2 and  $\phi\text{X174}$ ) in two porous media (a sand and a soil). We found that mineral-associated organic matter significantly promoted the transport of one virus (MS-2) but not the other ( $\phi\text{X174}$ ) in a phosphate-buffered saline solution. Similarly, MS-2 was retained less in sand columns with increasing concentrations of dissolved humic acid, while little effect was observed for  $\phi\text{X174}$ .

under the same conditions. The two viruses have different surface properties and thus exhibited different reactivity to the metal oxides present on sand particles and were affected differently by organic matter. Because the organic matter used in the study was negatively charged and hydrophilic, blocking of virus sorption sites and increasing of virus-medium electrostatic repulsion arising from modification of the sand and virus surface by organic matter are probably responsible for the facilitated transport. For dissolved humic acid, its competition for sorption sites with viruses was an additional mechanism involved. This study suggests that the effect of organic matter varied depending on the organic material properties and the type of viruses involved. As a general trend, the effect of organic matter was dominated by electrostatic rather than hydrophobic interactions

79. **Autolysis and autoaggregation in *Pseudomonas aeruginosa* colony morphology mutants.** D'Argenio, D. A., Calfee, M. W., Rainey, P. B., Pesci, E. C. (2002). *Journal of Bacteriology* 184:6481-6489. Two distinctive colony morphologies were noted in a collection of *Pseudomonas aeruginosa* transposon insertion mutants. One set of mutants formed wrinkled colonies of autoaggregating cells. Suppressor analysis of a subset of these mutants showed that this was due to the action of the regulator WspR and linked this regulator (and the chemosensory pathway to which it belongs) to genes that encode a putative fimbrial adhesin required for biofilm formation. WspR homologs, related in part by a shared GGDEF domain, regulate cell surface factors, including aggregative fimbriae and exopolysaccharides, in diverse bacteria. The second set of distinctive insertion mutants formed colonies that lysed at their center. Strains with the most pronounced lysis overproduced the *Pseudomonas quinolone* signal (PQS), an extracellular signal that interacts with quorum sensing. Autolysis was suppressed by mutation of genes required for PQS biosynthesis, and in one suppressed mutant, autolysis was restored by addition of synthetic PQS. The mechanism of autolysis may involve activation of the endogenous prophage and phage-related pyocins in the genome of strain PAO1. The fact that PQS levels correlated with autolysis suggests a fine balance in natural populations of *P. aeruginosa* between survival of the many and persistence of the few.
80. **Uneven growth and different susceptibility to viruses among bacteria increase estimates of virus production in the East Sea based on TEM observation.** Huang, C. Y., Cho, B. C. (2002). *Aquatic Microbial Ecology* 27:211-218. We developed a theory that uneven distribution of bacterial growth rates and different susceptibility to viral infection in bacterial community could result in higher estimates of virus production based on transmission electron microscopy (TEM) observation (*VPTEM*) compared to estimates obtained by neglecting uneven growth and different susceptibilities in the bacterial community. We tested this idea by classifying bacteria into 4 groups based on morphotypes (i.e. rods, cocci, curved shapes, and spirillae) and enumerating the frequency of visibly infected cells (FVIC) and the frequency of dividing cells (FDC; an indirect measure of the growth rates) in the 4 groups in the East Sea samples ( $n = 15$ ). FVIC and FDC varied between different morphotypes and were highest in cocci. Further, FVIC and estimated growth rates of bacterial morphotypes were significantly correlated. The presence of a fast-growing bacterial group (apparently more susceptible to viral infection) in the bacterial community substantially increased (1.2 to 2.8-fold) the estimates of *VPTEM* in comparison to those obtained by using the mean growth rate of the bacterial community. Until now the differences between virus production measured by virus decay rates (*VPD*) and *VPTEM* have been thought to be explained by adsorption of viruses to particles, degradation of viruses due to enzymes and inactivation of viruses caused by sunlight. It seems that uneven growth and different susceptibility to viruses in the bacterial community might be another additional explanation for the discrepancy between *VPD* and *VPTEM*.
81. **Flow cytometric analysis of an *Emiliana huxleyi* bloom terminated by viral infection.** Jacquet, S., Heldal, M., Iglesias-Rodriguez, D., Larsen, A., Wilson, W. H. (2002). *Aquatic Microbial Ecology* 27:111-124. During a field mesocosm experiment conducted in coastal waters off western Norway, 11 m<sup>3</sup> enclosures were filled with unfiltered seawater and enriched daily with different nitrate and phosphate concentrations in order to induce a bloom of the coccolithophorid *Emiliana huxleyi* under different nutrient regimes. Flow cytometry (FCM) analysis was performed 5 times d<sup>-1</sup> in order to follow the initiation, development and termination of the bloom as well as the production of large virus-like particles (LVLPs) identified as *E. huxleyi* viruses (*EhV*). *EhV* production was observed first in the enclosure where N was in excess, and P limitation induced a lower burst size compared to nitrate-replete enclosures. These observations suggest a critical role for both P and N in *E. huxleyi*-*EhV* interactions. Concomitant to *EhV* production, a shift was observed between the original population (coccolith-bearing cells) towards a population characterized by the same chlorophyll *a* (chl *a*) fluorescence but with lower right angle light scatter values. This population is likely to correspond to either senescent cells losing their coccoliths or cells characterized by a lower production of coccoliths possibly due to viral infection. At the end of experiment, a significant proportion of *E. huxleyi* had survived after the end of the bloom. This suggests either the presence of a resistant form of the coccolithophorid or a change in the dominance of different host and/or viral strains during the bloom. A periodical pattern in virus production was recorded with virus number decreasing during the second part of the day suggesting that virus production may be synchronized to the daily light cycle. Our results provide new insights towards the understanding of the relationship between a key marine species and its specific virus.
82. **Bacteriophages isolated from activated sludge process and their polyvalency.** Kahn, M. A., Satoh, H., Katayama, H., Kurisu, F., Mino, T. (2002). *Water Research* 36:3364-3370. In this study, bacteriophages were isolated from activated sludge and their host range was studied. Bacterial isolates were obtained from an activated sludge process treating urban sewage, and bacteriophages were obtained by plaque assay using the bacterial isolates obtained in this study as the host. Out of 15 bacteria isolated, 9 supported plaque formation. The host range test was conducted with a combination of 8 bacteriophage isolates and 9 bacterial isolates. All of the 8 bacteriophages tested were found to form plaques on more than 1 host, and 4 of them formed plaques on both Gram-positive and Gram-negative bacterial isolates. Three of the 8 bacteriophages failed to form plaques on their original bacterial host. The experimental result indicates that bacteriophages are an active part of the activated sludge microbial ecosystem, having a very close ecological relationship with their host bacteria.
83. **[The resistance conferred by the R/M system LlaBIII against bacteriophages].** Kong, J., Josephsen, J., Ma, G. R. (2002). *Acta Microbiologica Sinica* 42:246-250. LlaBIII, isolated from the naturally occurring plasmid pJW566 from *Lactococcus lactis* subsp. *cremoris* W56, encoded a restriction and modification (R/M) system. The plasmid pJK1 carrying the R/M system LlaBIII was transformed into *L. lactis* IL1403 with type I R/M system located on chromosome and the strain MG1614[pAW601] with AbiS gene on plasmid pAW601, respectively. The transformants obtained showed stacking resistance against bacteriophages. The plasmid pJK1 was transformed into industrial

strains *L. lactis* SMO86 and CHCC2281, and showed the EOP of the bacteriophages decreased by 10(-3) and 10(-5), respectively. The results indicated that the R/M system LlaBIII could protect strains from bacteriophages in dairy fermentation.

84. **Marine phage genomics.** Paul, J. H., Sullivan, M. B., Segall, A. M., Rohwer, F. (2002). *Comparative Biochemistry and Physiology part B Biochemistry & Molecular Biology* 133:463-476. Marine phages are the most abundant biological entities in the oceans. They play important roles in carbon cycling through marine food webs, gene transfer by transduction and conversion of hosts by lysogeny. The handful of marine phage genomes that have been sequenced to date, along with prophages in marine bacterial genomes, and partial sequencing of uncultivated phages are yielding glimpses of the tremendous diversity and physiological potential of the marine phage community. Common gene modules in diverse phages are providing the information necessary to make evolutionary comparisons. Finally, deciphering phage genomes is providing clues about the adaptive response of phages and their hosts to environmental cues.
85. **Coccolithovirus (*Phycodnaviridae*): characterisation of a new large dsDNA algal virus that infects *Emiliania huxleyi*.** Schroeder, D., Oke, J., Malin, G., Wilson, W. H. (2002). *Archives of Virology* 147:1685-1698. *Emiliania huxleyi*-specific viruses (EhV) were isolated from *E. huxleyi* blooms off the coast of Plymouth, UK, in July 1999 and July/August 2001, and from an *E. huxleyi* bloom induced during a mesocosm experiment in a fjord off Bergen, Norway, during June 2000. Transmission electron microscopy revealed that all 10 virus isolates are 170-200 nm in diameter with an icosahedral symmetry. Their density is approximately 1.2 in CsCl gradients and they have large double stranded DNA genomes approximately 410 kb in size. Phylogenetic analysis of the DNA polymerase genes of these viruses suggests that EhV belongs to a new genus within the family of algal viruses, Phycodnaviridae. We propose to name this new virus genus *Coccolithovirus*. Differences within members of the *Coccolithovirus* were elucidated by host range analysis of the virus isolates and sequence analysis of a gene fragment encoding part of their putative major capsid protein. All 10 virus isolates within this new genus only infected *E. huxleyi* strains that have previously been shown to exhibit low dimethylsulphoniopropionate lyase (DMSP-lyase) activity (CCMP1516, CCMP374 and L), while *E. huxleyi* strains with high DMSP-lyase activity (CCMP373 and CCMP379) were resistant to infection.
86. **Estimation of biologically damaging UV levels in marine surface waters with DNA and viral dosimeters.** Wilhelm, S. W., Jeffrey, W. H., Suttle, C. A., Mitchell, D. L. (2002). *Photochemistry and photobiology* 76:268-273. We have surveyed the biologically harmful radiation penetrating the water column along a transect in the western Gulf of Mexico using dosimeters consisting of intact viruses or naked calf-thymus DNA (ctDNA). The indigenous marine bacteriophage PWH3a-P1, which lytically infects the heterotrophic bacterium *Vibrio natriegens* (strain PWH3a), displayed decay rates for infectivity approaching  $1.0 \text{ h}^{-1}$  in surface waters when deployed in a seawater-based dosimeter. The accumulation of pyrimidine dimers in ctDNA dosimeters provided a strong correlation to these results, with pyrimidine dimers representing more than 0.3% (up to ca 3800 dimers  $\text{Mb}^{-1}$  DNA) of the total DNA in dosimeters exposed to sea surface levels of solar radiation. The results demonstrate a strong correlation between the dimer formation in the DNA dosimeters, the decay rates of viral infectivity and the penetration of UVB radiation into the water column. The decay of viral infectivity attenuated with depth in a manner similar to the decay of solar radiation and was still significant at 10 m in offshore oligotrophic water and at dimer frequencies less than 0.1% (ca 200-300 dimers  $\text{Mb}^{-1}$  DNA)
87. **Virus dynamics in a coccolithophore-dominated bloom in the North Sea.** Wilson, W. H., Tarran, G., Zubkoy, M. V. (2002). *Deep Sea Research Part II: Tropical Studies in Oceanography* 49:2951-2963. We used analytical flow cytometry (AFC) to determine virus concentrations through vertical profiles in a coccolithophore-dominated bloom in the northern North Sea during June 1999. We present the first high-intensity sampling data of viruses from a lagrangian survey to gain a unique insight into the temporal and spatial dynamics of viruses in an open-water sight. Virus abundances ranged from  $2.6 \times 10^5$  to  $5.4 \times 10^6 \text{ ml}^{-1}$ , which is within the range expected for open-water environments. The highest concentrations were invariably observed in surface waters. During the lagrangian experiment there was a net decrease in virus numbers, suggesting that they were actively infecting hosts. Large viruses could be easily discriminated from small viruses since there was at least an order of magnitude difference in their AFC side-scatter values. Large viruses, assumed to infect DMS-producing algae, did not appear to influence DMS/DMSP production. It is likely that microzooplankton out-competed viruses for coccolithophore prey/hosts. Lower small virus to bacteria ratios (VBR) were observed in a subsurface layer compared to the more productive surface layers. The subsurface layer was dominated by a species of  $\alpha$ -proteobacteria related to the genus *Roseobacter*, and the low VBR may indicate that viruses were infecting *Roseobacter* in this layer. Application of AFC is an excellent technique for high-definition sampling of virus communities, although it is recognised that we are working at the limit of detection for many small viruses using currently available nucleic acid stains.
88. **Inhibition of spontaneous induction of lambdoid prophages in *Escherichia coli* cultures: simple procedures with possible biotechnological applications.** Czyz, A., Los, M., Wrobel, B., Wegrzyn, G. (2001). *BMC biotechnology [electronic resource]* 1:1. BACKGROUND: Infections of bacterial cultures by bacteriophages are serious problems in biotechnological laboratories. Apart from such infections, prophage induction in the host cells may also be dangerous. *Escherichia coli* is a commonly used host in biotechnological production, and many laboratory strains of this bacterium harbour lambdoid prophages. These prophages may be induced under certain conditions leading to phage lytic development. This is fatal for further cultivations as relatively low, though still significant, numbers of phages may be overlooked. Thus, subsequent cultures of non-lysogenic strains may be infected and destroyed by such phage. RESULTS: Here we report that slow growth of bacteria decreases deleterious effects of spontaneous lambdoid prophage induction. Moreover, replacement of glucose with glycerol in a medium stimulates lysogenic development of the phage after infection of *E. coli* cells. A plasmid was constructed overexpressing the phage 434 *cl* gene, coding for the repressor of phage promoters which are necessary for lytic development. Overproduction of the *cl* repressor abolished spontaneous induction of the  $\lambda\text{imm}434$  prophage. CONCLUSIONS: Simple procedures that alleviate problems with spontaneous induction of lambdoid prophage and subsequent infection of *E. coli* strains by these phages are described. Low bacterial growth rate, replacement of glucose with glycerol in a medium and overproduction of the *cl* repressor minimise the risk of prophage induction during cultivation of lysogenic bacteria and subsequent infection of other bacterial strains.

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Contact [Steve Abedon](#) ([microdude+@osu.edu](mailto:microdude+@osu.edu)) with suggestions, criticisms, comments, or anything else that might help make this a better site.