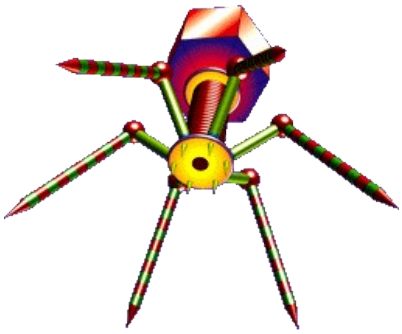

Bacteriophage Ecology Group (BEG) News

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

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Editorial

Editorials should be written on subjects relevant to The Bacteriophage Ecology Group as an organization, *BEG News* (either the concept or the current issue), 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 correspondence to abedon.1@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 any other document formats), and in English.

BEG: What we are, Where we are, Where we're going

The Bacteriophage Ecology Group (BEG) was born during the Summer of 1995 at the biannual Population Biology of Microorganisms Gordon Conference. The original group consisted of myself (Steve Abedon) plus a number of graduate students and post-docs including Brendan Bohannan, Greg Krukonis, Sharon Messenger, John Mittler, Tom Palys, and Ing-Nang Wang. At that moment I was in transition from a somewhat unsuccessful post-doc at the University of Pennsylvania (studying AIDS immunology of all things) to a tenure-track position in the department of Microbiology at The Ohio State University. Also at the time, I had a vague idea that service toward the profession counted for something, and that taking on a project such as BEG could contribute toward my college's service expectations.

Of course, as with all reasonably OK ideas, this one had its genesis long before the Summer of 1995. In fact, BEG's roots may be found in two locales. First, there is the obvious precedent of Max Delbrnck's Phage Group as a means of motivating camaraderie among researchers and to promote outstanding phage research ("Phage Group" → "Bacteriophage Ecology Group," get it?). Second, by working with mentors highly influenced by the phage group--Harris Bernstein, the man who (by some tangled turn of logic that I don't fully understand) gave his mother's "name" to the *amber* mutation (amber is the English *translation* of the German word "bernstein"), was my Ph.D. advisor and John Spizizen, Emory Ellis' first post-doc, was both my department head and on my Ph.D. committee--I found myself immersed in bacteriophagy but nevertheless isolated from bacteriophage ecologists. This isolation was perhaps more one of attitude than of geography since a mere one mile south of the Bernstein laboratory there were not one but two laboratories actively engaged in bacteriophage ecology research: Conrad Istock's group with their ecology of bacteriophages in soil and Chuck Gerba's applied bacteriophage ecology. As far as I am aware, none of us were extensively talking with each other! This travesty, combined with my ongoing frustration, during the late

1980s, early 1990s as I attempted to proselytize the relevance of ecology to molecular geneticists (my supposed Ph.D. area of concentration), resulted in an observation that would eventually become BEG: Bacteriophage ecologists seem to interact with just about anyone but other bacteriophage ecologists. The surprisingly large concentration of bacteriophage ecologists at the 1995 Gordon conference made me realize that not only should this sad situation change, but that it could.

Additionally, in the simpler systems of biology, it should be possible for the proximate causation people (e.g., molecular biologists, physiologists, and biochemists) to talk to the ultimate causation people (ecologists and evolutionists), and *vice versa*, and there aren't too many biological systems that are much simpler than bacteriophages. Thus, my agenda is both broader and more ambitious than just the organization and development of bacteriophage ecology: I additionally hope to merge bacteriophagy into a coherent whole. Or, more precisely, *re*merge these two camps since, in fact, the roots of bacteriophagy can be found in an organismal biology that embodied a concern for both philosophies (see, for example, the translation of FTlix d'Herelle, 1917, below).

BEG, from the start, was a child of the internet. BEG began with e-mail but by July of 1996 consisted of a web site. The bulk of the work involved in getting this web site into its current form began in the following months as a catharsis aimed at getting me past the dual crises of my mother's death (as well as both of her parents, my grandparents) and my ongoing inability to complete the set up of my laboratory (the most humorous delay involved the loss of my centrifuge during its shipment when a box containing a motorcycle apparently fell upon it). Part of this development included putting on line my collection of bacteriophage ecology references that I had been collecting and assembling since my graduate-school days. We are now up to 2344 references in this bibliography! Milestones in the further development of the BEG site included the incorporation of a search engine for these references (late Summer, 1998) and my obtaining the www.phage.org URL (ditto). These two events are correlated since it was my need to run the search engine on a Windows-based machine that forced me off of our (Unix) campus web server (now used as a mirror site) and it was my frustration employing an IP address for this new site, rather than an URL (plus my dislike of long URLs, e.g., www.mansfield.ohio-state.edu/~sabedon/), that motivated me to purchase www.phage.org. Right from that start BEG has also proudly emphasized bacteriophage ecologists and currently our membership consists of 40 individuals. My guess is that this represents about half of the world's bacteriophage ecologists. Where/who are the rest of you?

If creating a web presence for bacteriophage ecology represented phase II of BEG, then here allow me to introduce phase III: *Bacteriophage Ecology Group News*. *BEG News* represents a continuation of our efforts to forge bacteriophage ecology (indeed, all of bacteriophagy) into a cohesive discipline. My hope is to publish *BEG News* quarterly, as a single web page, with issues put to rest with whatever I have written or received as of July 1, October 1, January 1, or April 1. I envisage *BEG News* as a means of introducing BEG members to new members; to publicize newly published research, newly discovered links, and new features found on the BEG site; to remind people of upcoming meetings, to advertise (for free, of course) job positions available as well as job positions wanted; etc... Most important, though, is to foster communication between all of us. Toward that latter end, I would like to highly encourage the submission of material for publication in *BEG News*. For example, we all would like to hear of any developments that are relevant to phage ecology and those of you that are closest to these developments should consider writing up short articles. We additionally would appreciate the submission of notes on relevant bacteriophage ecology research that, for whatever reason, may not be published elsewhere or in a timely fashion. In other words, people, lets start talking to each other!

BEG News will be posted as it is drafted and suggestions as well editorial comments are welcome from all. Any material not completed by the quarterly deadlines will be scheduled for tentative publication in the subsequent issue. As usual, send any materials to me at abedon.1@osu.edu (microdude+@osu.edu works just as well). 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. I anxiously look forward to everybody's participation.

MicroDude, a.k.a., **Stephen T. Abedon**

Developer and Editor
The Bacteriophage Ecology Group
Dedicated to the ecology and evolutionary biology of the parasites of unicellular organisms (UOPs)

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New BEG Members

The BEG members list can be found on the BEG home page. As we add new members, these individuals will be introduced in this section. Note that, in fact, 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, i.e., individuals listed on the BEG home page, should be limited to individuals who are actively involved in science 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: abedon.1@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 list 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 T. 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: abedon.1@osu.edu and minimally include your name and e-mail address.

As follows is a complete list of current members.

name (home page links)	status	e-mail	address	other
Stephen T. Abedon	PI	microdude+ @osu.edu	Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44096	interests, publications, home page
Hans-W. Ackermann	PI	ackermann @mcb.ulaval.ca	Félix d'Hérelle Reference Center for Bacterial Viruses, Department of Medical Biology, Faculty of Medicine, Laval University, Quebec, Qc, Canada G1K 7P4	interests, publications
Norman G. Anderson	PI	norman @lsbc.com	Large Scale Biology Corporation, 9620 Medical Center Drive, Rockville, MD, 20950	interests, publications, home page
Luis Arn□iz Dur= de Paradfs	---	larnaiz @lix.intercom.es	Balmes, 412, 5□ 2□, 08022-BARCELONA -SPAIN-	---
Slava M. Belenkiy	---	slava.belenkiy @gtri.gatech.edu	Georgia Tech (home address: 4760 Trevino Circle, Duluth, GA 30136)	interests
Ralph Bickerdike	---	rbickerdike @plymouth.ac.uk	Flat 1, no. 1, Groveley Road, Westbourne, Bournemouth, Dorset, England, UK	---
Brendan J. Bohannan	PI	bohannan @stanford.edu	Department of Biological Sciences, 223C Herrin Laboratories, Stanford University, Stanford, CA 94305-5020	interests, publications, home page
James J. Bull	PI	bull @bull.zo.utexas.edu	University of Texas at Austin, NSF Org DEB, P.O. Box 7726, Austin, Texas 78713-7726	publications
Karin Carlson	PI	karinc @bmc.uu.se	Department of Microbiology, University of Uppsala Biomedical Center, Box 581, S-751 23 Uppsala, SWEDEN	interests, publications, home page
Nina Chanishvili	PI	Chanish @kheta.ge	Kazbegi street, 41, VERA region, 380079, Tbilisi, Georgia	interests, publications, home page
Frank Desiere	---	frank.desiere @rdls.nestle.com	NestlT Research Center, P. O. Box 44, CH-1000 Lausanne 26, SWITZERLAND	interests, publications, home page
Mike Dyall-Smith	PI	m.dyall-smith @microbiology.unimelb.edu.au	Department of Microbiology and Immunology, University of Melbourne, 3052 Australia	interests, publications, home page
Harold Eddleman	---	indbio @disknet.com	Palmyra, Indiana	interests, home page
Michael Feldgarden	---	mfeldgarden @wesleyan.edu	Dept. of Biology, Rm. 257, Hall-Atwater Labs., Lawn Ave., Wesleyan University, Middletown, CT 06459-0170	interests, publications
Stephen A. Gould	---	scxsag @szn1.nott.ac.uk	Microbiology Section Division of Food Sciences, School of Biological Sciences, University of Nottingham, Sutton Bonington Campus, Loughborough, Leics. LE12 5RD U.K.	interests,
Sidney Hayes	PI	hayess @duke.usask.ca	Department of Microbiology and Immunlogy, College of Medicine, University of Saskatchewan, Saskatoon, Saskatc hewan [SK] S7N 5E5, Canada	---
Jack Heinemann	PI	j.heinemann @botn.canterbury.ac.nz	Dept PAMS, University of Canterbury, Private Bag 4800, Christchurch, New Zealand	interests, publications, home page
Richard Herman	---	rherm @phagetx.com	Phage Therapeutics, Inc, 22116 23rd Drive SE, Bothell, Washington 98021	interests
Russell T. Hill	PI	hillr @umbi.umd.edu	Center of Marine Biotechnology, University of Maryland Biotechnology Institute, Suite 236, 701 East Pratt Street, Baltimore MD 21202	publications, home page
Jim Keen	PI	jk13114 @navix.net	USMARC, PO Box 166, Clay Center, NE 68933	interests, job opening
Munawwar Ali Khan	---	munawwar @env.t.u-tokyo.ac.jp	Department of Urban Engineering, The University of Tokyo, Japan	interests
Gregory P. Krukonis	---	krukonis @wesleyan.edu	Biology Department, Hall-Atwater Labs, Lawn Ave, Wesleyan University, Middletown, CT 06459	good press
Elizabeth (Betty) Kutter	PI	t4phage @elwha.evergreen.edu	Lab 1, The Evergreen State College, Olympia, WA 98505	interests, publications, home page
Nicholas H. Mann	PI	nm @dna.bio.warwick.ac.uk	Department of Biological Sciences, University of Warwick, Coventry CV4 7AL UK	interests, publications

W. Michael McShan	---	wmcshan @rex.uokhsc.edu	Dept. of Microbiology and Immunology, University of Oklahoma Health Sciences Center, BMSB 1053, 940 S.L. Young Blvd., Oklahoma City, OK 73130	interests, publications
Carl R. Merril	PI	merrilc @helix.nih.gov	Laboratory of Biochemical Genetics, NIMH, NIH, Bldg 10, Rm 2D54 Bethesda, MD 20892	publications
Sharon L. Messenger	---	messenger @mail.utexas.edu	Dept. of Zoology, University of Texas at Austin, Austin, TX 78712-1064	---
Monica Meyer	---	meyerpod @msu.edu	Michigan State University	interests
John E. Mittler	---	jmittler @t10.lanl.gov	Theoretical Biology & Biophysics, T-10 MS-K710, Los Alamos National Laboratory, Los Alamos, NM 87545	publications
Oladele (Dele) Abiola Ogunseitan	PI	oaogunse @uci.edu	Department of Environmental Analysis & Design, University of California at Irvine, CA 92697-7070	interests, publications
Thomas Palys	---	tpalys @eagle.wesleyan.edu	Biology Department, Hall-Atwater Labs, Lawn Ave, Wesleyan University, Middletown, CT 06459	interests
Elise Schnabel	---	palmerel @pilot.msu.edu	Michigan State University, Dept. of Botany and Plant Pathology, 103 Pesticide Research Center, East Lansing, MI 48824	interests
R.S. Sharma	---	shvetank @nde.vsnl.net.in	c/o Professor of C.R. Babu (Director, Centre for Environmental Management Degraded Ecosystem, University of Delhi), Department of Botany, University of Delhi, Delhi-110 007, INDIA	interests
Ruben Sommaruga	PI	ruben.sommaruga @uibk.ac.at	University of Innsbruck, Institute of Zoology & Limnology, Technikerstr. 25, A-6020 Innsbruck, Austria	interests, publications, home page
Curtis Suttle	PI	suttle @ocgy.ubc.ca	Oceanography, University of British Columbia, 6270 University Blvd., Vancouver, BC, V6T 1Z4, CANADA	interests, publications, home page
Elizabeth Thomas	---	thomasel @elwha.evergreen.edu	Lab 1, The Evergreen State College, Olympia, WA 98505	---
Gary A. Toranzos	PI	gtoranzo @upracd.upr.clu.edu	Department of Biology, P.O. Box 23360, University of Puerto Rico, San Juan, Puerto Rico 00931-3360	interests,
Ing-Nang Wang	---	inw0137 @unix.tamu.edu	Biochemistry and Biophysics Bldg., Texas A&M University, College Station, TX 77843	publications
K. Eric Wommack	---	wommack @umbi.umd.edu	COMB, 701 E. Pratt St., Baltimore, MD 21202	interests, publications, home page
Steven J. Zullo	---	zullo @helix.nih.gov	Laboratory of Biochemical Genetics, NIMH-NIH; Bldg. 10, Rm. 2D56; 9000 Rockville Pike, Bethesda, MD 20892	interests, publications, home page

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New Links

Links relevant to The Bacteriophage Ecology Group fall into a number of categories (e.g., see Bacteriophage Ecology Links on The Bacteriophage Ecology Group home page). Listed below are those links that overtly deal with phage ecology issues. With each issue of *BEG News* this list will be included, *in toto*, but updated with new links and with no-longer-working links both clearly indicated. If you know of a link that should be included on this page, or the whereabouts of a now-dead link, please let me know.

- Assessment of MS2 Bacteriophage Adsorption to Koch Membrane
- Bacteriophage Ecology Bibliography
- Bacteriophages (an overview)
- BioVir Laboratories (an environmental testing laboratory)
- Determination of Optimal Conditions for Bacteriophage Lysis of *Janthinobacterium lividum* Broth Cultures
- The effect of phosphate status on virus populations during a mesocosm study
- G. Eliava Institute of Bacteriophage (Tbilisi)
- Host Interactions and Growth Strategy of Aquatic Bacteriophages
- How the cholera bacterium got its virulence
- Lactobacillus Bacteriophage, Lay Discussion
- The Microbe Zoo | Dirtland | House of Horrors [featuring the strangler fungus, *Vampirococcus* and *Bdellovibrio*]
- MS2 Inactivation by Chlorine during Microgravity
- Nature of Things - The Virus that Cures [10/29/98 CBC TV broadcast]
- Optimal Conditions for Bacteriophage Lysis of *Janthinobacterium lividum*
- PhageBiotics Foundation

- Phage Therapeutics, Inc.
- Phage Therapy
- *Pseudomonas* Transduction in Wild (Fresh Water)
- Pseudolysogeny
- Return of a Killer [11/2/98 *U.S. News and World Report* article on phage therapy]
- Sunlight-induced DNA damage and in marine viral communities
- Tbilisi Institute for Bacteriophage
- The Curious Microbe: *Bdellovibrio*
- The Ecology of Computer Viruses
- The Isolation of T-Even Phages
- The Virus that Cures

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New Features

In this section I will highlight new or updated features of the BEG site. If you have any ideas of how either the BEG site or *BEG News* might be improved, please let me know.

new organization for BEG links:

In the course of putting together the New Links section of *BEG News* the links list on the BEG home page has been divided into a number of separate categories (Bacteriophage Ecology Links, Old-But-Still-Functional Links, Other Phage-Related Sites, Phage Books, Additional Sites of Possible Relevance to Phage Ecology, Dead Links, and Sites with Links to BEG). This change in emphasis and organization frees up the core bacteriophage ecology section to consider just those links that overtly deal with bacteriophage ecology (e.g., the list presented here under New Links). If your site should be included in any of these categories, but isn't, please let me know.

Raettig Pre-1966 Searchable Bibliography:

Since early this year, Jocelyn Witter has been steadily adding to the *Raettig Pre-1966 Searchable Bibliography*, working as a work-study student for me (S.T.A.). The *Raettig Pre-1966 Bibliography* consists of an estimated greater-than-95-percent-complete listing of all of the pre-1966 bacteriophage references, as assembled and then published in 1958 and 1967 by Dr. Med. Hansjnrgen Raettig (*Bakteriophagie 1917 bis 1956* and *Bakteriophagie 1957-1965*, respectably, Gustav Fischer Verlag, Stuttgart). There are a total of 11,405 numbered references in these volumes, with each publication consisting of approximately half of references plus a companion volume consisting of a detailed index (in German in the first volume and in both German and in English in the second). Our near-term goal is the enter the entire reference list and then to present the list in a searchable format, just as the BEG bibliography is currently presented. Note that the Raettig bibliography will be updated periodically (as data entry progresses; currently we have the first 1057 references entered). To search the incomplete database, choose the Raettig Pre-1966 option under "Search". In a subsequent issue of *BEG News* we hope to present a history of the Raettig bibliography as well as detailed directions on how to optimally use all of the BEG bibliographies.

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Upcoming Meetings

The BEG Meetings link will continue, but reminders about 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, please send this information for posting to abedon.1@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.

Microbial Population Biology Gordon Research Conference:

The biannual Microbial Population Biology Gordon Research Conference will be held July 18 through July 23, 1999, at Plymouth State College in Plymouth, New Hampshire. A list of sessions, speakers, and session chairs is available on the web. Don't forget your sunscreen, sunglasses, and bathing suits!

Evergreen International Phage Meeting:

No word yet on the dates of this biannual Olympia, Washington meeting. The above web link still refers to last year's (1998) meeting. Extrapolating into the future, we should expect a meeting some time in or about July of 2000. The 1998 meeting had a strong bacteriophage ecology presence and with luck (i.e., with your participation!) we will do even better in 2000. Stay tuned for more information as it becomes available.

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Jobs

The BEG Employment / Job Listings page will no longer be maintained. Instead, any job listings will be found in this section of *BEG News*. If you are looking to*fill* a bacteriophage-ecology related position or are in *search of* a bacteriophage-ecology related position, please feel free to advertise as such here (there will be no charge, of course). Legitimate information only, please, and *BEG News* cannot be held

responsible for any incorrect information supplied by posters. Send any information for posting to abedon.1@osu.edu or to "BEG Jobs," *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

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 abedon.1@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.

On an Invisible Microbe Antagonistic to the Dysentery Bacillus.

Felix d'Herelle

[Sur un microbe invisible antagonistic des bacilles dysentTroqes, *Comptes rendus Acad. Sci. Paris* 165(1917):373-375.]

From the feces of diverse patients convalescing from bacillary dysentery, and in one case from the urine, I have isolated an invisible microbe with the properties of antagonism to the bacillus of Shiga. This finding is particularly easy in the cases of common enteritis following dysentery; in convalescents who do not present this complication the disappearance of the anti-microbe quickly follows that of the pathogenic bacillus. In spite of numerous examinations, I have never found the antagonistic microbes either in the feces of dysenteritics during the disease period, or in the feces of normal subjects.

The isolation of the anti-Shiga microbe is simple: one inoculates a tube of bouillon with four to five drops of feces, incubates at 37°C for 18 hours, and then filters with a Chamberland L2 filter. A small quantity of the active filtrate added, either to a broth culture of Shiga bacillus, or to an emulsion of these bacillus in broth or even in physiological saline, provokes the arrest of the culture, the death of the bacillus then their lysis, which is complete after a period of time varying from hours to days depending on the amount of the culture and the quantity of the filtrate added.

The invisible microbe grows [*cultive*] in the lysed culture of Shiga bacillus because a trace of this liquid, placed in a new culture of Shiga, reproduces the same phenomenon with the same intensity: I have carried this out up to the present time with the first stock isolated for more than fifty successive transfers. The following experiment gives, moreover, the visible evidence that the antagonistic action is produced by a living germ: if one adds to a culture of Shiga a dilution of approximately one to a million of an already lysed culture, and if, immediately after, one spreads out on an agar slant a droplet of this culture, one obtains, after incubation, a coat of dysentery bacilli showing a certain number of circles about 1 mm in diameter, where the culture is void; these points can only represent the colonies of the antagonistic microbe: a chemical substance would not be able to concentrate at defined points. In working with measured quantities, I have seen that a lysed culture of Shiga contains five to six million of these filterable germs per cubic centimeter. One three-millionth of a cubic centimeter of the preceding culture from Shiga, or a single germ, introduced into a tube of broth, inhibits the culture of Shiga even when liberally inoculated; the same quantity added to a 10 cm^3 culture of Shiga sterilizes it and lyses it in five or six days.

The diverse stocks of the antagonistic microbe which I have isolated were originally active only against the bacillus of Shiga; through symbiotic culture [*culture en symbiose*] with the dysentery bacilli of Hiss or Flexner, I could, after several passages, render them antagonistic to these bacilli. I have not obtained any results working with other microbes: typhoid bacilli, paratyphoid bacilli, staphylococci, etc. The appearance of antagonism against the bacillus of Flexner or of Hiss is accompanied by a diminution followed by a loss of power against Shiga, this power being recoverable with its original intensity after several symbiotic cultures; the specificity of antagonistic action therefore is not inherent in the nature of the invisible microbe, but is acquired in the sick organism by symbiotic culture with the pathogenic bacillus. In the absence of dysentery bacilli the anti-microbe does not grow in any medium, it does not attack heat killed dysentery bacilli; in contrast it grows perfectly in an emulsion of washed bacilli in physiological salt solution: it results from these studies that the antidysentery microbe is an obligate bacteriophage [*un bactTriophage obligatoire*].

The anti-Shiga microbe does not show any pathogenic action on any of the animals tested. Cultures of Shiga lysed by the action of the invisible microbe, which are in reality cultures of the anti-microbe, possessed the property of immunizing a rabbit against a dose of Shiga bacilli which killed the controls in five days.

I have searched for evidence of such an anti-microbe from convalescents from typhoid fever: in two cases, one from the urine and the other from the feces, I have been successful in isolating a filterable microbe giving the clear lytic property with respect to bacillus of paratyphoid A, but always less marked than the anti-Shiga microbe. These properties are attenuated in successive culture.

In summary, in certain convalescents from dysentery, I have shown that the disappearance of the dysentery bacillus coincides with the appearance of an invisible microbe endowed with antagonistic properties with respect to the pathogenic bacillus. This microbe, the true microbe of immunity, is an obligatory bacteriophage; its parasitism is strictly specific, but if it is limited to one species at a given moment, it may develop antagonism in turn against diverse germs by accustomization. It appears therefore that in bacillary dysentery, next to the anti-tonic [sic] homologous immunity, emanating directly from the organism under attack, there exists a heterologous antimicrobial immunity produced by the antagonistic microorganism. It is probable that this phenomenon is not special to dysentery, but of a more general order because I have shown it can be found likewise, though less marked, in two case [sic] of paratyphoid fever.

reprinted with the permission of the author from
FTlix d'Herelle and the Origins of Molecular Biology
William C. Summers, 1999
Yale University Press
New Haven and London

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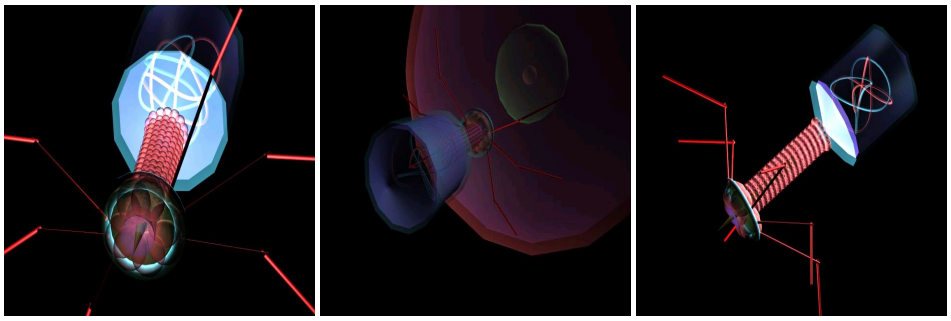
Letters

Letters should consist of comments, short statements, or personal editorials. Send all letters to abedon.1@osu.edu or to "Letters", 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 letters in English and all mailed or attached letters as Microsoft Word documents, if possible (I'll let you know if I have trouble converting any other document formats). In addition, to standard letters, BEG receives questions on a regular basis that may be addressed by BEG members. These questions are listed below. Anybody interested in answering these questions through *BEG News*, e-mail me at the following address: abedon.1@osu.edu. Alternatively, answer through the prompt following each question. Please note that these questions have not been edited for grammar, spelling, or clarity.

1. Here are some renderings of bacteriophages that I did in 3d Max 2.5 for a project for school (I'm a sophmore in High School). They may not be completly accurate but I thought it would be nice if I sent them to you. -Ed Clairmont (cyanide_plunge@hotmail.com)



These look much better as full size jpg's (esp. 1 & 3). Click on individual images to view them full size.

Questions

1. I am looking for T4 phage mutant capable of efficient generalized transduction - T4GT7. We need it for our E.coli strain construction experiments. Could you suggest where I can get this phage? Press to contact author of question.

2. Could phages be used in swimmingpool to prevent meningitis. (I forgot the specific bacteria, sorry) Because this is one of the biggist problems of swimming children or will the Cl in poolwater bestroy the phages like it does with most bacterias. Press to contact author of question.

3. How do you choose the 'package' of the phages. Because on the video by the BBC I could see there where pills, cremes and what are the main other 'ingredients' that lets us say the pills contain, phage nutrients? Press to contact author of question.

4. Because our faculty is agricultural there must be something in the work that deals with agricuture. Therefor, can you use phage in litter our in soil. One of the biggest problems in pest management is that bacterias like Nitrococcus and Nitromonas change the useful $NH4^{+}$ inot NO3- and this form is solvable in water so the pesticide floods out the soil. Let assume that these phages exist already, is it possible to stop this reaction by blokking the bacterias, our can 't you use phages at such a big scale. Press to contact author of question.

5. Do you know something about phage-kinetics? Does it follow the Michaelis-Menten equation? Are there anywhere graphics available of bacterial growth and bacterial growth after using different concentrations of phages? Press to contact author of question.

6. I'm a high school student... My interests are going to be fairly basic. Since Kindergarten I've been actively involved with science fairs, and for the past 2 years, the field of Microbiology, and since phages are rarely worked w/in my field I thought I should do some background research on some possible projects. Press to contact author of question.

7. I am student of Microbiology... I am from Guatemala, I□m looking for the procedure to isolate phages from feces. I have been looking for that technique but I can□t find nothing. Can you help me? Press to contact author of question.

8. I am a research from Plant Protection Institut, and I am doing my PhD in *Bacillus thuringiensis* phages. ...I am very interested in to obtain literature about bacteriophage (bacteriophage infections in industrial bioprocesses; influence of bacterial growth and culture media) because we have had some experiences in biopesticides production. Also, if you know to the Dr. S.B. Primrose, please, send me his email to contact him. Press to contact author of question.

9. We would like to set up a listing of any sites that have anything to do with bacteriophage info. A sort of clearing house. We are artists and are interested in detailed images (or "impressions of" type images) of bacteriophages. Press to contact author of question.

10. Is there a meeting ever held in the UK for people interested in phage therapy, and if there isnt would people in the UK be interested in maybe starting one here next year? Press to contact author of question.

11. I've been looking through your list of BEG links and came across this paper: PHENOTYPIC CONVERSIONS AS A RESULT OF PSEUDOLYSOGENY Julie J. Shaffer, John O. Schrader, and Tyler A. Kokjohn School of Biological Sciences, E151 Beadle Center, University of Nebraska-Lincoln, Lincoln, NE 68588-0666. I have an interest in the carrier state (what they call pseudolysogeny) and want to see what they are up to now. None of these authors are in the BEG list, they don't list an e-mail address, and I can't find them on the Uni.Nebraska-Lincoln staff directory. Do you have an e-mail address, or know whether they are still active? Press to contact author of question.

12. Do you know of anyone who is sequencing genomes of T3/T7-like phages. Press to contact author of question.

13. I am presently working on a paper on the effect of large hydropower projects on public health. These projects are now widely recognized to be responsible for dramatic increase in numerous waterborn diseases. These diseases are for the most part parasitic. Recent readings on the increasing interest of many scientist on the usefullness of bacteriophage to fight certain disease, got me thinking...could phage be found that would specifically attack parasites? Knowing the increasing

resistance of these parasites to chemical drugs, phages could become a very interesting tool to fight these debilitating diseases (malaria, bilhardioze, schistosomiasis, etc.). Press to contact author of question.

14. I am trying to find info about the life sequence and growth habits of the T1 phage, as well as info on how to prevent its growth and preventing it from contaminating my bacterial stocks. Any info you can provide, whether directly or in the form of a reference, would be much appreciated. Press to contact author of question.

15. Wondering if you might be able to give me some info on a bacteria called "Lwoff". It is named after Andre Lwoff at The Pasteur Institute. I think he was "The Father of Phage". I would like to know how and why it would become a human pathogen and if so, would an antibiotic kill it. Also what can it do to the body? Press to contact author of question.

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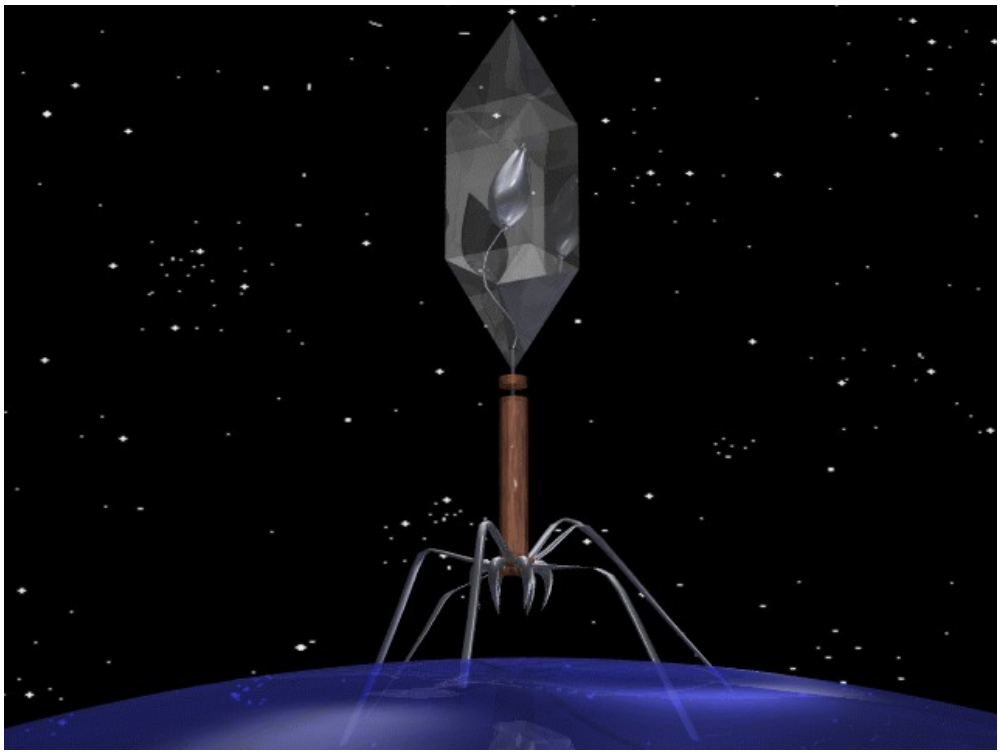
Phage Images

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 abedon.1@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.



The Face of the Phage

There is a conquering theme in all of nature. In regard to animals, this conquering is called survival; humans deem their conquests 'progress.' Of course, the humans never see themselves as animals, but that's another oddity of our species. There is in all of us a spirit of devouring, whether that be the consumption of knowledge, land, the minds of others, food, or in the case of the macrophage [sic?], life itself. Ahh, the macrophage [sic]...we call it a virus, a creature that destroys life to propagate its own DNA into the next generation. We being a judgmental people would probably look down upon the virus, making a moral judgement, and labeling these microbes 'evil.' Since we don't think of this most basic form in terms of responsibility or morality, the virus escapes our criticism.

The macrophage [sic] attacks a cell by using the cell's organelles to make copies of itself, over and over, until the cell finally ruptures and releases many more viruses. The only way it can propagate is to destroy, and in this way humans are not so different from Phage. The difference is, we do not have to destroy to create, as Phage does. Yet destruction, of both our world and ourselves is commonplace.

My argument is to never be so lulled by pride into believing that other life on earth is alien, and that we are nothing like the smallest of creatures. To look into yourself, aware of the darkness you might find, is a brave act. Perspective is made clear. Never hesitate to face yourself, the Phage, the macrophage... -anonymous

Editors note: I enjoy this image though I have no idea who the artist is (other than the URL to the page I found the image on). The text, I assume, is by the same individual. However, if I may correct the argument ever so slightly: To create is to change is to destroy. We humans mine the raw material of our procreation by destroying our environment just as inevitably as the phage destroys its (or, perhaps not just as inevitably, since not all nor, perhaps, even most phages are very good at completely destroying their environments). Just as with the phage, this destruction is sustainable long into the future, but only so long as our environments may be allowed to regenerate at least as fast as we destroy them.

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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, sending 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 (send to abedon.1@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). Also, be sure to indicate any listed publications that you feel should not be presented in the BEG Bibliography. This list is also present with available abstracts at the end of *BEG News*.

1. Effect of prey heterogeneity on the response of a food chain to resource enrichment. Bohannan, B.J.M., Lenski, R.E. (1999). *American Naturalist* 153:73-82. [PRESS FOR ABSTRACT]

2. Effect of resource supply rate on host-pathogen dynamics. Bohannan, B.J.M. (1999). ??? (eds) *Proceedings of the 8th International Symposium on Microbial Ecology*. [PRESS FOR ABSTRACT]

3. Epistatic interactions can lower the cost of resistance to multiple consumers. Bohannan, B.J.M., Travisano, M., Lenski, R.E. (1999). *Evolution* 53:292-295. [PRESS FOR ABSTRACT]

4. Unexplored reservoirs of pathogenic bacteria: protozoa and biofilms. Brown, M., Barker, J. (1999). *Trends in Microbiology* 7:???-??? [no abstract]

5. All the world's a phage. Hendrix, R.W., Smith, M.C.M., Burns, R.N., Ford, M.E., Hatfull, G.F. (1999). *Proc. Natl. Acad. Sci. USA* 96:2192-2197 [PRESS FOR ABSTRACT]

6. TB: the return of the phage. A review of fifty years of mycobacteriophage research. McNerney, R. (1999). *Int. J. Tuberc. Lung Dis.* 3:179-184. [PRESS FOR ABSTRACT]

7. Virus removal from sewage effluents during saturated and unsaturated flow through soil columns. Powelson, D.K., Gerba, C.P. (1999). *Water Research* 28:2175-2181. [PRESS FOR ABSTRACT]

8. *Felix d'Herelle and the Origins of Molecular Biology*. Summers, W.C. (1999). Yale University Press, New Haven, Connecticut.[no abstract]

9. Evaluation of virus removal in membrane separation processes using coliphage Q-beta. Urase, T., Yamamoto, K., Ohgaki, S. (1999). *Water Science and Technology* 28:9-15. [no abstract]

10. A phage DNA injection-blocking type resistance mechanism encoded by chromosomal DNA in *Lactococcus lactis* subsp. lactis PLM-18. ??? (1998). *Milchwissenschaft* 53:619-622. [PRESS FOR ABSTRACT]

11. In vivo transduction with Shiga toxin 1-encoding phage. Acheson, D.W.K., Reidl, J., Zhang, X., Keusch, G.T., Mekalanos, J.J., Waldor, M.K. (1998). *Infection and Immunity* 66:4496-4498. [no abstract]

12. Construction of multiple phage resistance in *Lactococcus lactis* subsp. lactis. Akcelik, M. (1998). *Advances in Food Sciences* 20:101-104. [PRESS FOR ABSTRACT]

13. Bacteriophages show promise as antimicrobial agents. Alisky, J., Iczkowski, K., Rapoport, A., Troitsky, N. (1998). *Journal of Infection* 36:5-15. [PRESS FOR ABSTRACT]

14. Phage resistance mechanisms in lactic acid bacteria. Allison, G.E., Klaenhammer, T.R. (1998). *International Dairy Journal* 8:207-226.[PRESS FOR ABSTRACT]

15. Peptide-guided cancer drugs show promise in mice. Barinaga, M. (1998). *Science* 279, 323-324. [PRESS FOR ABSTRACT]

16. Induction Studies on Thermophilic Phage. Barridge, B.D. (1998). The University of Nebraska - Lincoln. [no abstract]

17. Use of lytic bacteriophage for control of experimental *Escherichia coli* septicemia and meningitis in chickens and calves. Barrow, P., Lovell, M., Berchieri, A.jr. (1998). *Clinical and Diagnostic Laboratory Immunology* 5:294-298. [PRESS FOR ABSTRACT]

18. His1, and archaeal virus of the *Fuselloviridae* family that infects *Haloarcula hispanica*. Bath, C., Dyall-Smith, M.L. (1998). *J. Virol.* 72:9392-9395. [PRESS FOR ABSTRACT]

19. Modeling and analysis of a marine bacteriophage infection. Beretta, E., Kuang, Y. (1998). *Math. Biosci.* 149:57-76. [PRESS FOR ABSTRACT]

20. Microscale nutrient patches in planktonic habitats shown by chemotactic bacteria. Blackburn, N., Fenchel, T., Mitchell, J. (1998). *Science* 282:2254-2256. [PRESS FOR ABSTRACT]

21. Specific assays for bacteria using phage mediated release of adenylate kinase. Blasco, R., Murphy, M.J., Sanders, M.F., Squirrell, D.J. (1998). *Journal of Applied Microbiology* 84:661-666. [no abstract]

22. Response of model microbial communities to increased productivity. Bohannan, B.J.M. (1998). Michigan State Univeristy. [no abstract]

23. Effects of the abortive infection mechanism AbiK on the lactococcal phage p2. Boucher, I., Emond, E., Moineau, S. (1998). Denver, CO (USA). #1998 American Dairy Science Association (ADSA)/American Society of Animal Science (ASAS) Joint Meeting. 1998.[no abstract]

24. Description of two bacteriophages active against *Lotus rhizobia*. Bruch, C.W., Allen, O.N. (1998). *Proc. Am. Soil Sci. Soc.* 19:175-??? [no abstract]

25. Molecular ecology and evolution of *Streptococcus thermophilus* bacteriophages--a review. Brussow, H., Bruttin, A., Desiere, F., Lucchini, S., Foley, S. (1998). *Virus Genes* 16:95-109. [PRESS FOR ABSTRACT]

26. Viral escape from antisense RNA. Bull, J.J., Jacoboson, A., Badgett, M.R., Molineax, I.J. (1998). *Molecular Microbiology* 28:835-846. [PRESS FOR ABSTRACT]

27. The pleasures of pond scum. Carlson, S. (1998). *Scientific American* March, 96-98. [no abstract]

28. New cholera phages for *Vibrio cholerae* serovar O139. Chakrabarti, A.K., Ghosh, A.N., Sarkar, B.L. (1998). *Journal of Infection* 36:131-132. [no abstract]

29. Virus particle production in lysogenic bacteria exposed to protozoan grazing. Clarke, K.J. (1998). *FEMS Microbiology Letters* 166:177-180. [PRESS FOR ABSTRACT]

30. Increasing phage resistance of cheese starters: A case study using *Lactococcus lactis* DPC4268. Coffey, A., Coakley, M., McGarry, A., Fitzgerald, G.F., Ross, R.P. (1998). *Letters in Applied Microbiology* 26:51-55. [PRESS FOR ABSTRACT]

31. Effect of Environmental Factors upon a *Staphylococcus* Host-Phage System. Countryman, J.L. (1998). Stanford University. [no abstract]

32. Virulence of phage populations infecting *Halobacterium cutirubrum*. Daniels, L.L., Wais, A.C. (1998). *FEMS Microbiology Ecology* 25:129-134. [PRESS FOR ABSTRACT]

33. Phages infecting *Vibrio vulnificus* are abundant and diverse in oysters (*Crassostrea virginica*) collected from the Gulf of Mexico. Depaola, A., Motes, M.L., Chan, A.M., Suttle, C.A. (1998). *Applied & Environmental Microbiology* 64:346-351. [PRESS FOR ABSTRACT]

34. Evolution of *Streptococcus thermophilus* bacteriophage genomes by modular exchanges followed by point mutations and small deletions and insertions. Desiere, F., Lucchini, S., Brussow, H. (1998). *Virology* 241:345-356. [PRESS FOR ABSTRACT]

35. A leucine repeat motif in AbiA is required for resistance of *Lactococcus lactis* to phages representing three species. Dinsmore, P.K., O'Sullivan, D.J., Klaenhammer, T.R. (1998). *Gene* 212:5-11. [PRESS FOR ABSTRACT]

36. *E. coli*'s double life. Dixon, B. (1998). *ASM News* 64:616-617. [no abstract]

37. Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid pMRC01 from *Lactococcus lactis* DPC3147. Dougherty, B.A., Hill, C., Weidman, J.F., Richardson, D.R., Venter, J.C., Ross, R.P. (1998). *Molecular Microbiology* 29:1029-1038. [PRESS FOR ABSTRACT]

38. Delineating the specific influence of virus isoelectric point and size on virus adsorption and transport through sandy soils. Dowd, S.E., Pillai, S.D., Wang, S., Corapcioglu, M.Y. (1998). *Applied & Environmental Microbiology* 64:405-410. [PRESS FOR ABSTRACT]

39. AbiQ, an abortive infection mechanism from *Lactococcus lactis*. Emond, E., Dion, E., Walker, S.A., Vedamuthu, E.R., Kondo, J.K., Moineau, S. (1998). *Applied and Environmental Microbiology* 64:4748-4756. [PRESS FOR ABSTRACT]

40. Induction of the lysogenic phage encoding Cholera toxin in naturally occurring strains of toxigenic *Vibrio cholerae* O1 and O139. Faruque, S.M., Asadulghani, Abdul, A., Albert, M.J., Nasirul, I., Mekalanos, J.J. (1998). *Infection and Immunity* 66:3752-3757. [no abstract]

41. A short noncoding viral DNA element showing characteristics of a replication origin confers bacteriophage resistance to *Streptococcus thermophilus*. Foley, S., Lucchini, S., Zwahlen, M.C., Brussow, H. (1998). *Virology* 250:377-387. [PRESS FOR ABSTRACT]

42. Occurrence of a sequence in marine cyanophages similar to that of T4 gp20 and its application to PCR-based detection and quantification techniques. Fuller, N.J., Wilson, W.H., Joint, I.R., Mann, N.H. (1998). *Appl. Environ. Microbiol.* 64:2051-2060. [PRESS FOR ABSTRACT]

43. High titer, phage-neutralizing antibodies in bovine colostrum that prevent lytic infection of *Lactococcus lactis* in fermentations of phage-contaminated milk. Geller, B.L., Kraus, J., Schell, M.D., Hornsby, M.J., Neal, J.J., Ruch, F.E. (1998). *Journal of Dairy Science* 81:895-900. [PRESS FOR ABSTRACT]

44. Membrane receptor for prolate phages is not required for infection of *Lactococcus lactis* by small or large isometric phages. Geller, B.L. (1998). *Journal of Dairy Science* 81:2329-2335. [PRESS FOR ABSTRACT]

45. Predicting disinfection performance in continuous flow systems from batch disinfection kinetics. Haas, C.N., Joffe, J., Heath, M., Jacangelo, J., Anmangandla, U. (1998). *Water Science and Technology* 38:171-179. [PRESS FOR ABSTRACT]

46. Evaluation of alginate-encapsulated *Azotobacter chroococcum* as a phage-resistant and an effective inoculum. Hammad, A.M.M. (1998). *Journal of Basic Microbiology* 38:9-16. [PRESS FOR ABSTRACT]

47. Efficacy and mechanisms of action of sodium hypochlorite on *Pseudomonas aeruginosa* PAO1 phage F116. Hann, A.C., Baubet, V., Perrin, R. (1998). *Journal of Applied Microbiology* 85:925-932. [PRESS FOR ABSTRACT]

48. ??? Hausmann, R., Härle, E. (1998). *Proc. Eur. Biophys. Congr.* 1:467-??? [no abstract]

49. Optimising starter culture performance in NZ cheese plantsproduction. Heap, H.A. (1998). *Australian Journal of Dairy Technology* 53:74-78. [no abstract]

50. Phage as antibacterial tool. Holzman, D. (1998). *Genetic Engineering News* (October 15), 1-48. [no abstract]

51. Reassessment of medicinal phage……. Holzman, D. (1998). *ASM News* 64:620-622. [no abstract]

52. …Spurs companies to study therapeutic uses. Holzman, D. (1998). *ASM News* 64:622-623. [no abstract]

53. A comparison of two methods to recover phages from soil samples. Hu, T.L. (1998). *Bioresource Technology* 65:167-169. [PRESS FOR ABSTRACT]

54. Biofilm susceptibility to bacteriophage attack: the role of phage-borne polysaccharide depolymerase. Hughes, K.A., Sutherland, I.W., Jones, M.V. (1998). *Microbiology -Reading-* 45:3039-3047. [no abstract]

55. A novel filamentous phage, fs-2, of *Vibrio cholerae* O139. Ikema, M., Honma, Y. (1998). *Microbiology -Reading-* 144:1901-1906. [no abstract]

56. Mechanism of T4 Phage Restriction by a Thermosensitive Drug Resistant Factor RTSL. Ishaq, M. (1998). University of Pennsylvania. [no abstract]

57. Prevalence of broad-host-range lytic bacteriophages of *Sphaerotilus natans*, *Escherichia coli*, and *Pseudomonas aeruginosa*. Jensen, E.C., Schrader, H.S., Rieland, B., Thompson, T.L., Lee, K.W., Nickerson, K.W., Kokjohn, T.A. (1998). *Applied & Environmental Microbiology* 64:575-580. [PRESS FOR ABSTRACT]

58. Characterization of marine temperate phage-host systems isolated from Mamala Bay, Oahu, Hawaii. Jiang, S.C., Kellogg, C.A., Paul, J.H. (1998). *Applied & Environmental Microbiology* 64:535-542. [PRESS FOR ABSTRACT]

59. Significance of lysogeny in the marine environment: studies with isolates and a model of lysogenic phage production. Jiang, S.C., Paul, J.H. (1998). *Microbial Ecology* 35:235-243. [PRESS FOR ABSTRACT]

60. Gene transfer by transduction in the marine environment. Jiang, S.C., Paul, J.H. (1998). *Applied & Environmental Microbiology* 64:2780-2787. [PRESS FOR ABSTRACT]

61. Fluorescent *Escherichia coli* C for enumeration of coliphages from environmental samples. Jothikumar, N., Cliver, D.O. (1998). *BioTechniques* 24:546 [no abstract]

62. Characterization and possible functions of a new filamentous bacteriophage from *Vibrio cholerae* O139. Jouravleva, E.A., McDonald, G.A., Garon, C.F., Boesman-Finkelstein, M., Finkelstein, R.A. (1998). *Microbiology* 144:315-324. [PRESS FOR ABSTRACT]

63. The *Vibrio cholerae* mannose-sensitive hemagglutinin is the receptor for a filamentous bacteriophage from *V. cholerae* O139. Jouravleva, E.A., McDonald, G.A., Marsh, J.W., Taylor, R.K., Boesman-Finkelstein, M., Finkelstein, R.A. (1998). *Infection and Immunity* 66:2535-2539. [PRESS FOR ABSTRACT]

64. Phage display of a biologically active *Bacillus thuringiensis* toxin. Kasman, L.M., Lukowiak, A.A., Garczynski, S.F., McNall, R.J., Youngman, P., Adang, M.J. (1998). *Applied and Environmental Microbiology* 64:2995-3003. [no abstract]

65. Return of a killer. Koerner, B.I. (1998). *U.S.News and World Report* (November 2, 1998), 51-52. Phages may once again fight tough bacterial infections.[no abstract]

66. An experimental selection system to identify bacterial cells exhibiting a new DNA host specificity. Kunz, A., Meisel, A., Mackeldanz, P., Reuter, M., Krueger, D.H. (1998). *Biological Chemistry* 379:563-566. [PRESS FOR ABSTRACT]

67. Phage therapy: bacteriophages as antibiotics. Kutter, E. (1998). http://www.evergreen.edu/user/T4/PhageTherapy/Phagethea.html [no abstract]

68. Distribution of indicator bacteria and bacteriophages in shellfish and shellfish-growing waters. Legnani, P., Leoni, E., Lev, D., Rossi, R., Villa, G.C., Bisbini, P. (1998). *Journal of Applied Microbiology* 85:790-798. [PRESS FOR ABSTRACT]

69. The challenge of antibiotic resistance. Levy, S.B. (1998). *Scientific American* (March), 46-53. [PRESS FOR ABSTRACT]

70. The structural gene module in *Streptococcus thermophilus* bacteriophage ϕ Sfi11 shows a hierarchy of relatedness to *Siphoviridae* from a wide range of bacterial hosts. Lucchini, S., Desiere, F., Brussow, H. (1998). *Virology* 246:63-73. [PRESS FOR ABSTRACT]

71. Virus binding to brown algal spores and gametes visualized by DAPI fluorescence microscopy. Maier, I., Mueller, D.G. (1998). *Phycologia* 37:60-63. [PRESS FOR ABSTRACT]

72. Resistance of *Pseudomonas aeruginosa* PAO1 phage F116 to sodium hypochlorite. Maillard, J.Y., Hann, A.C., Perrin, R. (1998). *Journal of Applied Microbiology* 85:799-806. [PRESS FOR ABSTRACT]

73. Characterization of a novel cis-syn and trans-syn-II pyrimidine dimer glycosylase/AP lyase from a eukaryotic algal virus, *Paramecium bursaria* chlorella virus-1. McCullough, A.K., Romberg, M.T., Nyaga, S., Wei, Y., Wood, T.G., Taylor, J.S., Van Etten, J.L., Dodson, M.L., Lloyd, R.S. (1998). *Journal of Biological Chemistry [J. Biol. Chem.]* 273:13136-13142. [PRESS FOR ABSTRACT]

74. Synergistic effects of abiE or abiF from pNP40 when cloned in combination with abiD from pBF61. McLandsborough, L.A., Sechaud, L., McKay, L.L. (1998). *Journal of Dairy Science* 81:362-368. [PRESS FOR ABSTRACT]

75. Evidence of pseudolysogeny in a marine phage host system. McLaughlin, M.R., Paul, J.H. (1998). *Abstracts of the General Meeting of the American Society for Microbiology* 98:387-??? [no abstract]

76. Comparative survival of F^+ RNA coliphages, poliovirus type 1(PV1), and somatic salmonella phage (SSP) in advanced treated wastewater, groundwater and soil suspensions. Meschke, J.S., Sobsey, M.D. (1998). *Abstracts of the General Meeting of the American Society for Microbiology* 98:443-444. [no abstract]

77. Dynamics of the pseudolysogenic response in slowly growing cells of *Pseudomonas aeruginosa*. Miller, R.V. (1998). *Microbiology (Reading)* 144:2225-2232. [PRESS FOR ABSTRACT]

78. Abundance in sewage of bacteriophages that infect *Escherichia coli* 0157:H7 and that carry the Shiga toxin 2 gene. Muniesa, M., Jofre, J. (1998). *Applied and*

Environmental Microbiology 64:2443-2448. [PRESS FOR ABSTRACT]

79. A temperate phage with cohesive ends induced by mitomycin C treatment of *Lactobacillus casei*. Nakashima, Y., Hasuwa, H., Kakita, Y., Murata, K., Kuroiwa, A., Miake, F., Watanabe, K. (1998). *Archives of Virology* 143:1621-1626. [no abstract]

80. Comparison of the lysogeny modules from the temperate *Streptococcus thermophilus* bacteriophages TP-J34 and Sfi21: implications for the modular theory of phage evolution. Neve, H., Zenz, K.I., Desiere, F., Koch, A., Heller, K.J., Brussow, H. (1998). *Virology* 241:61-72. [PRESS FOR ABSTRACT]

81. Design of a phage-insensitive lactococcal dairy starter via sequential transfer of naturally occurring conjugative plasmids. O'Sullivan, D., Coffey, A., Fitzgerald, G.F., Hill, C., Ross, R.P. (1998). *Applied and Environmental Microbiology* 64:4618-4622. [no abstract]

82. Recovery of phages T1 and PP7, and poliovirus from water with a hollow-fiber, 50,000 molecular weight cut-off ultrafilter. Oshima, K., Ommani, A. (1998). *Abstracts of the General Meeting of the American Society for Microbiology* 98:438-??? [no abstract]

83. Genetic dynamics of *Salmonella typhi*-diversity in clonality. Pang, T. (1998). *Trends in Microbiology* 6:339-342. [PRESS FOR ABSTRACT]

84. The polyvalent staphylococcal phage í812: its host-range mutants and related phages. Pantucek, R., Rosypalova, A., Doskar, J., Kailerova, J., Ruzickova, V., Borecka, P., Snopkova, S., Horvath, R., Goetz, F., Rosypal, S. (1998). *Virology -New York-* 246:241-252. [no abstract]

85. Biological systems aimed at a control over environmental mutagenic load. Pererva, T.P., Miryuta, N.Y., Miryuta, A.Y., Aleksandrov, Y. (1998). *Dopovidi Natsional'noyi Akademiyi Nauk Ukrayiny* 188-192. [PRESS FOR ABSTRACT]

86. Abundance, morphology and distribution of planktonic virus-like particles in two high-mountain lakes. Pina, S., Creus, A., Ganzález, N., Gironés, R., Felip, M., Sommaruga, R. (1998). *Journal of Plankton Research* 20:2413-2421. [PRESS FOR ABSTRACT]

87. Viral pollution in the environment and in shellfish: Human adenovirus detection by PCR as an index of human viruses. Pina, S., Puig, M., Lucena, F., Jofre, J., Girones, R. (1998). *Applied and Environmental Microbiology* 64:3376-3382. [PRESS FOR ABSTRACT]

88. New method churns out TB mutants. Potera, C. (1998). *Science* 280, 1350-1351. [PRESS FOR ABSTRACT]

89. Complete sequence of the new lactococcal abortive phage resistance gene abiO. Prevots, F., Ritzenthaler, P. (1998). *Journal of Dairy Science* 81:1483-1485. [no abstract]

90. Nucleotide seqeunce and analysis of the new chromosomal abortive infection gene abiN of *Lactococcus lactis* subsp. cremoris S114. Prevots, F., Tolou, S., Delpech, B., Kaghad, M., Daloyau, M. (1998). *FEMS Microbiology Letters* 159:331-336. [PRESS FOR ABSTRACT]

91. Viral pollution in the environment and in shellfish: Human adenovirus detection by PCR as an index of human viruses. Puig, M., Lucena, F., Jofre, J., Girones, R. (1998). *Applied and Environmental Microbiology* 64:3376-3382. [PRESS FOR ABSTRACT]

92. Physicochemical characterization of phage adsorption to *Lactobacillus helveticus* ATCC 15807 cells. Quiberoni, A., Reinheimer, J.A. (1998). *Journal of Applied Microbiology* 85:762-768. [no abstract]

93. Genetic (RAPD-PCR) and technological diversities among wild *Lactobacillus helveticus* strains. Quiberoni, A., Tailliez, P., Quenee, P., Suarez, V., Reinheimer, J. (1998). *Journal of Applied Microbiology* 85:591-596. [PRESS FOR ABSTRACT]

94. Dynamics of the pseudolysogenic response in slowly growing cells of *Pseudomonas aeruginosa*. Ripp, S., Miller, R.V. (1998). *Microbiology (Reading)* 144:2225-2232. [PRESS FOR ABSTRACT]

95. Parvovirus B19-induced anemia as the presenting manifestation of X-linked hyper-IgM syndrome. Seyama, K., Kobayashi, R., Hasle, H., Apter, A.J., Rutledge, J.C., Rosen, D., Ochs, HD (1998). *Journal of Infectious Disease* 178:318-324. [PRESS FOR ABSTRACT]

96. Phenotypic mixing of pyocin R2 and bacteriophage PS17 in *Pseudomonas aeruginosa*. Shinomiya, T. (1998). *J. Virol.* 49:310-??? [no abstract]

97. Distinguishing human from animal faecal contamination in water: A review. Sinton, L.W., Finlay, R.K., Hannah, D.J. (1998). *New Zealand Journal of Marine and Freshwater Research* 32:323-348. [PRESS FOR ABSTRACT]

98. Phage therapy. Soothill, J.S. (1998). *Journal Of Pharmacy And Pharmacology* 50:36-36. [no abstract]

99. Lack of surface receptors not restriction-modification system determines F4 phage resistance in *Streptococcus bovis* II/1. Styriak, I., Pristas, P., Javorsky, P. (1998). *Folia Microbiologica* 43:35-38. [PRESS FOR ABSTRACT]

100. Temperate viruses and lysogeny in Lake Superior bacterioplankton. Tapper, M., Hicks, R.E. (1998). *Limnology and Oceanography* 43:95-103. [PRESS FOR ABSTRACT]

101. Role of the air-water-solid interface in bacteriophage sorption experiments. Thompson, S.S., Flury, M., Yates, M.V., Jury, W.A. (1998). *Applied & Environmental Microbiology* 64:304-309. [PRESS FOR ABSTRACT]

102. Is the major capsid protein of iridoviruses a suitable target for the study of viral evolution? Tidona, C.A., Schnitzler, P., Kehm, R., Darai, G. (1998). *Virus Genes* 16:59-66. [PRESS FOR ABSTRACT]

103. Identification and characterization of a newly isolated Shiga toxin 2-converting phage from Shiga toxin-producing *Escherichia coli*. Watarai, M., Sato, T., Kobayashi, M., Shimizu, T., Yamasaki, S., Tobe, T., Sasakawa, C., Takeda, Y. (1998). *Infection and Immunity* 66:4100-4107. [no abstract]

104. Significance of viral lysis and flagellate grazing as factors controlling bacterioplankton production in a eutrophic lake. Weinbauer, M.G., Hofle, M.G. (1998). *Applied and Environmental Microbiology* 64:431-438. [PRESS FOR ABSTRACT]

105. Population dynamics of phytoplankton and viruses in a phosphate-limited mesocosm and their effect on DMSP and DMS production. Wilson, W.H., Turner, S., Mann, N.H. (1998). *Estuarine, Coastal and Shelf Science* 56(Supplement a):49-59. [PRESS FOR ABSTRACT]

106. Ultrastructure, biological and physical-chemical properties of mycobacterial phage MTPH11. Zhilenkov, E.L., Shemyakin, I.G., Korobova, O.V., Stepanshina, V.A. (1998). Boston, MA (USA). 8th International Conference on Infectious Diseases. 1998.[no 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. **Effect of prey heterogeneity on the response of a food chain to resource enrichment. Bohannan, B.J.M., Lenski, R.E. (1999). *American Naturalist* 153:73-82**. We demonstrated that the presence of invulnerable prey can result in a shift in the balance between top-down and bottom-up control of a model food chain. Our model food chain consisted of the bacterium *Escherichia coli* and the bacteriophage T4 (a virus that feeds on *E. coli*) in chemostats supplied with different concentrations of glucose. The *E. coli* population consisted of individuals that were susceptible to predation by T4 ("edible" *E. coli*) and individuals that were resistant to predation by T4 ("inedible" *E. coli*). The equilibrium density of a hetergeneous prey population (consisting of edible and inedible *E. coli*) increased strongly in response to an enrichment of its resources. This response consisted of an increase in the inedible fraction of the prey population, but no change in the edible fraction. In contrast, a homogeneous prey population (edible *E. coli* only) increased only marginally. The equilibrium density of the predator population (bacteriophage T4) did not significantly increase in response to enrichment when its prey were heterogeneous, but it increased when its prey were homogeneous.

2. **Effect of resource supply rate on host-pathogen dynamics. Bohannan, B.J.M. (1999).** ??? **(eds) *Proceedings of the 8th International Symposium on Microbial Ecology*.** The dynamics of model host cell (*E. coli*) and model pathogen (bacteriophage) populations were studied in chemostats with different resource supply rates. Resource supply rate was manipulated by altering the concentration of the limiting resource (glucose) in the incoming media. Population responses to increased resource supply rate were influenced by the vulnerability of the host cells to infection. When the host cell population consisted entirely of cells equally vulnerable to infection, both pathogen and host cells responded to increased resource supply rate with an increase in their average densities. In contrast, when the host cell contained some cells that were less vulnerable to infection (i.e., partially phage-resistant *E. coli*), only the pathogen population responded to increased supply rate with a significant increase in average density. Furthermore, when the host cell population contained some cells completely invulnerable to infection (i.e., phage-resistant *E. coli*) only the host cell population responded to increased supply rate with an increase in average density. These responses were in general agreement with the predictions of mechanistic models of resource-consumer interactions.

3. **Epistatic interactions can lower the cost of resistance to multiple consumers. Bohannan, B.J.M., Travisano, M., Lenski, R.E. (1999). *Evolution* 53:292-295**. It is widely assumed that resistance to consumers (e.g., predators or pathogens) comes at a "cost"; i.e., that when the consumer is absent the resident organisms are less fit than their susceptible counterparts. It is unclear what factors determine this cost. We demonstrate that epistasis between genes that confer resistance to two different consumers can alter the cost of resistance. We used as a model system the bacterium *Escherichia coli* and two different viruses (bacteriophage), T4 and l, that prey upon *E. coli*. Epistasis tended to reduce the costs of multiple resistance in this system. However, the extent of cost savings and its statistical significance depended on the environment in which fitness was measured, whether the null hypothesis for gene interaction was additive or multiplicative, and subtle differences among mutations that conferred the same resistance phenotype.

4. **Unexplored reservoirs of pathogenic bacteria: protozoa and biofilms. Brown, M., Barker, J. (1999). *Trends in Microbiology* 7:???-???**

5. **All the world's a phage. Hendrix, R.W., Smith, M.C.M., Burns, R.N., Ford, M.E., Hatfull, G.F. (1999). *Proc. Natl. Acad. Sci. USA* 96:2192-2197** We report DNA and predicted protein sequence similarities, implying homology, among genes of dsDNA bacteriophages and prophages spanning broad phylogenetic range of host bacteria. The sequence matches reported here establish genetic connections not always direct, among the lambdoid phages of *Escherichia coli*, phage fC31 of *Streptomyces*, phages of *Mycobacterium*, a previously unrecognized cryptic prophage, fFlu, in the *Haemophilus influenzae* genome, and two small prophage-like elements fRv1 and fRV2, in the genome of *M. tuberculosis*. The results imply that these phage genomes, and very possibly all of the dsDNA tailed phages, share common ancestry. We propose a model for the genetic structure and dynamics of the global phage population in which all dsDNA phage genomes are mosaics with access by horizontal exchange, to a large common genetic pool, but in which access to the gene pool is not uniform for all phage.

6. **TB: the return of the phage. A review of fifty years of mycobacteriophage research. McNerney, R. (1999). *Int. J. Tuberc. Lung Dis.* 3:179-184**. The first mycobacteriophage was isolated in 1947, and since that time over 250 of these viruses have been identified. Phages have made a significant contribution to our knowledge of mycobacteria over the past 50 years, and following the development of typing techniques in the 1960s and 1970s they were widely used in epidemiological studies of tuberculosis. Unfortunately, attempts to use lytic phages therapeutically during tuberculosis infection have so far failed to elicit cure in experimentally infected animals. During the past decade phages have become important in molecular studies of mycobacteria, both in terms of studying phage biology and as tools in recombinant DNA technology, thus facilitating the investigation of mycobacterial pathogenesis. Today their potential as diagnostics reagents is also being realized with the development of exciting new techniques for rapid bacterial detection and drug susceptibility testing. This review outlines the history of these remarkable organisms, from their discovery fifty years ago to the current developments in rapid diagnostic techniques.

7. **Virus removal from sewage effluents during saturated and unsaturated flow through soil columns. Powelson, D.K., Gerba, C.P. (1999). *Water Research* 28:2175-2181**. Recharge of sewage effluents may lead to contamination of groundwater with viruses. The goal of this research was to quantify virus removal in representative subsurface transport conditions. Soil column and batch studies were conducted to evaluate how virus type, effluent type and water saturation affect virus adsorption and removal. Three viruses were used: MS2 and PRD1 bacteriophages and poliovirus type 1. In the first column study, secondary- or tertiary-treated sewage containing the viruses percolated through coarse-sand columns under unsaturated conditions. In the second column study, the viruses suspended in secondary-treated sewage percolated through the columns under saturated or unsaturated conditions. A batch adsorption study was conducted to determine equilibrium adsorption of these viruses to the sand. Effluent type had no significant effect on first-order virus removal coefficients or retardation of virus transport. Virus "removal" was considered to be inactivation or irreversible adsorption. Unsaturated conditions resulted in an average removal coefficient (mu^{-s} = 0.31 h^{-1}) more than three times greater than saturated conditions (mu^{-s}= 0.095 h^{-1}), a significant difference at the 0.01 level. Poliovirus had a greater retardation coefficient (R = 5.2) than the bacteriophages (MS2, R = 1.4; and PRD1, R = 2.2), a significant difference at the 0.001 level. Column retardations of virus transport were only 0.8-8.0% of that predicted by adsorption coefficients determined from the batch studies. Equations developed in this paper may aid in estimating virus removal during recharge of effluents if the water residence times in ponds, the vadose zone and the aquifer are known.

8. ***Felix d'Herelle and the Origins of Molecular Biology*. Summers, W.C. (1999). Yale University Press, New Haven, Connecticut.**

9. **Evaluation of virus removal in membrane separation processes using coliphage Q-beta. Urase, T., Yamamoto, K., Ohgaki, S. (1999). *Water Science and Technology* 28:9-15**.

10. **A phage DNA injection-blocking type resistance mechanism encoded by chromosomal DNA in *Lactococcus lactis* subsp. lactis PLM-18. ??? (1998). *Milchwissenschaft* 53:619-622**. *Lactococcus lactis* subsp. lactis strain PLM-18 has a phage resistance activity against variant ϕ la2 which resulted in phage DNA injection-blocking. After adsorption of variant ϕ la2 to PLM-18 and its plasmid free derivative MA-12 cells with the same adsorption rate (98.4%), phage DNA was detected in neither PLM-18 nor MA-12 cells while detecting variant ϕ la2 DNA in sensitive host LLA-111 after 5 min. following phage adsorption. However, electrotransformation of phage DNA into resistant hosts, PLM-18 and MA-12, resulted in release of phage progeny on the contrary of conventional infection assays.

11. **In vivo transduction with Shiga toxin 1-encoding phage. Acheson, D.W.K., Reidl, J., Zhang, X., Keusch, G.T., Mekalanos, J.J., Waldor, M.K. (1998). *Infection and Immunity* 66:4496-4498**.

12. **Construction of multiple phage resistance in *Lactococcus lactis* subsp. lactis. Akcelik, M. (1998). *Advances in Food Sciences* 20:101-104**. The conjugative 37.5 Kb plasmid encodes inhibition of phage adsorption (Ads^+) in *Lactococcus lactis* subsp. lactis P25, transferred into *L. lactis* subsp. lactis MA12 carrying chromosomally encoded inhibition of phage DNA injection (ϕ^+) type resistance. The Lac^+, Strr, Kmr, ϕ^+ and Ads^+ representative transconjugant PMA3 strain demonstrated full resistance to the prolate-headed phages which were not inhibited by ϕ^+ mechanism in the recipient strain MA12. Plasmid p2520L was found to be completely stable in the transconjugant strain PMA3 after growing this strain in 10% RSM for 75 generations.

13. **Bacteriophages show promise as antimicrobial agents. Alisky, J., Iczkowski, K., Rapoport, A., Troitsky, N. (1998). *Journal of Infection* 36:5-15**. The emergence of antibiotic-resistant bacteria has prompted interest in alternatives to conventional drugs. One possible option is to use bacteriophages (phage) as antimicrobial agents. We have conducted a literature review of all Medline citations from 1966-1996 that dealt with the therapeutic use of phage. There were 27 papers from Poland, the Soviet Union, Britain and the U.S.A. The Polish and Soviets administered phage orally, topically or systemically to treat a wide variety of antibiotic-resistant pathogens in both adults and children. Infections included suppurative wound infections, gastroenteritis, sepsis, osteomyelitis, dermatitis, empyemas and pneumonia; pathogens included *Staphylococcus*, *Streptococcus*, *Klebsiella*, *Escherichia*, *Proteus*, *Pseudomonas*, *Shigella* and *Salmonella* spp. Overall, the Polish and Soviets reported success rates of 80-95% for phage therapy, with rare, reversible gastrointestinal or allergic side effects. However, efficacy of phage was determined almost exclusively by qualitative clinical assessment of patients, and details of dosages and clinical criteria were very sketchy. There were also six British reports describing controlled trials of phage in animal models (mice, guinea pigs and livestock), measuring survival rates and other objective criteria. All of the British studies raised phage against specific pathogens then used to create experimental infections. Demonstrable efficacy against *Escherichia*, *Acinetobacter*, *Pseudomonas* and *Staphylococcus* spp. was noted in these model systems. Two U.S. papers dealt with improving the bioavailability of phage. Phage is sequestered in the spleen and removed from circulation. This can be overcome by serial passage of phage through mice to isolate mutants that resist sequestration. In conclusion, bacteriophages may show promise for treating antibiotic resistant pathogens. To facilitate further progress, directions for future research are discussed and a directory of authors from the reviewed papers is provided.

14. **Phage resistance mechanisms in lactic acid bacteria. Allison, G.E., Klaenhammer, T.R. (1998). *International Dairy Journal* 8:207-226**. Dairy fermentations involving *Lactococcus lactis* and more recently *Streptococcus thermophilus*, are commonly attacked by bacteriophages. Efforts to protect these dairy starter cultures have resulted in a significant body of knowledge about the bacteriophages, their interactions with the host, and natural phage defense mechanisms that have evolved within bacteria operating under the most dynamic and devastating phage environment faced by industrial fermentations. This paper will overview this area and discuss the novel genetic approaches that are now being investigated in an effort to provide long term phage protection to dairy starter cultures that are used extensively in the industry.

15. **Peptide-guided cancer drugs show promise in mice. Barinaga, M. (1998). *Science* 279, 323-324.** [This Research News item is on drugs developed using phages which were injected into mammalian blood streams. There is only a one sentence reference to the technique, however, and no references cited. Furthermore, the phages did not do any infecting while in the host. Instead, these were phages which displayed peptides on their capsids: "Phages were injected into an animal . . . to identify peptides that stuck to specific tissues."].

16. **Induction Studies on Thermophilic Phage. Barridge, B.D. (1998). The University of Nebraska - Lincoln.**

17. **Use of lytic bacteriophage for control of experimental *Escherichia coli* septicemia and meningitis in chickens and calves. Barrow, P., Lovell, M., Berchieri, A.jr. (1998). *Clinical and Diagnostic Laboratory Immunology* 5:294-298**. A lytic bacteriophage, which was previously isolated from sewage and which attaches to the K1 capsular antigen, has been used to prevent septicemia and a meningitis-like infection in chickens caused by a $K1^+$ bacteremic strain of *Escherichia coli*. Protection was obtained even when administration of the phage was delayed until signs of disease appeared. The phage was able to multiply in the blood. In newly borne colostrum-deprived calves given the *E. coli* orally, intramuscular inoculation of phage delayed appearance of the bacterium in the blood and lengthened life span. With some provisos there is considerable potential for this approach to bacterial-disease therapy.

18. **His1, and archaeal virus of the *Fuselloviridae* family that infects *Haloarcula hispanica*. Bath, C., Dyall-Smith, M.L. (1998). *J. Virol.* 72:9392-9395**. A novel archaeal virus, His1, was isolated from hypersaline waters in south-eastern Australia. It was lytic, grew only on *Ha. hispanica* (up to titres of 1011p.f.u./ml), and displayed a "lemon-shaped" morphology (74nm x 44nm) previously reported only for a virus of the extreme thermophiles (SSV1). The density of His1 was approximately 1.28g/ml - similar to that of SSV1 (1.24g/ml). Purified particles were resistant to low salt. The genome was linear, dsDNA and 14.9kb in size, which was similar in size to the genome of the SSV1 (ie. 15.5kb). Morphologically, this isolate clearly belongs to the recently proposed *Fuselloviridae* family of archaeal viruses. It represents the first member from the extremely halophilic archaea, and its host, *Ha. hispanica*, is one that can be readily manipulated genetically.

19. **Modeling and analysis of a marine bacteriophage infection. Beretta, E., Kuang, Y. (1998). *Math. Biosci.* 149:57-76**. A mathematical model for the marine bacteriophage infection is proposed and its essential mathematical features are analyzed. Since bacteriophage infection induces bacterial lysis which releases into the marine environment, on the average, 'b' viruses per cell, the parameter b epsilon (1, t infinity) or 'virus replication factor' is chosen as the main parameter on which the dynamics of the infection depends. We proved that a threshold b* exists beyond which the endemic equilibrium bifurcates from the free disease one. Still, for increasing b values the endemic equilibrium bifurcates toward a periodic solution. We proved that a compact attractor set omega within the positive cone exists and within omega the free disease equilibrium is globally stable whenever b < or = b*, whereas it becomes a strong uniform repeller for b > b*. A concluding discussion with numerical simulation is then presented.

20. **Microscale nutrient patches in planktonic habitats shown by chemotactic bacteria. Blackburn, N., Fenchel, T., Mitchell, J. (1998). *Science* 282:2254-2256**. Are nutrients available to microbial communities in micropatches long enough to influence growth and competition? And what are the sources

of such patches? To answer these questions, the swimming behavior of chemotactic bacteria in seawater samples was examined. Clusters of bacteria formed in conjunction with cell lysis and excretion by protozoa. These point sources of nutrients spread into spherical patches a few millimeters in diameter and sustained swarms of bacteria for about 10 minutes. Within that time, a large proportion of the nutrients was encountered by bacteria, chemotactic and nonchemotactic alike. Chemotaxis is advantageous for bacteria using patches over a certain size.

21. **Specific assays for bacteria using phage mediated release of adenylate kinase. Blasco, R., Murphy, M.J., Sanders, M.F., Squirrell, D.J. (1998).** ***Journal of Applied Microbiology*** **84:661-666**.

22. **Response of model microbial communities to increased productivity. Bohannan, B.J.M. (1998). Michigan State Univeristy.**

23. **Effects of the abortive infection mechanism AbiK on the lactococcal phage p2. Boucher, I., Emond, E., Moineau, S. (1998). Denver, CO (USA). #1998 American Dairy Science Association (ADSA)/American Society of Animal Science (ASAS) Joint Meeting. 1998.**

24. **Description of two bacteriophages active against** ***Lotus rhizobia*****. Bruch, C.W., Allen, O.N. (1998).** ***Proc. Am. Soil Sci. Soc.*** **19:175-???**

25. **Molecular ecology and evolution of** ***Streptococcus thermophilus*** **bacteriophages--a review. Brussow, H., Bruttin, A., Desiere, F., Lucchini, S., Foley, S. (1998).** ***Virus Genes*** **16:95-109**. Bacteriophages attacking *Streptococcus thermophilus*, a lactic acid bacterium used in milk fermentation, are a threat to the dairy industry. These small isometric-headed phages possess double-stranded DNA genomes of 31 to 45 kb. Yoghurt-derived phages exhibit a limited degree of variability, as defined by restriction pattern and host range, while a large diversity of phage types have been isolated from cheese factories. Despite this diversity all *S. thermophilus* phages, virulent and temperate, belong to a single DNA homology group. Several mechanisms appear to create genetic variability in this phage group. Site-specific deletions, one type possibly mediated by a viral recombinase/integrase, which transformed a temperate into a virulent phage, were observed. Recombination as a result of superinfection of a lysogenic host has been reported. Comparative DNA sequencing identified up to 10% sequence diversity due to point mutations. Genome sequencing of the prototype temperate phage ϕ Sfi21 revealed many predicted proteins which showed homology with phages from *Lactococcus lactis* suggesting horizontal gene transfer. Homology with phages from evolutionary unrelated bacteria like *E. coli* (e.g. lambdoid phage 434 and P1) and Mycobacterium ϕ L5 was also found. Due to their industrial importance, the existence of large phage collections, and the whole phage genome sequencing projects which are currently underway, the *S. thermophilus* phages may present an interesting experimental system to study bacteriophage evolution. [References: 48].

26. **Viral escape from antisense RNA. Bull, J.J., Jacoboson, A., Badgett, M.R., Molineax, I.J. (1998).** ***Molecular Microbiology*** **28:835-846**. RNA coliphage SP was propagated for several generations on a host expressing an inhibitory antisense RNA complementary to bases 31-270 of the positive-stranded genome. Phages evolved that escaped inhibition. Typically, these escape mutants contained 3-4 base substitutions, but different sequences were observed among different isolates. The mutations were located within three different types of structural features within the predicted secondary structure of SP genomic RNA: (i) hairpin loops; (ii) hairpin stems; and (iii) the 5' region of the phage genome complementary to the antisense molecule. Computer modelling of the mutant genomic RNAs showed that all of the substitutions within hairpin stems improved the Watson-Crick pairing of the stem. No major structural rearrangements were predicted for any of the mutant genomes, and most substitutions in coding regions did not alter the amino acid sequence. Although the evolved phage populations were polymorphic for substitutions, many substitutions appeared independently in two selected lines. The creation of a new, perfect, antisense RNA against an escape mutant resulted in the inhibition of that mutant but not of other escape mutants nor of the ancestral, unevolved phage. Thus, at least in this system, a population of viruses that evolved to escape from a single antisense RNA would require a cocktail of several antisense RNAs for inhibition.

27. **The pleasures of pond scum. Carlson, S. (1998).** ***Scientific American*** **March, 96-98.**

28. **New cholera phages for** ***Vibrio cholerae*** **serovar O139. Chakrabarti, A.K., Ghosh, A.N., Sarkar, B.L. (1998).** ***Journal of Infection*** **36:131-132**.

29. **Virus particle production in lysogenic bacteria exposed to protozoan grazing. Clarke, K.J. (1998).** ***FEMS Microbiology Letters*** **166:177-180**. Electron microscopy was used to investigate the apparent induction of virus particle production in bacteria undergoing digestion by ciliates. Results showed that numbers of bacteria containing virus particles increased by a factor of 25 when enclosed within ciliate food vacuoles. It was also found that 10% of these particles survived the digestion process to be released back into the aquatic habitat within faecal pellets. The possibility of virus gene transfer occurring between lysogenically infected bacteria that survive the ciliate digestive processes, is also considered.

30. **Increasing phage resistance of cheese starters: A case study using** ***Lactococcus lactis*** **DPC4268. Coffey, A., Coakley, M., McGarry, A., Fitzgerald, G.F., Ross, R.P. (1998).** ***Letters in Applied Microbiology*** **26:51-55**. This study serves as an example of strategies used to increase the phage resistance of an important Irish Cheddar cheese starter, *Lactococcus lactis* DPC4268. It describes the emergence and persistence of a lytic bacteriophage, 4268, that has a relatively large burst size and exhibits no homology to the most common phage types encountered in Irish cheese plants. Inherent difficulties were encountered that prevented the effective introduction of conjugative phage-resistance plasmids pNP40 and pMRCO1 to strain DPC4268. In fact, pNP40-associated Abi systems were naturally present in six of 19 starters. Control of phage 4268 was eventually achieved by generating a mutant of DPC4268, which was subsequently used for cheese manufacture.

31. **Effect of Environmental Factors upon a** ***Staphylococcus*** **Host-Phage System. Countryman, J.L. (1998). Stanford University.**

32. **Virulence of phage populations infecting** ***Halobacterium cutirubrum*****. Daniels, L.L., Wais, A.C. (1998).** ***FEMS Microbiology Ecology*** **25:129-134**. Phages of low virulence predominated culturable phage populations in a naturally occurring Jamaican salt pond with *Halobacterium cutirubrum* as host. These mutated rapidly in culture to higher virulence due to more rapid adsorption to host cells. Wild-type phages of low virulence, S50.2 and S41, with adsorption rate constants (K) of 1.15 and 1.21 times 10^{-11} ml min^{-1} mutated to produce highly virulent derivatives S50.2Vm and S41Vm with K= 2.60 and 2.61 times 10^{-11} ml min^{-1}, values similar to the most virulent wild-type phages S5100 and S4100, K= 2.61 and 2.55 times 10^{-11} ml min^{-1} respectively. Quantitative measures of intracellular phage development were constant among low and high virulence wild-type and mutant phages S50.2, S5100 and S50.2Vm with eclipse periods of 5.5 h, latent periods of 9 h and average apparent burst sizes of 60-65. We propose that the natural environment may select for slow adsorption to reduce the frequency of release of DNA from phage particles in response to encounters with non-host material.

33. **Phages infecting** ***Vibrio vulnificus*** **are abundant and diverse in oysters (*Crassostrea virginica*) collected from the Gulf of Mexico. Depaola, A., Motes, M.L., Chan, A.M., Suttle, C.A. (1998).** ***Applied & Environmental Microbiology*** **64:346-351**. Phages infecting *Vibrio vulnificus* were abundant (10^{-4} phages g of oyster $tissue^{-1}$) throughout the year in oysters (*Crassostrea virginica*) collected from estuaries adjacent to the Gulf of Mexico (Apalachicola Bay, Fla.; Mobile Bay, Ala.; and Black Bay, La.). Estimates of abundance ranged from 10^{-1} to 10^{-5}phages g of oyster $tissue^{-1}$ and were dependent on the bacterial strain used to assay the sample. *V. vulnificus* was near or below detection limits (lt 0.3 cell g^{-1}) from January through March and was most abundant ($10^{-3}$to 10^{-4}cells g^{-1}) during the summer and fall, when phage abundances also tended to be greatest. The phages isolated were specific to strains of *V. vulnificus*, except for one isolate that caused lysis in a few strains of *V. parahaemolyticus*. Based on morphological evidence obtained by transmission electron

microscopy, the isolates belonged to the *Podoviridae*, *Styloviridae*, and *Myoviridae*, three families of double-stranded DNA phages. One newly described morphotype belonging to the *Podoviridae* appears to be ubiquitous in Gulf Coast oysters. Isolates of this morphotype have an elongated capsid (mean, 258 nm; standard deviation, 4 nm; n = 35), with some isolates having a relatively broad host range among strains of *V. vulnificus*. Results from this study indicate that a morphologically diverse group of phages which infect *V. vulnificus* is abundant and widely distributed in oysters from estuaries bordering the northeastern Gulf of Mexico.

34. **Evolution of *Streptococcus thermophilus* bacteriophage genomes by modular exchanges followed by point mutations and small deletions and insertions. Desiere, F., Lucchini, S., Brussow, H. (1998). *Virology* 241:345-356**. Comparative sequence analysis of 40 % of the genomes from two prototype *Streptococcus thermophilus* bacteriophages (lytic group I phage fSfi19 and the cos-site containing temperate phage fSfi21) suggested two processes in the evolution of their genomes. In a first evolutionary distant phase the basic genome structure was apparently constituted by modular exchanges. Over the 17 kb long DNA segment analyzed in the present report we observed clusters of genes with similarity to genes from *Leuconostoc oenos* phage L10, *Lactococcus lactis* phage BK5-T and *Streptococcus pneumoniae* phage Dp-1. A chimeric protein was predicted for orf 1291 which showed similarity both to phage BK5-T and phage Dp-1. The very large orf 1626 gene product showed similarity to two adjacent genes from the *Lactobacillus delbrueckii* phage LL-H and further phage proteins (*Lactococcus lactis*, *Bacillus subtilis*). The similarities were localized to distinct parts of this apparently multifunctional protein. The putative fSfi19 lysin showed similarity both to lysins of phages and cellular enzymes. In a second evolutionary more recent phase the *S. thermophilus* phage genomes apparently diversified by point mutations and small deletions/insertions. Over the investigated 17 kb DNA region fSfi19 differed from fSfi21 by 10 % base pair changes, the majority of which were point mutations (mainly at the third codon position), while a third of the bp differences were contributed by small deletions/insertions. The bp changes were unevenly distributed: Over the *Leuconostoc* phage-related DNA the change rate was high, while over the *Lactococcus*- and *S. pneumoniae* phage-related DNA the change rate was low. We speculate that the degree of bp changes could provide relative time scales for the modular exchange reactions observed in *S. thermophilus* phages.

35. **A leucine repeat motif in AbiA is required for resistance of *Lactococcus lactis* to phages representing three species. Dinsmore, P.K., O'Sullivan, D.J., Klaenhammer, T.R. (1998). *Gene* 212:5-11**. The abiA gene encodes an abortive bacteriophage infection mechanism that can protect *Lactococcus* species from infection by a variety of bacteriophages including three unrelated phage species. Five heptad leucine repeats suggestive of a leucine zipper motif were identified between residues 232 and 266 in the predicted amino acid sequence of the AbiA protein. The biological role of residues in the repeats was investigated by incorporating amino acid substitutions via site-directed mutagenesis. Each mutant was tested for phage resistance against three phages, ϕ 31, sk1, and c2, belonging to species P335, 936, and c2, respectively. The five residues that comprise the heptad repeats were designated L234, L242, A249, L256, and L263. Three single conservative mutations of leucine to valine in positions L235, L242, and L263 and a double mutation of two leucines (L235 and L242) to valines did not affect AbiA activity on any phages tested. Non-conservative single substitutions of charged amino acids for three of the leucines (L235, L242, and L256) virtually eliminated AbiA activity on all phages tested. Substitution of the alanine residue in the third repeat (A249) with a charged residue did not affect AbiA activity. Replacement of L242 with an alanine elimination phage resistance against ϕ 31, but partial resistance to sk1 and c2 remained. Two single proline substitutions for leucines L242 and L263 virtually eliminated AbiA activity against all phages, indicating that the predicted alpha-helical structure of this region is important. Mutations in an adjacent region of basic amino acids had various effects on phage resistance, suggesting that these basic residues are also important for AbiA activity. This directed mutagenesis analysis of AbiA indicated that the leucine repeat structure is essential for conferring phage resistance against three species of lactococcal bacteriophages.

36. ***E. coli*'s double life. Dixon, B. (1998). *ASM News* 64:616-617**.

37. **Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid pMRC01 from *Lactococcus lactis* DPC3147. Dougherty, B.A., Hill, C., Weidman, J.F., Richardson, D.R., Venter, J.C., Ross, R.P. (1998). *Molecular Microbiology* 29:1029-1038**. The complete sequence of pMRC01, a large conjugative plasmid from *Lactococcus lactis* ssp. lactis DPC3147, has been determined. Using a shotgun sequencing approach, the 60,232 bp plasmid sequence was obtained by the assembly of 1056 underlying sequences (sevenfold average redundancy). Sixty-four open reading frames (ORFs) were identified. Analysis of the gene organization of pMRC01 suggests that the plasmid can be divided into three functional domains, with each approximately 20 kb region separated by insertion sequence (IS) elements. The three regions are (i) the conjugative transfer region, including a 16-gene Tra (transfer) operon; (ii) the bacteriocin production region, including an operon responsible for the synthesis of the novel bacteriocin lacticin 3147; and (iii) the phage resistance and plasmid replication region of the plasmid. The complete sequence of pMRC01 provides important information about these industrially relevant phenotypes and gives insight into the structure, function and evolution of large gram-positive conjugative plasmids in general. The completely sequenced pMRC01 plasmid should also provide a useful framework for the design of novel plasmids to be incorporated into starter strain improvement programmes for the dairy industry.

38. **Delineating the specific influence of virus isoelectric point and size on virus adsorption and transport through sandy soils. Dowd, S.E., Pillai, S.D., Wang, S., Corapcioglu, M.Y. (1998). *Applied & Environmental Microbiology* 64:405-410**. Many of the factors controlling viral transport and survival within the subsurface are still poorly understood. In order to identify the precise influence of viral isoelectric point on viral adsorption onto aquifer sediment material, we employed five different spherical bacteriophages (MS2, PRD1, Q beta, ϕ X174, and PM2) having differing isoelectric points (pI 3.9, 4.2, 5.3, 6.6, and 7.3 respectively) in laboratory viral transport studies. We employed conventional batch flowthrough columns, as well as a novel continuously recirculating column, in these studies. In a 0.78-m batch flowthrough column, the smaller phages (MS2, ϕ X174, and Q beta), which had similar diameters, exhibited maximum effluent concentration/initial concentration values that correlated exactly with their isoelectric points. In the continuously recirculating column, viral adsorption was negatively correlated with the isoelectric points of the viruses. A model of virus migration in the soil columns was created by using a one-dimensional transport model in which kinetic sorption was used. The data suggest that the isoelectric point of a virus is the predetermining factor controlling viral adsorption within aquifers. The data also suggest that when virus particles are more than 60 nm in diameter, viral dimensions become the overriding factor.

39. **AbiQ, an abortive infection mechanism from *Lactococcus lactis*. Emond, E., Dion, E., Walker, S.A., Vedamuthu, E.R., Kondo, J.K., Moineau, S. (1998). *Applied and Environmental Microbiology* 64:4748-4756**. *Lactococcus lactis* W-37 is highly resistant to phage infection. The cryptic plasmids from this strain were coelectroporated, along with the shuttle vector pSA3, into the plasmid-free host *L. lactis* LM0230. In addition to pSA3, erythromycin- and phage-resistant isolates carried pSRQ900, an 11-kb plasmid from *L. lactis* W-37. This plasmid made the host bacteria highly resistant (efficiency of plaquing $<10^{-8}$) to c2- and 936-like phages. pSRQ900 did not confer any resistance to phages of the P335 species. Adsorption, cell survival, and endonucleolytic activity assays showed that pSRQ900 encodes an abortive infection mechanism. The phage resistance mechanism is limited to a 2.2-kb EcoRV/BclI fragment. Sequence analysis of this fragment revealed a complete open reading frame (abiQ), which encodes a putative protein of 183 amino acids. A frameshift mutation within abiQ completely abolished the resistant phenotype. The predicted peptide has a high content of positively charged residues (pI = 10.5) and is, in all likelihood, a cytosolic protein. AbiQ has no homology to known or deduced proteins in the databases. DNA replication assays showed that phage c21 (c2-like) and phage p2 (936-like) can still replicate in cells harboring AbiQ. However, phage DNA accumulated in its concatenated form in the infected $AbiQ^+$ cells, whereas the $AbiQ^-$ cells contained processed (mature) phage DNA in addition to the concatenated form. The production of the major capsid protein of phage c21 was not hindered in the cells harboring AbiQ.

40. **Induction of the lysogenic phage encoding Cholera toxin in naturally occurring strains of toxigenic *Vibrio cholerae* O1 and O139. Faruque, S.M., Asadulghani, Abdul, A., Albert, M.J., Nasirul, I., Mekalanos, J.J. (1998). *Infection and Immunity* 66:3752-3757**.

41. **A short noncoding viral DNA element showing characteristics of a replication origin confers bacteriophage resistance to *Streptococcus thermophilus*. Foley, S., Lucchini, S., Zwahlen, M.C., Brussow, H. (1998). *Virology* 250:377-387**. A 302-bp noncoding DNA fragment from the DNA replication module of phage phiSfi21 was shown to protect the *Streptococcus thermophilus* strain Sfi1 from infection by 17 of 25 phages. The phage-inhibitory DNA possesses two determinants, each of which individually mediated phage resistance. The phage-inhibitory activity was copy number dependent and operates by blocking the accumulation of phage DNA. Furthermore, when cloned on a plasmid, the phiSfi21 DNA acts as an origin of replication driven by phage infection. Protein or proteins in the phiSfi21-infected cells were shown to interact with this phage-inhibitory DNA fragment, forming a retarded protein-DNA complex in gel retardation assays. A model in which phage proteins interact with the inhibitory DNA such that they are no longer available for phage propagation can be used to explain the observed bacteriophage resistance. Genome analysis of phiSfi19, a phage that is insensitive to the inhibitory activity of the phiSfi21-derived DNA, led to the characterisation of a variant putative phage replication origin that differed in 14 of 302 nucleotides from that of phiSfi21. The variant origin was cloned and exhibited an inhibitory activity toward phages that were insensitive to the phiSfi21-derived DNA. Copyright 1998 Academic Press.

42. **Occurrence of a sequence in marine cyanophages similar to that of T4 gp20 and its application to PCR-based detection and quantification techniques. Fuller, N.J., Wilson, W.H., Joint, I.R., Mann, N.H. (1998). *Appl. Environ. Microbiol.* 64:2051-2060**. Viruses are ubiquitous components of marine ecosystems and are known to infect unicellular phycoerythrin-containing cyanobacteria belonging to the genus *Synechococcus*. A conserved region from cyanophage genome was identified in three genetically distinct cyanomyoviruses, and a sequence analysis revealed that this region exhibited significant similarity to a gene encoding a capsid assembly protein (gp20) from the enteric coliphage T4. The results of a comparison of gene 20 sequences from three cyanomyoviruses and T4 allowed us to design two degenerate PCR primers, CPS1 and CPS2, which specifically amplified a 165-bp region from the majority of cyanomyoviruses tested. A competitive PCR (cPCR) analysis revealed that cyanomyovirus strains should be accurately enumerated, and it was demonstrated that quantification was log-linear over ca. 3 orders of magnitude. Different calibration curves were obtained for each of the three cyanomyovirus strains tested; consequently, cPCR performed with primers CPS1 and CPS2 could lead to substantial inaccuracies in estimates of phage abundance in natural assemblages. Further sequence analysis of cyanomyovirus gene 20 homologs would be necessary in order to design primers which do not exhibit phage-to-phage variability in priming efficiency. It was demonstrated that PCR products of the correct size could be amplified from seawater samples following 100x concentration and even directly without any prior concentration. Hence, the use of degenerate primers in PCR analysis of cyanophage populations should provide valuable data on the diversity of cyanophages in natural assemblages. Further optimization of procedures may ultimately lead to a sensitive assay which can be used to analyze natural cyanophage populations both quantitatively (by cPCR) and qualitatively following phylogenetic analysis of amplified products.

43. **High titer, phage-neutralizing antibodies in bovine colostrum that prevent lytic infection of *Lactococcus lactis* in fermentations of phage-contaminated milk. Geller, B.L., Kraus, J., Schell, M.D., Hornsby, M.J., Neal, J.J., Ruch, F.E. (1998). *Journal of Dairy Science* 81:895-900**. Antibodies against six phages of *Lactococcus lactis* were produced in six bovine colostra. Each colostrum neutralized its homologous phage. In addition, each colostrum neutralized a different phage. from the same species as its homologous phage, but either did not neutralize or weakly neutralized more distantly related lactococcal phages. The neutralization of heterologous phages correlated with the phage species but not with the strain on which the phage was grown. Blood serum from the same cows also neutralized homologous phages, but the titers were lower than that of the colostrum. Addition of colostrum to phage-contaminated milk prevented lysis of starter cultures of *L. lactis*. The titers of some of the colostra were sufficiently high that it may be economically practical to prepare antibodies from similar, high titer colostra for commercial use in factory bulk starter vats.

44. **Membrane receptor for prolate phages is not required for infection of *Lactococcus lactis* by small or large isometric phages. Geller, B.L. (1998). *Journal of Dairy Science* 81:2329-2335**. *Lactococcus lactis* contains a chromosomal gene (pip) for a membrane protein that serves as a receptor for the prolate bacteriophage c2 and other phages of the c2 species. A mutated allele of this receptor gene was used to replace the wild-type allele in *L. lactis* strains MM210, NCK 203, and C2. Allele replacement was confirmed by the presence of a restriction site marker in a polymerase chain reaction product from the mutated allele. The mutated pip derivative of strain C2 was completely resistant to phages of the c2 species but was fully sensitive to the small isometric phage sk1 of the 936 species, as expected. The mutated derivatives of MM210 and NCK203 were fully sensitive to the small isometric phages mm210b and 31 (p335 species) and to the large isometric phage 949 (949 species). These results show that pip is not required for infection by phages of species 936, p335, or 949. The resultant mutants grew as well as the parental strains in liquid media. The mutated derivatives of MM210 and C2 acidified and clotted milk as readily as the wild-type strains. These results show that phage receptor replacement in a commercial strain of *L. lactis* does not affect growth and acid production in milk.

45. **Predicting disinfection performance in continuous flow systems from batch disinfection kinetics. Haas, C.N., Joffe, J., Heath, M., Jacangelo, J., Anmangandla, U. (1998). *Water Science and Technology* 38:171-179**. Disinfection processes have often been characterized by the "CT" concept i.e., the product of disinfectant residual and contact time (perhaps as a function of pH, temperature, and other water quality variations) produces a given level of disinfection. The objective of this work was to develop and validate the use of reaction kinetic models for disinfection process design. Using bench scale (batch) kinetic information, and hydraulic characterization of pilot scale continuous disinfection processes, predictions of continuous process performance were made using a segregated flow model. These predictions were compared to independent experimental measurements of actual inactivation in pilot scale processes. Preammoniation, free residual chlorination, and ozonation were used on two waters from Portland, Oregon (US). Organisms used were *Giardia muris*, bacteriophage MS2, and *Escherichia coli*.

46. **Evaluation of alginate-encapsulated *Azotobacter chroococcum* as a phage-resistant and an effective inoculum. Hammad, A.M.M. (1998). *Journal of Basic Microbiology* 38:9-16**. The efficiency of free and alginate-encapsulated *Azotobacter chroococcum* in fixing nitrogen and their susceptibility to bacteriophages were studied in pure liquid cultures (in vitro) and under cultivated soil conditions (in vivo). Bacteriophages of *A. chroococcum* were isolated and were found to be common in soil of the Experimental Farm of Fac. Agric., Minia Univ., Egypt. In pure liquid cultures, the immobilized cells exhibited much higher nitrogenase activity (about 57 fold) than the free ones. The encapsulation system offered high protection to *A. chroococcum* against their phages. No nitrogenase activity was detected for the free cells in presence of phages. Under cultivated soil conditions, inoculation of maize plants (Zea mays, cv. GIZA 2) with immobilized *A. chroococcum*, markedly increased rhizosphere and rhizoplane *Azotobacter* population, significantly increased plant N% as well as dry weight/plant, compared to those inoculated with free cells. In free cells inoculated-plants, bacteriophages had a marked depressive effect on rhizosphere and rhizoplane *Azotobacter* population, significantly reduced plant N% and dry weight/plant, as compared to plants inoculated with free cells in absence of phages. In plants inoculated with immobilized cells, no significant effect for presence of phages was detected in plant N% and dry weight/plant, whereas, a slight reduction in rhizosphere and rhizoplane *Azotobacter* population was observed.

47. **Efficacy and mechanisms of action of sodium hypochlorite on *Pseudomonas aeruginosa* PAO1 phage F116. Hann, A.C., Baubet, V., Perrin, R. (1998). *Journal of Applied Microbiology* 85:925-932**. The *Pseudomonas aeruginosa* PAO1 phage F116 was used to investigate the viricidal activity and the mechanism of action of sodium hypochlorite. The bacteriophage was inactivated with a low concentration (0.0005% available chlorine) of the biocide prepared in tap water but it was less sensitive to a sodium hypochlorite solution prepared in ultra-pure water (0.0075% available chlorine). For all the effective concentrations of sodium hypochlorite (i.e. producing at least 4 log reduction in phage titre), F116 was readily inactivated within 30 s. Electron microscopical investigations of the phage particles challenged with sodium hypochlorite showed a wide variety of deleterious effects, some of which have not been previously observed with other biocides. The wide range of structural alterations observed suggested that sodium hypochlorite has multiple target sites against F116 bacteriophage. A 30 s exposure to sodium hypochlorite (0.001% available chlorine) produced severe damage, the number and severity of which increased with

a higher concentration (0.0075% available chlorine) and with a longer contact time. These observations suggested that sodium hypochlorite inactivated F116 bacteriophage by causing structural alterations to the phage head, tail and overall structure, hence possibly releasing the viral genome from damaged capsids in the surrounding media.

48. **??? Hausmann, R., Härle, E. (1998). *Proc. Eur. Biophys. Congr.* 1:467-???**

49. **Optimising starter culture performance in NZ cheese plantsproduction. Heap, H.A. (1998). *Australian Journal of Dairy Technology* 53:74-78**.

50. **Phage as antibacterial tool. Holzman, D. (1998). *Genetic Engineering News* (October 15), 1-48.**

51. **Reassessment of medicinal phage……. Holzman, D. (1998). *ASM News* 64:620-622**.

52. **…Spurs companies to study therapeutic uses. Holzman, D. (1998). *ASM News* 64:622-623**.

53. **A comparison of two methods to recover phages from soil samples. Hu, T.L. (1998). *Bioresource Technology* 65:167-169**. Environmental contamination caused by viruses has received extensive interest. The adsorption of viruses in soil can influence the extent of groundwater pollution. Many methods have been applied to detecting viruses in soil samples. Different elution methods lead to differences of viral titers. In this study, two elution methods were compared: glycine buffer and beef extract of phages from a soil sample. Experimental results indicated that, for both methods, the phage recovery increased with an increasing contact time between phages and soil sample. The phage recovery for the glycine buffer method increased only slightly when the elution time was increased from 2 to 10 min. However, the phage recovery for the beef extract method was higher when the elution time was increased to 6 min. At an elution time of 2 min., the glycine buffer method yielded a higher phage recovery than the beef extract method. Although both elution methods closely resembled each other in terms of the phage titers of an environmental sample, the glycine buffer method was simpler, faster, and would be more appropriate for detecting and enumerating phage when many soil or sediment samples are employed.

54. **Biofilm susceptibility to bacteriophage attack: the role of phage-borne polysaccharide depolymerase. Hughes, K.A., Sutherland, I.W., Jones, M.V. (1998). *Microbiology -Reading-* 45:3039-3047**.

55. **A novel filamentous phage, fs-2, of *Vibrio cholerae* O139. Ikema, M., Honma, Y. (1998). *Microbiology -Reading-* 144:1901-1906**.

56. **Mechanism of T4 Phage Restriction by a Thermosensitive Drug Resistant Factor RTSL. Ishaq, M. (1998). University of Pennsylvania.**

57. **Prevalence of broad-host-range lytic bacteriophages of *Sphaerotilus natans*, *Escherichia coli*, and *Pseudomonas aeruginosa*. Jensen, E.C., Schrader, H.S., Rieland, B., Thompson, T.L., Lee, K.W., Nickerson, K.W., Kokjohn, T.A. (1998). *Applied & Environmental Microbiology* 64:575-580**. Two bacteriophage collections were examined with regard to their ability to form plaques on multiple bacterial host species. Nine of 10 phages studied were found to be broad-host-range bacteriophages. These phages fell into two groups. Group 1, the SN series, was isolated from sewage treatment plant samples with *Sphaerotilus natans* ATCC 13338 as a host. The DNAs of these bacteriophages contained modified bases and were insensitive to cleavage by type I and II restriction endonucleases. The efficiency of plating of these bacteriophages was changed only slightly on the alternate host. Group 2, the BHR series, was isolated by a two-host enrichment protocol. These bacteriophages were sensitive to restriction, and their efficiency of plating was dramatically reduced on the alternate host. Our results suggest that a multiple-host enrichment protocol may be more effective for the isolation of broad-host-range bacteriophages by avoiding the selection bias inherent in single-host methods. At least two of the broad-host-range bacteriophages mediated generalized transduction. We suggest that broad-host-range bacteriophages play a key role in phage ecology and gene transfer in nature.

58. **Characterization of marine temperate phage-host systems isolated from Mamala Bay, Oahu, Hawaii. Jiang, S.C., Kellogg, C.A., Paul, J.H. (1998). *Applied & Environmental Microbiology* 64:535-542**. To understand the ecological and genetic role of viruses in the marine environment, it is critical to know the infectivity of viruses and the types of interactions that occur between marine viruses and their hosts. We isolated four marine phages from turbid plaques by using four indigenous bacterial hosts obtained from concentrated water samples from Mamala Bay, Oahu, Hawaii. Two of the rod-shaped bacterial hosts were identified as *Sphingomonas paucimobilis* and *Flavobacterium* sp. All of the phage isolates were tailed phages and contained double-stranded DNA. Two of the phage isolates had morphologies typical of the family *Siphoviridae*, while the other two belonged to the families *Myoviridae* and *Podoviridae*. The head diameters of these viruses ranged from 47 to 70.7 nm, and the tail lengths ranged from 12 to 146 nm. The burst sizes ranged from 7.8 to 240 phage/bacterial cell, and the genome sizes, as determined by restriction digestion, ranged from 36 to 112 kb. The members of the *Siphoviridae*, T-ϕ HSIC, and T-ϕ D0, and the member of the *Myoviridae*, T-ϕ D1B, were found to form lysogenic associations with their bacterial hosts, which were isolated from the same water samples. Hybridization of phage T-ϕ HSIC probe with lysogenic host genomic DNA was observed in dot blot hybridization experiments, indicating that prophage T-ϕ HSIC was integrated within the host genome. These phage-host systems are available for use in studies of marine lysogeny and transduction.

59. **Significance of lysogeny in the marine environment: studies with isolates and a model of lysogenic phage production. Jiang, S.C., Paul, J.H. (1998). *Microbial Ecology* 35:235-243**. The importance of lysogeny in marine microbial populations is just beginning to be understood. To determine the abundance of lysogens in bacterial populations, we studied the occurrence of lysogenic bacteria among bacterial isolates from a variety of marine environments. More than 116 bacteria isolated on artificial seawater nutrient agar plates were tested for the presence of inducible prophage by mitomycin C and UV radiation. Induction was determined as a decrease in culture absorbance at 600 nm, after treatment with inducing agents. Samples in which optical density decreased or remained the same after induction were further examined by transmission electron microscopy, for the presence of virus-like particles. More than 40% of the bacterial isolates contained inducible prophage, as determined by mitomycin C induction. A higher percentage of lysogenic bacteria was found in isolates from oligotrophic environments, compared to coastal or estuarine environments. These studies suggest that lysogenic bacteria are important components in marine microbial populations. However, a mathematical model based on viral and bacterial abundance and production rates suggests that, under normal conditions, lysogenic viral production contributes less than 0.02% of total viral production. Therefore, lysogens in the marine environment may serve as a source of viruses and only contribute significantly to viral production during natural induction events.

60. **Gene transfer by transduction in the marine environment. Jiang, S.C., Paul, J.H. (1998). *Applied & Environmental Microbiology* 64:2780-2787**. To determine the potential for bacteriophage-mediated gene transfer in the marine environment, we established transduction systems by using marine phage host isolates. Plasmid pQSR50, which contains transposon Tn5 and encodes kanamycin and streptomycin resistance, was used in plasmid transduction assays. Both marine bacterial isolates and concentrated natural bacterial communities were used as recipients in transduction studies. Transductants were detected by a gene probe complementary to the neomycin phosphotransferase (nptII) gene in Tn5. The transduction frequencies ranged from 1.33×10^{-7} to 5.13×10^{-9} transductants/PFU in studies performed with the bacterial isolates. With the mixed bacterial communities, putative transductants were detected in two of the six experiments performed. These putative transductants were confirmed and separated from indigenous antibiotic-resistant bacteria by colony hybridization probed with the nptII probe and by PCR amplification performed with two sets of primers specific for pQSR50. The frequencies of plasmid transduction in the mixed bacterial communities ranged from 1.58×10^{-8} to 3.7×10^{-8} transductants/PFU. Estimates of the transduction rate obtained by using a numerical model

suggested that up to 1.3 X 10^{14} transduction events per year could occur in the Tampa Bay Estuary. The results of this study suggest that transduction could be an important mechanism for horizontal gene transfer in the marine environment.

61. **Fluorescent *Escherichia coli* C for enumeration of coliphages from environmental samples. Jothikumar, N., Cliver, D.O. (1998). *BioTechniques* 24:546**

62. **Characterization and possible functions of a new filamentous bacteriophage from *Vibrio cholerae* O139. Jouravleva, E.A., McDonald, G.A., Garon, C.F., Boesman-Finkelstein, M., Finkelstein, R.A. (1998). *Microbiology* 144:315-324**. The emergence and rapid rise to dominance of *Vibrio cholerae* O139 in India and Bangladesh in 1992 led to the consideration that choleraphage might serve as both a selective mechanism and a means for horizontal transmission of genetic information. A filamentous phage '493' from O139 strain AJ27-493 has been purified and partially characterized. The phage was inactive on classical biotype *V. cholerae* O1 but it was active on El Tor biotype strains isolated prior to 1994 when El Tor re-emerged in Bangladesh. More recent El Tor isolates were all resistant to the phage. The phage was also active on O139 strains. Unlike the filamentous ctx ϕ, the receptor for 493 is not TcpA. The phage genome was a 9.3 kb closed circular single-stranded molecule containing a 0.4 kb double-stranded stem supporting a 2 kb single-stranded loop. A 283 bp fragment was cloned and used as a probe in Southern hybridization, in parallel with total phage 493 DNA. These probes hybridized both chromosomally and extrachromosomally with most O139 strains, but not with O1 strains. Infection of hybridization-negative El Tor or O139 strains resulted in the presence of hybridizing loci (both plasmid and chromosomal), in the appearance of an 18 kDa protein, and in marked alterations in colonial morphology. Phage 493 is clearly distinct from other O139 choleraphages which have been described. Phage 493 DNA hybridized with an encapsulated non-O1 (O31) strain (NRT36S) which was isolated before O139 was recognized. NRT36S also produces a phage which can infect El Tor strains with low efficiency. Further studies may reveal whether bacteriophage play a role in the emergence and the territoriality of new choleragenic vibrios.

63. **The *Vibrio cholerae* mannose-sensitive hemagglutinin is the receptor for a filamentous bacteriophage from *V. cholerae* O139. Jouravleva, E.A., McDonald, G.A., Marsh, J.W., Taylor, R.K., Boesman-Finkelstein, M., Finkelstein, R.A. (1998). *Infection and Immunity* 66:2535-2539**. We previously isolated from a 1994 isolate of *Vibrio cholerae* O139 a filamentous lysogenic bacteriophage, choleraphage 493, which inhibits pre-O139 but not post-O139 El Tor biotype *V. cholerae* strains in plaque assays. We investigated the role of the mannose-sensitive hemagglutinin (MSHA) type IV pilus as a receptor in phage 493 infection. Spontaneous, Tn5 insertion, and mshA deletion mutants are resistant to 493 infection. Susceptibility is restored by mshA complementation of deletion mutants. Additionally, the 493 phage titer is reduced by adsorption with MSHA-positive strains but not with a DELTAmshA1 strain. Monoclonal antibody against MSHA inhibits plaque formation. We conclude that MSHA is the receptor for phage 493. The emergence and decline of O139 in India and Bangladesh are correlated with the susceptibility and resistance of El Tor strains to 493. However, mshA gene sequences of post-O139 strains are identical to those of susceptible pre-O139 isolates, indicating that phage resistance of El Tor is not due to a change in mshA. Classical biotype strains are (with rare exceptions) hemagglutinin negative and resistant to 493 in plaque assays. Nevertheless, they express the mshA pilin gene. They can be infected with 493 and produce low levels of phage DNA, like post-O139 El Tor strains. Resistance to 493 in plaque assays is thus not equivalent to resistance to infection. The ability of filamentous phages, such as 493, to transfer large amounts of DNA provides them, additionally, with the potential for quantum leaps in both identity and pathogenicity, such as the conversion of El Tor to O139.

64. **Phage display of a biologically active *Bacillus thuringiensis* toxin. Kasman, L.M., Lukowiak, A.A., Garczynski, S.F., McNall, R.J., Youngman, P., Adang, M.J. (1998). *Applied and Environmental Microbiology* 64:2995-3003**.

65. **Return of a killer. Koerner, B.I. (1998). *U.S.News and World Report* (November 2, 1998), 51-52.** Phages may once again fight tough bacterial infections.

66. **An experimental selection system to identify bacterial cells exhibiting a new DNA host specificity. Kunz, A., Meisel, A., Mackeldanz, P., Reuter, M., Krueger, D.H. (1998). *Biological Chemistry* 379:563-566**. Restriction-modification enzymes interact with DNA sequences in a highly specific manner. Mutations within the DNA binding region of the enzymes could be expected to produce enzyme variants with changed DNA sequence specificities. We developed an efficient in vivo selection system that enabled us to detect one cell coding for a restriction-modification system with a new DNA sequence specificity in a background of more than 10^6 cells with the original DNA sequence specificity.

67. **Phage therapy: bacteriophages as antibiotics. Kutter, E. (1998). http://www.evergreen.edu/user/T4/PhageTherapy/Phagethea.html**

68. **Distribution of indicator bacteria and bacteriophages in shellfish and shellfish-growing waters. Legnani, P., Leoni, E., Lev, D., Rossi, R., Villa, G.C., Bisbini, P. (1998). *Journal of Applied Microbiology* 85:790-798**. Shellfish (mussels and clams) and shellfish-growing waters were examined for indicator bacteria according to the EC regulations, *Salmonella* spp., coliphages and anti-*Salmonella* phages. Samples were collected both from natural-growing areas along the coast and from authorized shellfish-harvesting beds. The coastal area was affected by organic pollution and extensive faecal contamination and, according to the legal requirements, was unsuitable for shellfish farming. The shellfish collected along the coast also showed faecal contamination at levels which did not conform to legal standards. No significant differences were observed between the frequency of isolation of somatic coliphages and indicator bacteria from sea water. In contrast, both the authorized and wild coastal shellfish were contaminated by coliphages at a significantly higher level than the corresponding bacteria) indicators for faecal contamination (chi2 test, $P < 0.01$), waters ($P < 0.001$), and sediments ($P < 0.05$), but no correlation was found in shellfish, thus Coliphage concentrations were significantly correlated with faecal indicators in marine of economic importance.

69. **The challenge of antibiotic resistance. Levy, S.B. (1998). *Scientific American* (March), 46-53.** Certain bacterial infections now defy all antibiotics. The resistance problem may be reversible, but only if society begins to consider how the drugs affect "good" bacteria as well as "bad". [this, technically, is not a bacteriophage ecology reference, but I'm including it in the BEG bibliography for those interested in questions of why bacteriophage therapy may again possess relevance; three volumes are referenced by this article which also address the antibiotic issue, and these, too, are now referenced by the BEG bibliography - STA].

70. **The structural gene module in *Streptococcus thermophilus* bacteriophage ϕ Sfi11 shows a hierarchy of relatedness to *Siphoviridae* from a wide range of bacterial hosts. Lucchini, S., Desiere, F., Brussow, H. (1998). *Virology* 246:63-73**. The structural gene cluster and the lysis module from lytic group II *Streptococcus thermophilus* bacteriophage ϕ Sfi11 was compared to the corresponding region from other *Siphoviridae*. The analysis revealed a hierarchy of relatedness. ϕ Sfi11 differed from the temperate *S. thermophilus* bacteriophage ϕ O1205 by about 10% at the nucleotide level. The majority of the changes were point mutations, mainly at the third base position. Only a single gene (orf 695) differed substantially between the two phages. Over the putative minor tail and lysis genes, ϕ Sfi11 and the lytic group 1 *S. thermophilus* ϕ Sfi19 shared regions with variable degrees of similarity. Orf 1291 from ϕ Sfi19 was replaced by four genes in ϕ Sfi11, two of which (orf 1000 and orf 695) showed a complicated pattern of similarity and nonsimilarity compared with ϕ Sfi19. The predicted orf 695 gp resembles the receptor-recognizing protein of T-even coliphages in its organization, but not its sequence. No sequence similarity was detected between ϕ Sfi11 and ϕ Sfi19 in the region covering the major head and tail genes. Comparison of the structural gene map of ϕ Sfi11 with that of *Siphoviridae* from gram-positive and -negative bacterial hosts revealed a common genomic organization. Sequence similarity was only found between ϕ Sfi11 and *Siphoviridae* from gram-positive hosts and correlated with the evolutionary distance between the bacterial hosts. Our data are compatible with the

hypothesis that the structural gene operon from *Siphoviridae* of the low G + C group of gram-positive bacteria is derived from a common ancestor.

71. **Virus binding to brown algal spores and gametes visualized by DAPI fluorescence microscopy. Maier, I., Mueller, D.G. (1998). *Phycologia* 37:60-63**. Several brown algae (Phaeophyceae) have been found to be regularly parasitized by viruses. These viruses are icosahedral, 120-180 nm in diameter, and have large genomes of double-stranded DNA in the range of 160-340 k base pairs (kbp). Their natural host range appears to be relatively narrow (Ivey et al. 1996; Mueller 1996; Kapp et al. 1997). Coleman et al. (1981) employed DAPI (4',6-diamidino-2-phenylindole) fluorescence staining for visualization and microspectrophotometric measurement of individual T_4 bacteriophage DNA, which is smaller than most brown algal viral genomes (166 kbp). Therefore, we expected this method to be sensitive enough for the localization of brown algal virus particles bound to their host cells. Stained virions could also be used to show if host specificity is reflected by the level of virus binding.

72. **Resistance of *Pseudomonas aeruginosa* PAO1 phage F116 to sodium hypochlorite. Maillard, J.Y., Hann, A.C., Perrin, R. (1998). *Journal of Applied Microbiology* 85:799-806**. The development of viral resistance to sodium hypochlorite was investigated using the *Pseudomonas aeruginosa* bacteriophage F116 as a model system. This phage was chosen because of its structural characteristics and former investigations conducted in this laboratory. F116 was shown to be sensitive to a sodium hypochlorite concentration of 0.0075 g l^{-1} (available chlorine) which produced a 5 log10 reduction in titre in a suspension test. Survival bacteriophages challenged with this sodium hypochlorite concentration were isolated, propagated and challenged again with the same and higher concentrations of the biocide. It was observed that progeny virions were becoming increasingly resistant to sodium hypochlorite challenges up to a concentration of 0.0175 g l^{-1} of available chlorine. It was also noticed that 1-2 log10 of F116 virions from resistant phage lysates remained sensitive to the biocide. An electron microscopical investigation of F116 resistant lysates showed that the phage resistance to sodium hypochlorite was not caused by F116 particles aggregation. Furthermore, no morphological difference between the sensitive and resistant F116 particles to sodium hypochlorite was identified.

73. **Characterization of a novel cis-syn and trans-syn-II pyrimidine dimer glycosylase/AP lyase from a eukaryotic algal virus, *Paramecium bursaria* chlorella Virus-1. McCullough, A.K., Romberg, M.T., Nyaga, S., Wei, Y., Wood, T.G., Taylor, J.S., Van Etten, J.L., Dodson, M.L., Lloyd, R.S. (1998). *Journal of Biological Chemistry [J. Biol. Chem.]* 273:13136-13142**. Endonuclease V from bacteriophage T4, is a cis-syn pyrimidine dimer-specific glycosylase. Recently, the first sequence homolog of T4 endonuclease V was identified from chlorella virus *Paramecium bursaria* chlorella virus-1 (PBCV-1). Here we present the biochemical characterization of the chlorella virus pyrimidine dimer glycosylase, cv-PDG. Interestingly, cv-PDG is specific not only for the cis-syn cyclobutane pyrimidine dimer, but also for the trans-syn-II isomer. This is the first trans-syn-II-specific glycosylase identified to date. Kinetic analysis demonstrates that DNAs containing both types of pyrimidine dimers are cleaved by the enzyme with similar catalytic efficiencies. Cleavage analysis and covalent trapping experiments demonstrate that the enzyme mechanism is consistent with the model proposed for glycosylase/AP lyase enzymes in which the glycosylase action is mediated via an imino intermediate between the C1' of the sugar and an amino group in the enzyme, followed by a beta -elimination reaction resulting in cleavage of the phosphodiester bond. cv-PDG exhibits processive cleavage kinetics which are diminished at salt concentrations greater than those determined for T4 endonuclease V, indicating a possibly stronger electrostatic attraction between enzyme and DNA. The identification of this new enzyme with broader pyrimidine dimer specificity raises the intriguing possibility that there may be other T4 endonuclease V-like enzymes with specificity toward other DNA photoproducts.

74. **Synergistic effects of abiE or abiF from pNP40 when cloned in combination with abiD from pBF61. McLandsborough, L.A., Sechaud, L., McKay, L.L. (1998). *Journal of Dairy Science* 81:362-368**. Two fragments conferring partial phage resistance were located on plasmid pNP40 from *Lactococcus lactis* ssp. lactis biovar diacetylactis DRC3 and cloned. A 2.3-kb PstI fragment from pNP40 containing abiF conferred partial phage resistance to prolate-headed phage c2, and a 4.8-kb PstI fragment of pNP40 containing abiE conferred partial phage resistance to small isometric-headed phage sk1. When each of the two fragments was cloned individually into a plasmid containing the abortive phage infection gene abiD from *L. lactis* ssp. lactis KR5, phage resistance was enhanced. When cloned with abiD, the 2.3-kb PstI fragment enhanced the resistance against prolate-headed phages, as was indicated by a 400-fold decrease in the efficiency of plating compared with that of abiD alone. When the 4.8-kb PstI fragment of pNP40 was cloned with abiD, resistance to small isometric-headed phages was enhanced, as was indicated by a greater than 50-fold decrease in efficiency of plating compared with that of abiD alone. The 4.8-kb PstI fragment of pNP40 cloned with abiD showed a large decrease (500- to 1000-fold) in efficiency of plating against prolate-headed phages, even though the 4.8-kb PstI fragment of pNP40 by itself conferred no resistance to the prolate-headed phages.

75. **Evidence of pseudolysogeny in a marine phage host system. McLaughlin, M.R., Paul, J.H. (1998). *Abstracts of the General Meeting of the American Society for Microbiology* 98:387-???**

76. **Comparative survival of F^+ RNA coliphages, poliovirus type 1(PV1), and somatic salmonella phage (SSP) in advanced treated wastewater, groundwater and soil suspensions. Meschke, J.S., Sobsey, M.D. (1998). *Abstracts of the General Meeting of the American Society for Microbiology* 98:443-444**.

77. **Dynamics of the pseudolysogenic response in slowly growing cells of *Pseudomonas aeruginosa*. Miller, R.V. (1998). *Microbiology (Reading)* 144:2225-2232**. Pseudolysogeny is an environmental condition in which the starved bacterial cell coexists in an unstable relationship with infecting viral genomes. As nutrients are supplied to the bacterium, the pseudolysogens resolve into either true lysogeny or active production of virions. The direct result of pseudolysogenic relationships is an extension of the effective phage half-lives in natural environments. In this paper a continuous culture model of interactions between bacterial host organisms and bacteriophages leading to pseudolysogeny is presented. The pseudolysogenic state was found to depend on the concentration of nutrients available to the host. As cells became more starved, the frequency of pseudolysogens increased. The dependence on overall nutrient concentration was more dramatic than the variation in the generation time (chemostat turnover time) of the host. Thus, it appears that pseudolysogeny is a legitimate strategy for environmental bacteriophages to adapt to survive periods of starvation of their host organisms. Consideration of pseudolysogeny as a survival strategy is important to the development of any comprehensive model of host-bacteriophage relationships in natural environments.

78. **Abundance in sewage of bacteriophages that infect *Escherichia coli* 0157:H7 and that carry the Shiga toxin 2 gene. Muniesa, M., Jofre, J. (1998). *Applied and Environmental Microbiology* 64:2443-2448**. Shiga toxin-converting bacteriophages are involved in the pathogenicity of some enteric bacteria, such as *Escherichia coli* O157:H7, but data on the occurrence and distribution of such phages as free particles in nature were not available. An experimental approach has been developed to detect the presence of the Shiga toxin 2 (Stx 2)-encoding bacteriophages in sewage. The Stx 2 gene was amplified by PCR from phages concentrated from 10-ml samples of sewage. Moreover, the phages carrying the Stx 2 gene were detected in supernatants from bacteriophage enrichment cultures by using an Stx 2-negative *E. coli* O157:H7 strain infected with phages purified from volumes of sewage as small as 0.02 mi. Additionally, the A subunit of Stx 2 was detected in the supernatants of the bacteriophage enrichment cultures, which also showed cytotoxic activity for Vero cells. By enrichment of phages concentrated from different volumes of sewage and applying the most-probable-number technique, it was estimated that the number of phages infectious for *E. coli* O157:H7 and carrying the Stx 2 gene was in the range of 1 to 10 per ml of sewage from two different origins. These values were approximately 1% of all phages infecting *E. coli* O157:H7.

79. **A temperate phage with cohesive ends induced by mitomycin C treatment of *Lactobacillus casei*. Nakashima, Y., Hasuwa, H., Kakita, Y., Murata, K., Kuroiwa, A., Miake, F., Watanabe, K. (1998). *Archives of Virology* 143:1621-1626**.

80. **Comparison of the lysogeny modules from the temperate *Streptococcus thermophilus* bacteriophages TP-J34 and Sfi21: implications for the modular theory of phage evolution. Neve, H., Zenz, K.I., Desiere, F., Koch, A., Heller, K.J., Brussow, H. (1998). *Virology* 241:61-72**. A 7.6-kb DNA segment covering the putative lysogeny module of the pac-site-containing temperate *Streptococcus thermophilus* bacteriophage TP-J34 was sequenced. Sequence alignment with the lysogeny module from the cos-site-containing *S. thermophilus* bacteriophage phiSfi21 revealed areas of high sequence conservation (e.g., over the int gene), interspersed with regions of low or no sequence similarity (e.g., over the cro gene). Four of the six sharp transition zones from high to low sequence conservation were found within open reading frames coding for the CI repressor, the Anti-repressor, the Immunity protein, and a protein of unknown function. The transition points in the cI and ant genes appear to separate gene segments coding for distinct functional domains of these proteins. In addition, these two transition points were located at or near the deletion sites observed in spontaneous phage phiSfi21 deletion mutants, thus suggesting these transition points as recombinational hotspots. Furthermore, the sequence at the transition point in the cI gene resembles the attachment site of the phage, suggesting the involvement of the phage integrase in at least some of the exchange reactions. Contrary to the initial formulation of the modular theory of phage evolution the unit of the evolutionary exchange in streptococcal phages is not a group of functional genes, but can be as small as a single gene. Exchange reactions can also occur within genes, possibly between gene segments encoding distinct protein domains.

81. **Design of a phage-insensitive lactococcal dairy starter via sequential transfer of naturally occurring conjugative plasmids. O'Sullivan, D., Coffey, A., Fitzgerald, G.F., Hill, C., Ross, R.P. (1998). *Applied and Environmental Microbiology* 64:4618-4622**.

82. **Recovery of phages T1 and PP7, and poliovirus from water with a hollow-fiber, 50,000 molecular weight cut-off ultrafilter. Oshima, K., Ommani, A. (1998). *Abstracts of the General Meeting of the American Society for Microbiology* 98:438-???**

83. **Genetic dynamics of *Salmonella typhi*-diversity in clonality. Pang, T. (1998). *Trends in Microbiology* 6:339-342**. "What mechanisms or selective pressures are acting on *S. typhi* to maintain such plasticity? It is thought that the evolution of virulence in *Salmonella* spp. is driven by plasmid- or phage-mediated horizontal transfer of genetic elements such as virulence genes and pathogenicity islands (reference). By itself, this mechanisms does not appear to be sufficient for the rapid pace of change and the high degree of genetic variability observed among pathogenic *Salmonella* spp. Rather, it has been proposed that *Salmonella* 'mutator' mutants can transiently increase their mutation rate (hypermutable state), which allows genetic variation to occur immediately after infection when the pathogen needs to survive, invade and colonize the human host (reference). This hypothesis is based on the results of recent studies showing that high mutation frequences (>1%) exist among *Escerhichia coli* and *Salmonella*, which is related to defects in methyl-directed mismatch repair (MMR) mechanisms (ditto)." p. 340 (emphasis mine; note otherwise that the article does not appear to have an abstract or summary).

84. **The polyvalent staphylococcal phage í812: its host-range mutants and related phages. Pantucek, R., Rosypalova, A., Doskar, J., Kailerova, J., Ruzickova, V., Borecka, P., Snopkova, S., Horvath, R., Goetz, F., Rosypal, S. (1998). *Virology -New York-* 246:241-252**.

85. **Biological systems aimed at a control over environmental mutagenic load. Pererva, T.P., Miryuta, N.Y., Miryuta, A.Y., Aleksandrov, Y. (1998). *Dopovidi Natsional'noyi Akademiyi Nauk Ukrayiny* 188-192**. Comparative analysis of RNA-containing MS2 phage, DNA-containing lambda phage and Drosophila melanogaster as possible test-objects for study of environmental mutagenic loading is carried out. According to the obtained results, MS2 phage is the most sensible to the combined mutagenic action of studied soil specimens, Drosophila is completely unsensible, while lambda phage is located on the intermediate position showing only an insignificant mutagenic response under experimental conditions.

86. **Abundance, morphology and distribution of planktonic virus-like particles in two high-mountain lakes. Pina, S., Creus, A., González, N., Gironés, R., Felip, M., Sommaruga, R. (1998). *Journal of Plankton Research* 20:2413-2421**. Direct counts of virus-like particles (VLP) by transmission electron microscopy revealed abundances of up to 3 x 10^7 ml^{-1} in the plankton of two remote high-mountain lakes in the Alps and in the Pyrenees. Most VLP were icosahedric without tail and with diameters between 40 and 90 nm, but also very large ones with diameter of up to 325 nm were observed. VLP outnumbered bacteria by a factor of 4.2 to 42.8 and bacterial cells were infected with large numbers (>50) of viral particles. This study constitutes the first report on aquatic viruses for alpine lakes and it suggests that they may be an important additional source of bacterial mortality in these systems.

87. **Viral pollution in the environment and in shellfish: Human adenovirus detection by PCR as an index of human viruses. Pina, S., Puig, M., Lucena, F., Jofre, J., Girones, R. (1998). *Applied and Environmental Microbiology* 64:3376-3382**. A study of the presence of human viruses (adenoviruses, enteroviruses, and hepatitis A viruses (HAVs)) in environmental and shellfish samples was carried out by applying DNA and cDNA amplification techniques by PCR. The detection of human adenoviruses by PCR was also examined as a potential molecular test to monitor viral pollution. The samples studied were urban and slaughterhouse sewage, river water, seawater, and shellfish. Enteroviruses were quantified by PFU in Buffalo green monkey kidney cells and fecal coliforms and phages of *Bacteroides fragilis* HSP40 were also evaluated in some of the samples. The amplification of viral DNA and cDNA has shown a high prevalence of human viruses that would not be detected by the use of classical techniques, such as the quantification of PFU in cell lines. The results of the analysis of slaughterhouse sewage samples together with the test of farm animal feces indicate that the adenoviruses and the HAVs detected in the environment are mostly of human origin. A significative correlation between the detection of human viruses by PCR and the values of bacteriophages of *B. fragilis* HSP40 in urban raw sewage was observed. Human adenoviruses were the viruses most frequently detected throughout the year, and all the samples that were positive for enteroviruses or HAVs were also positive for human adenoviruses. The results suggest that the detection of adenoviruses by PCR could be used as an index of the presence of human viruses in the environment where a molecular index is acceptable.

88. **New method churns out TB mutants. Potera, C. (1998). *Science* 280, 1350-1351.** "…viruses that naturally infect mycobacteria. With few such viruses available commercially, Jacobs turned to a handy source—his own backyard in the Bronx.¶ Bacterial viruses, or phages as they are called, are common soil dwellers, and so Jacobs screened soil from his yard looking for any that infect *M. tuberculosis* efficienty. He won the 'prokaryotic Lotto,' he says, in 1987 when he found a mutant bacteriophage that infects *M. tuberculosis* at a frequency seven orders of magnitude higher than its parent." [I know it is difficult to understand what exactly that last sentence is saying, but that is what it says---STA].

89. **Complete sequence of the new lactococcal abortive phage resistance gene abiO. Prevots, F., Ritzenthaler, P. (1998). *Journal of Dairy Science* 81:1483-1485**.

90. **Nucleotide seqeunce and analysis of the new chromosomal abortive infection gene abiN of *Lactococcus lactis* subsp. cremoris S114. Prevots, F., Tolou, S., Delpech, B., Kaghad, M., Daloyau, M. (1998). *FEMS Microbiology Letters* 159:331-336**. A 7.275-kb DNA fragment which encodes resistance by abortive infection (Abi^+) to bacteriophage was cloned from *Lactococcus lactis* subsp. cremoris S114. The genetic determinant for abortive infection was subcloned from this fragment. This gene was found to confer a reduction in efficiency of plating and plaque size for prolate-headed bacteriophage variant phi53 (group I homology) and for small isometric-headed bacteriophage variant phi59 (group III homology). This new gene, termed abiN, is predicted to encode a polypeptide of 178 amino acid residues with a deduced molecular mass of 20461 Da and an isoelectric point of 4.63. No homology with any previously described genes was found. A probe was used to determine the presence of this gene only in S114 from 31 strains tested.

91. **Viral pollution in the environment and in shellfish: Human adenovirus detection by PCR as an index of human viruses. Puig, M., Lucena, F.,**

Jofre, J., Girones, R. (1998). ***Applied and Environmental Microbiology*** **64:3376-3382**. A study of the presence of human viruses (adenoviruses, enteroviruses, and hepatitis A viruses (HAVs)) in environmental and shellfish samples was carried out by applying DNA and cDNA amplification techniques by PCR. The detection of human adenoviruses by PCR was also examined as a potential molecular test to monitor viral pollution. The samples studied were urban and slaughterhouse sewage, river water, seawater, and shellfish. Enteroviruses were quantified by PFU in Buffalo green monkey kidney cells and fecal coliforms and phages of *Bacteroides fragilis* HSP40 were also evaluated in some of the samples. The amplification of viral DNA and cDNA has shown a high prevalence of human viruses that would not be detected by the use of classical techniques, such as the quantification of PFU in cell lines. The results of the analysis of slaughterhouse sewage samples together with the test of farm animal feces indicate that the adenoviruses and the HAVs detected in the environment are mostly of human origin. A significative correlation between the detection of human viruses by PCR and the values of bacteriophages of *B. fragilis* HSP40 in urban raw sewage was observed. Human adenoviruses were the viruses most frequently detected throughout the year, and all the samples that were positive for enteroviruses or HAVs were also positive for human adenoviruses. The results suggest that the detection of adenoviruses by PCR could be used as an index of the presence of human viruses in the environment where a molecular index is acceptable.

92. **Physicochemical characterization of phage adsorption to *Lactobacillus helveticus* ATCC 15807 cells. Quiberoni, A., Reinheimer, J.A. (1998).** ***Journal of Applied Microbiology*** **85:762-768**.

93. **Genetic (RAPD-PCR) and technological diversities among wild *Lactobacillus helveticus* strains. Quiberoni, A., Tailliez, P., Quenee, P., Suarez, V., Reinheimer, J. (1998).** ***Journal of Applied Microbiology*** **85:591-596**. Diversity in 25 *Lactobacillus helveticus* strains isolated from natural whey cultures for Argentinian hard cheese production was studied by means of RAPD-PCR patterns and technological parameters (acidifying and proteolytic activities, salt tolerance, diacetyl, H_2O_2 and slime production, phage sensitivity). In the RAPD diversity study, 10 *Lact. helveticus* strains from the CNRZ collection were also included. The clustering of RAPD patterns from the Argentinian strains revealed the existence of two *Lact. helveticus* biotypes. Cluster 1 contained 22 strains (15 wild and seven CNRZ collection strains), Cluster 2 grouped 10 wild strains and Cluster 3 contained only three CNRZ collection strains. RAPD groups could be related to specific cheese-making characteristics (cheese plants). Analysis of technological characteristics in the Argentinian strains showed the occurrence of different natural variants. According to their capacity for growing in milk, they were classified as 'fast', 'intermediate' and 'slow' variants. Among the strains, low salt tolerance and widespread phage resistance were demonstrated. The genetic diversity (RAPD-PCR clustering) did not show any clear relationship with phenotypical diversity. Study of genetic and technological diversity allows a better characterization of wild strains belonging to *Lact. helveticus*.

94. **Dynamics of the pseudolysogenic response in slowly growing cells of *Pseudomonas aeruginosa*. Ripp, S., Miller, R.V. (1998).** ***Microbiology (Reading)*** **144:2225-2232**. Pseudolysogeny is an environmental condition in which the starved bacterial cell coexists in an unstable relationship with infecting viral genomes. As nutrients are supplied to the bacterium, the pseudolysogens resolve into either true lysogeny or active production of virions. The direct result of pseudolysogenic relationships is an extension of the effective phage half-lives in natural environments. In this paper a continuous culture model of interactions between bacterial host organisms and bacteriophages leading to pseudolysogeny is presented. The pseudolysogenic state was found to depend on the concentration of nutrients available to the host. As cells became more starved, the frequency of pseudolysogens increased. The dependence on overall nutrient concentration was more dramatic than the variation in the generation time (chemostat turnover time) of the host. Thus, it appears that pseudolysogeny is a legitimate strategy for environmental bacteriophages to adapt to survive periods of starvation of their host organisms. Consideration of pseudolysogeny as a survival strategy is important to the development of any comprehensive model of host-bacteriophage relationships in natural environments.

95. **Parvovirus B19-induced anemia as the presenting manifestation of X-linked hyper-IgM syndrome. Seyama, K., Kobayashi, R., Hasle, H., Apter, A.J., Rutledge, J.C., Rosen, D., Ochs, HD (1998).** ***Journal of Infectious Disease*** **178:318-324**. Parvovirus B19 (B19) can cause chronic anemia due to persistent infection in immunocompromised hosts who cannot produce neutralizing antibody necessary for clearing B19. Three patients with X-linked hyper-IgM syndrome (XHIM), who were all asymptomatic until they developed B19-induced chronic anemia at the ages of 8, 14, and 17 years, respectively, were found to have mutations of the CD40L gene, including a missense mutation (T254M), a nonsense mutation resulting in a new initiation codon and loss of the intracellular domain (R11X), and a splice site mutation (nt 309+2t-->a). Antibody responses to the T cell-dependent antigen, bacteriophage phiX174, were impaired, but neutralizing antibody titers were higher than in XHIM patients with classic phenotype. All 3 patients responded to intravenous immune globulin (IVIG) treatment. Certain mutations of the CD40L gene result in a mild XHIM phenotype that may become apparent following B19 infection in patients not on IVIG therapy and therefore not protected from B19 infection.

96. **Phenotypic mixing of pyocin R2 and bacteriophage PS17 in *Pseudomonas aeruginosa*. Shinomiya, T. (1998).** ***J. Virol.*** **49:310-???**

97. **Distinguishing human from animal faecal contamination in water: A review. Sinton, L.W., Finlay, R.K., Hannah, D.J. (1998).** ***New Zealand Journal of Marine and Freshwater Research*** **32:323-348**. Management of faecal contamination of water would be improved if sources could be accurately identified through water analysis. Human faeces are generally perceived as constituting a greater human health risk than animal faeces, but reliable epidemiological evidence is lacking. United States waterborne disease data suggest that human-specific enteric viruses account for over half the documented outbreaks. However, in New Zealand, where there is a high grazing animal:human ratio (increasing the relative importance of water-transmissible zoonoses), it seems prudent to assume that human and animal faecal pollution both constitute a risk to human health. Irrespective of the relative risks, the ability to identify sources would assist in overall management of microbial water quality. Faecal streptococci do not appear to provide reliable faecal source identification. Human and animal sources, respectively, may be distinguishable by two tests on *Bifidobacterium* spp.-growth at 45 degrees C in trypticase phytone yeast broth and sorbitol fermentation. Different species of Bacteroides tend to be present in humans and animals, but poor survival in water is a problem. Phages of the *Bacteroides fragilis* strain HSP40 appear to be human specific, but low counts in effluent in some countries, including New Zealand, may limit their usefulness. Different F-RNA phage subgroups appear to be associated with human and animal faecal sources. The actinomycete *Rhodococcus coprophilus* has potential as a grazing animal indicator but it is persistent, and existing culturing techniques are time consuming. The development of DNA-based techniques, such as polymerase chain reaction (PCR), may assist in the assay of some microbial faecal source indicators. Various faecal sterol isomers offer the possibility of distinguishing between human and animal sources, and even between different animals. Washing powder constituents such as fluorescent whitening agents, sodium tripolyphosphate and linear alkyl benzenes, offer useful human source identifiers. It is unlikely that any single determinant will be useful in all situations, but statistical analysis of appropriate "baskets" of microbial and chemical determinants offers the possibility of identifying and apportioning human and animal faecal inputs to natural waters.

98. **Phage therapy. Soothill, J.S. (1998).** ***Journal Of Pharmacy And Pharmacology*** **50:36-36**.

99. **Lack of surface receptors not restriction-modification system determines F4 phage resistance in *Streptococcus bovis* II/1. Styriak, I., Pristas, P., Javorsky, P. (1998).** ***Folia Microbiologica*** **43:35-38**. The resistance of *Streptococcus bovis* strain II/1, the producer of SbvI restriction endonuclease, to F4 phage infection was demonstrated by the double-agar-layer method. Despite the presence of restriction endonuclease SbvI which can cleave F4 phage DNA to numerous fragments in vitro, the evidence that adsorption inhibition is the most important defense mechanism in phage resistance of *S. bovis* II/1 strain was obtained by adhesion experiments in vivo. Electron microscopy of phage-host mixtures showed many phage particles on the bacterial surface of phage-sensitive *S. bovis* 47/3 control strain in comparison with no phage particles seen on *S. bovis* II/1 (phage-resistant) strain surface.

100. **Temperate viruses and lysogeny in Lake Superior bacterioplankton. Tapper, M., Hicks, R.E. (1998). *Limnology and Oceanography* 43:95-103**. The morphology and abundance of free viruses were measured in spring, summer, and fall at one site in Lake Superior. Free viral head sizes ranged from 10 to 70 nm and tail length ranged from 10 to 110 nm. The vast majority (98%) of free viral head sizes were <60 nm, smaller than reported in most freshwater habitats. Most of these free viruses (70%) had polyhedral heads and tails, indicative of bacteriophage. Free viral abundance only ranged from 0.1 to 9 X 10^6 viruses ml^{-1} in the surface microlayer (top 20 mum) and subsurface water (20m) in Lake Superior, but viruses were 2^{-15} times more abundant in the surface microlayer. This difference may be due to the enrichment of bacterial hosts, higher levels of UV light that induce temperate phage, or differences in viral burst sizes in the surface microlayer relative to subsurface water. Bacterioplankton were always more abundant than free viruses in both the surface microlayer and subsurface water, which resulted in some of the lowest virus-to-bacterium ratios reported for marine or freshwater environments. Temperate viruses from both habitats responded equally to mitomycin-C and UV light treatments used to induce prophage into lytic cycles. An estimated 0.1-7.4% of the bacterioplankton from this site in Lake Superior contained temperate prophage depending on viral burst sizes that were assumed. Three times more bacteria in the surface microlayer may contain temperate viruses compared to bacterioplankton in subsurface waters. In the western arm of Lake Superior, bacterioplankton infected by temperate phage may be more important for the survival of bacteriophage populations than as future carbon sources for new microbial production.

101. **Role of the air-water-solid interface in bacteriophage sorption experiments. Thompson, S.S., Flury, M., Yates, M.V., Jury, W.A. (1998). *Applied & Environmental Microbiology* 64:304-309**. Batch sorption experiments were carried out with the bacteriophages MS2 and ϕ-X174. Two types of reactor vessels, polypropylene and glass, were used. Consistently lower concentrations of MS2 were found in the liquid phase in the absence of soil (control blanks) than in the presence of soil after mixing. High levels of MS2 inactivation (apprx 99.9%) were observed in control tubes made of polypropylene (PP), with comparatively little loss of virus seen in PP tubes when soil was present. Minimal inactivation of MS2 was observed when the air-water interface was completely eliminated from PP control blanks during mixing. All batch experiments performed with reactor tubes made of glass demonstrated no substantial inactivation of MS2. In similar experiments, bacteriophage ϕ-X174 did not undergo inactivation in either PP or glass control blanks, implying that this virus is not affected by the same factors which led to inactivation of MS2 in the PP control tubes. When possible, phage adsorption to soil was calculated by the Freundlich isotherm. Our data suggest that forces associated with the air-water-solid interface (where the solid is a hydrophobic surface) are responsible for inactivation of MS2 in the PP control tubes. The influence of air-water interfacial forces should be carefully considered when batch sorption experiments are conducted with certain viruses.

102. **Is the major capsid protein of iridoviruses a suitable target for the study of viral evolution? Tidona, C.A., Schnitzler, P., Kehm, R., Darai, G. (1998). *Virus Genes* 16:59-66**. Iridoviruses are large cytoplasmic DNA viruses that are specific for different insect or vertebrate hosts. The major structural component of the non-enveloped icosahedral virus particles is the major capsid protein (MCP) which appears to be highly conserved among members of the family *Iridoviridae*, *Phycodnaviridae*, and African swine fever virus. The amino acid sequences of the known MCPs were used in comparative analyses to elucidate the phylogenic relationships between different cytoplasmic DNA viruses including three insect iridoviruses (Tipula iridescent virus, Simulium iridescent virus, Chilo iridescent virus), seven vertebrate iridoviruses isolated either from fish (lymphocystis disease virus, rainbow trout virus, European catfish virus, doctor fish virus), amphibians (frog virus 3), or reptiles (turtle virus 3, turtle virus 5), one member of the family *Phycodnaviridae* (*Paramecium bursaria* Chlorella virus type 1), and African swine fever virus. These analyses revealed that the amino acid sequence of the MCP is a suitable target for the study of viral evolution since it contains highly conserved domains, but is sufficiently diverse to distinguish closely related iridovirus isolates. Furthermore, the results suggest that a substantial revision of the taxonomy of iridoviruses based on molecular phylogeny is required.

103. **Identification and characterization of a newly isolated Shiga toxin 2-converting phage from Shiga toxin-producing *Escherichia coli*. Watarai, M., Sato, T., Kobayashi, M., Shimizu, T., Yamasaki, S., Tobe, T., Sasakawa, C., Takeda, Y. (1998). *Infection and Immunity* 66:4100-4107**.

104. **Significance of viral lysis and flagellate grazing as factors controlling bacterioplankton production in a eutrophic lake. Weinbauer, M.G., Hofle, M.G. (1998). *Applied and Environmental Microbiology* 64:431-438**. The effects of viral lysis and heterotrophic nanoflagellate (HNF) grazing on bacterial mortality were estimated in a eutrophic lake (Lake Plussee in northern Germany) which was separated by a steep temperature and oxygen gradient into a warm and oxic epilimnion and a cold and anoxic hypolimnion. Two transmission electron microscopy-based methods (whole-cell examination and thin sections) were used to determine the frequency of visibly infected cells, and a model was used to estimate bacterial mortality due to viral lysis. Examination of thin sections also showed that between 20.2 and 29.2% (average, 26.1%) of the bacterial cells were empty (ghosts) and thus could not contribute to viral production. The most important finding was that the mechanism for regulating bacterial production shifted with depth from grazing control in the epilimnion to control due to viral lysis in the hypolimnion. We estimated that in the epilimnion viral lysis accounted on average for 8.4 to 41.8% of the summed mortality (calculated by determining the sum of the mortalities due to lysis and grazing), compared to 51.3 to 91.0% of the summed mortality in the metalimninon and 88.5 to 94.2% of the summed mortality in the hypolimnion. Estimates of summed mortality values indicated that bacterial production was controlled completely or almost completely in the epilimnion (summed mortality, 66.6 to 128.5%) and the hypolimnion (summed mortality, 43.4 to 103.3%), whereas in the metalimnion viral lysis and HNF grazing were not sufficient to control bacterial production (summed mortality, 22.4 to 56.7%). The estimated contribution of organic matter released by viral lysis of cells into the pool of dissolved organic matter (DOM) was low; however, since cell lysis products are very likely labile compared to the bulk DOM, they might stimulate bacterial production. The high mortality of bacterioplankton due to viral lysis in anoxic water indicates that a significant portion of bacterial production in the metalimnion and hypolimnion is cycled in the bacterium-virus-DOM loop. This finding has major implications for the fate and cycling of organic nutrients in lakes.

105. **Population dynamics of phytoplankton and viruses in a phosphate-limited mesocosm and their effect on DMSP and DMS production. Wilson, W.H., Turner, S., Mann, N.H. (1998). *Estuarine, Coastal and Shelf Science* 56(Supplement a):49-59**. The effect of phosphate limitation on viral abundance, phytoplankton bloom dynamics and production of dimethylsulphoniopropionate (DMSP) and dimethyl sulphide (DMS) was investigated in seawater mesocosm enclosures, in a Norwegian fjord, during June 1995. Daily estimates of viral concentrations, based on transmission electron microscope (TEM) counts, varied on an apparently random basis in each of the enclosures. A large *Synechococcus* spp. bloom developed in an enclosure which was maintained at a high N:P ratio, simulating phosphate-deplete growth conditions. Following phosphate addition to this enclosure, there was a large increase in estimated virus numbers shortly before an apparent collapse of the *Synechococcus* bloom. It is tentatively suggested that lysogenic viruses were induced following phosphate addition to the phosphate-limited enclosures, and that these observations add to a growing body of evidence which supports the hypothesis that nutrient availability may be responsible for the switch between lysogeny and lytic production. High DMS concentrations and viral numbers were observed on the demise of the flagellate (predominantly *Emiliania huxleyi*) and diatom blooms, but overall there was no significant correlation. Highest concentrations of DMSP were associated with blooms of *E. huxleyi*, for which an intracellular concentration of 0.5 pg $cell^{-1}$ (SD, 0.06) was calculated. Good correlation of DMSP with *Synechococcus* spp. cell numbers was observed, suggesting that these species of picoplankton may be significant producers of DMSP. No effects of phosphate limitation on DMS and/or DMSP production were evident from the data.

106. **Ultrastructure, biological and physical-chemical properties of mycobacterial phage MTPH11. Zhilenkov, E.L., Shemyakin, I.G., Korobova, O.V., Stepanshina, V.A. (1998). Boston, MA (USA). 8th International Conference on Infectious Diseases. 1998.**

Acknowledgements

Thanks to the people responsible for producing *T4 News* for modeling the need in the phage community for an ongoing newsletter. Thanks to Steven Joyce for suggesting that I might attempt a bacteriophage-ecology newsletter. Thanks to Paul Hyman and Jocelyn Witter for reading and commenting on drafts of this page. Thanks to Bill Summers for making the translation of the d'Herelle article available to the phage community, as well as for his fine new book on Felix d'Herelle.

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