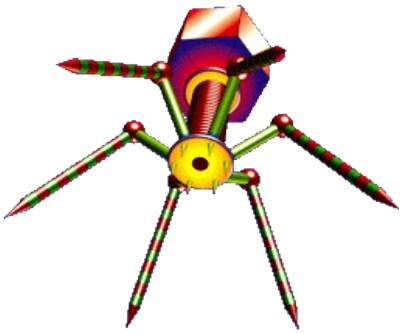

Bacteriophage Ecology Group (BEG) News

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

October 1, 2000 issue (volume 6)

At this site you will find . . .

contents | BEG News (006) | top of page

Editorial

Editorials should be written on subjects relevant to The Bacteriophage Ecology Group as an organization, to *BEG News* (either the concept or a given issue of *BEG News*), or the science of Bacteriophage Ecology. While my assumption is that I will be writing the bulk of these editorials, I wish to encourage as many people as possible to seek to relieve me of this duty, as often as possible. Additionally, I welcome suggestions of topics that may be addressed. Please address all correspondences to 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 other document formats), and in English.

Which Ecology are You?

For some time whenever I've been asked that simple question, "What exactly is it that you do?" I've had a hard time coming up with an answer. I suppose that the simplest answer is that I am a microbiologist since I received my Ph.D. in a department of microbiology, I post-docced in a department of microbiology, and I now hold a faculty position in a department of microbiology. But this answer has never been terribly satisfying to me, and can be downright terrifying when this prompts individuals to ask questions pertaining to medical microbiology. I certainly am not a medical microbiologist (though I certainly wish I could pass for one). For a while I've answered that I am a microbial evolutionary ecologist. This is satisfying since I actually do see myself as an evolutionary ecologist and I do work with microbes. But there are four problems with this answer. The first is that it is not nearly specific enough. The second is that I don't have much formal training in evolutionary ecology. The third is, "Just what the heck is evolutionary ecology anyway?" And the fourth is that I live in a very small, conservative town located in the upper fringes of the U.S. Bible belt. The just what the heck is evolutionary ecology is actually rather easy to answer: I am interested in how evolution has adapted organisms to their environments.

But *microbial evolutionary ecologist* is just something I say when I'm trying to impress (overwhelm, drive crazy, etc.) non-biologists. When speaking with biologists, one is obliged to employ a touch more precision. One solution is to pick some topic that I've recently been interested in such as the evolution of lysis timing in T-even bacteriophages (actually, I've been interested in this topic for over a decade). However, too much precision can be excluding. It's always nice to fit oneself within a group. Obviously I can call myself a phage ecologist, and thereby include all of you in my defining group, but from experience I've noted that if there is one thing a phage ecologist yearns to do, it is to command the respect of biologists, e.g., ecologists, who don't work with phages. So, for example, in terms of phages, what constitutes organismal, population, community, or ecosystem ecology, and which ecology am I?

Clearly there is a big world out there of organismal phage biology and just as clearly much of that world has far more of a molecular bent than an ecological one. Nevertheless, I see a number of areas of phage organismal biology that I would equate without hesitation with phage organismal ecology, e.g., any circumstance in which a virion particle or phage-infected cell interacts chemically or physically with a component of an ecosystem in such a way that this interaction impacts on a phage growth parameter. Phage growth parameters include: (i) the duration of the phage eclipse period, (ii) the likelihood of reduction to lysogeny, (iii) the rate of progeny production once the eclipse period has ended, (iv) the timing of lysis, (v) the duration of the rise period, (vi) adsorption kinetics, (vii) phage inactivation kinetics, etc. That is, I see phage organismal ecology as being intimately entwined with the study of phage single-step growth (a.k.a., one-step growth) and survival along with all those complications on the phage life cycle introduced by such things as lysogeny, etc.

What, then, is phage population ecology? This I see as equivalent, minimally, to phage batch culture growth, either within a liquid medium or associated with a solid substrate. At the level of experimentation, what is the difference between phage organismal ecology and phage population ecology? In essence this comes down to a degree of control over phage adsorption including phage multiplicity considerations. That is, phage population ecology typically involves cultures that begin with multiplicities that are less than one while phage organismal ecology need not. In addition, the study of phage single-step growth typically involves a significant level of control over phage adsorption either during the initial addition of phages to hosts or following phage progeny release. Batch culture growth is the antithesis of such control and therefore can involve multiple rounds of phage adsorption and infection. Phage population ecology can also encompass phage growth in continuous culture so long as one does not dwell too greatly upon the doings of the bacterial hosts.

Phage community ecology considers the phage host as something more than simply a fancy nutrient or complex growth environment. Indeed, the concern of the phage community ecologist often (gasp!) has more to do with the welfare of bacteria than with their lovely little parasites, as well as that dreaded experimental complication: Coevolution! The practitioners of phage community ecology often employ such fancy set ups as phage-host chemostats. Still, other than the bias of phage community ecologists towards considerations of the bacteriophage host, much of phage growth within chemostats probably consists of brief periods of phage batch-culture-like excitement punctuating long intervals of waiting-for-those-dang-bacteria-populations-to-grow-back-to-a-decent-density boredom.

Ecosystem ecology is the consideration of the interactions between organisms as well as their interactions with their chemical and physical (abiotic) environment, e.g., nutrient movement through trophic structures. Clearly the impact of phages on the aquatic microbial loop is a fine and deservedly popular example of phage ecosystem ecology.

There is more, in my opinion, to phage ecology than just these examples. Phage systematics is highly relevant to an understanding of phage ecology and encompasses phage nucleic acid analysis as well as studies of bacteriophage comparative morphology, while phage therapy is an example of applied community ecology. Even phage behavioral ecology is not completely oxymoronic. My lack of sympathy for the plight of bacteria clearly limits my forays into community ecology and real ecosystems are much too complex for my blood. Perhaps, then, *I am a bacteriophage organismal or population ecologist with a no-doubt unfortunate weakness for considerations of behavior?* I wonder what my neighbors would say?

MicroDude, a.k.a., **Stephen T. Abedon**
is the Developer and Editor of The Bacteriophage Ecology Group web site which is dedicated to the ecology and evolutionary biology of the parasites of unicellular organisms (UOPs)

Editorial Archive

contents | BEG News (006) | top of page

New BEG Members

The BEG members list can be found at www.phage.org/beg_members.htm as well as 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, e.g., 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 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.

Please welcome our newest members

name (home page links)	status	e-mail	address
Ipek Kurtboke	PI	micropeace @hotmail.com	LPO Box 2093, Hawthorn, Melbourne, Victoria 3122, Australia
	interests:	The use of phages as ecological and taxonomical tools, in anti-viral research, and in bacteriophage therapy. I was the organizer of the ACTINOPHAGE workshop in the 11th International Symposium on the Biology of Actinomycetes held in Crete, Greece in October, 1999. My call for an international study on Actinophages has been accepted and similar workshops will be conducted in the forthcoming conferences. I would like to encourage the group members to inform me about their research work on actinophages if they are interested to be involved in this international study. (contents | BEG members | top of page)	
Brennan O'Banion	---	virukill @aol.com	University of Kentucky, 161 Oliver Raymond Bldg., Lexington, Ky 40506
	interests:	Iodine disinfection kinetics using the serotype 2, male-specific bacteriophage GA which shows a higher resistance to inactivation when compared to phages MS-2, Q beta, Phi-X174, and PRD1. Isoelectric focusing will be used to determine if a relationship can be found to tie resistance to the degree of conformational change, after iodination, in the molecular constituents of viral capsids. (contents | BEG members | top of page)	

contents | BEG News (006) | top of page

New Links

Links relevant to The Bacteriophage Ecology Group fall into a number of categories (e.g., see Bacteriophage Ecology Links at www.phage.org/beg_links.htm). Listed below are new links found on that page. 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.

New Bacteriophage Ecology (Etc.) Links

- Evergreen International Phage Meeting (2001 meeting at Evergreen)
- Bacteriophages Show Promise as Antimicrobial Agents
- *Helicobacter pylori*-antigen-binding fragments expressed on the filamentous M13 phage prevent bacterial growth
- Long-circulating bacteriophage as antibacterial agents
- Protective effects of bacteriophage on experimental *Lactococcus garvieae* infection in yellowtail
- Use of Lytic Bacteriophage for Control of Experimental *Escherichia coli* Septicemia and Meningitis in Chickens and Calves
- Bacteriophages Show Promise as Antimicrobial Agents
- *E coli* Septicemia
- Long-circulating bacteriophage as antibacterial agents
- Phage Therapy / Tau Neutrino Science Friday
- Protective effects of bacteriophage on experimental *Lactococcus garvieae* infection in yellowtail
- Recent Phage Therapy Articles and Publications
- Results of Bacteriophage Treatment of Suppurative Bacterial Infections 1. General Evaluation of Results
- Results of Bacteriophage Treatment of Suppurative Bacterial Infections In the Years 1981 - 1986
- Smaller Fleas ... *Ad Infinitum*: Therapeutic bacteriophage redux
- Use of Lytic Bacteriophage for Control of Experimental *Escherichia coli* Septicemia and Meningitis in Chickens and Calves
- The Virus that Cures

contents | BEG News (006) | top of page

New Features

In this section I 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.

Phage Modeling References:

This page contains references to papers that attempt to mathematically model various aspects of bacteriophage ecology, etc. Please let me know of any such references that I may have missed.

contents | BEG News (006) | top of page

Upcoming Meetings

The BEG Meetings link will continue. Reminders of upcoming meetings will be placed in this section of *BEG News*. If you know of any meetings that might be of interest to BEG members, or would like to recap a meeting that you've attended, then please send this information for posting to 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.

Evergreen International Phage Meeting

Next Summer's phage meeting has been scheduled for August 8-13, 2001. The web page for this meeting can be found at http://www.evergreen.edu/user/T4/2001Meet.html. As always, this will be *the* meeting that brings together phage people with the widest possible array of interests - from the ecological to the molecular - in a setting of rain forest spender in the city that *Time Magazine* dubbed the "Hippest town in the West".

contents | BEG News (006) | top of page

Jobs

The BEG Employment / Job Listings page is no longer being 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.

Postdoctoral Position Bacterial-Bacteriophage Genetics

A two-year postdoctoral position in bacterial-bacteriophage genetics is available to investigate inter-species gene transfer within the *Burkholderia cepacia* complex using bacteriophages with inter-species host range. This is a Cystic Fibrosis Foundation funded position and is a collaborative project between the laboratories of John J. LiPuma, M.D. (U. Michigan-Medical School) and Carlos F. Gonzalez, Ph.D. (Texas A&M University). Candidates should have previous training in molecular biology, bacterial genetics, biochemistry, or virology. Send curriculum vitae, names, telephone numbers, and e-mail addresses of three references to Carlos F. Gonzalez, Department of Plant Pathology and Microbiology, 120 Peterson Bldg., Texas A&M University, College Station, Texas, 77843, Office: 979-845-8462, Fax: 979-845-6483; email cf-gonzalez@tamu.edu.

POST-DOCTORAL FELLOWSHIP - 11/4/00

New position, available immediately, for a recent Ph.D. with experience in microbiology and molecular biology. Prefer experience with oral bacteria and/or bacteriophages of gram-positives. Newly-funded (NIDCR, NIH) project involves isolating, cloning and characterizing the lysis genes of phages of Actinomyces naeslundii and Streptococcus mutans, and expressing and characterizing their gene products. Must have experience in isolating, purifying and characterizing prokaryotic DNAs and recombinant DNA techniques, including cloning in phage and plasmid vectors, manipulation and use of protein expression vectors and DNA/protein sequence analysis. Long-range goals include evaluating the therapeutic potential of purified phage lysins (a new twist on phage therapy!) and investigating the ecological role of phages in the oral cavity. Competitive salary + benefits. For more information or to apply (C.V. plus names and telephone numbers of 3 references), contact: Allan Delisle, Ph.D., Dept. of Oral & Craniofacial Biological Sciences, School of Dentistry, University of Maryland, Baltimore, Baltimore, MD 21201, e-mail: ald001@dental.umaryland.edu, phone: 410-706-7538, fax: 410-706-0193.

POSITION ANNOUNCEMENT: AVAILABILITY: IMMEDIATE

Post-doctoral position in *Salmonella* and enterohemorragic *E.coli* (EHEC) phage ecology and phage therapy: Position available to investigate the natural history, field ecology and diagnostic and/or therapeutic potential of bacteriophages specific for *Salmonella typhimurium* and EHEC O157, O111, and O26 in the livestock production environment. Will involve both lab and field based research. Ideal candidate will be a PhD microbiologist with experience in isolating and characterizing bacteriophages from the field. Previous work experience with Salmonella and EHEC is not necessary. Two year position with annual extensions possible. Annual salary of approx. $38,000 + benefits. Starting date: negotiable, but prefer between prior to Sept 2000. Interested candidates should contact Jim Keen, Animal Health Research Unit, USMARC, Clay Center, NE 68933; Ph: 402-762-4343; Email: keen@email.marc.usda.gov for additional information.

Harmful Algal Blooms and Marine Virology Postdoctoral Position

A postdoctoral position is available immediately to participate in a three-year project to investigate the use of algal and viral biomarkers in sediment cores to reconstruct the frequency and extent of occurrence of blooms of the toxic alga, *Heterosigma akashiwo*. Harmful algal blooms are a worldwide problem with enormous ecological and economic consequences. There is evidence the incidence and severity of blooms has increased in the last few decades as the result of environmental change. As well, the introduction and range expansion of harmful algal species is of great concern, but is often hard to document. The goal is to develop new approaches to hindcast the occurrence of toxic algal blooms. The successful candidate will develop and apply quantitative PCR-based methods to determine the distribution in sediment cores of cysts and viruses that are specific to *Heterosigma akashiwo*. The successful candidate will join an active laboratory of about 15 individuals investigating natural viral communities and viral mediated processes. **Applicants should provide a cover letter, CV and contact information for two references. Applicants must be within 3 years of being awarded a PhD. For further information, please contact Curtis Suttle, Department of Earth & Ocean Sciences Oceanography), University of British Columbia, 6270 University Blvd, Vancouver, BC, V6T 1Z4 Canada. Phone (604) 822-8610; Fax (604) 822-6091. APPLICATIONS BY EMAIL ARE PREFERRED: SUTTLE@EOS.UBC.CA.**

Bacteriophage diversity and horizontal gene transfer in the marine environment

See http://www.jobs.ac.uk/jobfiles/AC901.html for details. Interested candidates should contact Dr. Nick Mann (tel. +44-(0)24 7652

3526; fax +44- (0)24 7652 3701; Email: N.H.Mann@warwick.ac.uk for additional information. Closing date: November 2, 2000.

contents | BEG News (006) | top of page

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.

Bacteriophages: A Model System for Human Viruses

It is important to assess and control the presence of viruses and their inactivation from surfaces (e.g. inanimate surfaces, body tissues, nosocomial equipment) and water (e.g. drinking, sewage and sea water). Since the detection and use of mammalian viruses can be fastidious, bacteriophages (bacterial viruses) offer potential alternatives in the following areas:

1. Bacteriophages as a model system

Alongside the use of bacteriophages as index micro-organisms, their development and their employment as analogues of human viruses are due to the advantages they present. Bacteriophages infect only bacterial cells and are therefore not pathogenic. Their infection cycle is more rapid than that of human viruses, and complex and expensive culture media are not needed for their propagation. Also, the lytic infection cycle ends with lysis of the bacterial host, subsequently forming plaques, which are easy to assess, whereas the lysogenic cycle ends ultimately with the expression of 'foreign genes' in the host cell, providing a tool for the study of gene transfer. Finally, bacteriophages are widespread in the environment and are extremely diversified in their structure and can thus be used to study a variety of viruses of higher organisms.

2. Bacteriophages as an index system for enteric pathogens

The index function of bacteriophages is used to predict the possible presence of pathogenic organisms. In this respect several phages have been investigated as potential index systems for the contamination of swimming pools, and ground, drinking, sewage and shellfish water by faecal micro-organisms such as enteroviruses (Hedberg and Osterholm 1993). Three major groups of phages have been considered to achieve this function: somatic, F-RNA and *Bacteriodes fragilis* bacteriophages. The last two are thought to be the most adequate as index micro-organisms (Havelaar and Pot-Hogeboom 1988; Havelaar 1993; Nasser *et al.* 1995). *Bacteroides fragilis* phages appear to be of particular interest due to their faecal origin (Grabow *et al.* 1995). However, Callahan *et al.* (1995) recently described the use of somatic salmonella bacteriophages as index micro-organisms for enteric viruses in sea water. Therefore, the use of bacteriophages as index organisms depends upon the type of waters which are contaminated with pathogenic viruses. Furthermore, their use has to be subjected to several well-defined criteria (Havelaar 1993).

3. Bacteriophages as an indicator system for enteric viral pathogens.

The indicator function of bacteriophages is used to predict the efficacy of antimicrobial treatments. In this respect, coliphages, such as MS2 and f2 (Kott *et al.* 1972; Tartera *et al.* 1988; Maillard *et al.* 1994; Havelaar *et al.* 1995), have been widely studied, mainly to monitor the 'removal' of human enteroviruses (i.e., poliovirus, human rotavirus, hepatitis A virus and adenovirus) from various water sources. However, Finch and Fairbain (1991) showed that MS2 treatment by ozone was not indicative of the inactivation of poliovirus type-3. Therefore, the use of bacteriophages as indicators depends upon the type of antimicrobial treatments and the type of viruses investigated. Other bacteriophages such as the *Bact. Fragilis* phages have also been considered as indicators for enteroviral contamination because of their resistance to decontamination processes (Abad *et al.* 1994; Armon and Kott 1995; Bosh *et al.* 1995; Jofre *et al.* 1995a, b).

4. Bacteriophages as tools for studying mechanisms of viral disinfection.

Bacteriophages are also potential tools for studying rapidly and accurately the mechanisms of action of viricidal processes. Several biocides, as well as heat and radiation, have been tested against coliphages such as MS2 (Davies *et al.* 1993) and K (Maillard *et al.* 1994) and pseudomonad phages such as F116 (Maillard *et al.* 1993) and phi6 (Woolwine and Gerberding 1995). Bacteriophages are used as an investigating tool mainly because of their structure but also because of some particularly features. In this respect, Rheinbaben *et al.* (1992) investigated the disinfection of lactococcal phages P001, P008 and P109 and φX174 coliphage because of their thermal stability at high temperatures (i.e. 55-60°C). Woolwine and Gerberding (1995) studied the inactivation of the *Pseudomonas syringae* phi6 phage because of the presence of a surrounding envelope. The *Ps. Aeruginosa* F116 phage is currently being used as a tool for investigating the mechanism of the viricidal action of biocides. Its well-defined complex structure and its large size have been used to identify damage to the phage structure (Maillard *et al.* 1995a) after exposure to antimicrobial agents. Furthermore, F116 phage is also able to transduce. Maillard *et al.* (1995b) showed that the transduction process was extremely sensitive to disinfection.

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Submissions Archive

contents | BEG News (006) | top of page

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 by clicking the authors name. Please note that these questions have not been edited for grammar, spelling, or clarity.

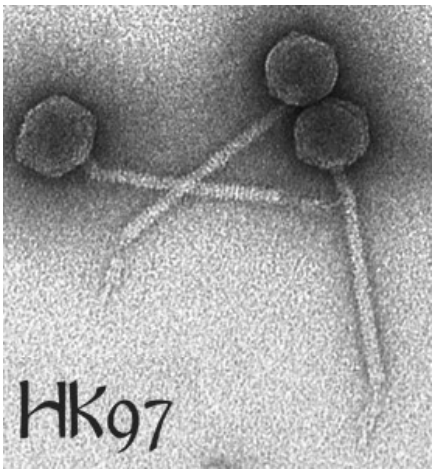
Questions

No entry.

contents | BEG News (006) | top of page

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.



For more on phage HK97 click here.

Phage Image Archive

- BEG Phage Images Page
- The Face of the Phage
- Bacteriophage T2 by H.-W. Ackermann
- SSV1-Type Phage
- Saline Lake Bacteriophage - David Bird
- Coliphage LG1 - Larry Goodridge
- Bacteriophage HK97 - Bob Duda

contents | BEG News (006) | top of page

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. **The murky origin of Snow White and her T-even dwarfs**. Abedon, S.T. (2000). *Genetics* **155**:481-486. [PRESS FOR ABSTRACT]

2. **SNDV, a novel virus of the extremely thermophilic and acidophilic archaeon Sulfolobus**. Arnold, H.P., Ziese, U., Zillig, W. (2000). *Virology* **272**:409-416. [PRESS FOR ABSTRACT]

3. **A proposal for the reclassification of *Bdellovibrio stolpii* and *Bdellovibrio starrii* into a new genus, *Bacteriovorax* gen. nov. as *Bacteriovorax stolpii* comb. nov. and *Bacteriovorax starrii* comb. nov., respectively**. Baer, M.L., Ravel, J., Chun, J., Hill, R.T., Williams, H.N. (2000). *Int J Syst Evol Microbiol* **50 Pt 1**:219-224. [PRESS FOR ABSTRACT]

4. **A bacteriophage-like particle from *Bartonella bacilliformis***. Barbian, K.D., Minnick, M.F. (2000). *Microbiology* **146 (Pt 3)**:599-609. [PRESS FOR ABSTRACT]

5. **Diversity in the arrangement of the CTX prophages in classical strains of *Vibrio cholerae* O1**. Basu, A., Mukhopadhyay, A.K., Garg, P., Chakraborty, S., Ramamurthy, T., Yamasaki, S., Takeda, Y., Nair, G.B. (2000). *FEMS Microbiol. Let.* **182**:35-40. [PRESS FOR ABSTRACT]

6. **The complete cDNA sequence of a type II *Trichomonas vaginalis* virus**. Bessarab, I.N., Liu, H.W., Ip, C.F., Tai, J.H. (2000). *Virology* **267**:350-359. [PRESS FOR ABSTRACT]

7. **Thermal and chemical inactivation of indigenous *Streptococcus thermophilus* bacteriophages isolated from Argentinian dairy plants**. Binetti, A.G., Reinheimer, J.A. (2000). *Journal of Food Protection* **63**:509-515. [PRESS FOR ABSTRACT]

8. **Characterization of mesophilic mixed starter cultures used for the manufacture of aged cheddar cheese**. Bissonnette, F., Labrie, S., Deveau, H., Lamoureux, M., Moineau, S. (2000). *Journal of Dairy Science* **83**:620-627. [PRESS FOR ABSTRACT]

9. **Linking genetic change to community evolution: insights from studies of bacteria and bacteriophage**. Bohannan, B.J.M., Lenski, R.E. (2000). *Ecological Letters* **3**:362-377. [PRESS FOR ABSTRACT]

10. **Pressure cycling technology: a novel approach to virus inactivation in plasma**. Bradley, D.W., Hess, R.A., Tao, F., Sciaba-Lentz, L., Remaley, A.T., Laugharn, J.J., Manak, M. (2000). *Transfusion* **40**:193-200. [PRESS FOR ABSTRACT]

11. **Big-benefit mutations in a bacteriophage inhibited with heat**. Bull, J.J., Badgett, M.R., Wichman, H.A. (2000). *Molecular Biology and Evolution* **17**:942-950. [PRESS FOR ABSTRACT]

12. **Selective accumulation may account for shellfish-associated viral illness**. Burkhardt, W., Calci, K.R. (2000). *Appl. Environ. Microbiol.* **66**:1375-1378. [PRESS FOR ABSTRACT]

13. **Development and evaluation of a phage typing scheme for *Vibrio cholerae* O139**. Chakrabarti, A.K., Ghosh, A.N., Nair, G.B., Niyogi, S.K., Bhattacharya, S.K., Sarkar, B.L. (2000). *Journal of Clinical Microbiology* **38**:44-49. [PRESS FOR ABSTRACT]

14. **Development of a genetically modified bacteriophage for use in tracing sources of pollution**. Daniell, T.J., Davy, M.L., Smith, R.J. (2000). *Journal of Applied Microbiology* **88**:860-869. [PRESS FOR ABSTRACT]

15. **Effect of deleterious mutation-accumulation on the fitness of RNA bacteriophage MS2**. de, l.P., Elena, S.F., Moya, A. (2000). *Int J Org Evolution* **54**:686-691. [PRESS FOR ABSTRACT]

16. **Characterization of a Phage Resistance Plasmid, pLKS, of Silage-Making *Lactobacillus plantarum* NGRI0101**. Eguchi, T., Doi, K., Nishiyama, K., Ohmomo, S., Ogata, S. (2000). *Biosci. Biotech. Biochem.* **64**:751-756. [no abstract]

17. **Computation, prediction, and experimental tests of fitness for bacteriophage T7 mutants with permuted genomes**. Endy, D., You, L., Yin, J., Molineux, I.J. (2000). *Proc. Natl. Acad. Sci. USA* **97**:5375-5380. [PRESS FOR ABSTRACT]

18. **Sunlight-Induced Propagation of the Lysogenic Phage Encoding Cholera Toxin**. Faruque, S.M., Rahman, A.M.M., Waldor, M.K., Sack, D.A. (2000). *Infect. Immun.* **68**:4795-4801. [no abstract]

19. **Intramuscular immunization with genetically inactivated (ghosts) *Actinobacillus pleuropneumoniae* serotype 9 protects pigs against homologous aerosol challenge and prevents carrier state**. Hensel, A., Huter, V., Katinger, A., Raza, P., Strnistschie, C., Roesler, U., Brand, E., Lubitz, W. (2000). *Vaccine* **18**:2945-2955. [PRESS FOR ABSTRACT]

20. **The *Streptococcus thermophilus* autolytic phenotype results from a leaky prophage**. Husson-Kao, C., Mengaud, J., Cesselin, B., van, S.D., Benbadis, L., Chapot-Chartier, M.P. (2000). *Appl. Environ. Microbiol.* **66**:558-565. [PRESS FOR ABSTRACT]

21. **Characterization of *Streptococcus thermophilus* strains that undergo lysis under unfavourable environmental conditions**. Husson-Kao, C., Mengaud, J., Gripon, J.C., Benbadis, L., Chapot-Chartier, M.P. (2000). *Int. J. Food Microbiol.* **55**:209-213. [PRESS FOR ABSTRACT]

22. **Structures of virus and virus-like particles**. Johnson, J.E., Chiu, W. (2000). *Current Opinion in Structural Biology* **10**:229-235. [PRESS FOR ABSTRACT]

23. **[Coliphages inactivation using chitosan derivatives]**. Kochkina, Z.M., Surgucheva, N.A., Chirkov, S.N. (2000). *Mikrobiologiia* **69**:261-265. [PRESS FOR ABSTRACT]

24. **[Effect of chitosan derivatives on the reproduction of Coliphages T2 and T7]**. Kochkina, Z.M., Chirkov, S.N. (2000). *Mikrobiologiia* **69**:257-260. [PRESS FOR ABSTRACT]

25. **Morphology of bacteriophages of E. Hammarström's set for typing *Shigella sonnei***. Krzywy, T., Kucharewicz-Krukowska, A., Slopek, S. (2000). *Arch. Immunol. Ther. Exp. (Warsz)* **20**:73-83. [no abstract]

26. **Forced retroevolution of an RNA bacteriophage**. Licis, N., Balklava, Z., Van, D.J. (2000). *Virology* **271**:298-306. [PRESS FOR ABSTRACT]

27. **Molecular characterization of a bacteriophage (Chp2) from *Chlamydia psittaci***. Liu, B.L., Everson, J.S., Fane, B., Giannikopoulou, P., Vretou, E., Lambden, P.R., Clarke, I.N. (2000). *J. Virol.* **74**:3464-3469. [PRESS FOR ABSTRACT]

28. **Complete nucleotide sequence, molecular analysis and genome structure of *Listeria monocytogenes* bacteriophage A118: implications for phage evolution**. Loessner, M.J., Inman, R.B., Lauer, P., Calendar, R. (2000). *Molecular Microbiology* **35**:324-340? [no abstract]

29. **Conversion of *Vibrio eltor* MAK757 to classical biotype: role of phage PS166**. Mitra, S.N., Mukhopadhyay, R., Ghosh, A.N., Ghosh, R.K. (2000).

Virology **273**:36-43. [PRESS FOR ABSTRACT]

30. **Characterization of the DNA replication module of bacteriophage A2 and use of its origin of replication as a defense against infection during milk fermentation by Lactobacillus casei**. Moscoso, M., Suarez, J.E. (2000). *Virology* **273**:101-111. [PRESS FOR ABSTRACT]

31. **Independent contrasts succeed where ancestor reconstruction fails in a known bacteriophage phylogeny**. Oakley, T.H., Cunningham, C.W. (2000). *Evolution Int J Org Evolution* **54**:397-405. [PRESS FOR ABSTRACT]

32. **Lateral gene transfer and the nature of bacterial innovation**. Ochman, H., Lawrence, J.G., Groisman, E.A. (2000). *Nature* **405**:299-304. [PRESS FOR ABSTRACT]

33. **Identification of virus-specific vesicles in Giardiavirus-infected *Giardia lamblia***. Ong, S.J., Tai, J.H. (2000). *Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih Chinese* **33**:9-13. [PRESS FOR ABSTRACT]

34. **Genotypic variations of Shiga toxin-converting phages from enterohaemorrhagic *Escherichia coli* O157: H7 isolates**. Osawa, R., Iyoda, S., Nakayama, S.I., Wada, A., Yamai, S., Watanabe, H. (2000). *J. Med. Microbiol.* **49**:565-574. [PRESS FOR ABSTRACT]

35. **Epidemiologic Subtyping of *Escherichia coli* Serogroup O157 Strains Isolated in Ontario by Phage Typing and Pulsed-Field Gel Electrophoresis**. Preston, M.A., Johnson, W., Khakhria, R., Borczyk, A. (2000). *Journal of Clinical Microbiology* **38**:2366-2368. [no abstract]

36. **The complete genomic sequence of the marine phage Roseophage SIO1 shares homology with nonmarine phages**. Rohwer, F., Segall, A., Steward, G., Seguritan, V., Breitbart, M., Wolven, F., Azam, F. (2000). *Limnology and Oceanography* **45**:408-418. [PRESS FOR ABSTRACT]

37. **Bacterial indicator occurrence and the use of an F+ specific RNA coliphage assay to identify fecal sources in Homosassa Springs, Florida**. Rose, J.B., Stokes, R. (2000). *Microb. Ecol.* **39**:56-64.

38. **Characterization of AbiR, a novel multicomponent abortive infection mechanism encoded by plasmid pKR223 of *Lactococcus lactis* subsp. lactis KR2**. Twomey, D.P., De, U.P., McKay, L.L., O'Sullivan, D.J. (2000). *Appl. Environ. Microbiol.* **66**:2647-2651. [PRESS FOR ABSTRACT]

39. **Genus *Chlorovirus* (*Phycodnaviridae*).** Van Etten, J.L. (2000). p. ???-??? *The Springer Index of Viruses*. Springer-Verlag, Berlin.[no abstract]

40. **An explosive antisense RNA strategy for inhibition of a lactococcal bacteriophage**. Walker, S.A., Klaenhammer, T.R. (2000). *Appl. Environ. Microbiol.* **66**:310-319. [PRESS FOR ABSTRACT]

41. **Morphology and general characteristics of phages specific for *Astragalus cicer rhizobia***. Wdowiak, S., Malek, W., Gr, adka, M. (2000). *Current Microbiology* **40**:110-113. [PRESS FOR ABSTRACT]

42. **Design and evolution of artificial M13 coat proteins**. Weiss, G.A., Sidhu, S.S. (2000). *Journal of Molecular Biology* **300**:213-219. [PRESS FOR ABSTRACT]

43. **An exfoliative toxin A-converting phage isolated from *Staphylococcus aureus* strain ZM**. Yoshizawa, Y., Sakurada, J., Sakurai, S., Machida, K., Kondo, I., Masuda, S. (2000). *Microbiology and Immunology* **44**:189-191. [PRESS FOR ABSTRACT]

44. **Iron modulates phenotypic variation and phosphorylation of P270 in double-stranded RNA virus-infected *Trichomonas vaginalis***. Alderete, J.F. (1999). *Infect. Immun.* **67**:4298-4302. [PRESS FOR ABSTRACT]

45. **Transduction of antibiotic resistance in *Pseudomomas aeruginosa*: relationship between lytic and transducing activity of phage isolate AP-423**. Blahova, J., Kralikova, K., Krcmery, V.S., Jezek, P. (1999). *Acta Virol.* **43**:395-398. [PRESS FOR ABSTRACT]

46. **The primary immunity determinant in modulating the lysogenic immunity of the filamentous bacteriophage cf [published erratum appears in J Mol Biol 1999 Nov 5;293(4):987]**. Cheng, C.M., Wang, H.J., Bau, H.J., Kuo, T.T. (1999). *Journal of Molecular Biology* **287**:867-876. [PRESS FOR ABSTRACT]

47. **Procaryotic infections in the mussel *Mytilus galloprovinciallis* and in its parasite the turbellarian *Urastoma cyprinae***. Comps, M., Tige, G. (1999). *Diseases of Aquatic Organisms* **38**:211-217. [PRESS FOR ABSTRACT]

48. **The *Vibrio cholerae* O139 Calcutta bacteriophage CTXphi is infectious and encodes a novel repressor**. Davis, B.M., Kimsey, H.H., Chang, W., Waldor, M.K. (1999). *J. Bacteriol.* **181**:6779-6787. [PRESS FOR ABSTRACT]

49. **The catalytic group-I introns of the psbA gene of *Chlamydomonas reinhardtii* : core structures, ORFs and evolutionary implications**. Holloway, S.P., Deshpande, N.N., Herrin, D.L. (1999). *Current Genetics* **36**:69-78. [PRESS FOR ABSTRACT]

50. **Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic *Escherichia coli* O157:H7 derived from the Sakai outbreak**. Makino, K., Yokoama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Kurokawa, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Lida, T., Yamamoto, K., Onishi, M., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C., Shinagawa, H. (1999). *Genes and Genetic Systems* **74**:227-239. [PRESS FOR ABSTRACT]

51. **Vibriophage KVP40 and coliphage T4 genomes share a homologous 7-kbp region immediately upstream of the gene encoding the major capsid protein**. Matsuzaki, S., Kuroda, M., Kimura, S., Tanaka, S. (1999). *Archives of Virology* **144**:2007-2012. [PRESS FOR ABSTRACT]

52. **Comparative study of techniques used to recover viruses from residual urban sludge**. Mignotte, B., Maul, A., Schwartzbrod, L. (1999). *Journal of Virological Methods* **78**:71-80. [PRESS FOR ABSTRACT]

53. **Isolation of additional bacteriophages with genomes of segmented double-stranded RNA**. Mindich, L., Qiao, X., Qiao, J., Onodera, S., Romantschuk, M., Hoogstraten, D. (1999). *J. Bacteriol.* **181**:4505-4508. [PRESS FOR ABSTRACT]

54. **Codon usage and lateral gene transfer in *Bacillus subtilis***. Moszer, I., Rocha, E.P., Danchin, A. (1999). *Curr Opin Microbiol* **2**:524-528. [PRESS FOR ABSTRACT]

55. **High bacterial diversity in permanently cold marine sediments**. Ravenschlag, K., Sahm, K., Pernthaler, J., Amann, R. (1999). *Appl. Environ. Microbiol.* **65**:3982-3989. [PRESS FOR ABSTRACT]

56. **Rapid film-based determination of antibiotic susceptibilities of *Mycobacterium tuberculosis* strains by using a luciferase reporter phage and the Bronx Box**. Riska, P.F., Su, Y., Bardarov, S., Freundlich, L., Sarkis, G., Hatfull, G., Carriere, C., Kumar, V., Chan, J., Jacobs, W.J. (1999). *Journal of Clinical Microbiology* **37**:1144-1149.

57. **Prophage carriage as a molecular epidemiological marker in *Streptococcus pneumoniae***. Severina, E., Ramirez, M., Tomasz, A. (1999). *Journal of Clinical Microbiology* **37**:3308-3315. [PRESS FOR ABSTRACT]

58. **(Methodic approaches to studing marine bacteria and viruses interaction) Metodicheskie podkhody k izucheniyu protsessa vzaimodejstviya morskikh bakterij i virusov**. Stepanova, O.A., Shaida, V.G. (1999). *Ehkologiya morya. Kiev [Ehkol. Morya]* **48**:96-99. [PRESS FOR ABSTRACT]

59. **[Successful treatment with bacteriophage in purulent cerebrospinal meningitis in a newborn]**. Stroj, L., Weber-Dabrowska, B., Partyka, K., Mulczyk, M., Wojcik, M. (1999). *Neurologia I Neurochirurgia Polska* **33**:693-698. [PRESS FOR ABSTRACT]

60. **Bacteriophage inactivation at the air-water-solid interface in dynamic batch systems**. Thompson, S., Yates, M.V. (1999). *Applied and Environmental Microbiology [Appl. Environ. Microbiol.]* **65**:1186-1190. [PRESS FOR ABSTRACT]

61. **Changes in bacterial and eukaryotic community structure after mass lysis of filamentous cyanobacteria associated with viruses**. van, H.E., Zwart, G., van, A.M., Gons, H.J., Ebert, J., Laanbroek, H.J. (1999). *Appl. Environ. Microbiol.* **65**:795-801. [PRESS FOR ABSTRACT]

62. **Increased synthesis of an Escherichia coli membrane protein suppresses F exclusion of bacteriophage T7**. Wang, W.F., Margolin, W., Molineux, I.J. (1999). *Journal of Molecular Biology* **292**:501-512. [PRESS FOR ABSTRACT]

63. **Bioluminescence-based assays for detection and characterization of bacteria and chemicals in clinical laboratories**. Billard, P., DuBow, M.S. (1998). *Clinical Biochemistryy* **31**:1-14.

64. **Origin, adaptation and evolutionary pathways of fungal viruses**. Ghabrial, S.A. (1998). *Virus Genes* **16**:119-131. [PRESS FOR ABSTRACT]

65. ***Legionella pneumophila* kills human phagocytes but not protozoan host cells by inducing apoptotic cell death**. Hagele, S., Hacker, J., Brand, B.C. (1998). *FEMS Microbiol. Let.* **169**:51-58. [PRESS FOR ABSTRACT]

66. **A novel filamentous phage, fs-2, of *Vibrio cholerae* O139**. Ikema, M., Honma, Y. (1998). *Microbiology* **144 (Pt 7)**:1901-1906. [PRESS FOR ABSTRACT]

67. **Genetic diversity and DNA repair of marine vibriophages.** Kellogg, C.A. (1998). Ph.D. Thesis, University of South Florida, FL, USA. [PRESS FOR ABSTRACT]

68. **High-temperature inducible cell-free transcription and replication of double-stranded RNAs within the parasitic protozoan *Cryptosporidium parvum***. Khramtsov, N.V., Upton, S.J. (1998). *Virology* **245**:331-337. [PRESS FOR ABSTRACT]

69. **Complete DNA sequence and detailed analysis of the *Yersinia pestis* KIM5 plasmid encoding murine toxin and capsular antigen**. Lindler, L.E., Plano, G.V., Burland, V., Mayhew, G.F., Blattner, F.R. (1998). *Infect. Immun.* **66**:5731-5742. [PRESS FOR ABSTRACT]

70. **Group I introns found in Chlorella viruses: biological implications**. Nishida, K., Suzuki, S., Kimura, Y., Nomura, N., Fujie, M., Yamada, T. (1998). *Virology* **242**:319-326. [PRESS FOR ABSTRACT]

71. **Phage typing of *Lactococcus garvieae* (formally *Enterococcus seriolicida*) a pathogen of cultured yellowtail**. Park, K.H., Kato, H., Nakai, T., Muroga, K. (1998). *Fisheries science. Tokyo [Fish. Sci.]* **64**:62-64. [PRESS FOR ABSTRACT]

72. **Coinfection of a fungal pathogen by two distinct double-stranded RNA viruses**. Preisig, O., Wingfield, B.D., Wingfield, M.J. (1998). *Virology* **252**:399-406. [PRESS FOR ABSTRACT]

73. **The use of luciferase-reporter phage for antibiotic-susceptibility testing of mycobacteria**. Riska, P.F., Jacobs, W.J. (1998). *Methods in Molecular Biology* **101**:431-455.

74. **Bacterioplankton dynamics in Lake Constance (Bodensee): Substrate utilization, growth control, and long-term trends.** Simon, M., Bunte, C., Schulz, M., Weiss, M., Wuensch, C. (1998). E. Baeuerle and U. Gaedke (eds.), *Archiv fuer Hydrobiologie. Spec. issue: Ergebnisse der Limnologie*. Schweizerbart'sche Verlagsbuchhandlung, Stuttgart (FRG).[PRESS FOR ABSTRACT]

75. **The specific and sensitive detection of bacterial pathogens within 4 h using bacteriophage amplification**. Stewart, G.S., Jassim, S.A., Denyer, S.P., Newby, P., Linley, K., Dhir, V.K. (1998). *Journal of Applied Microbiology* **84**:777-783. [PRESS FOR ABSTRACT]

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

77. **Effect of plating medium and phage storage on mutant frequency and titer in the lambda cII transgenic mutation assay**. Zimmer, D.M., Harbach, P.R., Mattes, W.B., Aaron, C.S. (1998). *ironmental and Molecular Mutagenesis* **32**:325-330. [PRESS FOR ABSTRACT]

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. **The murky origin of Snow White and her T-even dwarfs. Abedon, S.T. (2000). *Genetics* 155:481-486**. The T-even bacteriophages—T2, T4, and T6—represent facile experimental systems that are both relatively complex and meticulously well defined. They played essential roles in the birth and early nurturing of the field of molecular genetics, and could serve similarly as model organisms for ecology. Identification of the source habitat from which these phages were isolated would be satisfying from an ecological as well as historical perspective. Here I infer, mostly from published materials, the habitats from which these three phages were isolated, plus I delve into the history of their host, *Eschcerichia coli* B. [TOP OF PAGE]

2. **SNDV, a novel virus of the extremely thermophilic and acidophilic archaeon Sulfolobus. Arnold, H.P., Ziese, U., Zillig, W. (2000). *Virology* 272:409-416**. We describe a novel virus, SNDV (*Sulfolobus neozealandicus* droplet-shaped virus), of the crenarchaeotal archaeon *Sulfolobus*, which was found in a carrier state in a *Sulfolobus* strain isolated from a field sample from New Zealand. SNDV particles are droplet-shaped and densely covered by thin tail fibers at their pointed ends. The virion consists of a core and a coat. The latter has the appearance of a beehive and has a surface that is either helically ribbed or a stack of hoops. The genome is cccDNA of 20 kb, which is modified by dam-like methylation. It is cleaved by only a few type II restriction enzymes e.g., DpnI but not MboI, demonstrating an N(6)-methylation of the adenine residue in GATC sequences. The DNA-modifying system differentiates between virus and host. We postulate a virus-encoded methylase that is active on hemimethylated DNA. The host range of SNDV is confined to few *Sulfolobus* strains from New Zealand. The virus persists in an unstable carrier state rather than as a prophage. Due to its uniqueness we propose to assign it to a novel virus family termed Guttaviridae. [TOP OF PAGE]

3. **A proposal for the reclassification of *Bdellovibrio stolpii* and *Bdellovibrio starrii* into a new genus, *Bacteriovorax* gen. nov. as *Bacteriovorax stolpii* comb. nov. and *Bacteriovorax starrii* comb. nov., respectively. Baer, M.L., Ravel, J., Chun, J., Hill, R.T., Williams, H.N. (2000). *Int J Syst Evol Microbiol* 50 Pt 1:219-224**. Bdellovibrios are unique bacteria with the ability to prey upon a wide variety of susceptible Gram-negative bacteria. Micro-organisms exhibiting this trait have been included in the genus *Bdellovibrio* despite their isolation from diverse habitats and relatively unstudied taxonomic relatedness. In this study, 16S rDNA sequences were compared from known terrestrial *Bdellovibrio* species, *Bdellovibrio bacteriovorus* 100T, *Bdellovibrio stolpii* Uki2T and *Bdellovibrio starrii* A3.12T in order to study their phylogenetic relationship. The two sequences from *B. stolpii* Uki2T and *B. starrii* A3.12T were 90.0% similar to each other but exhibited only 81.7% and 81.2% similarity, respectively to *B. bacteriovorus* 100T. Phylogenetic analysis indicated that *B. bacteriovorus* 100T clustered in a separate clade from *B. starrii* A3.12T and B. stolpii Uki2T, demonstrating only a distant relationship between *B. bacteriovorus* 100T and the other two recognized type species. DNA-DNA hybridization experiments also demonstrated <4% hybridization between these three species. On the basis of the results obtained from the phylogenetic analysis and DNA-DNA hybridization studies, it is proposed that *B. stolpii* Uki2T and *B. starrii* A3.12T should be transferred to a new genus, *Bacteriovorax* gen. nov. as *Bacteriovorax stolpii* comb. nov. and *Bacteriovorax starrii* comb. nov., respectively. It is also proposed that the type species for the new genus *Bacteriovorax* should be *Bacteriovorax stolpii* comb. nov. [TOP OF PAGE]

4. **A bacteriophage-like particle from *Bartonella bacilliformis*. Barbian, K.D., Minnick, M.F. (2000). *Microbiology* 146 (Pt 3):599-609**. *Bartonella bacilliformis* and *Bartonella henselae*, the respective agents of Oroya fever and cat-scratch disease in humans, are known to produce bacteriophage-like particles (BLPs) that package 14 kbp segments of the host chromosome. Data from this study suggest that other *Bartonella* species including *Bartonella quintana*, *Bartonella doshiae* and *Bartonella grahamii* also contain similar BLPs, as evidenced by the presence of a 14 kbp extrachromosomal DNA element in their genomes, whereas *Bartonella elizabethae* and *Bartonella clarridgeiae* do not. A purification scheme utilizing chloroform, DNase I and centrifugation was devised to isolate BLPs from *B. bacilliformis*. Intact BLPs were observed by transmission electron microscopy and were round to icosahedral in shape and approximately 80 nm in diameter. RFLP and Southern blot analysis of BLP DNA from *B. bacilliformis* suggest that packaging, while non-selective, is less than the near-random packaging previously reported for the *B. henselae* phage. Data also suggest that the linear, double-stranded BLP DNA molecules have blunt ends with noncovalently closed termini. Packaging of the BLP DNA molecules into a protein coat appears to be closely related to nucleic acid synthesis, as unpackaged phage DNA is not detectable within the host cell. SDS-PAGE analysis of purified BLPs from *B. bacilliformis* showed three major proteins with apparent molecular masses of 32, 34 and 36 kDa; values that closely correspond to proteins found in *B. henselae* BLPs. Western blot analysis performed with patient convalescent serum showed that BLP proteins are slightly immunogenic in humans. To determine if BLPs contribute to horizontal gene transfer, mutants of *B. bacilliformis* were generated by allelic exchange with an internal fragment of the 16S-23S rDNA intergenic spacer region and a suicide vector construct, termed pKB1. BLPs from one of the resultant strains were able to package the mutagenized region containing the kanamycin-resistance cassette; however, numerous approaches and attempts at intraspecies transduction using these BLPs were unsuccessful. [TOP OF PAGE]

5. **Diversity in the arrangement of the CTX prophages in classical strains of *Vibrio cholerae* O1. Basu, A., Mukhopadhyay, A.K., Garg, P., Chakraborty, S., Ramamurthy, T., Yamasaki, S., Takeda, Y., Nair, G.B. (2000). *FEMS Microbiol. Let.* 182:35-40**. This study reports the results of a molecular analysis of the CTX prophages in classical biotype strains of *Vibrio cholerae* O1 of clinical origin isolated between 1970 and 1979 in India. All strains were sensitive to group IV classical phage and polymyxin B but resistant to group 5 El Tor phage. These phenotypic traits are consistent to that exhibited by the classical biotype. PCR studies reconfirmed their biotype assignment and showed the presence of intact CTX prophages and the presence of the recently described toxin linked cryptic plasmid. Restriction fragment length polymorphism of rRNA genes and pulsed-field gel electrophoresis showed clonal diversity among the strains. The most notable observation was the finding that one strain (GP13) has three CTX prophages while another (GP147) has four CTX prophages. This is the first time heterogeneity is reported in the arrangement of the CTX prophages among classical strains of V. cholerae O1. [TOP OF PAGE]

6. **The complete cDNA sequence of a type II *Trichomonas vaginalis* virus. Bessarab, I.N., Liu, H.W., Ip, C.F., Tai, J.H. (2000). *Virology* 267:350-359**. *Trichomonas vaginalis* viruses (TVV), which may regulate P270 gene expression in the protozoan pathogen *T. vaginalis*, are a group of divergent double-stranded (ds) RNA viruses. In the present study, the complete 4674-bp cDNA sequence of a 4.6-kb ds RNA from a newly identified TVV2-1 isolate was determined. The sequence of the plus-strand mRNA contains four open reading frames, which encode overlapping cap and pol genes in the reading frame 2 and reading frame 1, respectively, and two putative serine-threonine-rich basic proteins VP3 and VP4 in the third reading frame. An 85-kDa capsid protein and a 160-kDa CAP-POL fusion protein were identified in crude viruses by Western blotting experiments using antisera raised against gene-specific oligopeptides. In conjunction with the presence of a potential ribosomal slippery heptanucleotide G GGC CCC within the overlap of the cap and pol genes, these observations suggest that the pol gene of TVV2-1 is translated via a -1 ribosomal frameshifting event during translation of the cap gene. Our results also provide insight into the conservation among divergent dsRNA species from TVV and suggest that the genome of TVV2-1 may encode two extra genes in addition to the cap and pol genes. [TOP OF PAGE]

7. **Thermal and chemical inactivation of indigenous *Streptococcus thermophilus* bacteriophages isolated from Argentinian dairy plants. Binetti, A.G., Reinheimer, J.A. (2000). *Journal of Food Protection* 63:509-515**. Thermal and chemical resistance of five autochthonal bacteriophages of *Streptococcus thermophilus*, isolated from Cuartirolo cheese wheys and yogurt, was investigated. Times to obtain 99% inactivation of phages (T99) at 63 degrees C and 72 degrees C in three suspension media (enriched tryptic soy broth, reconstituted commercial nonfat skim milk, and tris magnesium gelatin buffer) were determined.

The thermal resistance was dependent on the phages studied but not detectable counts (<10 PFU/ml) were only achieved by heating at 90 degrees C during 5 min. The data obtained for the three assayed media did not permit verifying significant differences among them. Sodium hypochlorite (100 ppm) provided a fast inactivation of bacteriophage particles (<10 PFU/ml after 5 min). Ethanol, at concentrations of 75% and 100%, was also effective for phage destruction. Isopropanol was slightly less effective than ethanol at the same concentrations. Peracetic acid (0.15%) was also a very effective agent for phage inactivation. The results showed that these autochthonal bacteriophages were not completely inactivated neither by normal pasteurization treatments nor by some biocides commonly used in disinfection, except sodium hypochlorite and peracetic acid. The practical implications of these findings have pointed out the necessity of recognizing the importance of establishing adequate conditions to assure effective thermal and chemical treatments in dairy plants and laboratory environments. [TOP OF PAGE]

8. **Characterization of mesophilic mixed starter cultures used for the manufacture of aged cheddar cheese. Bissonnette, F., Labrie, S., Deveau, H., Lamoureux, M., Moineau, S. (2000). *Journal of Dairy Science* 83:620-627**. Seventy-one different *Lactococcus lactis* subsp. cremoris strains were isolated from seven mesophilic mixed starters used in the manufacture of aged Cheddar cheese in Canada. Based on plasmid profiles and growth in milk (with or without glucose, Casamino Acids or both), two mixed starters were highly heterogeneous, containing at least 18 to 24 distinct *L. lactis* strains. Three mixed starters were comprised of seven to nine strains, whereas two starters were relatively homogeneous, containing two or three strains. Many strains with similar plasmid profiles behaved differently during growth in milk, indicating variability in the phenotypes. Only 20% of the strains could grow in plain milk, whereas 30% could not grow in milk supplemented with glucose and Casamino Acids. Twenty-five lactococcal bacteriophages were also isolated from whey samples with single strains as hosts. Eighteen phages belonged to the 936 species and seven to the c2 species. Thirteen strains were insensitive to all 25 phages. Almost all sensitive strains were phage species-specific. The 936-like phages had a broader host range. [TOP OF PAGE]

9. **Linking genetic change to community evolution: insights from studies of bacteria and bacteriophage. Bohannan, B.J.M., Lenski, R.E. (2000). *Ecological Letters* 3:362-377**. A major goal of community ecology is to link biological processes at lower scales with community patterns. Microbial communities are especially powerful model systems for making these links. In this article, we review recent studies of laboratory communities of bacteria and bacteriophage (viruses that infect bacteria). We focus on the ecology and evolution of bacteriophage-resistance as a case study demonstrating the relationship between specific genes, individual interactions, population dynamics, community structure, and evolutionary change. In laboratory communities of bacteria and bacteriophage, bacteria rapidly evolve resistance to bacteriophage infection. Different resistance mutations produce distinct resistance phenotypes, differing, for example, in whether resistance is partial or complete, in the magnitude of the physiological cost associated with resistance, and in whether the mutation can be countered by a host-range mutation in the bacteriophage. These differences determine whether a mutant can invade, the effect its invasion has on the population dynamics of sensitive bacteria and phage, and the resulting structure of the community. All of these effects, in turn, govern the community's response to environmental change and its subsequent evolution. [TOP OF PAGE]

10. **Pressure cycling technology: a novel approach to virus inactivation in plasma. Bradley, D.W., Hess, R.A., Tao, F., Sciaba-Lentz, L., Remaley, A.T., Laugharn, J.J., Manak, M. (2000). *Transfusion* 40:193-200**. BACKGROUND: Hydrostatic-pressure virus inactivation is a novel approach to the inactivation of pathogens in plasma and blood-derived components, that retains the therapeutic properties of these products. STUDY DESIGN AND METHODS: A custom-built apparatus was used to pressurize human plasma samples spiked with lambda phage. Phage titer and plasma protein activities were monitored after pressure treatment. RESULTS: Pressure-mediated inactivation of lambda phage was found to be an effective means for virus inactivation, particularly when performed at near-zero (0 degrees C) temperatures, rather than at temperatures above 20 degrees C and below -40 degrees C. The efficiency of inactivation was improved by an increase in applied pressure and repeated cycling from atmospheric to high pressure. In contrast, activities of plasma proteins alkaline phosphatase and total amylase did not vary with temperature and remained within 29 percent and 6 percent, respectively, of starting values after the same pressure treatments. By combining cycling, near-zero temperatures, and high pressure, phage titers in serum were reduced approximately 6 log after 10 to 20 minutes of treatment. Activities of plasma proteins IgG, IgM, and factor X were at 104 percent, 89 percent, and 80 percent, respectively, of starting values after 20 minutes of the same temperature and pressure treatment. CONCLUSION: High-pressure procedures may be useful for the inactivation of viruses in blood and other protein-containing components. [TOP OF PAGE]

11. **Big-benefit mutations in a bacteriophage inhibited with heat. Bull, J.J., Badgett, M.R., Wichman, H.A. (2000). *Molecular Biology and Evolution* 17:942-950**. High temperature inhibits the growth of the wild-type bacteriophage phiX174. Three different point mutations were identified that each recovered growth at high temperature. Two affected the major capsid protein (residues F188 and F242), and one affected the internal scaffolding protein (B114). One of the major capsid mutations (F242) is located in a beta strand that contacts B114 in the procapsid during viral maturation, whereas the other capsid mutation (F188) is involved in subunit interactions at the threefold axis of symmetry. Selective coefficients of these mutations ranged from 13.9 to 3.8 in the inhibitory, hot environment, but all mutations reduced fitness at normal temperature. The selective effect of one of the mutations (F242) was evaluated at high temperature in four different genetic backgrounds and exhibited epistasis of diminishing returns: as log fitness of the background genotype increased from -0.1 to 4.1, the fitness boost provided by the F242 mutation decreased from 3.9 to 0. 8. These results support a model in which viral fitness is bounded by an upper limit and the benefit of a mutation is scaled according to the remaining opportunity for fitness improvement in the genome. [TOP OF PAGE]

12. **Selective accumulation may account for shellfish-associated viral illness. Burkhardt, W., Calci, K.R. (2000). *Appl. Environ. Microbiol.* 66:1375-1378**. From 1991 through 1998, 1,266 cases of shellfish-related illnesses were attributed to Norwalk-like viruses. Seventy-eight percent of these illnesses occurred following consumption of oysters harvested from the Gulf Coast during the months of November through January. This study investigated the ability of eastern oysters (*Crassostrea virginica*) to accumulate indicator microorganisms (i.e., fecal coliforms, Escherichia coli, Clostridium perfringens, and F(+) coliphage) from estuarine water. One-week trials over a 1-year period were used to determine if these indicator organisms could provide insight into the seasonal occurrence of these gastrointestinal illnesses. The results demonstrate that oysters preferentially accumulated F(+) coliphage, an enteric viral surrogate, to their greatest levels from late November through January, with a concentration factor of up to 99-fold. However, similar increases in accumulation of the other indicator microorganisms were not observed. These findings suggest that the seasonal occurrence of shellfish-related illnesses by enteric viruses is, in part, the result of seasonal physiological changes undergone by the oysters that affect their ability to accumulate viral particles from estuarine waters. [TOP OF PAGE]

13. **Development and evaluation of a phage typing scheme for *Vibrio cholerae* O139. Chakrabarti, A.K., Ghosh, A.N., Nair, G.B., Niyogi, S.K., Bhattacharya, S.K., Sarkar, B.L. (2000). *Journal of Clinical Microbiology* 38:44-49**. The scenario of cholera that existed previously changed in 1992 and 1993 with the emergence of toxigenic *Vibrio cholerae* O139 in India. The genesis of the new serogroup formed the impetus to search for O139 phages in and around the country. A total of five newly isolated phages lytic to *V. cholerae* O139 strains were used for the development of this phage typing scheme. These phages differed from each other and also differed from the existing O1 phages in their lytic patterns, morphologies, restriction endonuclease digestion profiles, and immunological criteria. With this scheme, 500 *V. cholerae* O139 strains were evaluated for their phage types, and almost all strains were found to be typeable. The strains clustered into 10 different phage types, of which type 1 (38.2%) was the dominant type, followed by type 2 (22.4%) and type 3 (18%). Additionally, a comparative study of phage types in 1993 and 1994 versus those from 1996 to 1998 for O139 strains showed a higher percentage of phage type 1 (40.5%), followed by type 3 (18.8%) during the period between 1993 and 1994, whereas phage type 2 (32. 1%) was the next major type during the period from 1996 to 1998. This scheme comprising five newly isolated phages would be another useful tool in the study of the epidemiology of cholera caused by *V. cholerae* O139. [TOP OF PAGE]

14. **Development of a genetically modified bacteriophage for use in tracing sources of pollution. Daniell, T.J., Davy, M.L., Smith, R.J. (2000).**

***Journal of Applied Microbiology* 88:860-869**. Bacteriophage are frequently used as biotracers to identify the source of water pollutants. Genetic manipulation of bacteriophage M13mp18 has been used to enhance this technique by creating a library in which each recombinant bacteriophage genome contains a unique identification sequence. Techniques that identify a recombinant bacteriophage by the presence of the identification sequence, including polymerase chain reaction, restriction site polymorphism and plaque hybridization, have been developed. Recombinant bacteriophage can be used to test a large number of suspected sources simultaneously. The identification sequence also eliminates confusion with natural bacteriophage present in water samples. The performance of the modified bacteriophage and the techniques were assessed in simulated field trials on a restricted site carried out under a consent for environmental release of a genetically modified organism. The techniques were also field tested at sites in northwest England using wild-type M13 bacteriophage. [TOP OF PAGE]

15. **Effect of deleterious mutation-accumulation on the fitness of RNA bacteriophage MS2. de, l.P., Elena, S.F., Moya, A. (2000). *Int J Org Evolution* 54:686-691**. RNA viruses show the highest mutation rate in nature. It has been extensively demonstrated that, in the absence of purifying selection, RNA viruses accumulate deleterious mutations at a high rate. However, the parameters describing this accumulation are, in general, poorly understood. The present study reports evidences for fitness declines by the accumulation of deleterious mutations in the bacteriophage MS2. We estimated the rate of fitness decline to be as high as 16% per bottleneck transfer. In addition, our results agree with an additive model of fitness effects. [TOP OF PAGE]

16. **Characterization of a Phage Resistance Plasmid, pLKS, of Silage-Making *Lactobacillus plantarum* NGRI0101. Eguchi, T., Doi, K., Nishiyama, K., Ohmomo, S., Ogata, S. (2000). *Biosci. Biotech. Biochem.* 64:751-756**. [TOP OF PAGE]

17. **Computation, prediction, and experimental tests of fitness for bacteriophage T7 mutants with permuted genomes. Endy, D., You, L., Yin, J., Molineux, I.J. (2000). *Proc. Natl. Acad. Sci. USA* 97:5375-5380**. We created a simulation based on experimental data from bacteriophage T7 that computes the developmental cycle of the wild-type phage and also of mutants that have an altered genome order. We used the simulation to compute the fitness of more than 10^5 mutants. We tested these computations by constructing and experimentally characterizing T7 mutants in which we repositioned gene 1, coding for T7 RNA polymerase. Computed protein synthesis rates for ectopic gene 1 strains were in moderate agreement with observed rates. Computed phage-doubling rates were close to observations for two of four strains, but significantly overestimated those of the other two. Computations indicate that the genome organization of wild-type T7 is nearly optimal for growth: only 2.8% of random genome permutations were computed to grow faster, the highest 31% faster, than wild type. Specific discrepancies between computations and observations suggest that a better understanding of the translation efficiency of individual mRNAs and the functions of qualitatively "nonessential" genes will be needed to improve the T7 simulation. In silico representations of biological systems can serve to assess and advance our understanding of the underlying biology. Iteration between computation, prediction, and observation should increase the rate at which biological hypotheses are formulated and tested. [TOP OF PAGE]

18. **Sunlight-Induced Propagation of the Lysogenic Phage Encoding Cholera Toxin. Faruque, S.M., Rahman, A.M.M., Waldor, M.K., Sack, D.A. (2000). *Infect. Immun.* 68:4795-4801**. [TOP OF PAGE]

19. **Intramuscular immunization with genetically inactivated (ghosts) *Actinobacillus pleuropneumoniae* serotype 9 protects pigs against homologous aerosol challenge and prevents carrier state. Hensel, A., Huter, V., Katinger, A., Raza, P., Strnistschie, C., Roesler, U., Brand, E., Lubitz, W. (2000). *Vaccine* 18:2945-2955**. Bacterial ghosts are empty cell envelopes achieved by the expression of a cloned bacteriophage lysis gene and, unlike classical bacterins, suffer no denaturing steps during their production. These properties may lead to a superior presentation of surface antigens to the immune system. Currently available porcine *Actinobacillus pleuropneumoniae* vaccines afford only minimal protection by decreasing mortality but not morbidity. Pigs which survive infection can still be carriers of the pathogen, so a herd once infected remains infected. Carrier pigs harbour *A. pleuropneumoniae* in their nasal cavities, in their tonsils, or within lung lesions. A dose-defined nose-only aerosol infection model for pigs was used to study the immunogenic and protective potential of systemic immunization with ghosts made from *A. pleuropneumoniae* serotype 9 reference strain CVI 13261 against an homologous aerogenous challenge. Pigs were vaccinated twice intramuscularly with a dose of 5x10(9) CFU ghosts (GVPs) or formalin-inactivated *A. pleuropneumoniae* bacterins (BVPs). After 2 weeks vaccinated pigs and non-vaccinated placebo controls (PCs) were challenged with a dose of 10(9) CFU by aerosol. The protective efficacy of immunization was evaluated by clinical, bacteriological, serological and post-mortem examinations. Bronchoalveolar lavage in pigs was performed during the experiment to obtain lavage samples (BALF) for assessment of local antibodies. Isotype-specific antibody responses in serum and BALF were determined by ELISAs based on whole-cell antigen. Immunization with ghosts did not cause clinical side-effects. After aerosol challenge PCs developed fever and pleuropneumonia. GVPs or BVPs were found to be fully protected against clinical disease or lung lesions in both vaccination groups, whereas colonization of the respiratory tract with *A. pleuropneumoniae* was only prevented in GVPs. Specific immunoglobins against *A. pleuropneumoniae* were not detectable in BALF after immunization. A significant systemic increase of IgM, IgA, IgG(Fc'), or IgG(H+L) antibodies reactive with *A. pleuropneumoniae* was measured in GVPs and BVPs when compared to the non-exposed controls. BVPs reached higher titers of IgG(Fc') and IgG(H+L) than GVPs. However, prevention of carrier state in GVPs coincided with a significant increase of serum IgA when compared to BVPs. These results suggest that immunization with ghosts, that bias antibody populations specific to non-denaturated surface antigens, may be more efficacious in protecting pigs against colonization and infection than bacterins. [TOP OF PAGE]

20. **The *Streptococcus thermophilus* autolytic phenotype results from a leaky prophage. Husson-Kao, C., Mengaud, J., Cesselin, B., van, S.D., Benbadis, L., Chapot-Chartier, M.P. (2000). *Appl. Environ. Microbiol.* 66:558-565**. *Streptococcus thermophilus* autolytic strains are characterized by a typical bell-shaped growth curve when grown under appropriate conditions. The cellular mechanisms involved in the triggering of lysis and the bacteriolytic activities of these strains were investigated in this study. Lactose depletion and organic solvents (ethanol, methanol, and chloroform) were shown to trigger a premature and immediate lysis of M17 exponentially growing cells. These factors and compounds are suspected to act by altering the cell envelope properties, causing either the permeabilization (organic solvents) or the depolarization (lactose depletion) of the cytoplasmic membrane. The autolytic character was shown to be associated with lysogeny. Phage particles, most of which were defective, were observed in the culture supernatants after both mitomycin C-induced and spontaneous lysis. By renaturing sodium dodecyl sulfate-polyacrylamide gel electrophoresis, a bacteriolytic activity was detected at 31 kDa exclusively in the autolytic strains. This enzyme was detected during both growth and spontaneous lysis with the same intensity. We have shown that it was prophage encoded and homologous to the endolysin Lyt51 of the streptococcal temperate bacteriophage phi01205 (M. Sheehan, E. Stanley, G. F. Fitzgerald, and D. van Sinderen, Appl. Environ. Microbiol. 65:569-577, 1999). It appears from our results that the autolytic properties are conferred to the *S. thermophilus* strains by a leaky prophage but do not result from massive prophage induction. More specifically, we propose that phagic genes are constitutively expressed in almost all the cells at a low and nonlethal level and that lysis is controlled and achieved by the prophage-encoded lysis proteins. [TOP OF PAGE]

21. **Characterization of *Streptococcus thermophilus* strains that undergo lysis under unfavourable environmental conditions. Husson-Kao, C., Mengaud, J., Gripon, J.C., Benbadis, L., Chapot-Chartier, M.P. (2000). *Int. J. Food Microbiol.* 55:209-213**. The autolysis of starter lactic acid bacteria appears as a promising way to enhance the flavour of fermented dairy products. The present work was aimed at investigating the autolysis phenomenon in *Streptococcus thermophilus*, a thermophilic lactic acid bacteria involved in the starters used for the production of yoghurts, Italian and Swiss-type cheeses. Out of 146 strains screened for their aptitude to spontaneously lyse at the end of growth in M17 medium containing lactose in limited concentration, six strains, among which is the type strain CNRZ 1358, were found to be highly autolytic. These autolytic strains are characterized by a typical bell-shaped growth curve. Lysis of the type strain, which was studied as the model, was triggered under unfavourable environmental conditions, such as lactose depletion and NaCl or organic solvents addition. The lysogenic character of this strain was evidenced. Taken together, our results indicate that the autolytic phenotype in *S.*

thermophilus is linked to the lysogenic character but does not result from the massive prophage induction under stressing conditions. [TOP OF PAGE]

22. **Structures of virus and virus-like particles. Johnson, J.E., Chiu, W. (2000). *Current Opinion in Structural Biology* 10:229-235**. Virus structures continue to be the basis for mechanistic virology and serve as a paradigm for solutions to problems concerning macromolecular assembly and function in general. The use of X-ray crystallography, electron cryomicroscopy and computational and biochemical methods has provided not only details of the structural folds of individual viral components, but also insights into the structural basis of assembly, nucleic acid packaging, particle dynamics and interactions with cellular molecules. [TOP OF PAGE]

23. **[Coliphages inactivation using chitosan derivatives]. Kochkina, Z.M., Surgucheva, N.A., Chirkov, S.N. (2000). *Mikrobiologiia* 69:261-265**. The effect of chitosan fragments with different degrees of polymerization and the chemical derivatives of chitosan differing in the number of amino groups and total molecule charge on phages T2, T4, and T7 was studied. The interaction of chitosan with bacteriophage particles inactivated them to the extent dependent on the chemical properties of chitosan and its concentration. Phage T2 was found to be most susceptible to inactivation by chitosan. The polycationic nature of chitosan plays an important role in the inactivation of phages. It is assumed that the abnormal rearrangement of the basal plate of phages, the loss of long tail fibers, and probably, modification of the receptor-recognizing phage proteins may be responsible for the inactivation of coliphages by chitosan. [TOP OF PAGE]

24. **[Effect of chitosan derivatives on the reproduction of Coliphages T2 and T7]. Kochkina, Z.M., Chirkov, S.N. (2000). *Mikrobiologiia* 69:257-260**. The effect of chitosan derivatives with different degrees of polymerization and deamination, as well as of chitosan 6-O-sulfate and chitosan N-succinate-6-O-sulfate, on the reproduction of coliphages T2 and T7 in Escherichia coli and on the growth of this bacterium was studied. Chitosan derivatives decreased the yield of coliphages and exhibited bactericidal activity. The efficiency of inhibition of viral infection and the bactericidal activity of chitosan were found to be dependent on the degree of its polymerization. At the same time, there was no correlation between the degree of chitosan deamination and the extent of inhibition of viral infection. Anionic chitosan derivatives virtually did not possess antiviral or bactericidal activity. It is assumed that chitosan blocks some stages of phage reproduction. The decrease in the phage-producing ability of *E. coli* may also be due to the bactericidal effect of chitosan. [TOP OF PAGE]

25. **Morphology of bacteriophages of E. Hammarström's set for typing *Shigella sonnei*. Krzywy, T., Kucharewicz-Krukowska, A., Slopek, S. (2000). *Arch. Immunol. Ther. Exp. (Warsz)* 20:73-83**. [TOP OF PAGE]

26. **Forced retroevolution of an RNA bacteriophage. Licis, N., Balklava, Z., Van, D.J. (2000). *Virology* 271:298-306**. The operator hairpin ahead of the replicase gene in RNA bacteriophage MS2 contains overlapping signals for binding the coat protein and ribosomes. Coat protein binding inhibits further translation of the gene and forms the first step in capsid formation. The hairpin sequence was partially randomized to assess the importance of this structure element for the bacteriophage and to monitor alternative solutions that would evolve on the passaging of mutant phages. The evolutionary reconstruction of the operator failed in the majority of mutants. Instead, a poor imitation developed containing only some of the recognition signals for the coat protein. Three mutants were of particular interest in that they contained double nonsense codons in the lysis reading frame that runs through the operator hairpin. The simultaneous reversion of two stop codons into sense codons has a very low probability of occurring. Therefore the phage solved the problem by deleting the nonsense signals and, in fact, the complete operator, except for the initiation codon of the replicase gene. Several revertants were isolated with activities ranging from 1% to 20% of wild type. The operator, long thought to be a critical regulator, now appears to be a dispensable element. In addition, the results indicate how RNA viruses can be forced to step back to an attenuated form. [TOP OF PAGE]

27. **Molecular characterization of a bacteriophage (Chp2) from *Chlamydia psittaci*. Liu, B.L., Everson, J.S., Fane, B., Giannikopoulou, P., Vretou, E., Lambden, P.R., Clarke, I.N. (2000). *J. Virol.* 74:3464-3469**. Comparisons of the proteome of abortifacient *Chlamydia psittaci* isolates from sheep by two-dimensional gel electrophoresis identified a novel abundant protein with a molecular mass of 61.4 kDa and an isoelectric point of 6.41. C-terminal sequence analysis of this protein yielded a short peptide sequence that had an identical match to the viral coat protein (VP1) of the avian chlamydiaphage Chp1. Electron microscope studies revealed the presence of a 25-nm-diameter bacteriophage (Chp2) with no apparent spike structures. Thin sections of chlamydia-infected cells showed that Chp2 particles were located to membranous structures surrounding reticulate bodies (RBs), suggesting that Chp2 is cytopathic for ovine C. psittaci RBs. Chp2 double-stranded circular replicative-form DNA was purified and used as a template for DNA sequence analysis. The Chp2 genome is 4,567 bp and encodes up to eight open reading frames (ORFs); it is similar in overall organization to the Chp1 genome. Seven of the ORFs (1 to 5, 7, and 8) have sequence homologies with Chp1. However, ORF 6 has a different spatial location and no cognate partner within the Chp1 genome. Chlamydiaphages have three viral structural proteins, VP1, VP2, and VP3, encoded by ORFs 1 to 3, respectively. Amino acid residues in the phiX174 procapsid known to mediate interactions between the viral coat protein and internal scaffolding proteins are conserved in the Chp2 VP1 and VP3 proteins. We suggest that VP3 performs a scaffolding-like function but has evolved into a structural protein. [TOP OF PAGE]

28. **Complete nucleotide sequence, molecular analysis and genome structure of *Listeria monocytogenes* bacteriophage A118: implications for phage evolution. Loessner, M.J., Inman, R.B., Lauer, P., Calendar, R. (2000). *Molecular Microbiology* 35:324-340?** [TOP OF PAGE]

29. **Conversion of *Vibrio eltor* MAK757 to classical biotype: role of phage PS166. Mitra, S.N., Mukhopadhyay, R., Ghosh, A.N., Ghosh, R.K. (2000). *Virology* 273:36-43**. Temperate phage PS166 infection of *Vibrio eltor* MAK757 resulted in complete changes in all biotype-specific determinants. About 10% of the PS166 lysogens of MAK757 lost their eltor-specific determinants, namely, the ability to produce soluble hemolysin, cell-associated hemagglutinin for chicken erythrocytes, and resistance to polymyxin B, as well as resistance to Mukherjee's group IV phage and sensitivity to eltor phage e4. These lysogens were found to have acquired the properties of classical strains, most significantly becoming sensitive to group IV phage but resistant to eltor-specific e4. The remainder of these lysogens, however, retained their parental biotype and serotype but acquired auxotrophy for glycine and histidine. The differential behavior of the two types of lysogen was due to the integration of the phage PS166 genome at different locations in the host chromosome. A 800-bp BglII fragment was found to contain the attP site. Phage PS166 has a polyhedral head (95 nm in diameter) and a contractile tail (98 nm in length). The phage chromosome is a linear double-stranded DNA of 110 kb and a G + C content of 58.7%. [TOP OF PAGE]

30. **Characterization of the DNA replication module of bacteriophage A2 and use of its origin of replication as a defense against infection during milk fermentation by Lactobacillus casei. Moscoso, M., Suarez, J.E. (2000). *Virology* 273:101-111**. Adjacent to the lysis/lysogeny cassette of the A2 phage genome lies a stretch of over 8 kb, which contains a series of genes probably involved in DNA replication. Fifteen open reading frames (orfs) were identified, 13 of which are encoded on the main coding strand and only two on the complementary strand. Database searches and comparative analyses allowed the identification of an open reading frame (orf455) that shows similarity with DNA helicases and contains a variant zinc-finger motif known from the phage T7 helicase/primase. Orf770 showed similarity to putative plasmid and phage DNA primases. Downstream of orf770 is a noncoding 258-bp region rich in direct and inverted repeats, which specifically binds to proteins whose synthesis is induced during phage infection. When present in a plasmid, this region can direct a partial bacteriophage resistance phenotype due to interference with phage DNA replication, both under laboratory conditions and during milk fermentation. It is deduced that this stretch contains the origin of replication of phage A2. [TOP OF PAGE]

31. **Independent contrasts succeed where ancestor reconstruction fails in a known bacteriophage phylogeny. Oakley, T.H., Cunningham, C.W. (2000). *Evolution Int J Org Evolution* 54:397-405**. Methods of ancestor reconstruction are important tools for evolutionary inference that are difficult to test empirically because ancestral states are rarely known with certainty. We evaluated reconstruction methods for continuous phenotypic characters using taxa from

an experimentally generated bacteriophage phylogeny. Except for one slowly evolving character, the estimated ancestral states of continuous phenotypic characters were highly inaccurate and biased, even when including a known ancestor at the root. This error was caused by a directional trend in character evolution and by rapid rates of character evolution. Computer simulations confirmed that such factors affect reconstruction of continuous characters in general. We also used phenotypic viral characters to evaluate two methods that attempt to estimate the correlation between characters during evolution. Whereas a nonphylogenetic regression was relatively inaccurate and biased, independent contrasts accurately estimated the correlation between characters with little bias. [TOP OF PAGE]

32. **Lateral gene transfer and the nature of bacterial innovation. Ochman, H., Lawrence, J.G., Groisman, E.A. (2000). *Nature* 405:299-304**. Unlike eukaryotes, which evolve principally through the modification of existing genetic information, bacteria have obtained a significant proportion of their genetic diversity through the acquisition of sequences from distantly related organisms. Horizontal gene transfer produces extremely dynamic genomes in which substantial amounts of DNA are introduced into and deleted from the chromosome. These lateral transfers have effectively changed the ecological and pathogenic character of bacterial species. [TOP OF PAGE]

33. **Identification of virus-specific vesicles in Giardiavirus-infected *Giardia lamblia*. Ong, S.J., Tai, J.H. (2000). *Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih Chinese* 33:9-13**. Giardiavirus (GLV), which infects the parasitic protozoan *Giardia lamblia*, is a nonsegmented double-stranded (ds) ribonucleic acid (RNA) virus. We previously purified two distinct types of related GLV from infected *G. lamblia*, and showed differential export of one of the viruses from infected cells. In the present study, fractionation of cell lysate was performed, revealing the presence of viruses in the membranous fraction. Distribution of viral antigens in the infected cells was examined by immunocytochemistry. The signal was enriched in certain regions of the cytoplasm, suggesting that a portion of GLV is confined to certain cellular compartments. A significantly reduced signal was also detected in the nuclei. We directly observed the viruses in the infected cells by electron microscopy. Consistent with previous observations, virus-like particles were clearly observed in some membranous vesicles in the cytoplasm at 48 h postinfection, and virus-like particles were again seen in the cytoplasm and then in the nuclei toward the late phase of virus infection. The virus-associated vesicles and some electron-dense nuclear structures were only observed in virus-infected cells, suggesting that virus infection may induce ultrastructural alteration of *G. lamblia*. [TOP OF PAGE]

34. **Genotypic variations of Shiga toxin-converting phages from enterohaemorrhagic *Escherichia coli* O157: H7 isolates. Osawa, R., Iyoda, S., Nakayama, S.I., Wada, A., Yamai, S., Watanabe, H. (2000). *J. Med. Microbiol.* 49:565-574**. Pulsed-field gel electrophoresis (PFGE) analysis revealed that enterohaemorrhagic *Escherichia coli* (EHEC) O157:H7 strains had considerable variations in their genomes. This study investigated whether or not the molecular profile of Shiga toxin (Stx) 1- and Stx2-converting phages isolated from EHEC O157:H7 strains, derived from various sources in the USA and Japan, corresponded to the variations of host strains' genotypes as determined by PFGE. A total of 51 Stx-converting phages including 12 Stx1-converting phages and 37 Stx2-converting phages was isolated from seven USA isolates and 20 Japanese isolates. The average Dice coefficient values showed 44% similarity between phage DNAs in Stx2-converting phages digested with SmaI and 55% in Stx1-converting phages digested with HindIII, indicating considerable variation among phage DNA. In particular, restriction fragment length polymorphism (RFLP) patterns of Stx2-converting phage DNA varied according to the PFGE type of their host strain, which suggests that the phage genomes have altered their genotypic characteristics with those of host genomes. However, there are several exceptions: the RFLP patterns of some Stx2-converting phages were quite similar irrespective of the different genotypes of the host strains, indicating that horizontal transfer of Stx2-converting phage may also occur under some circumstances. [TOP OF PAGE]

35. **Epidemiologic Subtyping of *Escherichia coli* Serogroup O157 Strains Isolated in Ontario by Phage Typing and Pulsed-Field Gel Electrophoresis. Preston, M.A., Johnson, W., Khakhria, R., Borczyk, A. (2000). *Journal of Clinical Microbiology* 38:2366-2368**. [TOP OF PAGE]

36. **The complete genomic sequence of the marine phage Roseophage SIO1 shares homology with nonmarine phages. Rohwer, F., Segall, A., Steward, G., Seguritan, V., Breitbart, M., Wolven, F., Azam, F. (2000). *Limnology and Oceanography* 45:408-418**. Viruses are ubiquitous components of the marine environment, frequently reaching concentrations of 10^7-10^8 viruses per milliliter of surface seawater The majority of these viral particles are bacteriophages (phages). Although the oceans are probably the largest pool of bacteriophages on the planet, the evolutionary relationships of marine phages to phages from other environments are unknown. To address this issue, we have completely sequenced the genome of the lytic marine phage, Roseophage SIO1, that infects the heterotrophic marine bacterium *Roseobacter* SIO67. This phage has an isometric capsid with a diameter of approximately 43 nm, a short tail, a buoyant density of 1.49 g cm^{-3} in CsCl, and a 39,906-bp dsDNA genome. Sequence similarities and relative positions within the genome suggest that three of the open reading frames (ORFs) are homologous to the primase, DNA polymerase, and endodeoxyribonuclease I proteins of coliphages T3 and T7. The results are consistent with the mosaic theory of phage evolution and indicate a genetic link between marine and nonmarine phages. Additionally, basic life histories of marine phages can be elucidated by comparison of complete genomes to those of other extensively studied phages (e.g., lambda, T4, T7). The DNA replication machinery of Roseophage SIO1 shows a clear homology with that of coliphages T3 and T7, suggesting that the process of DNA replication may be similar among these phages. The Roseophage SIO1 genome also encodes four predicted proteins involved in phosphate metabolism (RP PhoH, RP ribonucleotide reductase, RP Thy1, and RP endodeoxyribonuclease I) suggesting that phosphate recycling is important to Roseophage SIO1's life cycle. Other interesting clues about Roseophage SIO1's life history come from the absence of certain expected protein regions. For example, we have not been able to identify the Roseophage SIO1 structural proteins (e.g., capsid proteins) by homology to other phages. It is also conspicuous that the Roseophage SIO1 genome lacks a recognizable RNA polymerase, an essential component of T3 and T7 life cycles. Analysis of the Roseophage SIO1 genome shows that marine and nonmarine phages are genetically related but basic life histories may be significantly different. [TOP OF PAGE]

37. **Bacterial indicator occurrence and the use of an F+ specific RNA coliphage assay to identify fecal sources in Homosassa Springs, Florida. Rose, J.B., Stokes, R. (2000). *Microb. Ecol.* 39:56-64**. [TOP OF PAGE]

38. **Characterization of AbiR, a novel multicomponent abortive infection mechanism encoded by plasmid pKR223 of *Lactococcus lactis* subsp. lactis KR2. Twomey, D.P., De, U.P., McKay, L.L., O'Sullivan, D.J. (2000). *Appl. Environ. Microbiol.* 66:2647-2651**. The native lactococcal plasmid pKR223 encodes two distinct phage resistance mechanisms, a restriction and modification (R/M) system designated LlaKR2I and an abortive infection mechanism (Abi) which affects prolate-headed-phage proliferation. The nucleotide sequence of a 16,174-bp segment of pKR223 encompassing both the R/M and Abi determinants has been determined, and sequence analysis has validated the novelty of the Abi system, which has now been designated AbiR. Analysis of deletion and insertion clones demonstrated that AbiR was encoded by two genetic loci, separated by the LlaKR2I R/M genes. Mechanistic studies on the AbiR phenotype indicated that it was heat sensitive and that it impeded phage DNA replication. These data indicated that AbiR is a novel multicomponent, heat-sensitive, "early"-functioning Abi system and is the first lactococcal Abi system described which is encoded by two separated genetic loci. [TOP OF PAGE]

39. **Genus *Chlorovirus* (*Phycodnaviridae*). Van Etten, J.L. (2000).** p. **???-??? *The Springer Index of Viruses*. Springer-Verlag, Berlin.** [TOP OF PAGE]

40. **An explosive antisense RNA strategy for inhibition of a lactococcal bacteriophage. Walker, S.A., Klaenhammer, T.R. (2000). *Appl. Environ. Microbiol.* 66:310-319**. The coding regions of six putative open reading frames (ORFs) identified near the phage phi31 late promoter and the right cohesive end (cos) of lactococcal bacteriophage phi31 were used to develop antisense constructs to inhibit the proliferation of phage phi31. Two middle-expressed ORFs

(ORF 1 and ORF 2) and four late-expressed ORFs (ORF 3 through ORF 6) were cloned individually between the strong Lactobacillus P6 promoter and the T7 terminator (T(T7)) to yield a series of antisense RNA transcripts. When expressed on a high-copy-number vector from a strong promoter, the constructs had no effect on the efficiency of plaquing (EOP) or the plaque size of phage phi31. To increase the ratio of antisense RNA to the targeted sense mRNA appearing during a phage infection, the antisense cassettes containing the late-expressed ORFs (ORF 3 through ORF 6) were subcloned to pTRK360, a low-copy-number vector containing the phage phi31 origin of replication, ori31. ori31 allows for explosive amplification of the low-copy-number vector upon phage infection, thereby increasing levels of antisense RNA transcripts later in the lytic cycle. In addition, the presence of ori31 also lowers the burst size of phage phi31 fourfold, resulting in fewer sense, target mRNAs being expressed from the phage genome. The combination of ori31 and P6::anti-ORF 4H::T(T7) resulted in a threefold decrease in the EOP of phage phi31 (EOP = 0.11 +/- 0.03 [mean +/- standard deviation]) compared to the presence of ori31 alone (EOP = 0.36). One-step growth curves showed that expression of anti-ORF 4H RNA decreased the percentage of successful centers of infection (75 to 80% for ori31 compared to 35 to 45% for ori31 plus anti-ORF 4H), with no further reduction in burst size. Growth curves performed in the presence of varying levels of phage phi31 showed that ori31 plus anti-ORF 4H offered significant protection to *Lactococcus lactis*, even at multiplicities of infection of 0.01 and 0.1. These results illustrate a successful application of an antisense strategy to inhibit phage replication in the wake of recent unsuccessful reports. [TOP OF PAGE]

41. **Morphology and general characteristics of phages specific for *Astragalus cicer rhizobia*. Wdowiak, S., Malek, W., Gr, adka, M. (2000). *Current Microbiology* 40:110-113**. Three newly isolated phages, K1, K2, and C1, specific for *A. cicer rhizobia* were characterized by their morphology, host range, rate of adsorption, restriction endonuclease patterns, and DNA molecular weights. All three phages were classified to the morphological group B of Bradley's (Siphoviridae family) on the basis of presence of hexagonal in outline heads and long noncontractile tails. Phages K1, K2, and C1 are related by host range and restriction endonuclease patterns. The molecular weights of phage DNAs estimated from restriction enzyme digests were in the range from 64.6 kb to 68.5 kb. [TOP OF PAGE]

42. **Design and evolution of artificial M13 coat proteins. Weiss, G.A., Sidhu, S.S. (2000). *Journal of Molecular Biology* 300:213-219**. Using simple design and selective pressure, we have evolved an artificial M13 bacteriophage coat protein. M13 coat proteins first reside in the bacterial inner membrane and subsequently surround the DNA core of the assembled virus. The artificial coat protein (ACP) was designed and evolved to mimic both functions of the natural M13 coat proteins, but with an inverted orientation. ACP is a non-functional coat protein because it is not required for the production of phage particles. Instead, it incorporates into a phage coat which still requires all the natural coat proteins for structural integrity. In contrast with other M13 coat proteins, which can display polypeptides as amino-terminal fusions, ACP permits the carboxy-terminal display of large polypeptides. The results suggest that viruses can co-opt host membrane proteins to acquire new coat proteins and thus new functions. In particular, M13 bacteriophage can be engineered for new functions, such as carboxy-terminal phage display. [TOP OF PAGE]

43. **An exfoliative toxin A-converting phage isolated from *Staphylococcus aureus* strain ZM. Yoshizawa, Y., Sakurada, J., Sakurai, S., Machida, K., Kondo, I., Masuda, S. (2000). *Microbiology and Immunology* 44:189-191**. Exfoliative toxin A (ETA) causes staphylococcal scalded-skin syndrome in children. The gene for ETA was believed to be coded by the chromosomal DNA. We isolated temperate phages from an ETA-producing strain, ZM, using a restriction minus strain, 1039, as an indicator. One of the prophages, designated phi-ZM-1 mediated lysogenic conversion of ETA. The polymerase chain reaction assay of the eta gene revealed that phage phi-ZM-1 carries the structural gene for ETA. [TOP OF PAGE]

44. **Iron modulates phenotypic variation and phosphorylation of P270 in double-stranded RNA virus-infected *Trichomonas vaginalis*. Alderete, J.F. (1999). *Infect. Immun.* 67:4298-4302**. *Trichomonas vaginalis* infected with a double-stranded RNA virus undergoes phenotypic variation on the basis of surface versus cytoplasmic expression of the immunogenic protein P270. Examination of batch cultures by flow cytofluorometry with monoclonal antibody (MAb) to P270 yields both fluorescent and nonfluorescent trichomonads. Greater numbers and intensity of fluorescent organisms with surface P270 reactive with MAb were evident in parasites grown in medium depleted of iron. Placement of iron-limited organisms in medium supplemented with iron gave increased numbers of nonfluorescent trichomonads. Purified subpopulations of trichomonads with and without surface P270 obtained by fluorescence-activated cell sorting reverted to nonfluorescent and fluorescent phenotypes when placed in high- and low-iron media, respectively. No similar regulation by iron of P270 was evident among virus-negative *T. vaginalis* isolates or virus-negative progeny trichomonads derived from virus-infected isolates. Equal amounts of P270 were detectable by MAb on immunoblots of total proteins from identical numbers of parasites grown in low- and high-iron media. Finally, P270 was found to be highly phosphorylated in high-iron parasites. Iron, therefore, plays a role in modulating surface localization of P270 in virus-harboring parasites. [TOP OF PAGE]

45. **Transduction of antibiotic resistance in *Pseudomomas aeruginosa*: relationship between lytic and transducing activity of phage isolate AP-423. Blahova, J., Kralikova, K., Krcmery, V.S., Jezek, P. (1999). *Acta Virol.* 43:395-398**. Isolation and propagation of a wild type phage, isolate AP-423, from an apparently lysogenic strain of *Pseudomonas aeruginosa*, resistant to a series of anti-pseudomonadal antibiotics, and its use for transduction of resistance determinants is described. The phage isolate AP-423 showed a phenomenon of host restriction, i.e. it was lysogenic only for some of the recipient strains tested. Its transduction capacity, both in sets of genes transduced and frequency of transduction, was different in two recipient strains of *P. aeruginosa*. This phage showed also some restriction in titers, to which it could be propagated, only in certain recipient strains. [TOP OF PAGE]

46. **The primary immunity determinant in modulating the lysogenic immunity of the filamentous bacteriophage cf [published erratum appears in J Mol Biol 1999 Nov 5;293(4):987]. Cheng, C.M., Wang, H.J., Bau, H.J., Kuo, T.T. (1999). *Journal of Molecular Biology* 287:867-876**. Bacteriophage cf is the first single-stranded DNA phage that has been shown to set up a stable lysogenic state with its genome integrated into the host chromosome. From the isolation and characterization of a virulent mutant, cf-tv2, we report the first investigation into the mechanisms of the immunity established by the filamentous bacteriophage. The mutation in cf-tv2 enables the phage to produce plaques on lawns of cf lysogenic cells. The mutation was defined as a 49-nucleotide deletion located in a 0.59 kb NcoI/KpnI fragment of cf replicative form DNA. Two messages, cM1 and cM2, transcribed from the immunity region of wild-type cf but in opposite directions, were detected. In cf-tv2, the 49-nucleotide deletion abolishes cM2 transcription. The primer extension assay suggests a possible RNA-RNA interaction directed by base-pairing of the cM1 and cM2 RNAs. A frameshift mutation of the open reading frame ORF 165, encoded by cM2, resulted in a 10(5) plating efficiency on the cf lysogen. These observations suggest that both RNA-RNA interaction and repressor protein inhibition are involved in the mechanism of cf immunity. A model is proposed for the regulation of cf immunity. [TOP OF PAGE]

47. **Procaryotic infections in the mussel *Mytilus galloprovinciallis* and in its parasite the turbellarian *Urastoma cyprinae*. Comps, M., Tige, G. (1999). *Diseases of Aquatic Organisms* 38:211-217**. Mussels *Mytilus galloprovincialis* from the Thau lagoon (Mediterranean coast of France) were regularly sampled to determine the prevalence and intensity of parasitic infections. Microscopically, hepatopancreatic tubules of the mussel appeared infected by a rickettsia-like organism (RLO). Each RLO were surrounded by 2 unit membranes, and colonies composed of several bacteria were enclosed within a vacuolar membrane of the host cell. In addition, examination by transmission electron microscopy revealed that the RLO was infected by phage particles. Histological investigations of the turbellarian Urastoma cyprinae parasitizing the mussels have shown that this ectoparasite was also infected by 2 types of procaryotes, a chlamydia-like organism (CLO) and a mollicute-like organism (MLO). The CLO displayed characteristic developmental stages of the Chlamydiales and was secondarily infected by electron-dense particles presumed to be phage particles. The MLO exhibited some morphological characteristics of the mollicutes, in that the microorganisms were bounded by a single membrane sharing a trilaminar structure. Neither of these microorganisms have previously been reported in Platyhelminthes. [TOP OF PAGE]

48. **The *Vibrio cholerae* O139 Calcutta bacteriophage CTXphi is infectious and encodes a novel repressor. Davis, B.M., Kimsey, H.H., Chang, W.,**

Waldor, M.K. (1999). *J. Bacteriol.* 181:6779-6787. CTXphi is a lysogenic, filamentous bacteriophage. Its genome includes the genes encoding cholera toxin (ctxAB), one of the principal virulence factors of *Vibrio cholerae*; consequently, nonpathogenic strains of *V. cholerae* can be converted into toxigenic strains by CTXphi infection. O139 Calcutta strains of *V. cholerae*, which were linked to cholera outbreaks in Calcutta, India, in 1996, are novel pathogenic strains that carry two distinct CTX prophages integrated in tandem: CTX(ET), the prophage previously characterized within El Tor strains, and a new CTX Calcutta prophage (CTX(calc)). We found that the CTX(calc) prophage gives rise to infectious virions; thus, CTX(ET)phi is no longer the only known vector for transmission of ctxAB. The most functionally significant differences between the nucleotide sequences of CTX(calc)phi and CTX(ET)phi are located within the phages' repressor genes (rstR(calc) and rstR(ET), respectively) and their RstR operators. RstR(calc) is a novel, allele-specific repressor that regulates replication of CTX(calc)phi by inhibiting the activity of the rstA(calc) promoter. RstR(calc) has no inhibitory effect upon the classical and El Tor rstA promoters, which are instead regulated by their cognate RstRs. Consequently, production of RstR(calc) renders a CTX(calc) lysogen immune to superinfection by CTX(calc)phi but susceptible (heteroimmune) to infection by CTX(ET)phi. Analysis of the prophage arrays generated by sequentially integrated CTX phages revealed that pathogenic V. cholerae O139 Calcutta probably arose via infection of an O139 CTX(ET)phi lysogen by CTX(calc)phi. [TOP OF PAGE]

49. **The catalytic group-I introns of the psbA gene of *Chlamydomonas reinhardtii* : core structures, ORFs and evolutionary implications. Holloway, S.P., Deshpande, N.N., Herrin, D.L. (1999). *Current Genetics* 36:69-78**. The sequences and predicted secondary structures of the four catalytic group-I introns in the psbA gene of *Chlamydomonas reinhardtii*, Cr.psbA-1-Cr.psbA-4, have been determined. Cr.psbA-1 and Cr.psbA-4 are subgroup-IA1 introns and have similar secondary structures, except at the 3 end where Cr.psbA-1 contains a large inverted-repeat domain. Cr.psbA-4 is closely related to intron 1 of the *Chlamydomonas moewusii* psbA gene, with which it shares the same location, high nucleotide identity in the core, and an identically placed ORF that shows 58% amino-acid identity. Cr.psbA-2 is a subgroup-IA3 intron, and shows similarities to the *Chlamydomonas eugametos* rRNA intron, Ce.LSU-1. Cr.psbA-3 is a subgroup-IA2 intron, and is remarkably similar to the T4 phage intron, sunY. Interestingly, a degenerate version of Cr.psbA-3 is located in the intergenic region between the chloroplast petA and petD genes. All four introns contain ORFs, which potentially code for basic proteins of 11-38 kDa. The ORFs in introns 2 and 3 contain variants of the GIY-YIG motif; however, the Cr.psbA-2 ORF is free-standing, whereas the Cr.psbA-3 ORF is contiguous and in-frame with the upstream exon. The Cr.psbA-4 ORF contains an H-N-H motif, and possibly a GIY-YIG motif. These data indicate that the *C. reinhardtii* psbA introns have multiple origins, and illustrate some of the evolutionary DNA dynamics associated with group-I introns in *Chlamydomonas*. [TOP OF PAGE]

50. **Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic *Escherichia coli* O157:H7 derived from the Sakai outbreak. Makino, K., Yokoama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Kurokawa, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Lida, T., Yamamoto, K., Onishi, M., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C., Shinagawa, H. (1999). *Genes and Genetic Systems* 74:227-239**. The enterohemorrhagic *Escherichia coli* (EHEC) O157:H7 strain RIMD 0509952, derived from an outbreak in Sakai city, Japan, in 1996, produces two kinds of verotoxins, VT1 and VT2, encoded by the stx1 and stx2 genes. In the EHEC strains, as well as in other VT-producing E. coli strains, the toxins are encoded by lysogenic bacteriophages. The EHEC O157:H7 strain RIMD 0509952 did not produce plaque-forming phage particles upon inducing treatments. We have determined the complete nucleotide sequence of a prophage, VT2-Sakai, carrying the stx2A and stx2B genes on the chromosome, and presumed the putative functions of the encoded proteins and the cis-acting DNA elements based on sequence homology data. To our surprise, the sequences in the regions of VT2-Sakai corresponding to the early gene regulators and replication proteins, and the DNA sequences recognized by the regulators share very limited homology to those of the VT2-encoding 933W phage carried by the EHEC O157:H7 strain EDL933 reported by Plunkett et al. (J. Bacteriol., p1767-1778, 181, 1999), although the sequences corresponding to the structural components are almost identical. These data suggest that these two phages were derived from a common ancestral phage and that either or both of them underwent multiple genetic rearrangements. An IS629 insertion was found downstream of the stx2B gene and upstream of the lysis gene S, and this might be responsible for the absence of plaque-forming activity in the lysate obtained after inducing treatments. [TOP OF PAGE]

51. **Vibriophage KVP40 and coliphage T4 genomes share a homologous 7-kbp region immediately upstream of the gene encoding the major capsid protein. Matsuzaki, S., Kuroda, M., Kimura, S., Tanaka, S. (1999). *Archives of Virology* 144:2007-2012**. Vibriophage KVP40, a large tailed DNA phage morphologically similar to T-even coliphages, has a major capsid protein (Mcp) homologous to the equivalent protein, gp23(*), of coliphage T4. The sequence analysis was extended to a 7-kbp region immediately upstream of the mcp gene encoding the precursor of Mcp. The region as a whole was fairly homologous to the corresponding region of the T4 genome and contained 8 ORFs homologous to T4 genes 17, 18, 19, 20, 67, 68, 21, and 22 in the same order as in T4. These findings thus strongly suggest that these two phages are phylogenetically related. [TOP OF PAGE]

52. **Comparative study of techniques used to recover viruses from residual urban sludge. Mignotte, B., Maul, A., Schwartzbrod, L. (1999). *Journal of Virological Methods* 78:71-80**. Eight virus extraction techniques were compared on three types of residual urban sludge for simultaneous detection of infectious enteroviruses, somatic coliphages, F-specific RNA bacteriophages and *Bacteroides fragilis* bacteriophages. The highest virus counts were found in extracts obtained using three extraction techniques described by respectively using a 10% beef extract solution at pH 9 and sonication, using a 0.3 M NaCl/7% beef extract solution at pH 7.5 and freon, and finally using a 0.1 M borate buffer/3% beef extract solution at pH 9 and sonication. [TOP OF PAGE]

53. **Isolation of additional bacteriophages with genomes of segmented double-stranded RNA. Mindich, L., Qiao, X., Qiao, J., Onodera, S., Romantschuk, M., Hoogstraten, D. (1999). *J. Bacteriol.* 181:4505-4508**. Eight different bacteriophages were isolated from leaves of *Pisum sativum*, *Phaseolus vulgaris*, *Lycopersicon esculentum*, *Daucus carota sativum*, *Raphanus sativum*, and *Ocimum basilicum*. All contain three segments of double-stranded RNA and have genomic-segment sizes that are similar but not identical to those of previously described bacteriophage phi6. All appear to have lipid-containing membranes. The base sequences of some of the viruses are very similar but not identical to those of phi6. Three of the viruses have little or no base sequence identity to phi6. Two of the viruses, phi8 and phi12, contain proteins with a size distribution very different from that of phi6 and do not package genomic segments of phi6. Whereas phi6 attaches to host cells by means of a pilus, several of the new isolates attach directly to the outer membrane. Although the normal hosts of these viruses seem to be pseudomonads, those viruses that attach directly to the outer membrane can establish carrier states in *Escherichia coli* or *Salmonella typhimurium*. One of the isolates, phi8, can form plaques on heptoseless strains of *S. typhimurium*. [TOP OF PAGE]

54. **Codon usage and lateral gene transfer in *Bacillus subtilis*. Moszer, I., Rocha, E.P., Danchin, A. (1999). *Curr Opin Microbiol* 2:524-528**. *Bacillus subtilis* possesses three classes of genes, differing by their codon preference. One class corresponds to prophages or prophage-like elements, indicative of the existence of systematic lateral gene transfer in this organism. The nature of the selection pressure that operates on codon bias is beginning to be understood. [TOP OF PAGE]

55. **High bacterial diversity in permanently cold marine sediments. Ravenschlag, K., Sahm, K., Pernthaler, J., Amann, R. (1999). *Appl. Environ. Microbiol.* 65:3982-3989**. A 16S ribosomal DNA (rDNA) clone library from permanently cold marine sediments was established. Screening 353 clones by dot blot hybridization with group-specific oligonucleotide probes suggested a predominance of sequences related to bacteria of the sulfur cycle (43.4% potential sulfate reducers). Within this fraction, the major cluster (19.0%) was affiliated with *Desulfotalea* sp. and other closely related psychrophilic sulfate reducers isolated from the same habitat. The cloned sequences showed between 93 and 100% similarity to these bacteria. Two additional groups were frequently encountered: 13% of the clones were related to *Desulfuromonas palmitatis*, and a second group was affiliated with *Myxobacteria* spp. and *Bdellovibrio* spp. Many clones (18.1%) belonged to the gamma subclass of the class Proteobacteria and were closest to symbiotic or free-living sulfur oxidizers. Probe target groups were further characterized by amplified rDNA restriction analysis to determine diversity within the groups and within the clone library. Rarefaction

analysis suggested that the total diversity assessed by 16S rDNA analysis was very high in these permanently cold sediments and was only partially revealed by screening of 353 clones. [TOP OF PAGE]

56. **Rapid film-based determination of antibiotic susceptibilities of *Mycobacterium tuberculosis* strains by using a luciferase reporter phage and the Bronx Box. Riska, P.F., Su, Y., Bardarov, S., Freundlich, L., Sarkis, G., Hatfull, G., Carriere, C., Kumar, V., Chan, J., Jacobs, W.J. (1999). *Journal of Clinical Microbiology* 37:1144-1149**. Detecting antibiotic resistance in *Mycobacterium tuberculosis* is becoming increasingly important with the global recognition of drug-resistant strains and their adverse impact on clinical outcomes. Current methods of susceptibility testing are either time-consuming or costly; rapid, reliable, simple, and inexpensive methods would be highly desirable, especially in the developing world where most tuberculosis is found. The luciferase reporter phage is a unique reagent well-suited for this purpose: upon infection with viable mycobacteria, it produces quantifiable light which is not observed in mycobacterial cells treated with active antimicrobials. In this report, we describe a modification of our original assay, which allows detection of the emitted light with a Polaroid film box designated the Bronx Box. The technique has been applied to 25 *M. tuberculosis* reference and clinical strains, and criteria are presented which allow rapid and simple discrimination among strains susceptible or resistant to isoniazid and rifampin, the major antituberculosis agents. [TOP OF PAGE]

57. **Prophage carriage as a molecular epidemiological marker in *Streptococcus pneumoniae*. Severina, E., Ramirez, M., Tomasz, A. (1999). *Journal of Clinical Microbiology* 37:3308-3315**. The great majority of clinical isolates of *Streptococcus pneumoniae* carry prophages that may be identified through their hybridization with a DNA probe specific for the pneumococcal lytA gene (M. Ramirez, E. Severina, and A. Tomasz, J. Bacteriol. 181:3618-3625, 1999). We now show that the lytA hybridization pattern of chromosomal SmaI digests is stable for a given strain during extensive serial culturing in the laboratory; the pattern is specific for the strain's clonal type, as defined by pulsed-field gel electrophoretic (PFGE) pattern, and variations in PFGE subtypes may be explained by changes in the number and chromosomal localization of this prophage(s). These observations indicate that the lytA hybridization pattern may be used as a molecular epidemiological marker that offers additional resolution of the genetic background of *S. pneumoniae* strains. [TOP OF PAGE]

58. **(Methodic approaches to studing marine bacteria and viruses interaction) Metodicheskie podkhody k izucheniyu protsessa vzaimodejstviya morskikh bakterij i virusov. Stepanova, O.A., Shaida, V.G. (1999). *Ehkologiya morya. Kiev [Ehkol. Morya]* 48:96-99**. Comparative study of interaction between marine bacteria and viruses with the employment of microcalorimetry and Bioscreen-C automatic analyzer has demonstrated higher sensitivity of microcalorimetric method. Thus method permits studying the dynamics of virus -- bacterium interaction at the level of both lytic phage infection and a variety of enzymatic and other functions induced by lysogeny as the result of viral deoxyribonucleic acid integration into bacterial. [TOP OF PAGE]

59. **[Successful treatment with bacteriophage in purulent cerebrospinal meningitis in a newborn]. Stroj, L., Weber-Dabrowska, B., Partyka, K., Mulczyk, M., Wojcik, M. (1999). *Neurologia I Neurochirurgia Polska* 33:693-698**. The subject of this report is the case of purulent meningitis in new-born caused by *Klebsiella pneumoniae*. As the intensive antibiotic therapy turned out to be ineffective phage therapy was applied. Oral administration of specific phage preparate for the period of 5 weeks resulted in complete sterilization of cerebrospinal fluid and unquestionable improvement of child's health. However, after several ventriculopunctures some complications appeared (haemorrhage into central nervous system, extra infection). They were treated in standard way. Because of increasing internal hydrocephalus and necessity of operation, the child was sent to suitable hospital for further treatment. [TOP OF PAGE]

60. **Bacteriophage inactivation at the air-water-solid interface in dynamic batch systems. Thompson, S., Yates, M.V. (1999). *Applied and Environmental Microbiology [Appl. Environ. Microbiol.]* 65:1186-1190**. Bacteriophages have been widely used as surrogates for human enteric viruses in many studies on virus transport and fate. In this investigation, the fates of three bacteriophages, MS2, R17, and phi X174, were studied in a series of dynamic batch experiments. Both MS2 and R17 readily underwent inactivation in batch experiments where solutions of each phage were percolated through tubes packed with varying ratios of glass and Teflon beads. MS2 and R17 inactivation was the result of exposure to destructive forces at the dynamic air-water-solid interface. phi X174, however, did not undergo inactivation in similar studies, suggesting that this phage does not accumulate at air-water interfaces or is not affected by interfacial forces in the same manner. Other batch experiments showed that MS2 and R17 were increasingly inactivated during mixing in polypropylene tubes as the ionic strength of the solution was raised (phi X174 was not affected). By the addition of Tween 80 to suspensions of MS2 and R17, phage inactivation was prevented. Our data suggest that viral inactivation in simple dynamic batch experiments is dependent upon (i) the presence of a dynamic air-water-solid interface (where the solid is a hydrophobic surface), (ii) the ionic strength of the solution, (iii) the concentration of surface active compounds in the solution, and (iv) the type of virus used. [TOP OF PAGE]

61. **Changes in bacterial and eukaryotic community structure after mass lysis of filamentous cyanobacteria associated with viruses. van, H.E., Zwart, G., van, A.M., Gons, H.J., Ebert, J., Laanbroek, H.J. (1999). *Appl. Environ. Microbiol.* 65:795-801**. During an experiment in two laboratory-scale enclosures filled with lake water (130 liters each) we noticed the almost-complete lysis of the cyanobacterial population. Based on electron microscopic observations of viral particles inside cyanobacterial filaments and counts of virus-like particles, we concluded that a viral lysis of the filamentous cyanobacteria had taken place. Denaturing gradient gel electrophoresis (DGGE) of 16S ribosomal DNA fragments qualitatively monitored the removal of the cyanobacterial species from the community and the appearance of newly emerging bacterial species. The majority of these bacteria were related to the Cytophagales and actinomycetes, bacterial divisions known to contain species capable of degrading complex organic molecules. A few days after the cyanobacteria started to lyse, a rotifer species became dominant in the DGGE profile of the eukaryotic community. Since rotifers play an important role in the carbon transfer between the microbial loop and higher trophic levels, these observations confirm the role of viruses in channeling carbon through food webs. Multidimensional scaling analysis of the DGGE profiles showed large changes in the structures of both the bacterial and eukaryotic communities at the time of lysis. These changes were remarkably similar in the two enclosures, indicating that such community structure changes are not random but occur according to a fixed pattern. Our findings strongly support the idea that viruses can structure microbial communities. [TOP OF PAGE]

62. **Increased synthesis of an *Escherichia coli* membrane protein suppresses F exclusion of bacteriophage T7. Wang, W.F., Margolin, W., Molineux, I.J. (1999). *Journal of Molecular Biology* 292:501-512**. Increased synthesis of the protein FxsA alleviates the exclusion of T7 in cells harboring the F plasmid. In contrast to wild-type or cells defective in fxsA, overexpression of fxsA+ allows T7 to form plaques at normal efficiency even though the burst size is reduced to about half that obtained on the isogenic F- strain. No defect in DNA synthesis was observed but late protein synthesis remains partially inhibited and a reduced level of cell leakiness, a prominent feature of F+ cells abortively infected by T7, persists. The FxsA protein is shown to be a cytoplasmic membrane protein. How T7 avoids exclusion by F in cells that exhibit increased levels of FxsA is discussed in terms of its membrane localization. [TOP OF PAGE]

63. **Bioluminescence-based assays for detection and characterization of bacteria and chemicals in clinical laboratories. Billard, P., DuBow, M.S. (1998). *Clinical Biochemistryy* 31:1-14**. OBJECTIVES: To survey recent advances in the application of bioluminescence to public health problems. The usefulness of bacterial (lux) and eucaryotic (luc) luciferase genes is presented, along with several examples that demonstrate their value as "reporters" of many endpoints of clinical concern. CONCLUSIONS: The development of new technologies for monitoring biological and chemical contaminants is in continuous progress. Recent excitement in this area has come from the use of genes encoding enzymes for bioluminescence as reporter systems. Applications of the recombinant luciferase reporter phage concept now provide a sensitive approach for bacterial detection, their viability, and sensitivity to antimicrobial agents. Moreover, a number of fusions of the lux and luc genes to stress inducible genes in different bacteria can allow a real-time measurement of gene expression and determination of cellular viability, and also constitute a new tool to detect toxic chemicals and their bioavailability. [TOP OF PAGE]

64. **Origin, adaptation and evolutionary pathways of fungal viruses. Ghabrial, S.A. (1998). *Virus Genes* 16:119-131**. Fungal viruses or mycoviruses are widespread in fungi and are believed to be of ancient origin. They have evolved in concert with their hosts and are usually associated with symptomless infections. Mycoviruses are transmitted intracellularly during cell division, sporogenesis and cell fusion, and they lack an extracellular phase to their life cycles. Their natural host ranges are limited to individuals within the same or closely related vegetative compatibility groups. Typically, fungal viruses are isometric particles 25-50 nm in diameter, and possess dsRNA genomes. The best characterized of these belong to the family Totiviridae whose members have simple undivided dsRNA genomes comprised of a coat protein (CP) gene and an RNA dependent RNA polymerase (RDRP) gene. A recently characterized totivirus infecting a filamentous fungus was found to be more closely related to protozoan totiviruses than to yeast totiviruses suggesting these viruses existed prior to the divergence of fungi and protozoa. Although the dsRNA viruses at large are polyphyletic, based on RDRP sequence comparisons, the totiviruses are monophyletic. The theory of a cellular self-replicating mRNA as the origin of totiviruses is attractive because of their apparent ancient origin, the close relationships among their RDRPs, genome simplicity and the ability to use host proteins efficiently. Mycoviruses with bipartite genomes (partitiviruses), like the totiviruses, have simple genomes, but the CP and RDRP genes are on separate dsRNA segments. Because of RDRP sequence similarity, the partitiviruses are probably derived from a totivirus ancestor. The mycoviruses with unencapsidated dsRNA-like genomes (hypoviruses) and those with bacilliform (+) strand RNA genomes (barnaviruses) have more complex genomes and appear to have common ancestry with plant (+) strand RNA viruses in supergroup 1 with potyvirus and sobemovirus lineages, respectively. The La France isometric virus (LIV), an unclassified virus with multipartite dsRNA genome, is associated with a severe die-back disease of the cultivated mushroom. LIV appears to be of recent origin since it differs from its host in codon usage. [TOP OF PAGE]

65. ***Legionella pneumophila* kills human phagocytes but not protozoan host cells by inducing apoptotic cell death. Hagele, S., Hacker, J., Brand, B.C. (1998). *FEMS Microbiol. Let.* 169:51-58**. *Legionella pneumophila* is a facultative intracellular parasite able to replicate within and to kill a variety of eukaryotic cells. One possible killing mechanism is the induction of programmed cell death. Based on electron microscopy and flow cytometry studies using the phosphatidylserine binding protein annexin V, we could demonstrate that *L. pneumophila* is able to induce apoptosis in human monocytes which was clearly dependent on the multiplicity of infection, the time postinfection and the intracellular location of the bacteria. Furthermore, it became evident that Legionella-induced apoptosis does not require the TNF-alpha mediated signal-transduction pathway. By studying infection in *Acanthamoeba castellanii*, we found that *L. pneumophila* is not able to induce programmed cell death in their natural host cells indicating that different mechanisms are responsible for host cell killing in protozoan and human cells. [TOP OF PAGE]

66. **A novel filamentous phage, fs-2, of *Vibrio cholerae* O139. Ikema, M., Honma, Y. (1998). *Microbiology* 144 (Pt 7):1901-1906**. A novel filamentous bacteriophage, fs-2, was isolated from *Vibrio cholerae* O139 strain MDO14. The fs-2 phage was a long filamentous particle 1200 nm long and 7 nm wide. The purified phage formed a turbid plaque when spotted on a lawn of the host organisms. The plaque-formation activity was stable following heating to 70 degrees C but was inhibited by treatment with chloroform. fs-2 had a single-stranded DNA genome and was converted to a double-stranded replicative form in the host cell. Almost all *V. cholerae* O139 and O1 El Tor biotype strains tested were sensitive to the phage, but most O1 classical strains and non-O1 non-O139 strains were resistant. The fs-2 genome comprised 8651 nucleotides containing nine open reading frames, five of which had predicted protein products partially homologous to the reported protein products of other filamentous phages. Although the extent of the homology was not particularly high, the genetic organization of other filamentous phages appears to be preserved in fs-2. The phage was not integrated into the chromosome of its host, but a 715 nucleotide fragment located in the large intergenic region of fs-2 was highly homologous to a part of region RS2 (repetitive sequence 2) of the *V. cholerae* CTX phi sequence which is speculated to be required for integration of the phage into the *V. cholerae* chromosome at a specific site. [TOP OF PAGE]

67. **Genetic diversity and DNA repair of marine vibriophages. Kellogg, C.A. (1998). Ph.D. Thesis, University of South Florida, FL, USA.** Viruses are the numerically dominant organisms in the global ocean. The objectives of this study investigate the dynamics of a marine bacteriophage species, the Phi 16-like vibriophages: (1) To determine the genetic diversity of vibriophage isolates from geographically diverse environments, (2) To enumerate this virus in a variety of environments and correlate the phage counts with a number of parameters, (3) To determine if the levels of spatial genetic diversity detected in the first study were comparable to the seasonal genetic variations occurring over a year at one local sampling site, (4) To study the host repair mechanisms which allow these viruses to survive inactivation by ultraviolet radiation. Sixty-nine vibriophages were isolated from waters surrounding Florida and Hawaii on *Vibrio parahaemolyticus* st. 16, and were determined by DNA hybridization to be genetically related. The Tampa Bay population of Phi 16-like vibriophages was positively correlated to temperature (r=0.669), but in other environments the phages also showed a dependence on bacterial abundance and a negative correlation to viral direct counts. The concentration of these phages varied seasonally in Tampa Bay, constituting a fraction of the total viral community ranging from 10^{-10} to 10^{-7}. These viruses were primarily estuarine, although a few isolates have been found offshore and as deep as 1500 m. During the year-long genetic study in Tampa Bay, a 484 bp fragment was amplified from 165 isolates. The fragments were sorted into operational taxonomic units (OTUs) and representatives were sequenced. These sequences were compared to sequences of the geographic isolates. The genetic similarities ranged from 83% to 100%, showing that there was as much diversity temporally in Tampa Bay as there is spatially across all the sampling locations. Vibrio parahaemolyticus st. 16 clearly demonstrates photoreactivation and excision repair of the phages. Compared to *V. parahaemolyticus* HER1165 phages, the Phi 16-like vibriophages are more efficiently repaired, and have higher G+C contents. One HER1165 phage, which was most sensitive to UV damage and showed no photoreactivation (vp12) was found to have a G+C content of only 16%. All phage inactivation coefficients correlated with G+C content (r=0.955) suggesting that AT rich genomes are more UV sensitive. [TOP OF PAGE]

68. **High-temperature inducible cell-free transcription and replication of double-stranded RNAs within the parasitic protozoan *Cryptosporidium parvum*. Khramtsov, N.V., Upton, S.J. (1998). *Virology* 245:331-337**. Sporozoites of the protozoan parasite, *Cryptosporidium parvum*, were found to contain free, full-size plus strands transcribed from two extrachromosomal, cytoplasmic, virus-like double-stranded RNAs (dsRNAs). Cell-free transcription and replication of both dsRNAs were observed in crude sporozoite lysates. RNA polymerase activity was found to be dependent upon addition of Mg2+ or Mn2+, as well as the four ribonucleoside triphosphates, and was insensitive to inhibitors of cellular DNA-dependent RNA polymerase. Semiconservative transcription of the dsRNAs (plus strand synthesis) was observed at a wide range of temperatures, with an optimum of 50 degrees C. In contrast, replication (minus strand synthesis) was detected only at 50 and 60 degrees C. [TOP OF PAGE]

69. **Complete DNA sequence and detailed analysis of the *Yersinia pestis* KIM5 plasmid encoding murine toxin and capsular antigen. Lindler, L.E., Plano, G.V., Burland, V., Mayhew, G.F., Blattner, F.R. (1998). *Infect. Immun.* 66:5731-5742**. *Yersinia pestis*, the causative agent of plague, harbors at least three plasmids necessary for full virulence of the organism, two of which are species specific. One of the *Y. pestis*-specific plasmids, pMT1, is thought to promote deep tissue invasion, resulting in more acute onset of symptoms and death. We determined the entire nucleotide sequence of *Y. pestis* KIM5 pMT1 and identified potential open reading frames (ORFs) encoded by the 100,990-bp molecule. Based on codon usage for known yersinial genes, homology with known proteins in the databases, and potential ribosome binding sites, we determined that 115 of the potential ORFs which we considered could encode polypeptides in *Y. pestis*. Five of these ORFs were genes previously identified as being necessary for production of the classic virulence factors, murine toxin (MT), and the fraction 1 (F1) capsule antigen. The regions of pMT1 encoding MT and F1 were surrounded by remnants of multiple transposition events and bacteriophage, respectively, suggesting horizontal gene transfer of these virulence factors. We identified seven new potential virulence factors that might interact with the mammalian host or flea vector. Forty-three of the remaining 115 putative ORFs did not display any significant homology with proteins in the current databases. Furthermore, DNA sequence analysis allowed the determination of the putative replication and partitioning regions of pMT1. We identified a single 2,450-bp region within pMT1 that could function as the origin of replication, including a RepA-like protein similar to RepFIB, RepHI1B, and P1 and P7 replicons. Plasmid partitioning function was located ca. 36 kb from the putative origin of replication and was most similar to the parABS bacteriophage P1 and

P7 system. *Y. pestis* pMT1 encoded potential genes with a high degree of similarity to a wide variety of organisms, plasmids, and bacteriophage. Accordingly, our analysis of the pMT1 DNA sequence emphasized the mosaic nature of this large bacterial virulence plasmid and provided implications as to its evolution. [TOP OF PAGE]

70. **Group I introns found in Chlorella viruses: biological implications. Nishida, K., Suzuki, S., Kimura, Y., Nomura, N., Fujie, M., Yamada, T. (1998). *Virology* 242:319-326**. More than 80 group I introns were detected and characterized in Chlorella viruses isolated from various locations in Japan; the overall average frequency of viruses containing the group I intron was 8.0%. Although most of these introns were inserted in the gene for either transcriptional elongation factor TFIIS (approximately 60%) or URF 14.2 (unidentified open reading frame coding for a 14.2-kDa polypeptide) (approximately 40%), in a few cases, the gene for the major capsid protein Vp52 contained an intron. These introns were biologically active (self-splicing) both in vivo and in vitro. Viruses that contained introns almost usually contained only one, but more than two introns coexisted in several virus isolates. Nucleotide sequence analysis showed that the intron sequences have diverged under strong constraint of the exon genes: introns in the same gene showed more than 99% sequence identity, whereas introns in different genes were only 72-78% identical. Phylogenetic analysis suggested relatedness of these introns to those found in the rRNA genes of a variety of organisms including green algae, red algae, red algae, yeasts, fungi, and protozoa. [TOP OF PAGE]

71. **Phage typing of *Lactococcus garvieae* (formally *Enterococcus seriolicida*) a pathogen of cultured yellowtail. Park, K.H., Kato, H., Nakai, T., Muroga, K. (1998). *Fisheries science. Tokyo [Fish. Sci.]* 64:62-64**. Bacteriophages of *Lactococcus garvieae*, designated as PLgW and PLgS, were isolated from sea water and sediment samples by an enrichment method. Morphological and genomic features of these phages were in agreement with those of the *L. garvieae* phage, designated as PLgY, belonging to the family Siphoviridae that was detected in an *L. garvieae* strain isolated from diseased yellowtail Seriola quinqueradiata in the previous study. One hundred and eleven strains of *L. garvieae* examined were divided into 14 phage types (A similar to N) by using the phage isolates which were differentiated from each other in the infectivity, with a major phage type (type A) containing 73 strains. One phage type (type N) consisting of 9 bacterial strains was insensitive to any of the phages used. However, there were no apparent correlations between the phage types and the geographical sources of the bacterial strains or between phage types and the antigenic forms (KC- and KG+). [TOP OF PAGE]

72. **Coinfection of a fungal pathogen by two distinct double-stranded RNA viruses. Preisig, O., Wingfield, B.D., Wingfield, M.J. (1998). *Virology* 252:399-406**. Unsegmented double-stranded (ds)RNA viruses belonging to the family Totiviridae persistently infect protozoa and fungi. In this study, two totiviruses were found to coinfect the filamentous fungus Sphaeropsis sapinea, a well known pathogen of pines. Isometric, virus-like particles approximately 35 nm in diameter were isolated from extracts of this fungus. The nucleotide sequences of the genomes of the two S. sapinea RNA viruses named SsRV1 and SsRV2 were established. The linear genomes of 5163 and 5202 bp, respectively, are identically organized with two large, overlapping ORFs. The 5' located ORF1 probably encodes the coat protein, whereas the gene product of ORF2 shows the typical features of RNA-dependent RNA polymerases. The absence of a pseudoknot and a slippery site at the overlapping region between ORF1 and ORF2, as well as the shortness of that region, leads us to suggest that the translation of ORF2 of both viruses is internally initiated. The mode of translation and the genomic organization are similar to those of *Helminthosporium victoriae* 190S virus (Hv190SV; Huang, S., and Ghabrial, S. A. (1996). Proc. Natl. Acad. Sci. USA 93, 12541-12546). Hv190SV thus appears to be closely related to the SsRVs. Interestingly, based on amino acid sequence homology SsRV1 is more closely related to Hv190SV than to SsRV2. [TOP OF PAGE]

73. **The use of luciferase-reporter phage for antibiotic-susceptibility testing of mycobacteria. Riska, P.F., Jacobs, W.J. (1998). *Methods in Molecular Biology* 101:431-455**. [TOP OF PAGE]

74. **Bacterioplankton dynamics in Lake Constance (Bodensee): Substrate utilization, growth control, and long-term trends. Simon, M., Bunte, C., Schulz, M., Weiss, M., Wuensch, C. (1998).** In **Baeuerle, E. and Gaedke, U.** (eds.), ***Archiv fuer Hydrobiologie. Spec. issue: Ergebnisse der Limnologie*. Schweizerbart'sche Verlagsbuchhandlung, Stuttgart (FRG).** The authors studied the dynamics of bacterioplankton growth and the factors controlling it in Lake Constance between 1982 and 1997, but mainly during the last 8 years. In the course of this time, the lake experienced a significant oligotrophication due to an efficient decrease in the phosphorus load. The large changes in nutrient load and concomitant qualitative and quantitative changes in the phytoplankton community made it a particularly interesting time to study bacterial growth dynamics. Both bacterial production (BP) and bacterial numbers (BN) showed persistent annual patterns throughout the period. In most years, highest rates of BP and BN occurred towards the end of the phytoplankton spring bloom. During the clear-water phase, BP and BN varied depending on the grazing pressure by daphnids and decreased towards its end. During summer, BP and BN increased again and to varying extents until the autumnal decline. In 1995 and 1997, highest rates occurred in summer (August, September). In particular, BN remained lower in summer than during the previous part of the season. During the spring bloom, BP was closely correlated either to the biomass of ciliates or of daphnids, but only weakly to chlorophyll, indicating that grazing and thus release of dissolved organic matter by these two herbivores was the most important factor in bottom-up control of bacterial growth at this time. Dissolved free and combined amino acids as well as dissolved free and combined carbohydrates constituted the pool of labile dissolved organic matter to a great extent and were always the major bacterial substrates utilized. At maxima of BP amino acids were preferred whereas carbohydrates were utilized to a greater extent at high and declining bacterial numbers. The bacterial growth efficiency changed seasonally, but in general ranged between 20 and 40 %. During most of the growing season, bacterioplankton growth was co-limited by phosphorus and organic carbon whereas during winter only organic carbon was limiting. Temperature has relatively little direct impact on bacterioplankton growth in the epilimnion because the bacterial assemblages adapted fairly well to the changing ambient temperatures. In the deeper water, temperature directly controlled BP during most of the year. The major loss factors of bacterioplankton comprised phage-induced mortality and grazing by heterotrophic nanoflagellates (HNF), ciliates, and daphnids. On average, phages accounted for 1-24 % of total mortality whereas grazing by HNF for 52-68 %, by ciliates for 14-19 %, and by daphnids for 9-12 %. During the clear-water phase, however, grazing by daphnids dominated by more than 50 %. During oligotrophication, the annual ratio of BP/primary production (PP) integrated from 0 to 20 m varied between 0.09 and 0.29, but without a clear-cut trend. In 1995 and 1996, bacterial growth rates were enhanced and the biomasses of daphnids and autotrophic picoplankton reduced as compared to the previous years. This suggests that grazing control of BP by HNF became more important than before in this late stage of oligotrophication. [TOP OF PAGE]

75. **The specific and sensitive detection of bacterial pathogens within 4 h using bacteriophage amplification. Stewart, G.S., Jassim, S.A., Denyer, S.P., Newby, P., Linley, K., Dhir, V.K. (1998). *Journal of Applied Microbiology* 84:777-783**. This paper describes a novel approach, termed the 'phage amplification assay', for the rapid detection and identification of specific bacteria. The technique is based on the phage lytic cycle with plaque formation as the assay end-point. It is highly sensitive, quantitative and gives results typically within 4 h. The assay comprises four main stages: (1) phage infection of target bacterium; (2) destruction of exogenous phage; (3) amplification of phage within infected host and (4) plaque formation from infected host with the aid of helper bacteria. A key component of this assay is a potent virucidal agent derived from natural plant extracts, pomegranate rind extract (PRE). In combination with ferrous sulphate PRE can bring about an 11 log-cycle reduction in phage titre within 3 min. This is achieved without any injury to the infected target bacteria. Subsequently, any resulting plaques are derived only from infected target organisms. Data are presented for a range of bacterial hosts including *Pseudomonas aeruginosa*, *Salmonella typhimurium* and *Staphylococcus aureus*. The detection limit for *Ps. aeruginosa* was 40 bacteria ml^{-1} in a time of 4 h and 600 bacteria m^{-1} for *Salm. typhimurium*. Application of the principles of this technology to other bacterial genera is discussed. [TOP OF PAGE]

76. **Temperate viruses and lysogeny in Lake Superior bacterioplankton. Tapper, M.A., Hicks, R.E. (1998). *Limnology and Oceanography [Limnol. Oceanogr.]* 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 less than or equal to 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 super(6) viruses ml super(-1) in the surface microlayer (top 20 mu m) and subsurface water (20 m) 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. [TOP OF PAGE]

77. **Effect of plating medium and phage storage on mutant frequency and titer in the lambda cII transgenic mutation assay. Zimmer, D.M., Harbach, P.R., Mattes, W.B., Aaron, C.S. (1998). *ironmental and Molecular Mutagenesis* 32:325-330**. We examined several experimental parameters of the lambda cI/cII transgenic mutation assay. In the assay, clear plaque lambda phage mutants are identified in a positive selection scheme following rescue of the lambda/LIZ shuttle vector from frozen tissues of Big Blue" transgenic mice. Mutant frequency and titer of phage from various tissues of control and ENU-treated animals was essentially the same on LB or TB1 plating medium, and storage of isolated DNA at 4 degrees C for up to 4 months did not affect either mutant frequency or titer. Storage of packaged phage for 28 days at 4 degrees C did not affect titer. The mean mutant frequency of packaged phage stored 28 days at 4 degrees C was consistently higher than phage plated the same day as packaging (day 0), though the difference was statistically significant in only two of the four samples tested. Reconstruction experiments in which numerically defined titers of known cII mutants were plated on both G1217 and G1225 E. coli strains and incubated at 37 degrees C or 24 degrees C showed highest titers on G1217 at 37 degrees C. The fraction of the G1217, 37 degrees C titer seen in the other strains and conditions varied widely with the cII mutation. [TOP OF PAGE]

contents | BEG News (006) | top of page

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