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Bacteriophage Ecology Group (BEG) News

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

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January 1, 2003 issue (volume 15)

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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.

The Phage Manifesto

by Ry Young, Dept. of Biochemistry & Biophysics, Texas A&M University

It is critical that NIH and NSF develop plans for a major expansion of research in phage biology.

Bacteriophages are

- Key factors in microbial pathogenesis,
- Major tools in biotechnology,
- Integral components in global ecology, and, potentially,
- Powerful weapons against the rising tide of drug-resistant bacterial pathogens and microbial bioweapons.

Unfortunately, there are few laboratories ready to engage any of these issues. Classical phage biology, supported by many NIH and NSF grants, dominated molecular biology into the 1970's and generated much of its core knowledge base. Now support for phage biology has been reduced to a mere handful of grants, mostly to principal investigators already late in their careers. The scheduled extinction of the NIH study section responsible for most phage biology grant proposals merely puts a end to an era of unabated decline in bacteriophage research.

Many factors contributed to this decline, including the highly visible exodus from the field of many prominent scientists who viewed phage as powerful experimental tools and means to an end, rather than an intrinsically important component of modern microbiology. In any case, there are very few young scientists with training in phage biology, and fewer still being

trained, especially in the United States. Thus, although the general scientific community thinks that phage biology is a mature field, the reality is that very little is known about any bacteriophages outside of a few classic systems. In a real sense, the new phage biology that is needed for progress in such diverse areas as bacterial genomics, marine ecology, microbial pathogenesis and phage-based therapeutics lacks a fundamental base, because we do not know that our detailed knowledge of the classic coliphages can be extended to phages of other bacteria. In fact, recent results suggest otherwise:

- A *Bordetella* phage was described which apparently uses an HIV-type reverse transcriptase to mutagenize its own tail fiber gene (*Science* ***295:****2091*).
- Classically, filamentous phages were thought to be exclusively virulent until it was shown that active cholera derives from the induction of an M13-like prophage of *V. cholerae* (*Science* ***272:****5270*).
- The shiga-like toxin of hemorrhagic *E. coli* turns out to be a phage protein and its release is caused by phage lysis (*Molec. Microbiol.* ***44:****957*).

These and other developments suggest that our knowledge of bacteriophages is an inch wide and a mile deep.

The NIH, NSF and other national funding agencies are the only forces capable of attracting young scientists to phage biology, which is in a kind of potentially still-born infancy. Concrete steps would be to

> ***Promulgate RFAs in aspects of phage biology of many different bacterial genera and to assign the responsibility for research proposals in bacteriophage biology to new peer review entities with appropriate expertise.***

Failure to take action will cause serious delays in developing a component of modern microbiology critical to our understand of bacterial pathogenesis and ecology. Moreover, public perception is primed to appreciate bacteriophage as an ally, and a natural one at that, in the struggle against bacterial disease and bioterrorism. Phage biology, once a great American intellectual province, should languish no more.

Please Help by Signing our Phage Manifesto On-Line Petition

View List of Supporters of Phage-Biology Research

Editorial Archive

- BEG: What we are, Where we are, Where we're going by Stephen T. Abedon
- When Grown *In Vitro*, do Parasites of Multicellular Organisms (MOPs) become Unicellular Organism Parasites (UOPs)? by Stephen T. Abedon
- Bacteriophages as Model Systems by Stephen T. Abedon
- 2000 and Sun: A Phage Odyssey by Stephen T. Abedon
- Lytic, Lysogenic, Temperate, Chronic, Virulent, Quoi? by Stephen T. Abedon
- Which Ecology are You? by Stephen T. Abedon
- *Science* NetWatch October 13, 2000
- The Best of Times, the Worst of Times by Ry Young
- Naming Bacteriophages by Hans-Wolfgang Ackermann and Stephen T. Abedon
- The Bacteriophage Rise by Stephen T. Abedon
- Mathematics for Microbiologists by Stephen T. Abedon
- Shipping Phages by Hans-Wolfgang Ackermann
- Calling a Phage a "Phage" by Stephen T. Abedon
- Phage or Phages by Hans-Wolfgang Ackermann
- The Phage Manifesto by Ry Young

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New BEG Members

The BEG members page can be found at www.phage.org/beg_members.htm. There are two ways of "joining" BEG. One, the "traditional" way, is to have your name listed on the web page and on the list server. The second, the "non-traditional" way, is to have your name only listed on the list server. The latter I refer to as "non-members" on that list. Members, e.g., individuals listed on the BEG members list page, should be limited to individuals who are actively involved in science (research, instruction, outreach, industry) and who can serve as a phage ecology resource to interested individuals. If you have an interest in phage ecology but no real expertise in the area, then you should join as a non-member. To join as a member, please contact BEG using the following link: 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 page up to date including supplying on a reasonably timely basis the full references of your new phage ecology publications. Reprints can also be sent to *The Bacteriophage Ecology Group*, care of Stephen Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. To join BEG as a non-member, please contact BEG using the following link: 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
Donna May A. dela Cruz	---	dmadc11 @hotmail.com	The Philippines
	interests:	Comparative virulence of phages of enteric bateria found in soil and water habitats. (contents | BEG members | top of page)	
Doug Escribano	---	describa @ic.sunysb.edu	200 Pinehurst Ave, #4H New York, NY 10033 (at Marine Science Research Ctr, SUNY Stony Brook)
	interests:	Marine bacteriophage ecology and evolution. (contents | BEG members | top of page)	
Michael McMenamy	---	m.mcmenamy @qub.ac.uk	Queens University Belfast, School of Agriculture and Food Science, Food Science Department, Food Microbial Technology, Belfast BT9 5PX, N. Ireland
	interests:	The lysogenic / lytic switch and induction of temperate phage by food-compatible / non-mutagenic methods as a means of controlling food-borne pathogens. (contents | BEG members | top of page)	
Lemuel Benedict R. Non	PI	icho_bade @hotmail.com	Department of Biology, Mindanao State University, Fatima, General Santos City, Philippines, 9500
	interests:	Bacteriophage therapy of *Escherichia coli*-infected bacteremic mice. (contents | BEG members | top of page)	
Andrew Scott	---	stxaes @nottingham.ac.uk	48 City Road, Beeston, Notts, UK, NG9 2LQ
	interests:	Analysis of phage resistant *Campylobacter*. (contents | BEG members | top of page)	

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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.

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

Evergreen International Phage Meeting

Next Summer's phage meeting has been scheduled for July 23-27, 2003. Information pertaining to the meeting may be found at http://www.evergreen.edu/phage/. This meeting will bring together phage people with the widest possible array of interests - from the ecological to the molecular - in a setting of rain forest spender. Click here for a tour of The Evergreen State College.

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Jobs

Looking for job? Looking to fill a position? Please send advertisement and information to abedon.1@osu.edu or to "Jobs", 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 information as text (e.g., as an e-mail) or as Microsoft Word documents, if possible (I'll let you know if I have trouble converting any other document formats), and in English. I will update this section as I receive material, regardless of what date this issue of BEG News goes live.

Click here for International Society for Microbial Ecology Employment Listings.

Click here for American Association for the Advancement of Science Employment Listings.

Click here for AAAS "Microbial Ecology" Search.

Click here for AAAS "Ecology and Microbiology" Search.

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Submissions

Submissions are non-editorial items describing or highlighting some aspect of bacteriophage ecology including news pieces, historical pieces, reviews, and write-ups of research. Peer review of submissions is possible and a desire for peer review should be indicated. Send all submissions to abedon.1@osu.edu or to "Submissions", Bacteriophage Ecology Group News, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. Please send all submissions as Microsoft Word documents, if possible (I'll let you know if I have trouble converting any other document formats), and in English.

Pioneering genetic researcher Gisela Mosig dies

Gisela Mosig, 72, a pioneering genetic researcher and distinguished faculty member, died Jan. 12 at Alive Hospice. She had been undergoing cancer treatment for two years.

Mosig, a researcher and teacher at Vanderbilt for the past 38 years, was a central figure in understanding the role that DNA recombination plays in the replication of DNA and in the evolution of genomes. She had well over 100 publications in scientific journals.

One of the few women scientists of her era in molecular biology, she blazed the trail for others who followed. Mosig was a professor in the Department of Molecular Biology, which recently became the Biological Sciences Department. She was named professor emerita in May 2002.

Born in the Saxony region of Germany, Mosig grew up on a farm, where she first became interested in biology and genetics. After World War II, her home fell under East German rule.

In high school, she got a strange introduction to how ideology can affect the scientific quest for truth. Overnight her instructors stopped teaching Mendel's scientifically accepted rules of genetic inheritance and switched to a theory, espoused by Stalin's chief agronomist, T.D. Lysenko, that environment could change genes.

This difficult atmosphere helped her decide to escape East Germany. In 1948, when she was just 18, she managed to cross by bicycle into West Germany, carrying only the possessions that would fit on her bike.

In West Germany, she began her university studies. She did her undergraduate work at the University of Bonn and her graduate work, studying plant genetics, at the University of Cologne, where she was awarded her doctorate in 1959.

At Cologne, Mosig met Gus Doermann, a distinguished Vanderbilt biologist. He inspired her to study the genetics of a virus, bacteriophage T4, and recruited her to take a postdoctoral fellowship working in his lab at Vanderbilt. Studies with bacteriophage T4 led various labs to make some of the groundbreaking discoveries in understanding how genes function.

From 1962 to 1965, Mosig was a research associate at the Carnegie Institution Laboratory in Cold Spring Harbor, N.Y., where she worked with Nobel laureate Alfred Hershey. With Hershey's approval and support, she challenged lab dogma about the way the T4 virus's DNA recombined.

This zest for re-examining and challenging scientific dogma continued when Mosig became an independent scientist and faculty member at Vanderbilt in 1965. She shared her philosophy with the many students she taught and inspired over the years.

Mosig's achievements earned her many honors. She recently gave an invited lecture to a National Academy of Sciences colloquium, published in the Proceedings of the National Academy of Sciences USA. In recognition of her many contributions, her colleagues elected her a fellow of the American Society of Microbiology in 1994.

At Vanderbilt, she was honored for both her research and her teaching, winning the Earl Sutherland Prize for Achievement in Research in 1995 and the Outstanding Graduate Teaching Award in 1989.

Recently, an interview with Mosig was included as a chapter in a textbook on genetics. Asked how she maintained her enthusiasm for science for so long, she said, "I have been so privileged to work on and teach something that interests me most. It far exceeded any expectation that I had when I grew up. Is it surprising that I am enthusiastic about it?"

Mosig's interests extended far beyond science. She was a patron of the arts and environmental causes, and her adventurous spirit led her to travel around the world.

Mosig is survived by a large family in Germany: three brothers and four sisters, 16 nieces and nephews and 22 grandnieces and grandnephews.

Over the years Mosig hosted four of the younger generation of her family as they spent a semester or more studying in Nashville. Her niece, Kristina Mosig, studied at Belmont University. Nephews Ruediger and Axel Mosig attended the University School of Nashville. Her grandniece, Julianne Schubert, attended the University School just last year.

Mosig is also remembered by the many scientists whom she taught by example to love science and revere the truth.

Burial will be private. A memorial service will be held later in Nashville. In lieu of flowers, donations can be made to Alive Hospice of Nashville, the Nashville Symphony or the Tennessee Conservation League.

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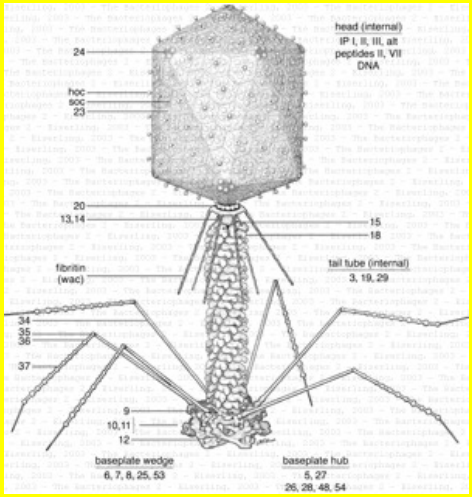
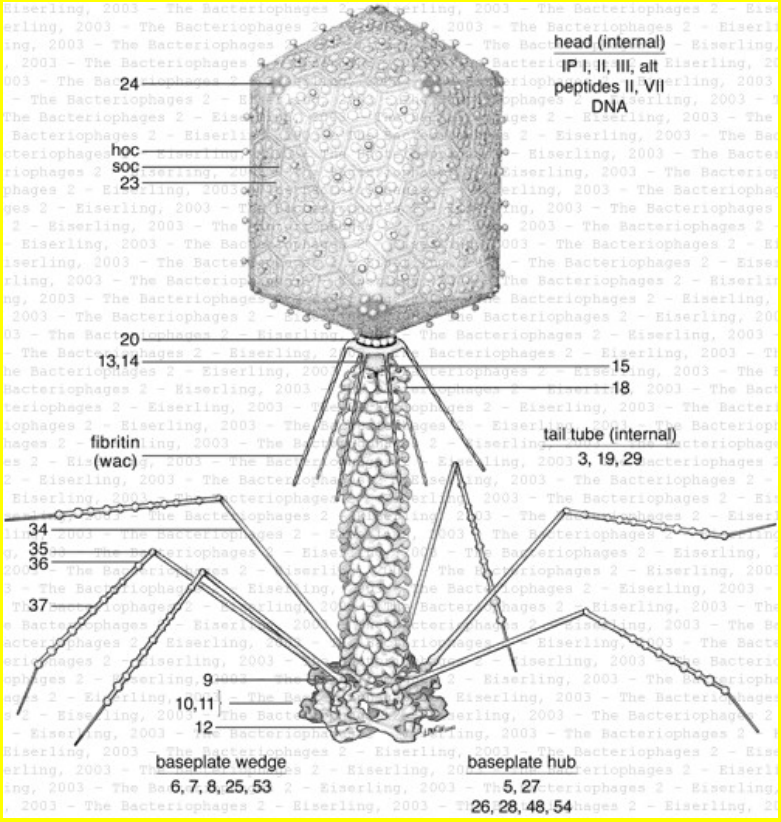
We would like to collect more on Gisela for our next issue of BEG News.
Colleagues, former grad students, friends, relatives, Please send any and all photos and reminiscences to microdude+@osu.edu
or by snail-mail to Stephen T. Abedon, The Ohio State University, 1680 University Dr., Mansfield, OH 44906. Many thanks.
Please also pass on this request to any interested parties that you may be aware of:
http://www.phage.org/bgnws015.htm#gisela_mosig

Updated Eiserling T4 Virion



Above and below are updates (circa late 2002) of the classic drawing of the bacteriophage T4 virion, kindly brought to us by Fred Eiserling (who is also responsible for the original). Fred

would like us to employ these watermarked images far and wide, so please feel free to copy and use them. An unwatermarked version is due to be published in the upcoming *The Bacteriophages* edition 2 (Oxford University Press). For your convenience we are providing the image in a number of sizes: small (300x316 and as shown above; 47 KB), medium (500x526 and as shown below; 118 KB), large (800x842; 262 KB), and extra large (1100x1158; 440 KB). Fred can be contacted at frede@college.ucla.edu .



Submissions Archive

- On an Invisible Microbe Antagonistic to the Dysentery Bacillus by Felix d'Herelle
- Obituary: Hansjürgen Raettig - Collector of Bacteriophage References (October 12, 1911 - December 1, 1997)
- Some Quotations
- Bacteriophages: A Model System for Human Viruses
- How Big is 10^{30}?
- Selling Phage Candy
- A List of Phage Names
- An Expanded Overview of Phage Ecology
- Rendering Phage Heads
- The Contractile-Tail Sheath, In Three Dimensions
- Eye On The Needle: Phage T4 Puncturing Point May Answer Penetrating Questions
- Pioneering genetic researcher Gisela Mosig dies
- Updated Eiserling T4 Virion

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Phage Images

Please send any phage images that you would like to present in this section to "Phage Images," *The Bacteriophage Ecology Group*, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. Alternatively, you may scan the images yourself and send them as an attachment to abedon.1@osu.edu. Please save all scans in gif or jpg formats and preferably with an image size (in terms of width, height, and kbytes) that will readily fit on a standard web page. No copyrighted material without permission, please!

Phage Image Archive

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

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New Publications

New bacteriophage publications are listed below. Each quarter not-yet-listed publications from the previous two years will be presented along with their abstracts. The indicator "???" denotes, of course, that specific information is not yet in the BEG Bibliography. Please help in the compilation of the BEG Bibliography by supplying any updated information, correcting any mistakes, and, of course, sending the references to your bacteriophage ecology publications, as well as the references to any bacteriophage ecology publications that you know of but which are not yet in the bibliography (send to abedon.1@osu.edu or to "BEG Bibliography," *Bacteriophage Ecology Group News*, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906). Also, be sure to indicate any listed publications that you feel should not be presented in the BEG Bibliography. This list is also present with available abstracts at the end of *BEG News*.

1. Strategies for improving the efficacy of bacteriophages for controlling bacterial spot of tomato. Balogh, B. (2002) Ph.D. dissertation, University of Florida. [PRESS FOR ABSTRACT]

2. R391: a conjugative integrating mosaic comprised of phage, plasmid, and transposon elements. Boltner, D., MacMahon, C., Pembroke, J. T., Strike, P., Osborn, A. M. (2002). *Journal of Bacteriology* 184:5158-5169. [PRESS FOR ABSTRACT]

3. PCR-based method for detecting viral penetration of medical exam gloves. Broyles, J. M., O'Connell, K. P., Korniewicz, D. M. (2002). *Journal of Clinical Microbiology* 40:2725-2728. [PRESS FOR ABSTRACT]

4. Effect of surfactants on the survival and sorption of viruses. Chattopadhyay, D., Chattopadhyay, S., Lyon, W. G., Wilson, J. T. (2002). *Environmental Science and Technology* 36:4017-4024. [PRESS FOR ABSTRACT]

5. Effect of exopolysaccharides on phage-host interactions in *Lactococcus lactis*. Deveau, H., Van Calsteren, M. R., Moineau, S. (2002). *Applied and Environmental Microbiology* 68:4364-4369. [PRESS FOR ABSTRACT]

6. Sunlight-induced propagation of the lysogenic phage encoding cholera toxin. Faruque, S. M., Asadulghani, Rhaman M. M., Waldor, M. K., Sack, D. A. (2002). *Infection and Immunity* 68:4795-4801. [PRESS FOR ABSTRACT]

7. Evolution of DNA polymerase families: evidences for multiple gene exchange between cellular and viral proteins. Filee, J., Forterre, P., Sen-Lin, T., Laurent, J. (2002). *Journal of Molecular Evolution* 54:763-773. [PRESS FOR ABSTRACT]

8. Bacteriophages: evolution of the majority. Hendrix, R. W. (2002). *Theoretical Population Biology* 61:471-480. [PRESS FOR ABSTRACT]

9. Reduction of enteric microbes in flushed swine wastewater treated by a biological aerated filter and UV irradiation. Hill, V. R., Kantardjieff, A., Sobsey, M. D., Westerman, P. W. (2002). *Water Environment Research* 74:91-99. [PRESS FOR ABSTRACT]

10. Dietary influences on bacteriophage numbers in the rumen. Klieve, A. V., Turner, A. F., Heck, G. L. (1998). *Animal Production in Australia (Proceedings of the Australian Society of Animal Production)* 22:341. [NO ABSTRACT]

11. Phagotherapy: myths and realities. Krylov, V. (2002). *Russian Academy of Sciences Presidium—Science in Russia* 4:40-46. [PRESS FOR ABSTRACT]

12. A novel sustained-release matrix based on biodegradable poly(ester amide)s and impregnated with bacteriophages and an antibiotic shows promise in management of infected venous stasis ulcers and other poorly healing wounds. Markoishvili, K., Tsitlanadze, G., Katsarava, R., Morris, J. G. Jr, Sulakvelidze, A. (2002). *International Journal of Dermatology* 41:453-458. [PRESS FOR ABSTRACT]

13. Detection of antibodies against the four subtypes of ebola virus in sera from any species using a novel antibody-phage indicator

assay. Meissner, F., Maruyama, T., Frentsch, M., Hessell, A. J., Rodriguez, L. L., Geisbert, T. W., Jahrling, P. B., Burton, D. R., Parren, P. W. H. I. (2002). *Virology* 300:236-243. [PRESS FOR ABSTRACT]

14. Temperate phages in *Salmonella enterica* serovar *Typhimurium*: implications for epidemiology. Mmolawa, P. T., Willmore, R., Thomas, C. J., Heuzenroeder, M. W. (2002). *International Journal of Medical Microbiology* 291:633-644. [NO ABSTRACT]

15. Phages of lactic acid bacteria: From genomics to industrial applications. Moineau, S., Tremblay, D., Labrie, S. (2002). *ASM News* 68:388-393. [PRESS FOR ABSTRACT]

16. Depuration dynamics of viruses in shellfish. Muniain-Mujika, I., Girones, R., Tofino-Quesada, G., Calvo, M., Lucena, F. (2002). *International Journal of Food Microbiology* 77:125-133. [PRESS FOR ABSTRACT]

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

18. A minimized M13 coat protein defines the requirements for assembly into the bacteriophage particle. Roth, T. A., Weiss, G. A., Eigenbrot, C., Sidhu, S. S. (2002). *Journal of Molecular Biology* 322:357-367. [PRESS FOR ABSTRACT]

19. Kinetic modeling of virus transport at the field scale. Schijven, J. F., Simunek, J. (2002). *J. Contaminant Hydrology* 55:113-135. [PRESS FOR ABSTRACT]

20. Fighting Foam with Phages? Thomas, J. A., Soddell, J. A., Kurtboke, D. I. (2002). *Water Science and Technology* 46:511-553. [PRESS FOR ABSTRACT]

21. [Defective lysogeny in *Erwinia carotovora*]. Tovkach, F. I. (2002). *Mikrobiologija (Microbiologiia)* 71:359-367. [PRESS FOR ABSTRACT]

22. *Lactococcus lactis* DPC5598, a plasmid-free derivative of a commercial starter, provides a valuable alternative host for culture improvement studies. Trotter, M., Ross, R. P., Fitzgerald, G. F., Coffey, A. (2002). *Journal of Applied Microbiology* 93:134-143. [PRESS FOR ABSTRACT]

23. In vivo generation of hybrids between different species of RNA phages. van Meerten, D., Groeneveld, H., Miller, D. M. J., Marechal, G. B., Tsareva, N. V., Olsthoorn, R. C. L., de la Pena, M., van Duin, J. (2002). *Journal of General Virology* 83:1223-1235. [PRESS FOR ABSTRACT]

24. Functional analysis of heterologous holin proteins in a lDS genetic background. Vukov, N., Scherer, S., Hibbert, E., Loessner, M. J. (2000). *FEMS Microbiology Letters* 184:179-186. [PRESS FOR ABSTRACT]

25. Human neutrophils and their products induce Shiga toxin production by enterohemorrhagic *Escherichia coli*. Wagner, P. L., Acheson, D. W., Waldor, M. K. (2001). *Infection and Immunity* 69:1934-1937. [PRESS FOR ABSTRACT]

26. Seasonal variation in lysogeny as depicted by prophage induction in Tampa Bay, Florida. Williamson, S. J., Houchin, L. A., McDaniel, L., Paul, J. H. (2002). *Applied and Environmental Microbiology* 68:4307-4314. [PRESS FOR ABSTRACT]

27. Phylogenetic diversity of marine cyanophage isolates and natural virus communities as revealed by sequences of viral capsid assembly protein gene g20. Zhong, Y., Chen, F., Wilhelm, S. W., Poorvin, L., Hodson, R. E. (2002). *Applied and Environmental Microbiology* 68:1576-1584. [PRESS FOR ABSTRACT]

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New Publications with Abstracts

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

1. **Strategies for improving the efficacy of bacteriophages for controlling bacterial spot of tomato. Balogh, B. (2002) Ph.D. dissertation, University of Florida.** Bacterial spot, caused by the bacterium *Xanthomonas campestris* pv. *vesicatoria*, is one of the major tomato diseases in Florida. The disease is routinely controlled by the application of copper-mancozeb, a mixture of chemical pesticides; however, there is no adequate control measure when the environmental conditions are conducive for disease development. A novel method for controlling this disease is the application of a mixture of bacteriophages, viruses that infect bacteria. However, these control agents are rapidly degraded by harmful environmental factors such as sunlight or desiccation, which delimits the efficacy of phage treatment. It has been hypothesized that the efficacy of phage treatment could be enhanced if the longevity of the viruses was increased. ¶ Three formulations were developed that enhanced the longevity of bacteriophages on plant foliage. These formulations were (i) PCF (0.5% pregelatinized corn flour (PCPF 400, Lauhoff Grain Co., Danville, IL) + 0.5% sucrose), (ii) Casecrete (0.5% Casecrete NH-400, a water-soluble casein protein polymer (American Casein Company, Burlington, NJ)+ 0.5% sucrose + 0.25% PCPF 400)), and (iii) skim milk (0.75% powdered skim milk + 0.5% sucrose). The use of these formulations resulted in a 4,700, 38,500 and 100,000-fold increase in phage populations two days after application compared to the non-formulated phage populations. ¶ The PCF, Casecrete and skim milk formulations and the non-formulated phages all significantly reduced disease severity in field trials on tomato compared to the standard copper-mancozeb treatment by 22, 33, 27 and 19%, respectively. The PCF and the Casecrete formulations reduced the disease severity compared to the non-formulated phage by 11 and 21% in average in three field experiments, respectively. The skim milk formulation reduced the disease severity by 10% compared to the non-formulated phage application in one field experiment. ¶ The co-application of skim milk-formulated phages and copper-mancozeb treatment resulted in a superior disease control efficacy, which was significantly better than the control achieved by any of the treatments. The integration of phage application with Actigard treatment resulted in a significant increase in efficacy only with the PCF formulation but not with Casecrete

formulation. The lowest phage titer that significantly reduced disease development in greenhouse experiment was 10^6 PFU/ml.

(See http://etd.fcla.edu/etd/uf/2002/UFE1000106/balogh_b.pdf for full text of Balogh's dissertation)

2. **R391: a conjugative integrating mosaic comprised of phage, plasmid, and transposon elements. Boltner, D., MacMahon, C., Pembroke, J. T., Strike, P., Osborn, A. M. (2002). *Journal of Bacteriology* 184:5158-5169.** The conjugative, chromosomally integrating element R391 is the archetype of the IncJ class of mobile genetic elements. Originally found in a South African Providencia rettgeri strain, R391 carries antibiotic and mercury resistance traits, as well as genes involved in mutagenic DNA repair. While initially described as a plasmid, R391 has subsequently been shown to be integrated into the bacterial chromosome, employing a phage-like integration mechanism closely related to that of the SXT element from Vibrio cholerae O139. Analysis of the complete 89-kb nucleotide sequence of R391 has revealed a mosaic structure consisting of elements originating in bacteriophages and plasmids and of transposable elements. A total of 96 open reading frames were identified; of these, 30 could not be assigned a function. Sequence similarity suggests a relationship of large sections of R391 to sequences from *Salmonella*, in particular those corresponding to the putative conjugative transfer proteins, which are related to the IncHI1 plasmid R27. A composite transposon carrying the kanamycin resistance gene and a novel insertion element were identified. Challenging the previous assumption that IncJ elements are plasmids, no plasmid replicon was identified on R391, suggesting that they cannot replicate autonomously

3. **PCR-based method for detecting viral penetration of medical exam gloves. Broyles, J. M., O'Connell, K. P., Korniewicz, D. M. (2002). *Journal of Clinical Microbiology* 40:2725-2728.** The test approved by the U.S. Food and Drug Administration for assessment of the barrier quality of medical exam gloves includes visual inspection and a water leak test. Neither method tests directly the ability of gloves to prevent penetration by microorganisms. Methods that use microorganisms (viruses and bacteria) to test gloves have been developed but require classical culturing of the organism to detect it. We have developed a PCR assay for bacteriophage phiX174 that allows the rapid detection of penetration of gloves by this virus. The method is suitable for use with both latex and synthetic gloves. The presence of glove powder on either latex or synthetic gloves had no effect on the ability of the PCR assay to detect bacteriophage DNA. The assay is rapid, sensitive, and inexpensive; requires only small sample volumes; and can be automated

4. **Effect of surfactants on the survival and sorption of viruses. Chattopadhyay, D., Chattopadhyay, S., Lyon, W. G., Wilson, J. T. (2002). *Environmental Science and Technology* 36:4017-4024.** There is an increasing concern about the protection of groundwater from contamination by enteric viruses and the prevention of outbreaks of waterborne diseases. Knowledge of survivability and transport of viruses from their point of origin is necessary to determine their potential effects on the neighboring groundwater systems. The distribution of virus is, in turn, dependent on the physical and chemical compositions of the surrounding soil and subsurface systems. For the present study, we have determined the effects of different surfactants (cationic, anionic, nonionic, and biological) and natural organic matter (NOM) on bacteriophages. Results indicated that surfactants and NOM adversely affect phage survival in binary systems, with surfactants being the most harmful. Studies with ternary systems also showed that the presence of surfactants reduced sorption of phages on sorbents either by occupying available sorption sites on the sorbent material or by displacing the sorbed phages from the sorbent surface. Water contact angles of the selected phages and different sorbent surfaces have been measured. Experimental data demonstrated that the sorption of hydrophobic viruses was favored by hydrophobic sorbents, while the sorption of hydrophilic viruses was favored by hydrophilic sorbents.

5. **Effect of exopolysaccharides on phage-host interactions in *Lactococcus lactis*. Deveau, H., Van Calsteren, M. R., Moineau, S. (2002). *Applied and Environmental Microbiology* 68:4364-4369.** In this study, we report that *Lactococcus lactis* strains producing exopolysaccharides (EPS) are sensitive to virulent phages. Eight distinct lytic phages (Q61 to Q68) specifically infecting Eps(+) strains were isolated in 47 buttermilk samples obtained from 13 North American factories. The eight phages were classified within the 936 species by the multiplex PCR method, indicating that these phages are not fundamentally distinct from those infecting Eps(-) L. lactis strains. The host range of these phages was determined with 19 Lactococcus strains, including 7 Eps(+) and 12 Eps(-) cultures. Three phages (Q62, Q63, and Q64) attacked only the Eps(+) strain SMQ-419, whereas the five other phages (Q61, Q65, Q66, Q67, and Q68) infected only the Eps(+) strain SMQ-420. The five other Eps(+) strains (H414, MLT2, MLT3, SMQ-461, and SMQ-575) as well as the 12 Eps(-) strains were insensitive to these phages. The monosaccharide composition of the polymer produced by the seven Eps(+) strains was determined. The EPS produced by strains MLT3, SMQ-419, and SMQ-575 contained glucose, galactose, and rhamnose. The EPS fabricated by H414 contained only galactose. The EPS made by MLT2, SMQ-420, and SMQ-461 contained glucose and galactose. These findings indicate that the sugar composition of the EPS has no effect on phage sensitivity. The plasmid encoding the eps operon was cured from the two phage-sensitive strains. The cured derivatives were still phage sensitive, which indicates that EPS are not necessary for phage infection. Phage adsorption assays showed that the production of EPS does not confer a significant phage resistance phenotype

6. **Sunlight-induced propagation of the lysogenic phage encoding cholera toxin. Faruque, S. M., Asadulghani, Rhaman M. M., Waldor, M. K., Sack, D. A. (2002). *Infection and Immunity* 68:4795-4801.** In toxigenic *Vibrio cholerae*, the cholera enterotoxin (CT) is encoded by CTXPhi, a lysogenic bacteriophage. The propagation of this filamentous phage can result in the origination of new toxigenic strains. To understand the nature of possible environmental factors associated with the propagation of CTXPhi, we examined the effects of temperature, pH, salinity, and exposure to direct sunlight on the induction of the CTX prophage and studied the transmission of the phage to potential recipient strains. Exposure of cultures of CTXPhi lysogens to direct sunlight resulted in approximately 10,000-fold increases in phage titers. Variation in temperature, pH, or salinity of the culture did not have a substantial effect on the induction of the prophage, but these factors influenced the stability of CTXPhi particles. Exposure of mixed cultures of CTXPhi lysogens and potential recipient strains to sunlight significantly increased both the in vitro and in vivo (in rabbit ileal loops) transduction of the recipient strains by CTXPhi. Included in these transduction experiments were two environmental nontoxigenic (CTXPhi(-)) strains of V. cholerae O139. These two O139 strains were transduced at high efficiency by CTXPhi, and the phage genome integrated into the O139 host chromosome. The resulting CTXPhi lysogens produced biologically active CT both in vitro and in rabbit ileal loops. This finding suggests a possible mechanism explaining the origination of toxigenic *V. cholerae* O139 strains from nontoxigenic progenitors. This study indicates that sunlight is a significant inducer of the CTX prophage and suggests that sunlight-induced transmission of CTXPhi may constitute part of a natural mechanism for the origination of new toxigenic strains of *V. cholerae*.

7. **Evolution of DNA polymerase families: evidences for multiple gene exchange between cellular and viral proteins. Filee, J., Forterre, P., Sen-Lin, T., Laurent, J. (2002). *Journal of Molecular Evolution* 54:763-773.** A phylogenetic analysis of the five major families of DNA polymerase is presented. Viral and plasmid sequences are included in this compilation along

with cellular enzymes. The classification by Ito and Braithwaite (Ito and Braithwaite 1991) of the A, B, C, D, and X families has been extended to accommodate the "Y family" of DNA polymerases that are related to the eukaryotic RAD30 and the bacterial UmuC gene products. After analysis, our data suggest that no DNA polymerase family was universally conserved among the three biological domains and no simple evolutionary scenario could explain that observation. Furthermore, viruses and plasmids carry a remarkably diverse set of DNA polymerase genes, suggesting that lateral gene transfer is frequent and includes non-orthologous gene displacements between cells and viruses. The relationships between viral and host genes appear very complex. We propose that the gamma DNA polymerase of the mitochondrion replication apparatus is of phage origin and that this gene replaced the one in the bacterial ancestor. Often there was no obvious relation between the viral and the host DNA polymerase, but an interesting exception concerned the family B enzymes: in which ancient gene exchange can be detected between the viruses and their hosts. Additional evidence for horizontal gene transfers between cells and viruses comes from an analysis of the small damage-inducible DNA polymerases. Taken together, these findings suggest a complex evolutionary history of the DNA replication apparatus that involved significant exchanges between viruses, plasmids, and their hosts

8. **Bacteriophages: evolution of the majority. Hendrix, R. W. (2002). *Theoretical Population Biology* 61:471-480.** The dsDNA-tailed bacteriophages are probably the largest evolving group in the Biosphere and they are arguably very ancient. Comparative examination of genomes indicates that the hallmark of phage evolution is horizontal exchange of sequences. This is accomplished, first, by rampant non-homologous recombination between different genomes and, second, by reassortment of the variant sequences so created through homologous recombination. The comparative analysis suggests mechanisms by which new genes can be added to phage genomes and by which genes with novel functions may be assembled from parts. Horizontal exchange of sequences occurs most frequently among closely related phages, but it also extends across the entire global population at lower frequency. Bacteriophages also have probable ancestral connections with viruses of eukaryotes and archaea

9. **Reduction of enteric microbes in flushed swine wastewater treated by a biological aerated filter and UV irradiation. Hill, V. R., Kantardjieff, A., Sobsey, M. D., Westerman, P. W. (2002). *Water Environment Research* 74:91-99.** An aerobic biofilter system was studied to assess its effectiveness for reducing enteric microbial indicators in flushed swine wastewater under different seasonal conditions. A laboratory-scale, low-pressure UV collimated beam apparatus was used to investigate the effectiveness of UV irradiation for inactivating enteric bacteria, coliphages, and bacterial spores in treated and untreated swine wastewater having unfiltered absorbances of 5 to 11 cm(-1) and total suspended solids concentrations of 500 to 1200 mg/L. Fecal coliforms, *Escherichia coli*, enterococci, somatic coliphages, and male-specific coliphages were reduced by 97 to 99% in the biofilter system when reactor water temperatures were between 23 and 32 degrees C. *Salmonella* were reduced by 95 to 97% when water temperatures were 17 to 32 degrees C. Of the six microbial indicators studied. *Clostridium perfringens* spores were typically reduced the least by the biofilter system. At an average absorbed UV irradiation dose of 13 mJ/cm2, maximum reductions of fecal coliforms, *E. coli*, enterococci, *C. perfringens* spores, and somatic coliphages in biofilter system effluent were 2.2, 2.1, 1.3, 0.2, and 2.3 log10, respectively. The results of this study show that the aerobic biofilter system can be an effective alternative for treatment of flushed swine waste. Ultraviolet irradiation can be effective for further reducing enteric microbe concentrations in biologically-treated swine waste, as well as in lower quality wastewaters, indicating its general potential for pathogen reductions in low-quality wastewaters intended for beneficial reuse

10. **Dietary influences on bacteriophage numbers in the rumen. Klieve, A. V., Turner, A. F., Heck, G. L. (1998). *Animal Production in Australia (Proceedings of the Australian Society of Animal Production)* 22:341.**

11. **Phagotherapy: myths and realities. Krylov, V. (2002). *Russian Academy of Sciences Presidium—Science in Russia* 4:40-46.** The current situation of uncontrolled uses of medicinal preparations, pollution of nature with toxic wastes and other adverse phenomena of this kind have produced what experts call another spiral in the eovlution of bacteria—the development of their multiple-resistant strains. As often as not, many expensive antibiotics of the last generation (vancomycin, imipenem, etc.) turn out to be powerless. And the way medical experts see it—the way out of this situation—consists in pioneering some alternative therapies. The most promising of these is believed to be phagotherapy—the use of specific bacterial viruses (bacteriophages or phages).

12. **A novel sustained-release matrix based on biodegradable poly(ester amide)s and impregnated with bacteriophages and an antibiotic shows promise in management of infected venous stasis ulcers and other poorly healing wounds. Markoishvili, K., Tsitlanadze, G., Katsarava, R., Morris, J. G. Jr, Sulakvelidze, A. (2002). *International Journal of Dermatology* 41:453-458.** Healing of poorly vascularized and venous stasis ulcers is often refractory to therapy, particularly when they are infected. Systemic antibiotic therapy may be of little benefit in this setting because of poor penetration of the antibiotic into the wound and the frequent associated emergence of bacterial strains resistant to common antimicrobial agents. Given the clinical significance of these problems, there is a need to explore alternative management approaches for these difficult-to-treat wounds. PhagoBioDerm is a novel wound-healing preparation consisting of a biodegradable polymer impregnated with an antibiotic and lytic bacteriophages, which was recently licensed for sale in the Republic of Georgia (one of the former Soviet Union republics). In 1999-2000, in Tbilisi, Georgia, 107 patients who had ulcers that had failed to respond to conventional therapy were treated with PhagoBioDerm alone or in combination with other interventions. The wounds/ulcers healed completely in 67 (70%) of 96 patients for whom follow-up data were available. In 22 cases in which microbiologic data were available, healing was associated with the concomitant elimination of, or a reduction in, specific pathogenic bacteria in the ulcers. Our findings suggest that this slow-release biopolymer is safe and of possible benefit in the management of refractory wounds, and they support the apparent utility of bacteriophages in this setting. Further studies, including carefully designed clinical trials, will be required to rigorously evaluate the efficacy of this novel wound dressing preparation

13. **Detection of antibodies against the four subtypes of ebola virus in sera from any species using a novel antibody-phage indicator assay. Meissner, F., Maruyama, T., Frentsch, M., Hessell, A. J., Rodriguez, L. L., Geisbert, T. W., Jahrling, P. B., Burton, D. R., Parren, P. W. H. I. (2002). *Virology* 300:236-243.** The natural host for Ebola virus, presumed to be an animal, has not yet been identified despite an extensive search following several major outbreaks in Africa. A straightforward approach used to determine animal contact with Ebola virus is by assessing the presence of specific antibodies in serum. This approach however has been made very difficult by the absence of specific reagents required for the detection of antibodies from the majority of wild animal species. In this study, we isolated a human monoclonal antibody Fab fragment, KZ51, that reacts with an immunodominant epitope on Ebola virus nucleoprotein (NP) that is conserved on all four Ebola virus subtypes. The antibody KZ51 represents a major specificity as sera from all convalescent patients tested (10/10) and sera from guinea pigs infected with each of the four Ebola virus subtypes competed strongly with KZ51 for binding to radiation-inactivated Ebola virus. These features allowed us to develop a novel assay for the detection of seroconversion irrespective of Ebola virus subtype or animal species. In this assay, the binding of KZ51 Fab-phage particles is used as an indicator assay and the presence of specific antibodies against Ebola virus in sera is indicated by binding competition. A prominent feature of the assay is that the

Fab-phage particles may be prestained with a dye so that detection of binding can be directly determined by visual inspection. The assay is designed to be both simple and economical to enable its use in the field

14. **Temperate phages in *Salmonella enterica* serovar *Typhimurium*: implications for epidemiology. Mmolawa, P. T., Willmore, R., Thomas, C. J., Heuzenroeder, M. W. (2002). *International Journal of Medical Microbiology* 291:633-644.**

15. **Phages of lactic acid bacteria: From genomics to industrial applications. Moineau, S., Tremblay, D., Labrie, S. (2002). *ASM News* 68:388-393.** Dairy microbiologists seek new ways to protet milk-fermenting microorganisms against damaging phages. Dairy microbiologists have been trying for more than 70 years to eleminate, or at least bring under better control, the bacteriophages that interfere with the manufacture of many fermented milk products. Products such as yogurt and cheese are manufactured through use of nonsporulating gram-positive microorganisms know as the lactic acid bacteria (LAB) (see p. 369). Among them are members of serveral genera, including *Lactococcus*, *Streptococcus*, *Lactobacillus*, and *Leuconostoc*. Large-scale fermentations of dairy products typically begin following inoculation with carefully seleted started cultures containing a mixture of 10^7 LAB per ml of milk. The choice of the LAB strains in starter cultures serves to control the fermentation and to yield high-quality produts. ¶ Annually, perhaps 10^{23} cells of LAB are used globally for such fermentations. Wtih this extensive commercial use, interest in studying LAB has increased to an unprecedented level in recent years. In fact, some researchers have even enthusiastically dubbed LAB "the bug of the new millenium." However, these commercial fermentative processes are vulnerable to specialized bacteriophages. A keen interest in overcoming this vulnerability is bolstering an established fascination for these microorganisms, and dairy microbiologists are learning to control phages in numerous ways. The phage diversity has led such researchers to a wide range of fundamental and applied studies, engaging them in the "ome" era of genome, proteome, and transcriptomes with the hope of developing novel anti-phage mechanisms. [= first two paragraphs]

16. **Depuration dynamics of viruses in shellfish. Muniain-Mujika, I., Girones, R., Tofino-Quesada, G., Calvo, M., Lucena, F. (2002). *International Journal of Food Microbiology* 77:125-133.** The consumption of shellfish has been associated with viral infections even in cases where shellfish complied with the current regulation, which is based on bacterial analysis. In this study, depuration rates of potential indicators and human viruses have been analysed in order to study the use of complementary parameters for evaluating the microbiological quality of depurated shellfish. Depuration of naturally highly polluted mussels has been evaluated and analyses for *Escherichia coli*, *Clostridium perfringens*, somatic coliphages, F-RNA phages and bacteriophages infecting *Bacteroides fragilis* RYC2056 and HSP40, human adenovirus, enterovirus have been done. Seawater of the depuration tank was disinfected by UV irradiation, ozone and passed through a skimmer and a biological filter. The correct functioning of the depuration tank was monitored by the quantification of total organic carbon (TOC), NH4+ and total aerobic bacteria in the seawater. To study the relation between the bacteriophages and the human viruses analysed, a logistic regression model was applied. F-RNA phages are significantly related to human adenoviruses and enteroviruses. Thus, they can be used as a complementary parameter for evaluating the efficiency of the depuration treatment. Somatic coliphages are also significantly associated with enteroviruses. Bacteriophages infecting *B. fragilis* HSP40 were analysed by the double-agar-layer (DAL) method, which quantifies infectious viruses, and by nested PCR, which detects the presence of the genome of these phages. The highest sensitivity of the molecular techniques was demonstrated and the results obtained are an indicator of a close relation between positive results by PCR and the presence of infectious viral particles in shellfish. All shellfish samples were negative for human viruses by PCR after 5 days of depuration treatment and the results obtained applying a regression model also showed negative results or nearly for F-RNA phages and bacteriophages infecting *B. fragilis* RYC2056. Thus, in this specific depuration treatment, 5 days may be necessary to assess the sanitary quality of shellfish

17. **Phage typing of *Lactococcus garvieae* (formerly *Enterococcus seriolicida*) a pathogen of cultured yellowtail. Park, K. H., Kato, H., Nakai, T., Muroga, K. (1998). *Fisheries Science (Tokyo)* 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 in the previous study. One hundred and eleven strains of *L. garvieae* examined were divided into 14 phage types (A~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 (KG and KG+).

18. **A minimized M13 coat protein defines the requirements for assembly into the bacteriophage particle. Roth, T. A., Weiss, G. A., Eigenbrot, C., Sidhu, S. S. (2002). *Journal of Molecular Biology* 322:357-367.** The M13 filamentous bacteriophage coat is a symmetric array of several thousand alpha-helical major coat proteins (P8) that surround the DNA core. P8 molecules initially reside in the host membrane and subsequently transition into their role as coat proteins during the phage assembly process. A comprehensive mutational analysis of the 50-residue P8 sequence revealed that only a small subset of the side-chains were necessary for efficient incorporation into a wild-type (wt) coat. In the three-dimensional structure of P8, these side-chains cluster into three functional epitopes: a hydrophobic epitope located near the N terminus and two epitopes (one hydrophobic and the other basic) located near the C terminus on opposite faces of the helix. The results support a model for assembly in which the incorporation of P8 is mediated by intermolecular interactions involving these functional epitopes. In this model, the N-terminal hydrophobic epitope docks with P8 molecules already assembled into the phage particle in the periplasm, and the basic epitope interacts with the acidic DNA backbone in the cytoplasm. These interactions could facilitate the transition of P8 from the membrane into the assembling phage, and the incorporation of a single P8 would be completed by the docking of additional P8 molecules with the second hydrophobic epitope at the C terminus. We constructed a minimized P8 that contained only nine non-Ala side-chains yet retained all three functional epitopes. The minimized P8 assembled into the wt coat almost as efficiently as wt P8, thus defining the minimum requirements for protein incorporation into the filamentous phage coat. The results suggest possible mechanisms of natural viral evolution and establish guidelines for the artificial evolution of improved coat proteins for phage display technology

19. **Kinetic modeling of virus transport at the field scale. Schijven, J. F., Simunek, J. (2002). *J. Contaminant Hydrology* 55:113-135.** Bacteriophage removal by soil passage in two field studies was re-analyzed with the goal to investigate differences between one- and two-dimensional modeling approaches, differences between one- and two-site kinetic sorption models, and the role of heterogeneities in the soil properties. The first study involved removal of bacteriophages MS2 and PRDI by dune recharge, while the second study represented removal of MS2 by deep well injection. In both studies, removal was higher during the first meters of soil passage than thereafter. The software packages HYDRUS-ID and HYDRUS-2D, which simulate water flow and solute transport in one- and two-dimensional variably saturated porous media, respectively, were used. The two codes were

modified by incorporating reversible adsorption to two types of kinetic sites. Tracer concentrations were used first to calibrate flow and transport parameters of both models before analyzing transport of bacteriophages. The one-dimensional one-site model did not fully describe the tails of the measured breakthrough curves of MS2 and PRD1 from the dune recharge study. While the one-dimensional one-site model predicted a sudden decrease in virus concentrations immediately after the peaks, measured data displayed much smoother decline and tailing. The one-dimensional two-site model simulated the overall behavior of the breakthrough curves very well. The two-dimensional one-site model predicted a more gradual decrease in virus concentrations after the peaks than the one-dimensional one-site model, but not as good as the one-dimensional two-site model. The dimensionality of the problem hence can partly explain the smooth decrease in concentration after peak breakthrough. The two-dimensional two-site model provided the best results. Values for k(att2) and k(det2) could not be determined at the last two of four monitoring wells, thus suggesting that either a second type of kinetic sites is present in the first few meters of dune passage and not beyond the second monitoring well, or that effects of soil heterogeneity and dimensionality of the problem overshadowed this process. Variations between single collector efficiencies were relatively small, whereas collision efficiencies varied greatly. This implies that the nonlinear removal of MS2 and PRD1 is mainly caused by variations in interactions between grain and virus surfaces rather than by physical heterogeneity of the porous medium. Similarly, a two-site model performed better than the one-site model in describing MS2 concentrations for the deep well injection study. However, the concentration data were too sparse in this study to have much confidence in the fitted parameters

20. **Fighting Foam with Phages? Thomas, J. A., Soddell, J. A., Kurtboke, D. I. (2002). *Water Science and Technology* 46:511-553.** Seventeen(17) phages infective for the mycolata were isolated from six samples of activated sludge using 21 prospective hosts from the genera *Dietzia*, *Nocardia*, *Rhodococcus*, *Tsukamurella* and *Mycobacterium*. Their morphology indicated that they were all members of the viral family Siphoviridae, but they varied in the size of the icosahedral head and length of non-contractile tail, suggesting they were different. This was confirmed by host-range studies with 47 strains of mycolata, which showed that each phage had a unique host-range, and this was polyvalent in the majority (15/17) of cases, with 12 infective for hosts representing two or three of the genera *Gordonia*, *Nocardia* and *Rhodococcus*. The potential for use of these phages in the control of foaming and other applications is discussed.

21. **[Defective lysogeny in *Erwinia carotovora*]. Tovkach, F. I. (2002). *Mikrobiologija (Microbiologiia)* 71:359-367.** The electron microscopic study of several *Erwinia carotovora* strains showed that the SOS-induced cells of this pectolytic phytopathogenic bacterium produce particular phage parts (tails, heads, and baseplates) but do not assemble them into fully functional phage particles. *E. carotovora* cells produced several times greater amounts of phage tails in response to induction by mitomycin C than in response to induction by nalidixic acid. The tails were 128-192 nm in length and 13-21 nm in diameter. Phage heads were characterized by four discrete ranges of diameters: 18, 55-59, 66-75, and 92-98 nm. The diameters of phage baseplates varied from 39 to 53 nm, depending on the particular strain. It was shown that cells of the same species may contain several different types of phage tails and heads. The structural organization of phage tails and baseplates in the nalidixic acid-induced lysate of *E. carotovora* J2 was studied in more detail. The data obtained suggest that pectolytic phytopathogenic erwinia are characterized by defective polylysogeny

22. ***Lactococcus lactis* DPC5598, a plasmid-free derivative of a commercial starter, provides a valuable alternative host for culture improvement studies. Trotter, M., Ross, R. P., Fitzgerald, G. F., Coffey, A. (2002). *Journal of Applied Microbiology* 93:134-143.** AIMS: To generate a plasmid-free derivative of an extensively used industrial starter strain *Lactococcus lactis* DPC4268, which could be used as a backbone strain for starter improvement programmes. METHODS AND RESULTS: DPC4268 containing four large plasmids was subjected to high temperature plasmid curing resulting in derivatives, each with a different plasmid complement of one, two or three different plasmids in addition to a plasmid-free derivative. Industrially relevant phenotypes were assigned to each plasmid on the basis of detailed phenotypic and genetic analyses and these were (a) proteinase activity (Prt, 60 kb) (b) lactose fermentation (Lac, 55 kb) (c) bacteriophage adsorption inhibition (Ads, 44 kb) and (d) type I restriction/modification (R/M, 40 kb). The plasmid-free variant of DPC4268 was shown to be transformable at frequencies comparable to the common laboratory strain L. lactis MG1614. Furthermore its genome was demonstrated to be significantly different from the laboratory strains *L. lactis* MG1614 and the recently sequenced *L. lactis* IL1403 genomes by pulsed-field gel electrophoresis. CONCLUSIONS: This study produced an easily transformable plasmid-free derivative which was genomically different from both MG1614 and IL1403. In addition, important plasmid-borne industrial traits, including two phage-resistance mechanisms, were identified in DPC4268. SIGNIFICANCE AND IMPACT OF THE STUDY: L. DPC4268 is a vitally important commercial strain used in the manufacture of Cheddar cheese. The generation of a plasmid-free derivative may provide an important backbone strain as a basis for future strain improvement purposes

23. **In vivo generation of hybrids between different species of RNA phages. van Meerten, D., Groeneveld, H., Miller, D. M. J., Marechal, G. B., Tsareva, N. V., Olsthoorn, R. C. L., de la Pena, M., van Duin, J. (2002). *Journal of General Virology* 83:1223-1235.** Hybrids between different species or genera of the single-stranded RNA coliphages have not been found in nature. Here, it has been shown that viable hybrids between different phage species can easily be generated in the laboratory by in vivo recombination. cDNA of species I phage MS2 located on a plasmid and lacking part of its 5' untranslated leader (5' UTR) was complemented with another plasmid carrying the 5' half of the genome of fr, a species I phage, or of KU1, a species II representative with low sequence similarity. When the two plasmids were present in the same cell there was spontaneous production of hybrid phages. Interestingly, these hybrids did not arise by a double or single crossover that would replace the missing MS2 sequences with those of fr or KU1. Rather, hybrids arose by attaching the complete 5' UTR of fr or KU1 to the 5' terminus of the defective MS2 phage. Several elements of the 5' UTR then occurred twice, one from KU1 (or fr) and the other from MS2. These redundant elements are in most cases deleted upon evolution of the hybrids. As a result, the 5' UTR of KU1 (or fr) then replaced that of MS2. It was earlier shown that this 5' UTR could assume two alternating structures that facilitated transient translation of the proximal maturation gene. Apparently, this timer function of the 5' UTR was exchangeable and could function independently of the rest of the genome. When hybrids were competed against wild-type, they were quickly outgrown, probably explaining their absence from natural isolates

24. **Functional analysis of heterologous holin proteins in a lDS genetic background. Vukov, N., Scherer, S., Hibbert, E., Loessner, M. J. (2000). *FEMS Microbiology Letters* 184:179-186.** Holins are small hydrophobic proteins causing non-specific membrane lesions at the end of bacteriophage multiplication, to promote access of the murein hydrolase to their substrate. We have established a lDS genetic system, which enables functional expression of holins from various phages in an isogenic phage l background, and allows qualitative evaluation of their ability to support lysis of *Escherichia coli* cells. Synthesis of Holins is under control of native l transcription and translation initiation signals, and the temperature-sensitive CIts857 repressor. A number of different holins were tested in this study. The opposing action of phage l S105 and S107 holin variants in lysis timing could be confirmed, whereas we found evidence for a functionally non-homologous dual translational start motif in the *Listeria* phage Hol500 holin, i.e., the Hol500-96 polypeptide starting at Met-1 revealed a more distinct lytic activity as compared

to the shorter product Hol500-93. The largest holin known, HolTW from a *Staphylococcus aureus* phage, revealed an early lysis phenotype in the lDSthf background, which conferred a plaque forming defect due to premature lysis. Mutant analysis revealed that an altered C-terminus and/or a V52L substitution were sufficient to delay lysis and enable plaque formation. These results suggest that the extensively charged HolTW C-terminus may be important in regulation of lysis timing. The gene 17.5 product of *E. coli* phage T7 was found to support sudden, saltatory cell lysis in the lDSthf background, which clearly confirms its holin character. In conclusion, lDSthf offers a useful genetic tool for studying the structure–function relationship of the extremely heterogeneous group of holin protein orthologs.

25. **Human neutrophils and their products induce Shiga toxin production by enterohemorrhagic *Escherichia coli*. Wagner, P. L., Acheson, D. W., Waldor, M. K. (2001). *Infection and Immunity* 69:1934-1937.** The Shiga toxins (Stx) are critical virulence factors for Escherichia coli O157:H7 and other serotypes of enterohemorrhagic E. coli (EHEC). These potent toxins are encoded in the genomes of temperate lambdoid bacteriophages. We recently demonstrated that induction of the resident Stx2-encoding prophage in an O157:H7 clinical isolate is required for toxin production by this strain. Since several factors produced by human cells, including hydrogen peroxide (H_2O_2), are capable of inducing lambdoid prophages, we hypothesized that such molecules might also induce toxin production by EHEC. Here, we studied whether H_2O_2 and also human neutrophils, an important endogenous source of H_2O_2, induced Stx2 expression by an EHEC clinical isolate. Both H_2O_2 and neutrophils were found to augment Stx2 production, raising the possibility that these agents may lead to prophage induction in vivo and thereby contribute to EHEC pathogenesis.

26. **Seasonal variation in lysogeny as depicted by prophage induction in Tampa Bay, Florida. Williamson, S. J., Houchin, L. A., McDaniel, L., Paul, J. H. (2002). *Applied and Environmental Microbiology* 68:4307-4314.** A seasonal study of the distribution of lysogenic bacteria in Tampa Bay, Florida, was conducted over a 13-month period. Biweekly water samples were collected and either were left unaltered or had the viral population reduced by filtration (pore size, 0.2 micro m) and resuspension in filtered (pore size, 0.2 micro m) water. Virus-reduced and unaltered samples were then treated by adding mitomycin C (0.5 micro g ml^{-1}) to induce prophage or were left untreated. In order to test the hypothesis that prophage induction was phosphate limited, additional induction experiments were performed in the presence and absence of phosphate. Induction was assessed as an increase in viral direct counts, relative to those obtained in controls, as detected by epifluorescence microscopy. Induction of prophage was observed in 5 of 25 (20%) unaltered samples which were obtained during or after the month of February, paralleling the results from a previous seasonal study. Induction of prophage was observed in 9 of 25 (36%) of the virus-reduced samples, primarily those obtained in the winter months, which was not observed in a prior seasonal study (P. K. Cochran and J. H. Paul, Appl. Environ. Microbiol. 64:2308-2312, 1998). Induction was noted in the months of lowest bacterial and primary production, suggesting that lysogeny was favored under conditions of poor host growth. Phosphate addition enabled prophage induction in two of nine (22%) experiments. These results indicate that prophage induction may occasionally be phosphate limited or respond to increases in phosphate concentration, suggesting that phosphate concentration may modulate the lysogenic response of natural populations

27. **Phylogenetic diversity of marine cyanophage isolates and natural virus communities as revealed by sequences of viral capsid assembly protein gene g20. Zhong, Y., Chen, F., Wilhelm, S. W., Poorvin, L., Hodson, R. E. (2002). *Applied and Environmental Microbiology* 68:1576-1584.** In order to characterize the genetic diversity and phylogenetic affiliations of marine cyanophage isolates and natural cyanophage assemblages, oligonucleotide primers CPS1 and CPS8 were designed to specifically amplify ca. 592-bp fragments of the gene for viral capsid assembly protein g20. Phylogenetic analysis of isolated cyanophages revealed that the marine cyanophages were highly diverse yet more closely related to each other than to enteric coliphage T4. Genetically related marine cyanophage isolates were widely distributed without significant geographic segregation (i.e., no correlation between genetic variation and geographic distance). Cloning and sequencing analysis of six natural virus concentrates from estuarine and oligotrophic offshore environments revealed nine phylogenetic groups in a total of 114 different g20 homologs, with up to six clusters and 29 genotypes encountered in a single sample. The composition and structure of natural cyanophage communities in the estuary and open-ocean samples were different from each other, with unique phylogenetic clusters found for each environment. Changes in clonal diversity were also observed from the surface waters to the deep chlorophyll maximum layer in the open ocean. Only three clusters contained known cyanophage isolates, while the identities of the other six clusters remain unknown. Whether or not these unidentified groups are composed of bacteriophages that infect different Synechococcus groups or other closely related cyanobacteria remains to be determined. The high genetic diversity of marine cyanophage assemblages revealed by the g20 sequences suggests that marine viruses can potentially play important roles in regulating microbial genetic diversity

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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.