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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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April 1, 2003 issue (volume 16)

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Editorial

The Félix d'Hérelle Phage Center Changes Hands

by Hans-Wolfgang Ackermann

The "Félix d'Hérelle Reference Center for Bacterial Viruses" was founded in 1982 by Dr. Hans-W. Ackermann, M.D., as a repository for type viruses of bacteriophage species (1). It was initially funded by grants of the National Research Council for Science and Engineering (NSERC) of Canada. Since 1995, after a funding crisis in Canadian Science, the Center has to rely on fees to cover its costs.

The Félix d'Hérelle Center is an instrument of the ICTV (International Committee on Taxonomy of Viruses). It collects and preserves type viruses of phage species and phages with interesting applications (typing, teaching, industrial) or properties (e.g., capsule-specificity or large DNA size). The collection contains about 430 bacteriophages and as many bacterial hosts belonging to over 50 genera. It is the largest phage collection in the world. Most phages are for acinetobacters, enterobacteria, bacilli, pseudomonads, rhizobia, and vibrios.

The Center seeks out interesting phages in the literature and requests deposits from the original investigators. Phages are examined in the electron microscope and depositors receive a complimentary micrograph. Phages are preserved (i) as lysates at +4°C and (ii) in 50% glycerol at -80°C and in liquid nitrogen. Host bacteria are preserved in 15% glycerol at -80° C and in liquid nitrogen. Phages are available without restrictions to any scientist. The Center has a collection of approximately 6000 books or articles, provides expertises, and accepts visitors for training.

Dr. Ackermann retired about two years ago. The new curator is Dr. Sylvain Moineau, Ph.D., of Science Faculty. He is a specialist of phages of lactic acid bacteria. Dr. Ackermann is staying on for advice and electron microscopy.

The Center, located for a long time at the Medical Faculty of Laval University, was recently moved to Science Faculty. Its new address is the Department of Biochemisty and Microbiology, Faculty of Science, Laval University, Quebec, Qc, Canada G1K 7P4, tel. (418) 656-2131, ext. 3112; fax (418) 656-2861 (collection.phages@bcm.ulaval.ca). Dr. Ackermann can be contacted at (ackermann@mcb.ulaval.ca).

1. Ackermann, H.-W., Martin, M., Vieu, J.-F., Nicolle, P. Félix d'Hérelle: his life and work and the foundation of a bacteriophage reference center. ASM News, 48, 346-348, 1982.

Editorial Archive

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

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.

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New BEG Members

Please welcome our newest members

name (home page links)	status	e-mail	address
Nadezda (Milos) Ilic	PI	nenadilic @ozemail.com.au	Sidney Water, Sidney, Australia
	interests:	New developments within Bacteriophage testing involving the detection, isolation and identification of Bacteriophages in water as indicators of water pollution, assessment of the water treatment processes and indirect indicators of the presence of enteric viruses. (contents | BEG members | top of page)	

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.

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Meetings

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.

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.

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Submissions

Sorry, no submission(s) this quarter.

Submissions Archive

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.

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Phage Images

Phage Image Archive

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

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!

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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. Elevated abundance of bacteriophage infecting bacteria in soil. Ashelford, K. E., Day, M. J., Fry, J. C. (2003). *Applied and Environmental Microbiology* 69:285-289. [PRESS FOR ABSTRACT]

2. Bacteriophage isolation from human saliva. Bachrach, G., Leizerovici-Zigmond, M., Zlotkin, A., Naor, R., Steinberg, D. (2003). *Letters in Applied Microbiology* 36:50-53. [PRESS FOR ABSTRACT]

3. Early lysis of *Lactobacillus helveticus* CNRZ 303 in Swiss cheese is not prophage-related. Deutsch, S. M., Neveu, A., Guezenec, S., Ritzenthaler, P., Lortal, S. (2003). *International Journal of Food Microbiology* 81:147-157. [PRESS FOR ABSTRACT]

4. Levels of male-specific RNA bacteriophage and *Escherichia coli* in molluscan bivalve shellfish from commercial harvesting areas. Dore, W. J., Mackie, M., Lees, D. N. (2003). *Letters in Applied Microbiology* 36:92-96. [PRESS FOR ABSTRACT]

5. Male-specific coliphages as an additional fecal contamination indicator for screening fresh carrots. Endley, S., Lu, L., Vega, E., Hume, M. E., Pillai, S. D. (2003). *Journal of Food Protection* 66:88-93. [PRESS FOR ABSTRACT]

6. Bacteriophages of *Erwinia amylovora*. Gill, J. J., Svircev, A. M., Smith, R., Castle, A. J. (2003). *Applied and Environmental Microbiology* 69:2133-2138. [PRESS FOR ABSTRACT]

7. [Bacteriophage therapy: Stalin's forgotten medicine]. Kaulen, H. (2003). *Dtsch Med Wochenschr* 128:307. [no abstract]

8. Experimental protection of mice against lethal *Staphylococcus aureus* infection by novel bacteriophage phi MR11. Matsuzaki, S., Yasuda, M., Nishikawa, H., Kuroda, M., Ujihara, T., Shuin, T., Shen, Y., Jin, Z., Fujimoto, S., Nasimuzzaman, M. D., Wakiguchi, H., Sugihara, S., Sugiura, T., Koda, S., Muraoka, A., Imai, S. (2003). *J Infect Dis* 187:613-624. [PRESS FOR ABSTRACT]

9. Coevolution of bacteriophage PP01 and *Escherichia coli* O157:H7 in continuous culture. Mizoguchi, K., Morita, M., Fischer, C. R., Yoichi, M., Tanji, Y., Unno, H. (2003). *Applied and Environmental Microbiology* 69:170-176. [PRESS FOR ABSTRACT]

10. Microbial contamination of two urban sandstone aquifers in the UK. Powell, K. L., Taylor, R. G., Cronin, A. A., Barrett, M. H.,

Pedley, S., Sellwood, J., Trowsdale, S. A., Lerner, D. N. (2003). *Water Research* 37:339-352. [PRESS FOR ABSTRACT]

11. Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of *Xylella fastidiosa*. Van Sluys, M. A., de Oliveira, M. C., Monteiro-Vitorello, C. B., Miyaki, C. Y., Furlan, L. R., Camargo, L. E. A., da Silva, A. C. R., Moon, D. H., Takita, M. A., Lemos, E. G. M., Machado, M. A., Ferro, M. I. T., da Silva, F. R., Goldman, M. H. S., Goldman, G. H., Lemos, M. V. F., El Dorry, H., Tsai, S. M., Carrer, H., Carraro, D. M., de Oliveira, R. C., Nunes, L. R., Siqueira, W. J., Coutinho, L. L., Kimura, E. T., Ferro, E. S., Harakava, R., Kuramae, E. E., Marino, C. L., Giglioti, E., Abreu, I. L., Alves, L. M. C., do Amaral, A. M., Baia, G. S., Blanco, S. R., Brito, M. S., Cannavan, F. S., Celestino, A. V., da Cunha, A. F., Fenille, R. C., Ferro, J. A., Formighieri, E. F., Kishi, L. T., Leoni, S. G., Oliveira, A. R., Rosa, V. E. J., Sassaki, F. T., Sena, J. A. D., de Souza, A. A., Truffi, D., Tsukumo, F., Yanai, G. M., Zaros, L. G., Civerolo, E. L., Simpson, A. J. G., Almeida, N. F. J., Setubal, J. C., Kitajima, J. P. (2003). *Journal of Bacteriology* 185:1018-1026. [PRESS FOR ABSTRACT]

12. A new phage may help control pathogens on fresh-cut produce. (2002). *Journal of environmental health* 64:59. [no abstract]

13. Treatment of post-burns bacterial infections by bacteriophages, specifically ubiquitous *Pseudomonas* spp. notoriously resistant to antibiotics. Ahmad, S. I. (2002). *Medical Hypotheses* 58:327-331. [PRESS FOR ABSTRACT]

14. Particle transport in a karst aquifer: natural and artificial tracer experiments with bacteria, bacteriophages and microspheres. Auckenthaler, A., Raso, G., Huggenberger, P. (2002). *Water Science and Technology* 46:131-138. [PRESS FOR ABSTRACT]

15. The fundamental contribution of phages to GAS evolution, genome diversification and strain emergence. Banks, D. J., Beres, S. B., Musser, J. M. (2002). *Trends in Microbiology* 10:515-521. [PRESS FOR ABSTRACT]

16. Characterization of six *Leuconostoc fallax* bacteriophages isolated from an industrial sauerkraut fermentation. Barrangou, R., Yoon, S. S., Breidt, F. Jr, Fleming, P., Klaenhammer, T. R. (2002). *Applied and Environmental Microbiology* 68:5452-5458. [PRESS FOR ABSTRACT]

17. Trade-offs and coexistence in microbial microcosms. Bohannan, B. J. M., Kerr, B., Jessup, C. M., Hughes, J. B., Sandvik, G. (2002). *Antonie van Leeuwenhoek* 81:107-115. [PRESS FOR ABSTRACT]

18. Fate of bacterial indicators, viruses and protozoan parasites in a wastewater multi-component treatment system. Bonadonna, L., Briancesco, R., Cataldo, C., Divizia, M., Donia, D., Pana, A. (2002). *the New Microbiologica* 25:413-420. [PRESS FOR ABSTRACT]

19. Common themes among bacteriophage-encoded virulence factors and diversity among the bacteriophages involved. Boyd, E. F., Brussow, H. (2002). *Trends in Microbiology* 10:521-529. [PRESS FOR ABSTRACT]

20. Performance of a novel Viresolve NFR virus filter. Brough, H., Antoniou, C., Carter, J., Jakubik, J., Xu, Y., Lutz, H. (2002). *Biotechnology Progress* 18:782-795. [PRESS FOR ABSTRACT]

21. The role of parasites in sympatric and allopatric host diversification. Buckling, A., Rainey, P. B. (2002). *Nature (London)* 420:496-499. [PRESS FOR ABSTRACT]

22. Antagonistic coevolution between a bacterium and a bacteriophage. Buckling, A., Rainey, P. B. (2002). *Proceedings of the Royal Society of London Series B Biological sciences* 269:931-936. [PRESS FOR ABSTRACT]

23. Dynamics of success and failure in phage and antibiotic therapy in experimental infections. Bull, J. J., Levin, B. R., DeRouin, T., Walker, N., Bloch, C. A. (2002). *BMC microbiology [electronic resource]* 2:35. [PRESS FOR ABSTRACT]

24. [Phenogenetic characterization of a group of giant Phi KZ-like bacteriophages of Pseudomonas aeruginosa]. Burkal'tseva, M. V., Krylov, V. N., Pleteneva, E. A., Shaburova, O. V., Krylov, S. V., Volkart, G., Sykilinda, N. N., Kurochkina, L. P., Mesianzhinov, V. V. (2002). *Genetika* 38:1470-1479. [PRESS FOR ABSTRACT]

25. Phenogenetic characterization of a group of giant fKZ-like bacteriophages of *Pseudomonas aeruginosa*. Burkal'tseva, M. V., Krylov, V. N., Pleteneva, E. A., Shaburova, O. V., Krylov, S. V., Volkart, G., Sykilinda, N. N., Kurochkina, L. P., Mesyanzhinov, V. V. (2002). *Russian Journal of Genetics* 38:1242-1250. [PRESS FOR ABSTRACT]

26. Genome plasticity in *Lactococcus lactis*. Campo, N., Dias, M. J., Daveran-Mingot, M. L., Ritzenthaler, P., Le Bourgeois, P. (2002). *Antonie van Leeuwenhoek* 82:123-132. [PRESS FOR ABSTRACT]

27. Genome analysis of an inducible prophage and prophage remnants integrated in the *Streptococcus pyogenes* strain SF370. Canchaya, C., Desiere, F., McShan, W. M., Ferretti, J. J., Parkhill, J., Brussow, H. (2002). *Virology* 302:245-258. [PRESS FOR ABSTRACT]

28. Phage therapy of local and systemic disease caused by *Vibrio vulnificus* in iron-dextran-treated mice. Cerveny, K. E., Depaola, A., Duckworth, D. H., Gulig, P. A. (2002). *Infection and Immunity* 70:6251-6262. [PRESS FOR ABSTRACT]

29. Isolation and genetic characterization of a novel filamentous bacteriophage, a deleted form of phage f237, from a pandemic *Vibrio parahaemolyticus* O4:K68 strain. Chan, B., Miyamoto, H., Taniguchi, H., Yoshida, S. I. (2002). *Microbiology and Immunology* 46:565-569. [PRESS FOR ABSTRACT]

30. Bacteriophage-resistance systems in dairy starter strains: molecular analysis to application. Coffey, A., Ross, R. P. (2002). *Antonie van Leeuwenhoek* 82:303-321. [PRESS FOR ABSTRACT]

31. Occurrence and levels of indicator bacteriophages in bathing waters throughout Europe. Contreras-Coll, N., Lucena, F., Mooijman, K., Havelaar, A., Pierz, V., Boque, M., Gawler, A., Holler, C., Lambiri, M., Mirolo, G., Moreno, B., Niemi, M., Sommer, R., Valentin, B., Wiedenmann, A., Young, V., Jofre, J. (2002). *Water Research* 36:4963-4974. [PRESS FOR ABSTRACT]

32. Comparative genomics of phages and prophages in lactic acid bacteria. Desiere, F., Lucchini, S., Canchaya, C., Ventura, M., Brussow, H. (2002). *Antonie van Leeuwenhoek* 82:73-91. [PRESS FOR ABSTRACT]

33. Time-delayed spread of viruses in growing plaques. Fort, J., Mendez, V. (2002). *Physical Review Letters* 89:178101. [PRESS FOR ABSTRACT]

34. *Bacteroides fragilis* and *Escherichia coli* bacteriophages in human faeces. Gantzer, C., Henny, J., Schwartzbrod, L. (2002). *International Journal of Hygiene and Environmental Health* 205:325-328. [PRESS FOR ABSTRACT]

35. Conserved filamentous prophage in *Escherichia coli* O18:K1:H7 and *Yersinia pestis* biovar orientalis. Gonzalez, M. D., Lichtensteiger, C. A., Caughlan, R., Vimr, E. R. (2002). *Journal of Bacteriology* 184:6050-6055. [PRESS FOR ABSTRACT]

36. [Action of *Spirulina platensis* on bacterial viruses]. Gorobets, O. B., Blinkova, L. P., Baturo, A. P. (2002). *Zh. Mikrobiol. Epidemiol. Immunobiol.* 18-21. [PRESS FOR ABSTRACT]

37. Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7. Hahn, M. W., Rausher, M. D., Cunningham, C. W. (2002). *Genetics* 161:11-20. [PRESS FOR ABSTRACT]

38. Effects of temperatures, pH-values, ultra-violet light, ethanol and chloroform on the growth of isolated thermophilic *Bacillus* phages. Hazem, A. (2002). *the New Microbiologica* 25:469-476. [PRESS FOR ABSTRACT]

39. Prevention of *Escherichia coli* respiratory infection in broiler chickens with bacteriophage (SPR02). Huff, W. E., Huff, G. R., Rath, N. C., Balog, J. M., Xie, H., Moore, P. A. J., Donoghue, A. M. (2002). *Poultry science* 81:437-441. [PRESS FOR ABSTRACT]

40. Prevention of *Escherichia coli* infection in broiler chickens with a bacteriophage aerosol spray. Huff, W. E., Huff, G. R., Rath, N. C., Balog, J. M., Donoghue, A. M. (2002). *Poultry science* 81:1486-1491. [PRESS FOR ABSTRACT]

41. Characterization of serracin P, a phage-tail-like bacteriocin, and its activity against *Erwinia amylovora*, the fire blight pathogen. Jabrane, A., Sabri, A., Compere, P., Jacques, P., Vandenberghe, I., Van Beeumen, J., Thonart, P. (2002). *Applied and Environmental Microbiology* 68:5704-5710. [PRESS FOR ABSTRACT]

42. Viral Trojan horse for combating tuberculosis. Johnston, N. (2002). *Drug discovery today* 7:333-335. [PRESS FOR ABSTRACT]

43. *Vibrio cholerae* phage K139: complete genome sequence and comparative genomics of related phages. Kapfhammer, D., Blass, J., Evers, S., Reidl, J. (2002). *Journal of Bacteriology* 184:6592-6601. [PRESS FOR ABSTRACT]

44. [Effect of bacteriophage on the lipid peroxidation process and antioxidant protective enzymes in experimental uveitis]. Karimova, M. Kh, Bakhritdinova, F. A. (2002). *Vestn Oftalmol* 118:38-40. [PRESS FOR ABSTRACT]

45. Deleterious impact of a virulent bacteriophage on survival and biocontrol activity of *Pseudomonas fluorescens* strain CHAO in natural soil. Keel, C., Ucurum, Z., Michaux, P., Adrian, M., Haas, D. (2002). *Molecular plant-microbe interactions : MPMI* 15:567-576. [PRESS FOR ABSTRACT]

46. Bacteriophage-host interaction in the enhanced biological phosphate removing activated sludge system. Khan, M. A., Satoh, H., Mino, T., Katayama, H., Kurisu, F., Matsuo, T. (2002). *Water Science and Technology* 46:39-43. [PRESS FOR ABSTRACT]

47. Bacteriophages isolated from activated sludge processes and their polyvalency. Khan, M. A., Satoh, H., Katayama, H., Kurisu, F., Mino, T. (2002). *Water Research* 36:3364-3370. [PRESS FOR ABSTRACT]

48. Preventing phage lysis of *Lactococcus lactis* in cheese production using a neutralizing heavy-chain antibody fragment from llama. Ledeboer, A. M., Bezemer, S., de Hiaard, J. J. W., Schaffers, I. M., Verrips, C. T., van Vliet, C., Dusterhoft, E. M., Zoon, P., Moineau, S., Frenken, L. G. J. (2002). *J Dairy Sci* 85:1376-1382. [PRESS FOR ABSTRACT]

49. Influence of flow rate on transport of bacteriophage in shale saprolite. McKay, L. D., Harton, A. D., Wilson, G. V. (2002). *Journal of Environmental Quality* 31:1095-1105. [PRESS FOR ABSTRACT]

50. Application of actinomycetes to soil to ameliorate water repellency. McKenna, F., El Tarabily, K. A., Petrie, S., Chen, C., Dell, B. (2002). *Letters in Applied Microbiology* 35:107-112. [PRESS FOR ABSTRACT]

51. Conservation of phage reference materials and water samples containing bacteriophages of enteric bacteria. Mendez, J., Jofre, J., Lucena, F., Contreras, N., Mooijman, K., Araujo, R. (2002). *Journal of Virological Methods* 106:215-224. [PRESS FOR ABSTRACT]

52. Evaluation of bacteriophages during the treatment of sludge. Mignotte-Cadiergues, B., Gantzer, C., Schwartzbrod, L. (2002). *Water Science and Technology* 46:189-194. [PRESS FOR ABSTRACT]

53. Microbial genome evolution: sources of variability. Mira, A., Klasson, L., Andersson, S. G. E. (2002). *Current Opinion in Microbiology* 5:506-512. [PRESS FOR ABSTRACT]

54. Characterization of a virulent bacteriophage specific for *Escherichia coli* O157:H7 and analysis of its cellular receptor and two tail fiber genes. Morita, M., Tanji, Y., Mizoguchi, K., Akitsu, T., Kijima, N., Unno, H. (2002). *FEMS Microbiol Lett* 211:77-83. [PRESS FOR ABSTRACT]

55. Contribution of microbial activity to virus reduction in saturated soil. Nasser, A. M., Glozman, R., Nitzan, Y. (2002). *Water Research* 36:2589-2595. [PRESS FOR ABSTRACT]

56. The dilemma of phage taxonomy illustrated by comparative genomics of Sfi21-like Siphoviridae in lactic acid bacteria. Proux, C., van Sinderen, D., Suarez, J., Garcia, P., Ladero, V., Fitzgerald, G. F., Desiere, F., Brussow, H. (2002). *Journal of Bacteriology* 184:6026-6036. [PRESS FOR ABSTRACT]

57. The dual role of wild phages for horizontal gene transfer among *Salmonella* strains. Rabsch, W., Mirold, S., Hardt, W. D., Tschape, H. (2002). *Berliner und Munchener tierarztliche Wochenschrift* 115:355-359. [PRESS FOR ABSTRACT]

58. Remarkable morphological diversity of viruses and virus-like particles in hot terrestrial environments. Rachel, R., Bettstetter, M., Hedlund, B. P., Haring, M., Kessler, A., Stetter, K. O., Prangishvili, D. (2002). *Archives of Virology* 147:2419-2429. [PRESS FOR ABSTRACT]

59. Column experiments to study nonlinear removal of bacteriophages by passage through saturated dune sand. Schijven, J. F., Hassanizadeh, S. M., de Bruin, H. A. M. (2002). *J. Contam. Hydrol* 58:243-259. [PRESS FOR ABSTRACT]

60. Two-site kinetic modeling of bacteriophages transport through columns of saturated dune sand. Schijven, J. F., Hassanizadeh, S. M., de Bruin, R. H. A. M. (2002). *Journal of contaminant hydrology* 57:259-279. [PRESS FOR ABSTRACT]

61. Improved method for recovery of bacteriophage from large volumes of water using negatively charged microporous filters. Scott, T. M., Lukasik, J., Farrah, S. R. (2002). *Canadian Journal of Microbiology* 48:305-310. [PRESS FOR ABSTRACT]

62. E.coli cell-cycle regulation by bacteriophage lambda. Sergueev, K., Court, D., Reaves, L., Austin, S. (2002). *Journal of Molecular Biology* 324:297-307. [PRESS FOR ABSTRACT]

63. Fates of bacteriophages and bacterial indicators in the Moselle river (France). Skraber, S., Gantzer, C., Maul, A., Schwartzbrod, L. (2002). *Water Research* 36:3629-3637. [PRESS FOR ABSTRACT]

64. Bacteriophage therapy. Stalin's forgotten cure. Stone, R. (2002). *Science* 298:728-731. [no abstract]

65. Bacteriophage therapy. Food and agriculture: testing grounds for phage therapy. Stone, R. (2002). *Science* 298:730. [no abstract]

66. Thermophilic lactic acid bacteria phages isolated from Argentinian dairy industries. Suarez, V. B., Quiberoni, A., Binetti, A. G., Reinheimer, J. A. (2002). *Journal of Food Protection* 65:1597-1604. [PRESS FOR ABSTRACT]

67. Emerging foodborne pathogens. Tauxe, R. V. (2002). *International Journal of Food Microbiology* 78:31-41. [PRESS FOR ABSTRACT]

68. New ways to treat bacterial infections. Taylor, P. W., Stapleton, P. D., Paul L.J. (2002). *Drug discovery today* 7:1086-1091. [PRESS FOR ABSTRACT]

69. Effect of phage therapy on the turnover and function of peripheral neutrophils. Weber-Dabrowska, B., Zimecki, M., Mulczyk, M., Gorski, A. (2002). *FEMS Immunology and Medical Microbiology* 34:135-138. [PRESS FOR ABSTRACT]

70. Modulation of the susceptibility of intestinal bacteria to bacteriophages in response to Ag43 phase variation -- a hypothesis. Wegrzyn, G., Thomas, M. S. (2002). *Medical Science Monitor* 8:HY15-HY18. [PRESS FOR ABSTRACT]

71. Bacteriophage HP2 of *Haemophilus influenzae*. Williams, B. J., Golomb, M., Phillips, T., Brownlee, J., Olson, M. V., Smith, A. L. (2002). *Journal of Bacteriology* 184:6893-6905. [PRESS FOR ABSTRACT]

72. Phage mediated horizontal transfer of the sopE1 gene increases enteropathogenicity of *Salmonella enterica* serotype Typhimurium for calves. Zhang, S., Santos, R. L., Tsolis, R. M., Mirold, S., Hardt, W. D., Adams, L. G., Baumler, A. J. (2002). *FEMS Microbiol Lett* 217:243-247. [PRESS FOR ABSTRACT]

73. Mutant bacteriophage with non-catalytic endosialidase binds to both bacterial and eukaryotic polysialic acid and can be used as probe for its detection. Aalto, J., Pelkonen, S., Kalimo, H., Finne, J. (2001). *Glycoconjugate Journal* 18:751-758. [PRESS FOR ABSTRACT]

74. Expression and immunogenicity of a liver stage malaria epitope presented as a foreign peptide on the surface of RNA-free MS2 bacteriophage capsids. Heal, K. G., Hill, H. R., Stockley, P. G., Hollingdale, M. R., Taylor-Robinson, A. W. (1999). *Vaccine* 18:251-258. [PRESS FOR ABSTRACT]

75. Generalized transduction of small *Yersinia enterocolitica* plasmids. Hertwig, S., Popp, A., Freytag, B., Lurz, R., Appel, B. (1999). *Applied and Environmental Microbiology* 65:3862-3866. [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. **Elevated abundance of bacteriophage infecting bacteria in soil. Ashelford, K. E., Day, M. J., Fry, J. C. (2003). *Applied and Environmental Microbiology* 69:285-289.** Here we report the first direct counts of soil bacteriophage and show that substantial populations of these viruses exist in soil (grand mean = 1.5 x 10^7 g^{-1}), at least 350-fold more than the highest

numbers estimated from traditional viable plaque counts. Adding pure cultures of a *Serratia* phage to soil showed that the direct counting methods with electron microscopy developed here underestimated the added phage populations by at least eightfold. So, assuming natural phages were similarly underestimated, virus numbers in soil averaged 1.5 x 10^8 g^{-1}, which is equivalent to 4% of the total population of bacteria. This high abundance was to some extent confirmed by hybridizing colonies grown on *Serratia* and *Pseudomonas* selective media with cocktails of phage infecting these bacteria. This showed that 8.9 and 3.9%, respectively, hybridized with colonies from the two media and confirmed the presence of phage DNA sequences in the cultivable fraction of the natural population. Thus, soil phage, like their aquatic counterparts, are likely to be important in controlling bacterial populations and mediating gene transfer in soil

2. **Bacteriophage isolation from human saliva. Bachrach, G., Leizerovici-Zigmond, M., Zlotkin, A., Naor, R., Steinberg, D. (2003). *Letters in Applied Microbiology* 36:50-53.** AIMS: To detect bacteriophages for Gram-positive oral pathogens in human saliva. METHODS AND RESULTS: Saliva samples from 31 donors were screened for the presence of bacteriophages for *Streptococcus sobrinus*, *Streptococcus mutans*, *Streptococcus salivarius*, *Actinomyces viscosus* and *Enterococcus faecalis*. Bacteriophages for *Enterococcus faecalis* were found in seven samples. *Enterococcus faecalis* phages were still present in saliva re-collected from one donor one month, and one year after initial saliva collection. CONCLUSIONS: The presence and stability of the *Enterococcus faecalis* bacteriophages in human saliva suggests a possible role of these bacteriophages in the oral ecosystem. SIGNIFICANCE AND IMPACT OF THE STUDY: Phage therapy as a way to control oral bacteria might be considered

3. **Early lysis of *Lactobacillus helveticus* CNRZ 303 in Swiss cheese is not prophage-related. Deutsch, S. M., Neveu, A., Guezenec, S., Ritzenthaler, P., Lortal, S. (2003). *International Journal of Food Microbiology* 81:147-157.** *Lactobacillus helveticus* is mainly used as starter in Swiss-type cheeses. Often, lysogenic strains are eliminated because of the risk of early lysis and acidification failure due to phage expression. On the other hand, *L. helveticus* lysis was shown to positively influence cheese proteolysis during ripening. In order to better assess the relationship between lysis and lysogeny, a prophage-cured derivative of *L. helveticus* CNRZ 303 was isolated (LH 303-G11) and relysogenised (LH 303-G11R), as demonstrated by hybridisation using the whole phage DNA as probe. The growth, lysis in buffered solutions and lytic activities in zymogram using either *Micrococcus luteus* or *L. helveticus* as substrate were identical between the mother strain and its cured derivatives. Only morphological differences were observed by scanning electron microscopy: the cells of the cured derivative were shorter in length. The mother strain and its cured and relysogenised derivatives were assayed in triplicate in experimental Swiss cheeses (scale 1:100). No differences were noted during the cheese making: the three strains exhibited identical kinetics of acidification, leading to similar cheeses at day 1 in terms of gross composition and pH. Phages were detected only in the cheeses made with the mother strain and the relysogenised derivative. The lysis of *L. helveticus*, estimated by viability decrease and release of the intracellular marker D-lactate deshydrogenase, started early before brining and continued during the cold room ripening. No obvious differences of lysis extent were observed. These results demonstrated for the first time that, in the case of LH 303, the extensive lysis observed in cheese is mainly due to autolysin activity and not to prophage induction

4. **Levels of male-specific RNA bacteriophage and *Escherichia coli* in molluscan bivalve shellfish from commercial harvesting areas. Dore, W. J., Mackie, M., Lees, D. N. (2003). *Letters in Applied Microbiology* 36:92-96.** AIMS: Current measures for controlling the public health risks associated with bivalve molluscan shellfish consumption rely on the use of *Escherichia coli* to indicate the sanitary quality of shellfish harvesting areas. However, it has been demonstrated that *E. coli* is an inadequate indicator of the viral risk associated with shellfish. An alternative indicator organism, male-specific RNA (FRNA) bacteriophage has been proposed for this role. This study compared the distribution of *E. coli* and FRNA bacteriophage in shellfish harvesting areas. METHODS AND RESULTS: A total of 608 shellfish samples from 49 shellfish harvesting areas were analysed for *E. coli* and FRNA bacteriophage using standard published methods. The geometric mean concentration of FRNA bacteriophage in all samples was over three times greater than that of *E. coli* (1800 and 538 counts/100 g for FRNA bacteriophage and *E. coli*, respectively). In contrast to *E. coli*, FRNA bacteriophage concentrations were strongly influenced by season with a geometric mean count of 4503 PFU/100 g in the winter (October-March) compared with 910 PFU/100 g in the summer (April-September). CONCLUSIONS: FRNA bacteriophage were present in shellfish at higher concentrations than *E. coli*. Elevated levels of FRNA bacteriophage observed in the winter concur with the known increased viral risk associated with shellfish harvested at that time of year in the UK. Levels of FRNA bacteriophage found in many shellfish from category B harvesting areas would not be eliminated by conventional treatment processes. SIGNIFICANCE AND IMPACT OF THE STUDY: Data from this study will inform future proposals to introduce FRNA bacteriophage as an indicator of the viral risk associated with shellfish

5. **Male-specific coliphages as an additional fecal contamination indicator for screening fresh carrots. Endley, S., Lu, L., Vega, E., Hume, M. E., Pillai, S. D. (2003). *Journal of Food Protection* 66:88-93.** The objective of this study was to evaluate the efficacy of male-specific (F+) coliphages as a fecal-contamination indicator for fresh carrots. The prevalence of specific pathogens and indicator organisms on the surface of carrots obtained from a farm, truck, and processing shed was studied. Twenty-five carrot samples collected from each of these locations were washed, and aliquots of the wash were analyzed for the presence of F+ coliphages, *Escherichia coli*, *Salmonella*, and *Shigella*. Additionally, the *Salmonella* isolates were genotyped using pulsed-field gel electrophoresis (PFGE). Our studies detected the presence of F+ coliphages, *E. coli*, and *Salmonella* on carrots. All samples, however, tested negative for *Shigella*. Although none of the carrot samples from the field were positive for *E. coli*, one sample was positive for *Salmonella*, and another was positive for F+ coliphages. From the truck, two carrot samples (8%) were positive for *Salmonella*, four (16%) were positive for F+ coliphages, and four (16%) were positive for *E. coli*. None of the carrot samples from the processing shed were positive for *Salmonella*. However, 2 carrot samples (8%) were positive for *E. coli*, and 14 carrot samples (56%) were positive for F+ coliphages. The PFGE results suggest that there were three distinct *Salmonella* genotypes among the carrot samples from the truck and that the *Salmonella* isolates identified on carrot samples from the field and truck locations were different. Microbiological screening of fresh produce such as carrots (which can be exposed to fecal contaminants in soils and water) should ensure the detection of both viral and bacterial contaminants. Overall, in this study, F+ coliphages were detected in 25% of the carrot samples, compared to *E. coli* (8%), *Salmonella* (4%), and *Shigella* (0%). The results suggest F+ coliphages can serve as a conservative indicator of fecally associated viruses on carrots. This suggests that in addition to *E. coli* screening, F+ coliphages should be included when produce such as carrots that are vulnerable to fecal contaminants are screened. Since the detection of specific enteric viral pathogens is expensive, screening for viral indicators of fecal contamination using F+ coliphages can be an economical approach to providing an additional level of assurance about the microbiological quality of fresh carrots

6. **Bacteriophages of *Erwinia amylovora*. Gill, J. J., Svircev, A. M., Smith, R., Castle, A. J. (2003). *Applied and***

***Environmental Microbiology* 69:2133-2138.** Fifty bacteriophage isolates of *Erwinia amylovora*, the causalagent of fire blight, were collected from sites in and aroundthe Niagara region of southern Ontario and the Royal BotanicalGardens, Hamilton, Ontario. Forty-two phages survived the isolation,purification, and storage processes. The majority of the phagesin the collection were isolated from the soil surrounding treesexhibiting fire blight symptoms. Only five phages were isolatedfrom infected aerial tissue in pear and apple orchards. To avoidany single-host selection bias, six bacterial host strains wereused in the initial isolation and enrichment processes. Molecularcharacterization of the phages with a combination of PCR andrestriction endonuclease digestions showed that six distinctphage types, described as groups 1 to 6, were recovered. Tenphage isolates were related to the previously characterized*E. amylovora* PEa1, with some divergence of molecular markersbetween phages isolated from different sites. A study of thehost ranges of the phages revealed that certain types were unableto efficiently lyse some *E. amylovora* strains and that someisolates were able to lyse the epiphytic bacterium *Pantoea agglomerans*.Representatives from the six molecular groups were studied byelectron microscopy to determine their morphology. The phagesexhibited distinct morphologies when examined by an electronmicroscope. Group 1 and 2 phages were tailed and contractile,and phages belonging to groups 3 to 6 had short tails or openingswith thin appendages. Based on morphotypes, the bacteriophagesof *E. amylovora* were placed in the order *Caudovirales*, in thefamilies *Myoviridae* and *Podoviridae*.

7. **[Bacteriophage therapy: Stalin's forgotten medicine]. Kaulen, H. (2003). *Dtsch Med Wochenschr* 128:307.**

8. **Experimental protection of mice against lethal *Staphylococcus aureus* infection by novel bacteriophage phi MR11. Matsuzaki, S., Yasuda, M., Nishikawa, H., Kuroda, M., Ujihara, T., Shuin, T., Shen, Y., Jin, Z., Fujimoto, S., Nasimuzzaman, M. D., Wakiguchi, H., Sugihara, S., Sugiura, T., Koda, S., Muraoka, A., Imai, S. (2003). *J Infect Dis* 187:613-624.** The protective effects of bacteriophages were assessed against experimental *Staphylococcus aureus* infection in mice. Of the *S. aureus* phages isolated in the study, phi MR11 was representatively used for all testing, because its host range was the most broad and it carries no genes for known toxins or antibiotic resistance. Intraperitoneal injections (8×10^8 cells) of *S. aureus*, including methicillin-resistant bacteria, caused bacteremia and eventual death in mice. In contrast, subsequent intraperitoneal administration of purified phi MR11 (MOI > or = 0.1) suppressed *S. aureus*-induced lethality. This lifesaving effect coincided with the rapid appearance of phi MR11 in the circulation, which remained at substantial levels until the bacteria were eradicated. Inoculation with high-dose phi MR11 alone produced no adverse effects attributable to the phage. These results uphold the efficacy of phage therapy against pernicious *S. aureus* infections in humans and suggest that phi MR11 may be a potential prototype for gene-modified, advanced therapeutic *S. aureus* phages

9. **Coevolution of bacteriophage PP01 and *Escherichia coli* O157:H7 in continuous culture. Mizoguchi, K., Morita, M., Fischer, C. R., Yoichi, M., Tanji, Y., Unno, H. (2003). *Applied and Environmental Microbiology* 69:170-176.** The interaction between Escherichia coli O157:H7 and its specific bacteriophage PP01 was investigated in chemostat continuous culture. Following the addition of bacteriophage PP01, E. coli O157:H7 cell lysis was observed by over 4 orders of magnitude at a dilution rate of 0.876 h^{-1} and by 3 orders of magnitude at a lower dilution rate (0.327 h^{-1}). However, the appearance of a series of phage-resistant *E. coli* isolates, which showed a low efficiency of plating against bacteriophage PP01, led to an increase in the cell concentration in the culture. The colony shape, outer membrane protein expression, and lipopolysaccharide production of each escape mutant were compared. Cessation of major outer membrane protein OmpC production and alteration of lipopolysaccharide composition enabled *E. coli* O157:H7 to escape PP01 infection. One of the escape mutants of *E. coli* O157:H7 which formed a mucoid colony (Mu) on Luria-Bertani agar appeared 56 h postincubation at a dilution rate of 0.867 h^{-1} and persisted until the end of the experiment (approximately 200 h). Mu mutant cells could coexist with bacteriophage PP01 in batch culture. Concentrations of the Mu cells and bacteriophage PP01 increased together. The appearance of mutant phage, which showed a different host range among the O157:H7 escape mutants than wild-type PP01, was also detected in the chemostat culture. Thus, coevolution of phage and *E. coli* O157:H7 proceeded as a mutual arms race in chemostat continuous culture

10. **Microbial contamination of two urban sandstone aquifers in the UK. Powell, K. L., Taylor, R. G., Cronin, A. A., Barrett, M. H., Pedley, S., Sellwood, J., Trowsdale, S. A., Lerner, D. N. (2003). *Water Research* 37:339-352.** Development of urban groundwater has historically been constrained by concerns about its quality. Rising urban water tables and overabstraction from rural aquifers in the UK have led to a renewed interest in urban groundwater, particularly the possibility of finding water of acceptable quality at depth. This study assessed the microbial quality of groundwater collected from depth-specific intervals over a 15-month period within the Permo-Triassic Sherwood Sandstone aquifers underlying the cities of Nottingham and Birmingham. Sewage-derived bacteria (thermotolerant coliforms, faecal streptococci and sulphite-reducing clostridia) and viruses (enteroviruses, Norwalk-like viruses, coliphage) were regularly detected to depths of 60 m in the unconfined sandstone and to a depth of 91 m in the confined sandstone. Microbial concentrations varied temporally and spatially but increased frequency of contamination with depth coincided with geological heterogeneities such as fissures and mudstone bands. Significantly, detection of Norwalk-like viruses and Coxsackievirus B4 in groundwater corresponded with seasonal variations in virus discharge to the sewer system. The observation of low levels of sewage-derived microbial contaminants at depth in the Triassic Sandstone aquifer is explained by the movement of infinitesimal proportions of bulk (macroscopic) groundwater flow along preferential pathways (e.g., fissures, bedding planes). The existence of very high microbial populations at source (raw sewage) and their extremely low detection limits at the receptor (multilevel piezometer) enable these statistically extreme (microscopic) flows to be traced. Rapid penetration of microbial contaminants into sandstone aquifers, not previously reported, highlights the vulnerability of sandstone aquifers to microbial contamination

11. **Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of *Xylella fastidiosa*. Van Sluys, M. A., de Oliveira, M. C., Monteiro-Vitorello, C. B., Miyaki, C. Y., Furlan, L. R., Camargo, L. E. A., da Silva, A. C. R., Moon, D. H., Takita, M. A., Lemos, E. G. M., Machado, M. A., Ferro, M. I. T., da Silva, F. R., Goldman, M. H. S., Goldman, G. H., Lemos, M. V. F., El Dorry, H., Tsai, S. M., Carrer, H., Carraro, D. M., de Oliveira, R. C., Nunes, L. R., Siqueira, W. J., Coutinho, L. L., Kimura, E. T., Ferro, E. S., Harakava, R., Kuramae, E. E., Marino, C. L., Giglioti, E., Abreu, I. L., Alves, L. M. C., do Amaral, A. M., Baia, G. S., Blanco, S. R., Brito, M. S., Cannavan, F. S., Celestino, A. V., da Cunha, A. F., Fenille, R. C., Ferro, J. A., Formighieri, E. F., Kishi, L. T., Leoni, S. G., Oliveira, A. R., Rosa, V. E. J., Sassaki, F. T., Sena, J. A. D., de Souza, A. A., Truffi, D., Tsukumo, F., Yanai, G. M., Zaros, L. G., Civerolo, E. L., Simpson, A. J. G., Almeida, N. F. J., Setubal, J. C., Kitajima, J. P. (2003). *Journal of Bacteriology* 185:1018-1026.** *Xylella fastidiosa* is a xylem-dwelling, insect-transmitted, gamma-proteobacterium that causes diseases in many plants, including grapevine, citrus, periwinkle, almond, oleander, and coffee. *X. fastidiosa* has an unusually broad host range, has an extensive geographical distribution throughout the American continent, and induces diverse disease phenotypes. Previous molecular analyses indicated three distinct groups of *X. fastidiosa* isolates that were expected to be genetically divergent. Here

we report the genome sequence of *X. fastidiosa* (Temecula strain), isolated from a naturally infected grapevine with Pierce's disease (PD) in a wine-grape-growing region of California. Comparative analyses with a previously sequenced *X. fastidiosa* strain responsible for citrus variegated chlorosis (CVC) revealed that 98% of the PD *X. fastidiosa* Temecula genes are shared with the CVC *X. fastidiosa* strain 9a5c genes. Furthermore, the average amino acid identity of the open reading frames in the strains is 95.7%. Genomic differences are limited to phage-associated chromosomal rearrangements and deletions that also account for the strain-specific genes present in each genome. Genomic islands, one in each genome, were identified, and their presence in other *X. fastidiosa* strains was analyzed. We conclude that these two organisms have identical metabolic functions and are likely to use a common set of genes in plant colonization and pathogenesis, permitting convergence of functional genomic strategies

12. **A new phage may help control pathogens on fresh-cut produce. (2002). *Journal of environmental health* 64:59.**

13. **Treatment of post-burns bacterial infections by bacteriophages, specifically ubiquitous *Pseudomonas* spp. notoriously resistant to antibiotics. Ahmad, S. I. (2002). *Medical Hypotheses* 58:327-331.** Post-burn microbial infections are a major problem in recovering from the trauma of third-degree burns, and the survival of patients can depend upon the severity of the burn and the infections encountered. Within 24 hours, patients can start suffering from opportunistic bacterial attacks, which can vary from simple infection, such as those easily treatable by antibiotics, to more complicated types, which may have natural or acquired resistance to drugs. Infection by multiple drug-resistant bacteria can create additional complexity to the problem. As an alternative to treating bacterial infections by antibiotics, bacteriophages have been in use in certain parts of the world, such as at Tbilisi in Georgia and in Poland, and this approach has now been more widely recognized. Results have shown that phage therapy has an 80% success rate against *Enterococcus* infections and up to 90% against *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Escherichia coli* and *Klebsiella pneumoniae*. Here it is proposed that bacteriophages can effectively be used for the treatment of post-burn infections, particularly the ubiquitous opportunistic pathogens, *Pseudomonas* spp., known to be notoriously resistant to a variety of antibiotics. This kind of treatment may be of particular importance in Third World countries where the incidence of burns and infections, due to lack of stringent safety regulations and proper hygiene respectively, may be more common and where cocktails of antibiotics may be less affordable. Phages that can possibly be employed in the treatment and their advantages compared to the use of antibiotics are also highlighted

14. **Particle transport in a karst aquifer: natural and artificial tracer experiments with bacteria, bacteriophages and microspheres. Auckenthaler, A., Raso, G., Huggenberger, P. (2002). *Water Science and Technology* 46:131-138.** Fast changes in spring water quality in karst areas are a major concern for production of drinking water and require detailed knowledge of the complex interaction between karst aquifer, transport behavior of microorganisms and water treatment. We have conducted artificial and natural particle transport experiments at a karst spring with bacteria, bacteriophages, microspheres, and pathogens. Transport of the investigated microorganisms, turbid matter and chemical pullutants as well as increase in discharge are strongly related to precipitation and the heterogeneity of the aquifer. The indicator bacteria *E. coli* revealed a significant correlation to verotoxin-producing *E coli* and *Cryptosporidium* spp. We conclude that artificial particle tracers can help identify 'hot spots' for microbial recharge and that system parameters in spring water such as turbidity, UV-extinction and increase in discharge can be key parameters for efficient raw water management

15. **The fundamental contribution of phages to GAS evolution, genome diversification and strain emergence. Banks, D. J., Beres, S. B., Musser, J. M. (2002). *Trends in Microbiology* 10:515-521.** The human bacterial pathogen group A *Streptococcus* (GAS) causes many different diseases including pharyngitis, tonsillitis, impetigo, scarlet fever, streptococcal toxic shock syndrome, necrotizing fasciitis and myositis, and the post-infection sequelae glomerulonephritis and rheumatic fever. The frequency and severity of GAS infections increased in the 1980s and 1990s, but the cause of this increase is unknown. Recently, genome sequencing of serotype M1, M3 and M18 strains revealed many new proven or putative virulence factors that are encoded by phages or phage-like elements. Importantly, these genetic elements account for an unexpectedly large proportion of the difference in gene content between the three strains. These new genome-sequencing studies have provided evidence that temporally and geographically distinct epidemics, and the complex array of GAS clinical presentations, might be related in part to the acquisition or evolution of phage-encoded virulence factors. We anticipate that new phage-encoded virulence factors will be identified by sequencing the genomes of additional GAS strains, including organisms non-randomly associated with particular clinical syndromes

16. **Characterization of six *Leuconostoc fallax* bacteriophages isolated from an industrial sauerkraut fermentation. Barrangou, R., Yoon, S. S., Breidt, F. Jr, Fleming, P., Klaenhammer, T. R. (2002). *Applied and Environmental Microbiology* 68:5452-5458.** Six bacteriophages active against *Leuconostoc fallax* strains were isolated from industrial sauerkraut fermentation brines. These phages were characterized as to host range, morphology, structural proteins, and genome fingerprint. They were exclusively lytic against the species *L. fallax* and had different host ranges among the strains of this species tested. Morphologically, three of the phages were assigned to the family Siphoviridae, and the three others were assigned to the family Myovidae: Major capsid proteins detected by electrophoresis were distinct for each of the two morphotypes. Restriction fragment length polymorphism analysis and randomly amplified polymorphic DNA fingerprinting showed that all six phages were genetically distinct. These results revealed for the first time the existence of bacteriophages that are active against *L. fallax* and confirmed the presence and diversity of bacteriophages in a sauerkraut fermentation. Since a variety of *L. fallax* strains have been shown to be present in sauerkraut fermentation, bacteriophages active against *L. fallax* are likely to contribute to the microbial ecology of sauerkraut fermentation and could be responsible for some of the variability observed in this type of fermentation

17. **Trade-offs and coexistence in microbial microcosms. Bohannan, B. J. M., Kerr, B., Jessup, C. M., Hughes, J. B., Sandvik, G. (2002). *Antonie van Leeuwenhoek* 81:107-115.** Trade-offs among the abilities of organisms to respond to different environmental factors are often assumed to play a major role in the coexistence of species. There has been extensive theoretical study of the role of such trade-offs in ecological communities but it has proven difficult to study such trade-offs experimentally. Microorganisms are ideal model systems with which to experimentally study the causes and consequences of ecological trade-offs. In model communities of *E. coli* B and T-type bacteriophage, a trade-off in *E. coli* between resistance to bacteriophage and competitive ability is often observed. This trade-off can allow the coexistence of different ecological types of *E. coli*. The magnitude of this trade-off affects, in predictable ways, the structure, dynamics and response to environmental change of these communities. Genetic factors, environmental factors, and gene-by-environment interactions determine the magnitude of this trade-off. Environmental control of the magnitude of trade-offs represents one avenue by which environmental change can alter community properties such as invasability, stability and coexistence

18. **Fate of bacterial indicators, viruses and protozoan parasites in a wastewater multi-component treatment system. Bonadonna, L., Briancesco, R., Cataldo, C., Divizia, M., Donia, D., Pana, A. (2002). *the New Microbiologica* 25:413-420.** The extent of reduction in selected microrganisms was tested at a multi-component wastewater treatment plant that treats sewage for a potential re-use in agriculture. The aim of the investigation was to evaluate possible reciprocal correlation among the different microrganisms and to compare the removal of two encysted pathogenic protozoa with that of microbial indicators, *Clostridium perfringens* spores, enteroviruses and bacteriophages. Samples collected included the raw wastewater, the chlorinated effluent and the effluent after an ultraviolet light treatment. All of the raw sewage samples were positive for *Cryptosporidium* oocysts and *Giardia* cysts, as well as for the other microorganisms tested but the bacteriophage B40-8. The data obtained confirm the removal efficiency of the entire process for indicator bacteria but also show the low and variable removal efficiency for the other microbial parameters, such as *Giardia* and *Cryptosporidium*, enteroviruses and *Clostridium perfringens* spores. Reciprocal correlation between *Cryptosporidium* and *Giardia* (oo)cysts and the other microbial groups was not demonstrated. The results confirm the resistance of *Clostridium perfringens* spores, enteroviruses and protozoa to chlorination and demonstrate the relative persistence of these organisms in the effluents even during the ultraviolet light treatment. The yields also emphasise the influence of the analytical method for the determination of protozoan parasites

19. **Common themes among bacteriophage-encoded virulence factors and diversity among the bacteriophages involved. Boyd, E. F., Brussow, H. (2002). *Trends in Microbiology* 10:521-529.** There are common themes among bacteriophage-encoded virulence factors, which include the well-characterized bacterial toxins and proteins that alter antigenicity as well as several new classes of bacteriophage-encoded proteins such as superantigens, effectors translocated by a type III secretion system, and proteins required for intracellular survival and host cell attachment. These virulence factors are encoded by a diversity of bacteriophages, members of the viral families Siphoviridae, Podoviridae, Myoviridae and Inoviridae, with some bacteriophages having characteristics of more than one virus family. The location of virulence genes within the bacteriophage genomes is non-random and consistent with an origin via imprecise prophage excision or as either transferable cassettes or integral components of the bacteriophage genome

20. **Performance of a novel Viresolve NFR virus filter. Brough, H., Antoniou, C., Carter, J., Jakubik, J., Xu, Y., Lutz, H. (2002). *Biotechnology Progress* 18:782-795.** Mammalian cell-expressed therapeutic proteins are particularly vulnerable to contamination by endogenous retrovirus-like particles (RVLPs). The Viresolve NFR filter was designed to meet the critical requirement of manufacturing a safe and virus-free therapeutic by retaining RVLPs by a minimum of six log reduction value (LRV). The NFR designation refers to retrovirus removal in a normal flow format. To qualify the product, we tested two model viruses: the 78 nm diameter phi6 bacteriophage and the 80-110 nm diameter Xenotropic Murine Leukemia Virus (X-MuLV). Robust retention was demonstrated over a wide range of process parameters. Viresolve NFR filters also retain other model adventitious viruses including 70-85 nm diameter Reovirus 3 (Reo3), 70-90 nm diameter Adenovirus 2 (Ad2), and 53 nm diameter PR772 by >6 LRV. In addition to these model viruses, the filter retains >7 LRV of both the mycoplasma Acholeplasma laidlawii and the bacterium Brevundimonas diminuta. Protein passage is shown to be consistently high (95-100%) for a variety of therapeutic protein products, including monoclonal antibodies. Characterization of the filter in specific applications is made simple by availability of ultralow surface area (5 cm(2)) disks, which are shown to scale linearly to the manufacturing scale pleated-filters. Viresolve NFR filters provide consistent water permeability performance (34-37 LMH/psi) and show very little plugging for all feedstocks evaluated. The Viresolve NFR filter incorporates Retropore, a unique asymmetric polyethersulfone membrane, the surface of which has been modified to minimize protein binding

21. **The role of parasites in sympatric and allopatric host diversification. Buckling, A., Rainey, P. B. (2002). *Nature (London)* 420:496-499.** Exploiters (parasites and predators) are thought to play a significant role in diversification, and ultimately speciation, of their hosts or prey. Exploiters may drive sympatric (within-population) diversification if there are a variety of exploiter-resistance strategies or fitness costs associated with exploiter resistance. Exploiters may also drive allopatric (between-population) diversification by creating different selection pressures and increasing the rate of random divergence. We examined the effect of a virulent viral parasite (phage) on the diversification of the bacterium *Pseudomonas fluorescens* in spatially structured microcosms. Here we show that in the absence of phages, bacteria rapidly diversified into spatial niche specialists with similar patterns of diversity across replicate populations. In the presence of phages, sympatric diversity was greatly reduced, as a result of phage-imposed reductions in host density decreasing competition for resources. In contrast, allopatric diversity was greatly increased as a result of phage-imposed selection for resistance, which caused populations to follow divergent evolutionary trajectories. These results show that exploiters can drive diversification between populations, but may inhibit diversification within populations by opposing diversifying selection that arises from resource competition

22. **Antagonistic coevolution between a bacterium and a bacteriophage. Buckling, A., Rainey, P. B. (2002). *Proceedings of the Royal Society of London Series B Biological sciences* 269:931-936.** Antagonistic coevolution between hosts and parasites is believed to play a pivotal role in host and parasite population dynamics, the evolutionary maintenance of sex and the evolution of parasite virulence. Furthermore, antagonistic coevolution is believed to be responsible for rapid differentiation of both hosts and parasites between geographically structured populations. Yet empirical evidence for host-parasite antagonistic coevolution, and its impact on between-population genetic divergence, is limited. Here we demonstrate a long-term arms race between the infectivity of a viral parasite (bacteriophage; phage) and the resistance of its bacterial host. Coevolution was largely driven by directional selection, with hosts becoming resistant to a wider range of parasite genotypes and parasites infective to a wider range of host genotypes. Coevolution followed divergent trajectories between replicate communities despite establishment with isogenic bacteria and phage, and resulted in bacteria adapted to their own, compared with other, phage populations

23. **Dynamics of success and failure in phage and antibiotic therapy in experimental infections. Bull, J. J., Levin, B. R., DeRouin, T., Walker, N., Bloch, C. A. (2002). *BMC microbiology [electronic resource]* 2:35.** BACKGROUND: In 1982 Smith and Huggins showed that bacteriophages could be at least as effective as antibiotics in preventing mortality from experimental infections with a capsulated *E. coli* (K1) in mice. Phages that required the K1 capsule for infection were more effective than phages that did not require this capsule, but the efficacies of phages and antibiotics in preventing mortality both declined with time between infection and treatment, becoming virtually ineffective within 16 hours. RESULTS: We develop quantitative microbiological procedures that (1) explore the in vivo processes responsible for the efficacy of phage and antibiotic treatment protocols in experimental infections (the Resistance Competition Assay, or RCA), and (2) survey the therapeutic potential of phages in vitro (the Phage Replication Assay or PRA). We illustrate the application and utility of these methods in a repetition of Smith and Huggins' experiments, using the *E. coli* K1 mouse thigh infection model, and applying treatments of phages or streptomycin. CONCLUSIONS: 1) The Smith and Huggins phage and antibiotic therapy results are quantitatively and qualitatively robust. (2) Our RCA values reflect the microbiological efficacies of the different phages and of streptomycin in preventing mortality, and reflect the decline in their efficacy with a delay in treatment. These results show specifically that bacteria become refractory to treatment over the term of infection. (3) The K1-specific and non-specific phages had similar replication

rates on bacteria grown in broth (based on the PRA), but the K1-specific phage had markedly greater replication rates in mouse serum

24. **[Phenogenetic characterization of a group of giant Phi KZ-like bacteriophages of Pseudomonas aeruginosa]. Burkal'tseva, M. V., Krylov, V. N., Pleteneva, E. A., Shaburova, O. V., Krylov, S. V., Volkart, G., Sykilinda, N. N., Kurochkina, L. P., Mesianzhinov, V. V. (2002). *Genetika* 38:1470-1479.** A comparative study was made of a group of *Pseudomonas aeruginosa* virulent giant DNA bacteriophages similar to phage phi KZ in several genetic and phenotypic properties (particle size, particle morphology, genome size, appearance of negative colonies, high productivity, broad spectrum of lytic activity, ability to overcome the suppressing effect of plasmids, absence of several DNA restriction sites, capability of general transduction, pseudolysogeny). We have recently sequenced the phage phi KZ genome (288,334 bp) [J. Mol. Biol., 2002, vol. 317, pp. 1-19]. By DNA homology, the phages were assigned to three species (represented by phage phi KZ, Lin68, and EL, respectively) and two new genera (phi KZ and EL). Restriction enzyme analysis revealed the mosaic genome structure in four phages of the phi KZ species (phi KZ, Lin21, NN, and PTB80) and two phages of the EL species (EL and RU). Comparisons with respect to phage particle size, number of structural proteins, and the N-terminal sequences of the major capsid protein confirmed the phylogenetic relatedness of the phages belonging to the phi KZ genus. The origin and evolution of the phi KZ-like phages are discussed. Analysis of protein sequences encoded by the phage phi KZ genome made it possible to assume wide migration of the phi KZ-like phages (wandering phages) among various prokaryotes and possibly eukaryotes. Since the phage phi KZ genome codes for potentially toxic proteins, caution must be exercised in the employment of large bacteriophages in phage therapy

25. **Phenogenetic characterization of a group of giant fKZ-like bacteriophages of *Pseudomonas aeruginosa*. Burkal'tseva, M. V., Krylov, V. N., Pleteneva, E. A., Shaburova, O. V., Krylov, S. V., Volkart, G., Sykilinda, N. N., Kurochkina, L. P., Mesyanzhinov, V. V. (2002). *Russian Journal of Genetics* 38:1242-1250.** A comparative study was made of a group of *Pseudomonas aeruginosa* virulent giant DNA bacteriophages similar to KZ in several genetic and phenotypic properties (particle size, particle morphology, genome size, appearance of negative colonies, high productivity, broad spectrum of lytic activity, ability to overcome the suppressing effect of plasmids, absence of several DNA restriction sites, capability of general transduction, pseudolysogeny). We have recently sequenced the phage KZ genome (288 334 bp) [*J. Mol. Biol.*, 2002, vol. 317, pp. 1-19]. By DNA homology, the phages were assigned to three species (represented by phages KZ, Lin68, and EL, respectively) and two new genera (KZ, LIN21, NN, and PTB80) and two phages of the EL species (EL and RU). Comparisons with respect to phage particle size, number of structural proteins, and the N-terminal sequences of the major capsid protein confirmed the phylogenetic relatedness of the phages belonging to the KZ genus. The origin and evolution of the KZ-like phages are discussed. Analysis of protein sequences encoded by the phage KZ genome made it possible to assume wide migration of the KZ-like phages (wandering phages) among various prokaryotes and possibly eukaryotes. Since the phage KZ genome codes for potentially toxic proteins, caution must be exercise in the empoyment of large bacteriophages in phage therapy.

26. **Genome plasticity in *Lactococcus lactis*. Campo, N., Dias, M. J., Daveran-Mingot, M. L., Ritzenthaler, P., Le Bourgeois, P. (2002). *Antonie van Leeuwenhoek* 82:123-132.** Comparative genome analyses contribute significantly to our understanding of bacterial evolution and indicate that bacterial genomes are constantly evolving structures. The gene content and organisation of chromosomes of lactic acid bacteria probably result from a strong evolutionary pressure toward optimal growth of these microorganisms in milk. The genome plasticity of *Lactococcus lactis* was evaluated at inter- and intrasubspecies levels by different experimental approaches. Comparative genomics showed that the lactococcal genomes are not highly plastic although large rearrangements (a.o. deletions, inversions) can occur. Experimental genome shuffling using a new genetic strategy based on the Cre-loxP recombination system revealed that two domains are under strong constraints acting to maintain the original chromosome organisation: a large region around the replication origin, and a smaller one around the putative terminus of replication. Future knowledge of the rules leading to an optimal genome organisation could facilitate the definition of new strategies for industrial strain improvement

27. **Genome analysis of an inducible prophage and prophage remnants integrated in the *Streptococcus pyogenes* strain SF370. Canchaya, C., Desiere, F., McShan, W. M., Ferretti, J. J., Parkhill, J., Brussow, H. (2002). *Virology* 302:245-258.** The mitomycin C inducible prophage SF370.1 from the highly pathogenic M1 serotype *Streptococcus pyogenes* isolate SF370 showed a 41-kb-long genome whose genetic organization resembled that of SF11-like pac-site Siphoviridae. Its closest relative was prophage NIH1.1 from an M3 serotype *S. pyogenes* strain, followed by *S. pneumoniae* phage MM1 and Lactobacillus phage phig1e, *Listeria* phage A118, and *Bacillus* phage SPP1 in a gradient of relatedness. Sequence similarity with the previously described prophages SF370.2 and SF370.3 from the same polylysogenic SF370 strain were mainly limited to the tail fiber genes. As in these two other prophages, SF370.1 encoded likely lysogenic conversion genes between the phage lysin and the right attachment site. The genes encoded the pyrogenic exotoxin C of *S. pyogenes* and a protein sharing sequence similarity with both DNases and mitogenic factors. The screening of the SF370 genome revealed further prophage-like elements. A 13-kb-long phage remnant SF370.4 encoded lysogeny and DNA replication genes. A closely related prophage remnant was identified in *S. pyogenes* strain Manfredo at a corresponding genome position. The two prophages differed by internal indels and gene replacements. Four phage-like integrases were detected; three were still accompanied by likely repressor genes. All prophage elements were integrated into coding sequences. The phage sequences complemented the coding sequences in all cases. The DNA repair genes mutL and mutS were separated by the prophage remnant SF370.4; prophage SF370.1 and S. pneumoniae phage MM1 integrated into homologous chromosomal locations. The prophage sequences were interpreted with a hypothesis that predicts elements of cooperation and an arms race between phage and host genomes

28. **Phage therapy of local and systemic disease caused by *Vibrio vulnificus* in iron-dextran-treated mice. Cerveny, K. E., Depaola, A., Duckworth, D. H., Gulig, P. A. (2002). *Infection and Immunity* 70:6251-6262.** *Vibrio vulnificus* is a gram-negative bacterium that contaminates filter-feeding shellfish such as oysters. After ingestion of contaminated oysters, predisposed people may experience highly lethal septicemia. Contamination of wounds with the bacteria can result in devastating necrotizing fasciitis, which can progress to septicemia. The extremely rapid progression of these diseases can render antibiotic treatment ineffective, and death is a frequent outcome. In this study, we examined the potential use of bacteriophages as therapeutic agents against *V. vulnificus* in an iron-dextran-treated mouse model of *V. vulnificus* infection. Mice were injected subcutaneously with 10 times the lethal dose of *V. vulnificus* and injected intravenously, either simultaneously or at various times after infection, with phages. Treatment of mice with phages could prevent death; systemic disease, as measured by CFU per gram of liver and body temperature; and local disease, as measured by CFU per gram of lesion material and histopathologic analysis. Two different phages were effective against three different *V. vulnificus* strains with various degrees of virulence, while a third phage that required the presence of seawater to lyse bacteria in vitro was ineffective at

treating mice. Optimum protection required that the phages be administered within 3 h of bacterial inoculation at doses as high as 10^8 PFU. One of the protective phages had a half-life in blood of over 2 h. These results demonstrate that bacteriophages have therapeutic potential for both localized and systemic infections caused by *V. vulnificus* in animals. This model should be useful in answering basic questions regarding phage therapy

29. **Isolation and genetic characterization of a novel filamentous bacteriophage, a deleted form of phage f237, from a pandemic *Vibrio parahaemolyticus* O4:K68 strain. Chan, B., Miyamoto, H., Taniguchi, H., Yoshida, S. I. (2002). *Microbiology and Immunology* 46:565-569.** We isolated a filamentous bacteriophage, VfO4K68, from the pandemic *Vibrio parahaemolyticus* strain belonging to 04:K68 serovar. The VfO4K68 DNA lacked a 1,893-bp fragment present in that of the distinctive region of f237, a filamentous phage isolated from a pandemic 03:K6 strain (Nasu, H. et al., J. Clin. Microbiol., 38, 2156-2161, 2000). The deletion resulted in the formation of a novel open reading frame (ORF) that possesses homology to the ORF 27 of ETA phage and staphylococcal enterotoxin E (SEE) of *Staphylococcus aureus*. VfO4K68 was able to infect the recipient 03:K6 serovar strains. These results suggest that VfO4K68 might act as a genetic transmitter and play some roles in the pandemic *V. parahaemolyticus* infection

30. **Bacteriophage-resistance systems in dairy starter strains: molecular analysis to application. Coffey, A., Ross, R. P. (2002). *Antonie van Leeuwenhoek* 82:303-321.** Starter inhibition by bacteriophage infection in dairy fermentations can limit the usage of specific bacterial strains used in the manufacture of Cheddar, Mozzarella and other cheeses and can result in substantial economic losses. A variety of practical measures to alleviate the problem of phage infection have been adopted over the years but has invariably resulted in a very limited number of strains which can withstand intensive usage in industry. The application of genetic techniques to improve the phage-resistance of starter cultures for dairy fermentations has been intensively studied for the last 20 years to a point where this approach now has significant potential to alleviate the problem. This paper highlights the recent findings and developments that have been described in the literature that will have an impact on improvement of the phage-resistance of starter cultures

31. **Occurrence and levels of indicator bacteriophages in bathing waters throughout Europe. Contreras-Coll, N., Lucena, F., Mooijman, K., Havelaar, A., Pierz, V., Boque, M., Gawler, A., Holler, C., Lambiri, M., Mirolo, G., Moreno, B., Niemi, M., Sommer, R., Valentin, B., Wiedenmann, A., Young, V., Jofre, J. (2002). *Water Research* 36:4963-4974.** Somatic coliphages, F-specific RNA bacteriophages, bacteriophages infecting *Bacteroides fragilis*, *Escherichia coli* and enterococci were counted in bathing waters in the late spring and summer. We tested fresh and marine bathing waters from North, South, East and West Europe expected to contain between 100 and 500 E. coli per 100 ml, although wider ranges were sometimes found. Bacteriophages were counted after concentration, since a preliminary study proved that this step was necessary to obtain positive counts. During monitoring, a first-line quality control with reference materials for bacteria and bacteriophages was performed by all the laboratories participating in the study. The same microbes were also counted in raw sewage samples from various areas in Europe, where the bacterial indicators and the three groups of bacteriophages were detected in roughly the same numbers. All groups of bacteriophages were detected in both fresh and marine bathing waters throughout Europe. Reliable and complete results from 147 samples showed that for log-transformed values, *E. coli* and bacteriophages were slightly correlated. However, the slope of the regression line changed according to *E. coli* concentration and the correlation diminished when this concentration was close to zero per 100 ml. The ratios between *E. coli* and phages in bathing waters differed significantly from those in sewage. The relative amounts of bacteriophages, mainly somatic coliphages and phages infecting *Bact. fragilis* RYC2056, increased in bathing waters with low *E. coli* concentration, especially in seawater samples containing < 100 *E. coli* per 100 ml. The relationship of bacteriophages with respect to enterococci paralleled that of bacteriophages with respect to *E. coli*. Somatic coliphages and bacteriophages infecting *Bact. fragilis* are useful to predict the presence of some pathogens with the same origin as present bacterial indicators but with higher survival rates

32. **Comparative genomics of phages and prophages in lactic acid bacteria. Desiere, F., Lucchini, S., Canchaya, C., Ventura, M., Brussow, H. (2002). *Antonie van Leeuwenhoek* 82:73-91.** Comparative phage genomics has become possible due to the availability of more than 100 complete phage genome sequences and the development of powerful bioinformatics tools. This technology, profiting from classical molecular-biology knowledge, has opened avenues of research for topics, which were difficult to address in the past. Now, it is possible to retrace part of the evolutionary history of phage modules by comparative genomics. The diagnosis of relatedness is hereby not uniquely based on sequence similarity alone, but includes topological considerations of genome organization. Detailed transcription maps have allowed in silico predictions of genome organization to be verified and refined. This comparative knowledge is providing the basis for a new taxonomic classification concept for bacteriophages infecting low G + C-content Gram-positive bacteria based on the genetic organization of the structural gene module. An Sfi21-like and an Sfi11-like genus of Siphoviridae is proposed. The gene maps of many phages show remarkable synteny in their structural genes defining a lambda super-group within Siphoviridae. A hierarchy of relatedness within the lambda super-group suggests elements of vertical evolution in Siphoviridae. Tailed phages are the result of both vertical and horizontal evolution and are thus fascinating objects for the study of molecular evolution. Prophage sequences integrated into the genomes of their bacterial host present theoretical challenges for evolutionary biologists. Prophages represent up to 10% of the genome in some LAB. In pathogenic streptococci prophages confer genes of selective value for the lysogenic cell. The lysogenic conversion genes are located between the lysin gene and the right phage attachment site. Non-attributed genes were found at the same genome position of prophages from lactic streptococci. These genes belong to the few prophage genes transcribed in the lysogen. Prophages from dairy bacteria might therefore also contribute to the evolutionary fitness of non-pathogenic LAB

33. **Time-delayed spread of viruses in growing plaques. Fort, J., Mendez, V. (2002). *Physical Review Letters* 89:178101.** The spread of viruses in growing plaques predicted by classical models is greater than that measured experimentally. There is a widespread belief that this discrepancy is due to biological factors. Here we show that the observed speeds can be satisfactorily predicted by a purely physical model that takes into account the delay time due to virus reproduction inside infected cells. No free or adjustable parameters are used

34. ***Bacteroides fragilis* and *Escherichia coli* bacteriophages in human faeces. Gantzer, C., Henny, J., Schwartzbrod, L. (2002). *International Journal of Hygiene and Environmental Health* 205:325-328.** Some bacteriophages found in human faeces are being evaluated as possible indicators of viral contamination of water. These bacteriophages include somatic coliphages and *Bacteroides fragilis* phages. The aims of this study were to determine the occurrence and concentrations of somatic coliphages and *Bacteroides fragilis* phages in the stools of a human population residing in eastern France (n = 193). Somatic coliphages were detected in 68% of the stools at a mean concentration of 4.3 x 10(3) PFU.g-1 and Bacteroides fragilis phages were detected in 11% of the stools at a mean concentration of 7 x 10(1) PFU.g-1. Statistical analysis showed no

correlation between the phage concentration and the age or sex of the human subject

35. **Conserved filamentous prophage in *Escherichia coli* O18:K1:H7 and *Yersinia pestis* biovar orientalis. Gonzalez, M. D., Lichtensteiger, C. A., Caughlan, R., Vimr, E. R. (2002). *Journal of Bacteriology* 184:6050-6055.** Microbial virulence is known to emerge by horizontal gene transfer mechanisms. Here we describe the discovery of a novel filamentous prophage, designated CUS-1, which is integrated into the chromosomal dif homologue of the high-virulence clone *Escherichia coli* O18:K1:H7. An homologous chromosomal element (CUS-2) in *Yersinia pestis* biovar orientalis is integrated at the same relative location as CUS-1; both lysogenic *E. coli* and *Y. pestis* strains produce particles with properties expected of single-stranded DNA virions. CUS(phi) is epidemiologically correlated with the emergence of K1 strains with increased virulence and with the *Y. pestis* biovar responsible for the current (third) plague pandemic

36. **[Action of *Spirulina platensis* on bacterial viruses]. Gorobets, O. B., Blinkova, L. P., Baturo, A. P. (2002). *Zh. Mikrobiol. Epidemiol. Immunobiol.* 18-21.** The impact of the biomass of the blue-green microalga (cyanobacterium) *S. platensis* on bacteriophage T4 (bacterial virus) has been evaluated. The study revealed that the addition of *S. platensis* biomass into the agar nutrient medium, followed by sterilization with 2% chloroform and thermal treatment, produced an inhibiting or stimulating effect on the reproduction of the bacteriophage in *Escherichia coli* B cells, depending on the concentration of *S. platensis* and the multiplicity of phage infection, as well as on the fact whether the microalgae were added during the first cycle of the development of the virus. The reproduction of the bacteriophage in *E. coli* B was influenced by the method and duration of the sterilization of the nutrient medium with *S. platensis*

37. **Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7. Hahn, M. W., Rausher, M. D., Cunningham, C. W. (2002). *Genetics* 161:11-20.** Experimental evolution of short-lived organisms offers the opportunity to study the dynamics of polymorphism over time in a controlled environment. Here, we characterize DNA polymorphism data over time for four genes in bacteriophage T7. Our experiment ran for 2500 generations and populations were sampled after 500, 2000, and 2500 generations. We detect positive selection, purifying ("negative") selection, and population expansion in our experiment. We also present a statistical test that is able to distinguish demographic from selective events, processes that are hard to identify individually because both often produce an excess of rare mutations. Our "heterogeneity test" modifies common statistics measuring the frequency spectrum of polymorphism (e.g., Fu and Li's D) by looking for processes producing different patterns on nonsynonymous and synonymous mutations. Test results agree with the known conditions of the experiment, and we are therefore confident that this test offers a tool to evaluate natural populations. Our results suggest that instances of segregating deleterious mutations may be common, but as yet undetected, in nature

38. **Effects of temperatures, pH-values, ultra-violet light, ethanol and chloroform on the growth of isolated thermophilic *Bacillus* phages. Hazem, A. (2002). *the New Microbiologica* 25:469-476.** Seven thermophilic Bacillus phages were characterized with reference to their host range, time of appearance, morphology of plaques, thermal inactivation, stability, lipid presence and inactivation by ultraviolet irradiation. Response surface methodology was adapted to describe the response of growth parameters to environmental changes. Most phages are susceptible to temperatures above 60 degrees C and inactivated immediately at 103 degrees C. Most phages are resistant to pH ranges 5 to 9 and almost all to pH 7 to 8. Both phages 46 and 80 were highly resistance to UV exposure for 13 minutes and 20 minutes, respectively. The presence of chloroform or 75% ethanol showed no effect on almost all isolated phages that indicate of possibility of the absence of lipids. The isolated phages were slow in their growth, possibly due to the lower gross growth efficiency

39. **Prevention of *Escherichia coli* respiratory infection in broiler chickens with bacteriophage (SPR02). Huff, W. E., Huff, G. R., Rath, N. C., Balog, J. M., Xie, H., Moore, P. A. J., Donoghue, A. M. (2002). *Poultry science* 81:437-441.** Bacteriophages are viruses that can infect and kill bacteria. Three studies were conducted to determine the efficacy of bacteriophage to prevent an Escherichia coli respiratory infection in broiler chickens. In the first study 3-d-old-birds were challenged with an air sac inoculation of 10^3 cfu of E. coli per mL mixed with either 10^3 or 10^6 pfu of bacteriophage, or 10^4 cfu E. coli mixed with 10^4 or 10^8 pfu of bacteriophage. In the second study, drinking water of birds to 1 wk of age was treated with 103 or 104 pfu of bacteriophage per mL and birds were air sac challenged with 103 cfu of E. coli, or water was treated with 10^4 or 10^6 pfu of bacteriophage per milliliter and birds were challenged with 10^4 cfu of E. coli. In the third study, birds were air sac challenged at 1 wk of age with 10^4 cfu of E. coli and given 10^5 or 10^6 pfu of bacteriophage per mL of water from 1 d of age to 2 wk of age. In Studies 1 and 2, there were two replicate pens per treatment with 10 birds per pen, and in Study 3, there were four replicate pens per treatment with 10 birds per pen. The studies were all concluded when the birds were 3 wk of age. In Study 1, BW was decreased at 1 and 2 wk of age in the birds that were challenged with 10^3 or 10^4 cfu of E. coli and was decreased at 2 wk of age in the birds challenged with 10^4 cfu of *E. coli* mixed with 10^4 pfu of the bacteriophage. Mortality was decreased from 80% in the birds challenged with 103 cfu of E. coli to 25 and 5% when mixed with 10^3 or 10^6 pfu of the bacteriophage, respectively. Mortality was decreased from 85% in birds challenged with 10^4 cfu of E. coli to 35% when mixed with 10^4 pfu of the bacteriophage, and no mortality occurred when mixed with 106 pfu of bacteriophage. There was essentially no protection observed in Studies 2 and 3 when the birds were challenged with 10^3 or 10^4 cfu of *E. coli* with bacteriophage present in their drinking water at any level. These data suggest that bacteriophage can protect birds from a respiratory challenge with *E. coli*, but that adding the bacteriophage to the drinking water offered no protection to the birds. The complete protection of the birds observed in Study 1 suggests that bacteriophage may possibly be developed as an alternative to antibiotic use in poultry

40. **Prevention of *Escherichia coli* infection in broiler chickens with a bacteriophage aerosol spray. Huff, W. E., Huff, G. R., Rath, N. C., Balog, J. M., Donoghue, A. M. (2002). *Poultry science* 81:1486-1491.** Bacteriophage to an *Escherichia coli* isolate that is pathogenic in poultry were isolated from municipal sewer treatment facilities or poultry processing plants. Three studies were conducted to determine the efficacy of aerosol administration of bacteriophage to prevent an *E. coli* respiratory infection in broiler chickens. In all three studies the experimental design consisted of nine treatments with three replicate pens of 10 birds. Three treatments were not challenged with *E. coli* and consisted of unsprayed birds, birds sprayed with a diluent control, and birds sprayed with a combination of two bacteriophages. Six treatments were challenged with *E. coli* by injecting 10^4 cfu into the thoracic air sac when birds were 7, 8, or 10 d of age after being sprayed at 7 d of age with either a diluent control or a combination of two bacteriophages. In Studies 1 and 2, BW at 2 wk of age of all the birds challenged with *E. coli*, regardless of spray treatment, were decreased significantly from the unchallenged controls, except in Study 2 for the birds sprayed with bacteriophage and challenged at 10 d of age. There was a significant decrease in mortality in Studies 1 and 2 when the birds were challenged with *E. coli* immediately after bacteriophage administration and in Study 2 in birds challenged at 10 d of age. In

Study 3 a suspected pre-existing *E. coli* infection resulted in mortality in the unchallenged, unsprayed controls, and in the diluent sprayed controls of 20 and 27%, respectively. The mortality in the unchallenged bacteriophage sprayed birds was 3%, representing a significant decrease. Mortality in Study 3 was significantly decreased in the bacteriophage-sprayed birds challenged with *E. coli* immediately or 1 d later but not 3 d after bacteriophage administration. The decrease in BW at 2 wk of age in challenged birds indicates that bacteriophage treatment did not provide complete protection; however, in all three studies mortality was significantly decreased, indicating that aerosol spray of bacteriophage may be practical for administration of bacteriophage and may provide an alternative to the use of antibiotics in poultry production

41. **Characterization of serracin P, a phage-tail-like bacteriocin, and its activity against *Erwinia amylovora*, the fire blight pathogen. Jabrane, A., Sabri, A., Compere, P., Jacques, P., Vandenberghe, I., Van Beeumen, J., Thonart, P. (2002). *Applied and Environmental Microbiology* 68:5704-5710.** *Serratia plymithicum* J7 culture supernatant displayed activity against many pathogenic strains of *Erwinia amylovora*, the causal agent of the most serious bacterial disease of apple and pear trees, fire blight, and against *Klebsiella pneumoniae*, *Serratia liquefaciens*, *Serratia marcescens*, and *Pseudomonas fluorescens*. This activity increased significantly upon induction with mitomycin C. A phage-tail-like bacteriocin, named serracin P, was purified from an induced culture supernatant of *S. plymithicum* J7. It was found to be the only compound involved in the antibacterial activity against sensitive strains. The N-terminal amino acid sequence analysis of the two major subunits (23 and 43 kDa) of serracin P revealed high homology with the Fels-2 prophage of *Salmonella enterica*, the coliphages P2 and 168, the phiCTX prophage of *Pseudomonas aeruginosa*, and a prophage of *Yersinia pestis*. This strongly suggests a common ancestry for serracin P and these bacteriophages

42. **Viral Trojan horse for combating tuberculosis. Johnston, N. (2002). *Drug discovery today* 7:333-335.** The emergence of pathogenic bacteria resistant to one or more antibiotics has outpaced the development of new drugs. Using bacteriophage, Raul Barletta (Dept of Veterinary and Biomedical Sciences, University of Nebraska, Lincoln, NE, USA) and colleagues at the California Pacific Medical Center (San Francisco, CA, USA) have devised a promising new approach to killing the intracellular pathogens *Mycobacterium avium*, which commonly afflicts AIDS patients, and *Mycobacterium tuberculosis*, the causative agent of tuberculosis. Their findings were presented at the *41st Interscience Conference on Antimicrobial Agents and Chemotherapy* hosted by the American Society for Microbiology in Chicago, IL, USA [1].

43. ***Vibrio cholerae* phage K139: complete genome sequence and comparative genomics of related phages. Kapfhammer, D., Blass, J., Evers, S., Reidl, J. (2002). *Journal of Bacteriology* 184:6592-6601.** In this report, we characterize the complete genome sequence of the temperate phage K139, which morphologically belongs to the Myoviridae phage family (P2 and 186). The prophage genome consists of 33,106 bp, and the overall GC content is 48.9%. Forty-four open reading frames were identified. Homology analysis and motif search were used to assign possible functions for the genes, revealing a close relationship to P2-like phages. By Southern blot screening of a Vibrio cholerae strain collection, two highly K139-related phage sequences were detected in non-O1, non-O139 strains. Combinatorial PCR analysis revealed almost identical genome organizations. One region of variable gene content was identified and sequenced. Additionally, the tail fiber genes were analyzed, leading to the identification of putative host-specific sequence variations. Furthermore, a K139-encoded Dam methyltransferase was characterized

44. **[Effect of bacteriophage on the lipid peroxidation process and antioxidant protective enzymes in experimental uveitis]. Karimova, M. Kh, Bakhritdinova, F. A. (2002). *Vestn Oftalmol* 118:38-40.** Experimental uveitis features distinct hyperlipoperoxidation in damaged eye tissues, blood serum and the liver. The activity of antioxidant defense (AOD) enzymes decreases in tissues and blood of experimental animals whereas catalase compensatorily activates in hepatic tissue. Experimental therapy of uveitis with gentamycin and bacteriophage results in reducing hyperlipoperoxidation, increased activity of AOD enzymes but no complete normalization is observed. This manifested in preservation of inflammations to a certain degree

45. **Deleterious impact of a virulent bacteriophage on survival and biocontrol activity of *Pseudomonas fluorescens* strain CHAO in natural soil. Keel, C., Ucurum, Z., Michaux, P., Adrian, M., Haas, D. (2002). *Molecular plant-microbe interactions : MPMI* 15:567-576.** Many biotic and abiotic factors affect the persistence and activity of beneficial pseudomonads introduced into soil to suppress plant diseases. One such factor may be the presence of virulent bacteriophages that decimate the population of the introduced bacteria, thereby reducing their beneficial effect. We have isolated a lytic bacteriophage (phi)GP100) that specifically infects the biocontrol bacterium *Pseudomonas fluorescens* CHA0 and some closely related *Pseudomonas strains*. phiGP100 was found to be a double-stranded-DNA phage with an icosahedral head, a stubby tail, and a genome size of approximately 50 kb. Replication of phiGP100 was negatively affected at temperatures higher than 25 degrees C. phiGP100 had a negative impact on the population size and the biocontrol activity of *P. fluorescens* strain CHA0-Rif (a rifampicin-resistant variant of CHA0) in natural soil microcosms. In the presence of phiGP100, the population size of strain CHA0-Rif in soil and on cucumber roots was reduced more than 100-fold. As a consequence, the bacterium's capacity to protect cucumber against a root disease caused by the pathogenic oomycete Pythium ultimum was entirely abolished. In contrast, the phage affected neither root colonization and nor the disease suppressive effect of a phiDGP100-resistant variant of strain CHA0-Rif. To our knowledge, this study is the first to illustrate the potential of phages to impair biocontrol performance of beneficial bacteria released into the natural soil environment

46. **Bacteriophage-host interaction in the enhanced biological phosphate removing activated sludge system. Khan, M. A., Satoh, H., Mino, T., Katayama, H., Kurisu, F., Matsuo, T. (2002). *Water Science and Technology* 46:39-43.** Bacteriophages were isolated from a laboratory scale enhanced biological phosphate removing (EBPR) activated sludge process, and their host range was examined. Bacterial isolates to host the bacteriophages were isolated from the EBPR activated sludge process. Bacteriophages were eluted from the EBPR activated sludge, enriched by incubation with the bacterial isolates, and then tested for plaque formation on each of the bacterial isolates. Out of 12 bacterial isolates isolated, 4 supported plaque formation. Four bacteriophages were obtained from the plaques. The host range test was conducted with the combination of the bacteriophage isolates and the bacterial isolates. Three of the bacteriophages were found to form plaques on more than one host, and one of them formed plaques on both gram +ve and gram -ve bacterial isolates. Two of the four bacteriophages failed to form plaques on their original bacterial host, indicating the existence of mutation on either both or one of the host and the bacteriophage. This study strongly suggests that bacteriophages are an active part of the activated sludge microbial ecosystem, having very complex interaction with their host bacteria

47. **Bacteriophages isolated from activated sludge processes and their polyvalency. Khan, M. A., Satoh, H., Katayama, H., Kurisu, F., Mino, T. (2002). *Water Research* 36:3364-3370.** In this study, bacteriophages were isolated from activated

sludge and their host range was studied. Bacterial isolates were obtained from an activated sludge process treating urban sewage, and bacteriophages were obtained by plaque assay using the bacterial isolates obtained in this study as the host. Out of 15 bacteria isolated, 9 supported plaque formation. The host range test was conducted with a combination of 8 bacteriophage isolates and 9 bacterial isolates. All of the 8 bacteriophages tested were found to form plaques on more than 1 host, and 4 of them formed plaques on both gram-positive and gram-negative bacterial isolates. Three of the 8 bacteriophages failed to form plaques on their original bacterial host. The experimental result indicates that bacteriophages are an active part of the activated sludge microbial ecosystem, having a very close ecological relationship with their host bacteria

48. **Preventing phage lysis of *Lactococcus lactis* in cheese production using a neutralizing heavy-chain antibody fragment from llama. Ledeboer, A. M., Bezemer, S., de Hiaard, J. J. W., Schaffers, I. M., Verrips, C. T., van Vliet, C., Dusterhoft, E. M., Zoon, P., Moineau, S., Frenken, L. G. J. (2002). *J Dairy Sci* 85:1376-1382.** Bacteriophage infection is still a persistent problem in large dairy processes despite extensive studies over the last decades. Consequently, new methods are constantly sought to prevent phage infection. In this paper, we show that phage neutralizing heavy-chain antibody fragments, obtained from Camelidae and produced at a large scale in the generally regarded as safe microorganism *Saccharomyces cerevisiae*, can effectively be used to impede phage induced lysis during a cheese process. The growth inhibition of the cheese starter culture by 10^5 pfu/ml cheese-milk of the small isometric-headed 936-type phage p2 was prevented by the addition of only 0.1 microg/ml (7 nM) of the neutralizing antibody fragment. The use of such antibody fragments in cheese manufacturing are a realistic and interesting option because of the small amount of antibody fragments that are needed. Moreover the antibodies are produced in a food grade microorganism and can easily be isolated from the fermentation liquid in a pure and DNA free form

49. **Influence of flow rate on transport of bacteriophage in shale saprolite. McKay, L. D., Harton, A. D., Wilson, G. V. (2002). *Journal of Environmental Quality* 31:1095-1105.** The objective of this study was to investigate the influence of flow rate on transport and retention of bacteriophage tracers in a fractured shale saprolite, which is a highly weathered, fine-grained subsoil that retains much of the fabric of the parent bedrock. Synthetic ground water containing PRD-1, MS-2, and bromide was passed through a saturated column of undisturbed shale saprolite at rates ranging from 0.0075 to 0.96 m d '. First arrival of the bacteriophage tracers in effluent samples in each of the experiments occurred within 0.01 to 0.04 pore volumes (PV) of the start of injection, indicating that bacteriophage were advectively transported mainly through fractures or macropores. Bacteriophage transport velocities, based on first arrival in the effluent, were very similar to fracture flow velocities calculated using the cubic law for flow in a fractured material. For MS-2, maximum concentration and mass of tracer recovered both increased steadily as flow rate increased. For PRD-1, these values initially increased, but were nearly constant at flow rates above 0.039 m d^{-1}, indicating that approximately 50% of the observed losses were independent of flow rate. Evaluation of the data indicates that physical straining and electrostatic or hydrophobic attachment to fracture or macropore walls were the dominant retention processes. Inactivation and gravitational settling playing secondary roles, except at the slowest flow rates. The study suggests that microbial contamination from sources such as septic fields and sewage ponds may pose a threat to the quality of ground water and surface water in areas with saprolitic subsoils

50. **Application of actinomycetes to soil to ameliorate water repellency. McKenna, F., El Tarabily, K. A., Petrie, S., Chen, C., Dell, B. (2002). *Letters in Applied Microbiology* 35:107-112.** AIMS: The aim of this study was to develop a novel isolation technique using a mixture of Bacillus and Streptomyces phages to selectively isolate wax-utilizing non-streptomycete actinomycetes effective in ameliorating water repellency in a problem soil. METHODS AND RESULTS: Phages added to a soil suspension reduced the dominance of Bacillus and Streptomyces isolates and significantly increased the number of non-streptomycete actinomycetes on isolation plates. Promising isolates, grown on a medium containing beeswax as sole carbon source, were selected for application to water repellent soil. Their addition significantly reduced water repellency. CONCLUSIONS: Phage application significantly increased the isolation of non-streptomycete actinomycetes. Wax-utilizing isolates were found to significantly reduce water repellency in a problem soil. SIGNIFICANCE AND IMPACT OF THE STUDY: The phage technique can be used for the routine isolation of non-streptomycete actinomycetes. Beeswax medium can be used to selectively isolate wax-utilizing micro-organisms with the potential to ameliorate water repellency in soil

51. **Conservation of phage reference materials and water samples containing bacteriophages of enteric bacteria. Mendez, J., Jofre, J., Lucena, F., Contreras, N., Mooijman, K., Araujo, R. (2002). *Journal of Virological Methods* 106:215-224.** The survival was determined in different conservation conditions of: somatic coliphages, F-specific RNA bacteriophages and phages infecting proposed as model micro-organisms for water quality control. Titres of phages of all groups either in pure culture phage suspensions or in naturally occurring phage suspensions were stable at (-70+/-10) degrees C and at (-20+/-5) degrees C when protected with glycerol. Moreover, phage analysis of stored suspensions demonstrated that their numbers were homogeneous, both between vials and within vials, and consequently they can be used as reference materials. Furthermore, changes in the storage temperature of the vials cause unpredictable changes in the numbers of bacteriophages. Consequently, phage reference materials and samples containing a quantitative number of phages must be maintained and dispatched at a constant temperature. Consequently, the results indicate that bacteriophages should be packed in dry ice during transport and storage. Finally, the number of phages in water samples stored at (5+/-3) degrees C in the dark does not decrease significantly during the first 72 h of storage. In addition, phage concentrates from natural samples obtained by adsorption-elution to cellulose nitrate filters and mixed with 10% glycerol were stable at least for 2 months at (-70+/-10) degrees C and at (-20+/-5) degrees C

52. **Evaluation of bacteriophages during the treatment of sludge. Mignotte-Cadiergues, B., Gantzer, C., Schwartzbrod, L. (2002). *Water Science and Technology* 46:189-194.** The aim of this work was to determine the effect of liming and composting on the fate of three bacteriophages (somatic coliphages, F-RNA phages, phages) considered as potential indicators of viral contamination. It was shown that the three bacteriophages studied exhibited variable densities in sludge. Somatic coliphages were most abundant (10^4 to 10^5 x 10 g^{-1} DM) then F-RNA bacteriophages (10^2 to 10^4 x 10 g^{-1} DM) and *Bacteroides fragilis* phages (10^1 to 10^2 x 10 g^{-1} DM). The efficacy of liming was found to be pH dependent but also sludge dependent. The pH allowing 99% elimination of somatic coliphage is close to 9 for solid sludges and close to 13.5 for liquid sludges. For composting, our findings clearly demonstrated that phage inactivation is very clearly temperature-dependent. For temperatures reaching 70 degrees, there is a 5 log reduction in somatic coliphages while for temperature in the 50-55 degrees C range, the drop off is only 2 log. Considering the efficacy of the treatment methods, it is clear that the well-established industrial procedures that reach temperatures in the 60-70 degrees C range totally inactivate all 3 phages tested and present in sludge before composting

53. **Microbial genome evolution: sources of variability. Mira, A., Klasson, L., Andersson, S. G. E. (2002). *Current Opinion in Microbiology* 5:506-512.** Comparative genome analyses of close relatives have yielded exciting insight into the sources of

microbial genome variability with respect to gene content, gene order and evolution of genes with unknown functions. The genomes of free-living bacteria often carry phages and repetitive sequences that mediate genomic rearrangements in contrast to the small genomes of obligate host-associated bacteria. This suggests that genomic stability correlates with the genomic content of repeated sequences and movable genetic elements, and thereby with bacterial lifestyle. Genes with unknown functions present in a single species tend to be shorter than conserved, functional genes, indicating that the fraction of unique genes in microbial genomes has been overestimated

54. **Characterization of a virulent bacteriophage specific for *Escherichia coli* O157:H7 and analysis of its cellular receptor and two tail fiber genes. Morita, M., Tanji, Y., Mizoguchi, K., Akitsu, T., Kijima, N., Unno, H. (2002). *FEMS Microbiol Lett* 211:77-83.** A virulent phage, named PP01, specific for *Escherichia coli* O157:H7 was isolated from swine stool sample. The phage concentration in a swine stool, estimated by plaque assay on *E. coli* O157:H7 EDL933, was 4.2x10(7) plaque-forming units per g sample. PP01 infects strains of *E. coli* O157:H7 but does not infect *E. coli* strains of other O-serogroups and K-12 strains. Infection of an *E. coli* O157:H7 culture with PP01 at a multiplicity of infection of two produced a drastic decrease of the optical density at 600 nm due to cell lysis. The further incubation of the culture for 7 h produced phage-resistant *E. coli* O157:H7 mutant. One PP01-resistant *E. coli* O157:H7 mutant had lost the major outer membrane protein OmpC. Complementation by ompC from a O157:H7 strain but not from a K-12 strain resulted in the restoration of PP01 susceptibility suggesting that the OmpC protein serves as the PP01 receptor. DNA sequences and homology analysis of two tail fiber genes, 37 and 38, responsible for the host cell recognition revealed that PP01 is a member of the T-ev en bacteriophages, especially the T2 family

55. **Contribution of microbial activity to virus reduction in saturated soil. Nasser, A. M., Glozman, R., Nitzan, Y. (2002). *Water Research* 36:2589-2595.** Application of wastewater to soil may result in the contamination of groundwater and soil with pathogenic microorganisms and other biological and chemical agents. This study was performed to determine the antiviral microbial activity of soil saturated with secondary effluent. Low concentrations (0.05mg/ml) of protease pronase resulted in the inactivation of more than 90% of seeded Cox-A9 virus, whereas Poliovirus type 1, Hepatitis A virus (HAV) and MS2 bacteriophages were found to be insensitive to the enzyme activity. Exposure of Cox A9 virus to *P. aeruginosa* extracellular enzymes resulted in 99% inactivation of the seeded virus. Hepatitis A virus was found to be as sensitive as the Cox A9 virus, whereas Poliovirus 1 and MS2 were found to be insensitive to P. aeruginosa extracellular enzymatic activity. Furthermore, the time required for 99% reduction (T99) of Cox A9 and MS-2 Bacteriophage, at 15 degrees C, in soil saturated with secondary effluent was found to be 7 and 21 days, respectively. Faster inactivation was observed for MS2 and Cox A9 in soil saturated with secondary effluent incubated at 30 degrees C, T99 of 2 and 0.3 days, respectively. Although the concentration of the total bacterial count in the soil samples increased from 10^3 cfu/g to 10^5 cfu/g after 20 days of incubation at 30 degrees C, the proteolytic activity was below the detection level. The results of this study indicate that the virucidal effect of microbial activity is virus type dependent. Furthermore microbial activity in the soil material can be enhanced by the application of secondary effluent at higher temperature. The results also showed that MS2 bacteriophage can be used to predict viral contamination of soil and groundwater

56. **The dilemma of phage taxonomy illustrated by comparative genomics of Sfi21-like Siphoviridae in lactic acid bacteria. Proux, C., van Sinderen, D., Suarez, J., Garcia, P., Ladero, V., Fitzgerald, G. F., Desiere, F., Brussow, H. (2002). *Journal of Bacteriology* 184:6026-6036.** The complete genome sequences of two dairy phages, *Streptococcus thermophilus* phage 7201 and *Lactobacillus casei* phage A2, are reported. Comparative genomics reveals that both phages are members of the recently proposed Sfi21-like genus of Siphoviridae, a widely distributed phage type in low-GC-content gram-positive bacteria. Graded relatedness, the hallmark of evolving biological systems, was observed when different Sfi21-like phages were compared. Across the structural module, the graded relatedness was represented by a high level of DNA sequence similarity or protein sequence similarity, or a shared gene map in the absence of sequence relatedness. This varying range of relatedness was found within Sfi21-like phages from a single species as demonstrated by the different prophages harbored by *Lactococcus lactis* strain IL1403. A systematic dot plot analysis with 11 complete *L. lactis* phage genome sequences revealed a clear separation of all temperate phages from two classes of virulent phages. The temperate lactococcal phages share DNA sequence homology in a patchwise fashion over the nonstructural gene cluster. With respect to structural genes, four DNA homology groups could be defined within temperate *L. lactis* phages. Closely related structural modules for all four DNA homology groups were detected in phages from *Streptococcus* or *Listeria*, suggesting that they represent distinct evolutionary lineages that have not uniquely evolved in *L. lactis*. It seems reasonable to base phage taxonomy on data from comparative genomics. However, the peculiar modular nature of phage evolution creates ambiguities in the definition of phage taxa by comparative genomics. For example, depending on the module on which the classification is based, temperate lactococcal phages can be classified as a single phage species, as four distinct phage species, or as two if not three different phage genera. We propose to base phage taxonomy on comparative genomics of a single structural gene module (head or tail genes). This partially phylogeny-based taxonomical system still mirrors some aspects of the current International Committee on Taxonomy in Virology classification system. In this system the currently sequenced lactococcal phages would be grouped into five genera: c2-, sk1, Sfi11-, r1t-, and Sfi21-like phages

57. **The dual role of wild phages for horizontal gene transfer among *Salmonella* strains. Rabsch, W., Mirold, S., Hardt, W. D., Tschape, H. (2002). *Berliner und Munchener tierarztliche Wochenschrift* 115:355-359.** *Salmonella* bacteriophages seem to mediate horizontal transfer of virulence functions among *Salmonella* strains in two different ways: by general transduction and also by lysogenic conversion. The majority of wild phages isolated from *Salmonella* strains belong to the P22 like phages and were able to transduce. Our data show that the lysogenic conversion is generally accompanied by changes in the susceptibility to the typing phages used for epidemiological purposes. Similar phage type conversions to *S. Typhimurium* DT104 could be detected upon lysogenization with two other *S. Typhimurium* strains. For some *S. Typhimurium* strains the typical phage pattern is actually associated with alterations of virulence characteristics. For example, all tested wild type isolates of phage types DT49 and DT204 were found to be SopE phi-lysogens. The Anderson typing phages interfere with the prophages and/or cryptic phages and so the complex genetic short-term evolution can be demonstrated in the lab. This is one reason for the successful application of phage typing in Salmonella epidemiology since the 50s

58. **Remarkable morphological diversity of viruses and virus-like particles in hot terrestrial environments. Rachel, R., Bettstetter, M., Hedlund, B. P., Haring, M., Kessler, A., Stetter, K. O., Prangishvili, D. (2002). *Archives of Virology* 147:2419-2429.** Electron microscopic studies of the viruses in two hot springs (85 degrees C, pH 1.5-2.0, and 75-93 degrees C, pH 6.5) in Yellowstone National Park revealed particles with twelve different morphotypes. This diversity encompassed known viruses of hyperthermophilic archaea, filamentous Lipothrixviridae, rod-shaped Rudiviridae, and spindle-shaped Fuselloviridae, and novel morphotypes previously not observed in nature. Two virus types resembled head-and-tail bacteriophages from the families Siphoviridae and Podoviridae, and constituted the first observation of these viruses in a hydrothermal environment. Viral

hosts in the acidic spring were members of the hyperthermophilic archaeal genus *Acidianus*

59. **Column experiments to study nonlinear removal of bacteriophages by passage through saturated dune sand. Schijven, J. F., Hassanizadeh, S. M., de Bruin, H. A. M. (2002). *J. Contam. Hydrol* 58:243-259.** In a recent field study on dune recharge, bacteriophages MS2 and PRD1 were found to be removed 3 log10 over the first 2.4 m and only 5 log10 over the next 27 m. To understand the causes of this nonlinear removal, column experiments were carried out under conditions similar to the field: same recharge water, temperature (5 +/- 3 degrees C) and pore water velocity (1.5 m day(-1)). Soil samples were taken along a streamline between the recharge canal and the first monitoring well. Bacteriophage phiX174 was included for comparison. The high initial removal in the field was found not to be due to heterogeneity of phage suspensions but to soil heterogeneity. Phage removal rates correlated strongly positively with soil organic carbon content, and relatively strongly positively with silt content and the presence of ferric oxyhydroxides. Soil organic carbon content, silt content and the presence of ferric oxyhydroxides were found to decrease exponentially with travel distance. Removal rates of phiX174 were found to be 3-10 times higher than those of MS2 and PRD1 due to the lower electrostatic repulsion that the less negatively charged phiX174 experiences. It is suggested that the high initial removal in the field is due to the presence of favorable sites for attachment formed by ferric oxyhydroxides that decrease exponentially with travel distance. Similar removal rates may be found at both laboratory and field scale. However, due to local variations at field scale detailed knowledge on soil heterogeneity may be needed to enable a reliable prediction of removal

60. **Two-site kinetic modeling of bacteriophages transport through columns of saturated dune sand. Schijven, J. F., Hassanizadeh, S. M., de Bruin, R. H. A. M. (2002). *Journal of contaminant hydrology* 57:259-279.** Breakthrough curves, on a semi-log scale, from tests in porous media with block-input of viruses, bacteria, protozoa and colloidal particles often exhibit a typical skewness: a rather slowly rising limb and a smooth transition of a declining limb to a very long tail. One-site kinetic models fail to fit the rising and declining limbs together with the tail satisfactorily. Inclusion of an equilibrium adsorption site does not seem to improve simulation results. This was encountered in the simulation of breakthrough curves from a recent field study on the removal of bacteriophages MS2 and PRD1 by passage through dune sand. In the present study, results of laboratory experiments for the study of this issue are presented. Breakthrough curves of salt and bacteriophages MS2, PRDI, and phiX174 in 1 D column experiments have been measured. One- and two-site kinetic models have been applied to fit and predict breakthrough curves from column experiments. The two-site model fitted all breakthrough curves very satisfactorily, accounting for the skewness of the rising limb as well as for the smooth transition of the declining limb to the tail of the breakthrough curve. The one-site model does not follow the curvature of the breakthrough tail, leading to an overestimation of the inactivation rate coefficient for attached viruses. Interaction with kinetic site 1 is characterized by relatively fast attachment and slow detachment, whereas attachment to and detachment from kinetic site 2 is fast. Inactivation of viruses and interaction with kinetic site 2 provide only a minor contribution to removal. Virus removal is mainly determined by the attachment to site 1. Bacteriophage phiX174 attached more than MS2 and PRD1, which can be explained by the greater electrostatic repulsion that MS2 and PRD1 experience compared to the less negatively charged phiX174

61. **Improved method for recovery of bacteriophage from large volumes of water using negatively charged microporous filters. Scott, T. M., Lukasik, J., Farrah, S. R. (2002). *Canadian Journal of Microbiology* 48:305-310.** Current virus-recovery procedures using negatively charged microporous filters provide an inexpensive, reliable method for the recovery and detection of enteroviruses from water and wastewater; however, adjustment of the test samples to pH 3.5 to promote enterovirus adsorption results in significant inactivation of bacteriophage and an inability to simultaneously recover them from large volumes of water using this procedure. Procedures specifically designed for the detection of bacteriophage are currently in use but generally are only effective for small volumes of water. Positively charged filters can be used to recover both enteroviruses and bacteriophage from large volumes of water at neutral pH; however, the filters are expensive. The addition of manganese chloride to test solutions at pH 3.5 prior to filtration through negatively charged Filterite filters allowed for sampling of larger volumes of water by reducing the inactivation of bacteriophage and increasing the recovery of PRD1, MS2, and naturally isolated bacteriophage by a factor of four or five when compared with recoveries from solutions without MnCl2. This method provides an inexpensive, reliable alternative to large-volume bacteriophage recovery procedures that use positively charged filters at neutral pH

62. **E.coli cell-cycle regulation by bacteriophage lambda. Sergueev, K., Court, D., Reaves, L., Austin, S. (2002). *Journal of Molecular Biology* 324:297-307.** We re-examined the old but surprising claim of Kourilsky and Knapp that transient expression of genes located downstream of the p(L) promoter of bacteriophage lambda can induce cell-cycle synchrony in a population of *Escherichia coli* cells. Although we were unable to reproduce a lasting synchrony, a cessation of division, followed by one or two fairly synchronous cell divisions was observed. This line up of the cell cycle was found to be due to two genetically separable events: a temporary block of cell division and, at the same time, a block to the initiation of new rounds of DNA replication. These blocks then release after about one mass doubling so that chromosome replication and cell division occur during a short time interval in all the cells in the population. The cell division block is a result of the transient expression of the lambda kil gene. The block to initiation of DNA replication requires a region that we term bin (blocks initiation) immediately upstream of the xis gene. The region consists of ea22 and ea8.5 and two small open reading frames (ORFs) that flank them. Deletion-substitution mutagenesis suggests that all four ORFs may be required for the initiation block. The ability of the phage to modify two aspects of the host cell cycle presumably reflects a stratagem that provides the phage with an advantage for lysogeny or lytic growth

63. **Fates of bacteriophages and bacterial indicators in the Moselle river (France). Skraber, S., Gantzer, C., Maul, A., Schwartzbrod, L. (2002). *Water Research* 36:3629-3637.** It has been suggested that bacteriophages can provide useful information about the pathogenic microorganisms, particularly enteric viruses, present in water. This information is complementary to that obtained from bacterial indicators of faecal contamination, which would be of great value for evaluating the risks associated with the use of certain types of water. Before bacteriophages can be used as indicators of faecal contamination, we need to confirm that bacteriophages give a different response to that given by the well-known bacteria indicators and to determine what happens to bacteriophages in river water. Indeed, drinking water is often produced from river water, either by natural filtration through the soil or after undergoing various treatments. We collected 96 river water samples from six different sites between February and November 2000. The samples were analysed for three faecal indicator bacteria (thermotolerant coliforms, enterococci and spores of sulphite-reducing anaerobes) and three types of bacteriophages (somatic coliphages, F-specific phages and *Bacteroides fragilis* phages). The densities of thermotolerant coliforms and enterococci depended mainly on physical factors such as flow rate and water temperature. High temperature and low flow rate led to a decrease in the density of these microorganisms, especially in the absence of a major input of faecal pollution. Conversely, the densities of somatic coliphages, F-specific phages and spores of sulphite-reducing anaerobes remained constant regardless of the flow rate and temperature. The density of *Bacteroides fragilis* phages was too low for unambiguous determination of their fate in river water

64. **Bacteriophage therapy. Stalin's forgotten cure. Stone, R. (2002). *Science* 298:728-731.**

65. **Bacteriophage therapy. Food and agriculture: testing grounds for phage therapy. Stone, R. (2002). *Science* 298:730.**

66. **Thermophilic lactic acid bacteria phages isolated from Argentinian dairy industries. Suarez, V. B., Quiberoni, A., Binetti, A. G., Reinheimer, J. A. (2002). *Journal of Food Protection* 65:1597-1604.** Sixty-one natural phages (59 of Streptococcus thermophilus and 2 of Lactobacillus delbrueckii subsp. bulgaricus) were isolated from Argentinian dairy plants from November 1994 to July 2000. Specifically, 17 yogurt samples (18% of all samples) and 26 cheese samples (79%) contained phages lytic to *S. thermophilus* strains. The number of viral particles found in samples ranged from 10^2 to 10^9 PFU/ml. The phages belonged to Bradley's group B or the Siphoviridae family (morphotype B1). They showed high burst size values and remarkably short latent periods. The results of this study show that phages were found more frequently in cheesemaking processes than in yogurt-making processes. The commercial streptococcus strains appeared to propagate more phages, whereas the natural strains propagated fewer phage strains. These results suggest that the naturally occurring cultures are inherently more phage resistant

67. **Emerging foodborne pathogens. Tauxe, R. V. (2002). *International Journal of Food Microbiology* 78:31-41.** The broad spectrum of foodborne infections has changed dramatically over time, as well-established pathogens have been controlled or eliminated, and new ones have emerged. The burden of foodborne disease remains substantial: one in four Americans is estimated to have a significant foodborne illness each year. The majority of these illnesses are not accounted for by known pathogens, so more must remain to be discovered. Among the known foodborne pathogens, those more recently identified predominate, suggesting that as more and more is learned about pathogens, they come under control. In addition to the emergence or recognition of new pathogens, other trends include global pandemics of some foodborne pathogens, the emergence of antimicrobial resistance, the identification of pathogens that are highly opportunistic, affecting only the most high-risk subpopulations, and the increasing identification of large and dispersed outbreaks. New pathogens can emerge because of changing ecology or changing technology that connects a potential pathogen with the food chain. They also can emerge de novo by transfer of mobile virulence factors, often through bacteriophage. Though this is rarely observed, it can be reconstructed. Better understanding of the ecology and dynamics of phage transmission among bacteria will help us to understand the appearance of new pathogens in the future. One may look for emerging foodborne pathogens among the silent zoonoses, and among the severe infections affecting the immunocompromised humans. We should expect the unexpected. In the past, separating human sewage and animal manure from human food and water supplies was critical to improving public health. Now, our health depends increasingly on the safety of the feed and water supplies for the animals themselves. The successes of the 20th century and the new challenges we face mean that public health vigilance, careful investigation of new problems, responsible attention to food safety from farm to table, and partnerships to bring about new foodborne disease control measures will be needed for the foreseeable future

68. **New ways to treat bacterial infections. Taylor, P. W., Stapleton, P. D., Paul L.J. (2002). *Drug discovery today* 7:1086-1091.** There is an urgent need for fresh approaches to the treatment of bacterial infections because of the changing patterns of infectious disease and the emergence of bacterial strains resistant to current antibiotics. Modification of the cell phenotype to sensitize bacteria to components of the hosts' immune system or to previously ineffective antibiotics could prevent the emergence of the resistant genotype. In addition, the use of light-activated antibacterial agents and lytic bacteriophage specific for key pathogens should be considered as safe and inexpensive alternatives to conventional treatment regimens for certain non-systemic infections

69. **Effect of phage therapy on the turnover and function of peripheral neutrophils. Weber-Dabrowska, B., Zimecki, M., Mulczyk, M., Gorski, A. (2002). *FEMS Immunology and Medical Microbiology* 34:135-138.** The aim of this investigation was to establish the impact of phage therapy on the turnover and function of circulating neutrophils in 37 patients with suppurative bacterial infections. We determined the levels of circulating neutrophils and their precursors before therapy, after 3 weeks of therapy, and at a distant time interval (3 months) following the beginning of therapy. In addition, we measured the ability of neutrophils to phagocytize *Staphylococcus aureus* in vitro. Eight healthy blood donors served as a control group. The results showed that, among the studied parameters, the significant changes involved neutrophil precursor count and the ability of neutrophils to phagocytize bacteria. The percentage of neutrophils in patients before therapy was lower than in healthy donors (mean 58.0, versus 61.4). This value dropped further in patients after 3 months of following the therapy (mean 55.6). The content of neutrophil precursors, on the other hand, was lower in healthy donors than in patients before therapy (mean 2.5, versus 3.8). After 3 weeks of the therapy and after 3 months, the levels of neutrophil precursors were significantly higher (mean 4.8 and 4.9, respectively) than in control donors. The phagocytic index was lower in patients before therapy than in control donors (mean 66.3, versus 70.1) and decreased further after 3 weeks of therapy (mean 59.0) and after 3 months (mean 59.6). The results of this investigation indicate that successful phage therapy accelerates the turnover of neutrophils, accompanied by a decrease in their ability to phagocytize bacteria

70. **Modulation of the susceptibility of intestinal bacteria to bacteriophages in response to Ag43 phase variation -- a hypothesis. Wegrzyn, G., Thomas, M. S. (2002). *Medical Science Monitor* 8:HY15-HY18.** *Escherichia coli* is a Gram-negative bacterium which colonizes the intestinal tract of man and other animals. In addition to being a part of the normal bacterial flora of the human intestine, there are a number of enteropathogenic strains of *E. coli* which cause infections ranging in consequence from diarrhoea to colitis. Antigen 43 (Ag43) is the major phase-variable protein in the outer membrane of *E. coli*. One benefit for bacteria resulting from phase variation of surface antigens is usually ascribed to evasion of host defences. However, results of recent studies indicate that infection of *E. coli* by different bacteriophages is inhibited in the presence of certain bile salts and carbohydrates (components present in the human intestine but absent in standard bacteriological media) when cells are in the 'OFF' state for production of Ag43. The inhibition of bacteriophage development was found to be due to a significant impairment in the process of phage adsorption and evidence was presented for the binding of phage to Ag43. Here we present a hypothesis that in the case of Ag43, phase-variation might benefit the host bacterium by modulating the susceptibility to phage infection in the gut. If this hypothesis is true, it may have important implications not only for basic research but also for development of bacteriophage therapy, a re-discovered method of treatment of patients with infectious diseases

71. **Bacteriophage HP2 of *Haemophilus influenzae*. Williams, B. J., Golomb, M., Phillips, T., Brownlee, J., Olson, M. V., Smith, A. L. (2002). *Journal of Bacteriology* 184:6893-6905.** Temperate bacteriophages effect chromosomal evolution of their bacterial hosts, mediating rearrangements and the acquisition of novel genes from other taxa. Although the *Haemophilus influenzae* genome shows evidence of past phage-mediated lateral transfer, the phages presumed responsible have not been identified. To date, six different *H. influenzae* phages are known; of these, only the HP1/S2 group, which lyosogenizes exclusively

Rd strains (which were originally encapsulated serotype d), is well characterized. Phages in this group are genetically very similar, with a highly conserved set of genes. Because the majority of *H. influenzae* strains are nonencapsulated (nontypeable), it is important to characterize phages infecting this larger, genetically more diverse group of respiratory pathogens. We have identified and sequenced HP2, a bacteriophage of nontypeable *H. influenzae*. Although related to the fully sequenced HP1 (and even more so to the partially sequenced S2) and similar in genetic organization, HP2 has a few novel genes and differs in host range; HP2 will not infect or lysogenize Rd strains. Genomic comparisons between HP1/S2 and HP2 suggest recent divergence, with new genes completely replacing old ones at certain loci. Sequence comparisons suggest that *H. influenzae* phages evolve by recombinational exchange of genes with each other, with cryptic prophages, and with the host chromosome

72. **Phage mediated horizontal transfer of the sopE1 gene increases enteropathogenicity of *Salmonella enterica* serotype Typhimurium for calves. Zhang, S., Santos, R. L., Tsolis, R. M., Mirold, S., Hardt, W. D., Adams, L. G., Baumler, A. J. (2002). *FEMS Microbiol Lett* 217:243-247.** Epidemiological evidence shows that the sopE1 gene is associated with *Salmonella Typhimurium* phage types causing epidemics in cattle. In this study we demonstrate that horizontal transfer of the sopE1 gene by lysogenic conversion with the SopEphi increased enteropathogenicity of *S. Typhimurium* in the bovine ligated ileal loop model. These data support the hypothesis that phage mediated horizontal transfer of the sopE1 gene contributes to the emergence of epidemic cattle-associated *S. Typhimurium* clones

73. **Mutant bacteriophage with non-catalytic endosialidase binds to both bacterial and eukaryotic polysialic acid and can be used as probe for its detection. Aalto, J., Pelkonen, S., Kalimo, H., Finne, J. (2001). *Glycoconjugate Journal* 18:751-758.** There is a molecular mimicry between the polysialic acid polysaccharide of bacterial pathogens causing sepsis and meningitis, and the carbohydrate units of the neural cell adhesion molecule NCAM. We investigated whether bacteriophage mutants with catalytically disabled endosialidase, which bind but do not cleave polysialic acid, could recognise and bind to bacterial and eukaryotic polysialic acid. In nitrocellulose dot blot assay the mutant bacteriophages, but not the wild-type phages, remained specifically bound to polysialic acid-containing bacteria including *Escherichia coli* K1 and K92, group B meningococci, *Mannheimia* (*Pasteurella*) *haemolytica* A2, and *Moraxella nonliquefaciens*. A minimum binding requirement was determined to be 10 sialyl residues in the polysialic acid chain. In Western blots the mutant phages specifically bound to the embryonic polysialylated form of NCAM, but not to the adult less sialylated form of the molecule. The mutant phages together with secondary anti-phage antibodies were subsequently successfully used in fluorescence microscopy of cultured cells and light microscopy of paraffin-embedded tissue sections as a probe for the eukaryotic polysialic acid. Thus, mutant bacteriophages of meningitis causing bacteria bind to and detect the molecularly mimicked polysialic acid of the neural cell adhesion molecule in host tissues

74. **Expression and immunogenicity of a liver stage malaria epitope presented as a foreign peptide on the surface of RNA-free MS2 bacteriophage capsids. Heal, K. G., Hill, H. R., Stockley, P. G., Hollingdale, M. R., Taylor-Robinson, A. W. (1999). *Vaccine* 18:251-258.** We have designed a novel vaccine strategy which enables display of short peptides expressed from chimeras of the gene encoding the coat protein of the RNA bacteriophage MS2 and inserted foreign DNA. MS2 coat protein has a beta-hairpin loop at the N-terminus which forms the most radially distinct feature of the mature capsid. The coat protein gene was modified to enable insertion of DNA at the central part of the beta-hairpin loop. Upon expression of the recombinant gene in *E. coli*, the MS2 coat protein subunits self-assemble into capsids, each comprising 180 copies of the monomer. This system was used to produce chimeras containing a putatively protective epitope, T1, from the immunodominant liver stage antigen-1 (LSA-1) of the malaria parasite *Plasmodium falciparum*. The immunogenicity of the native MS2 capsid and the recombinant construct was investigated in BALB/c (H-2(d)) mice. The native protein appeared to elicit both humoral and cellular immune responses, observed as a predominance of type 2 cytokines but with a mixed profile of immunoglobulin isotypes. In contrast, the LSA-1 chimera stimulated a type 1-polarised response, with significant upregulation of interferon-gamma, a finding which corroborates naturally acquired resistance to liver stage malaria. These results validate RNA phage capsid display of immunogenic determinants as a basis for the development of novel peptide vaccines and indicate that further evaluation of MS2 coat protein as a vector for malaria epitopes is merited

75. **Generalized transduction of small *Yersinia enterocolitica* plasmids. Hertwig, S., Popp, A., Freytag, B., Lurz, R., Appel, B. (1999). *Applied and Environmental Microbiology* 65:3862-3866.** To study phage-mediated gene transfer in *Yersinia*, the ability of *Yersinia* phages to transduce naturally occurring plasmids was investigated. The transduction experiments were performed with a temperate phage isolated from a pathogenic *Yersinia enterocolitica* strain and phage mixtures isolated from sewage. Small plasmids (4.3 and 5.8 kb) were transduced at a frequency of 10(-5) to 10(-7)/PFU. However, we could not detect the transduction of any indigenous virulence plasmid (ca. 72 kb) in pathogenic *Yersinia* strains. Transductants obtained by infection with the temperate phage were lysogenic and harbored the phage genome in their chromosomes

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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.