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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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Editorial

Editorials should be written on subjects relevant to The Bacteriophage Ecology Group as an organization, to *BEG News* (either the concept or a given issue of *BEG News*), or the science of Bacteriophage Ecology. While my assumption is that I will be writing the bulk of these editorials, I wish to encourage as many people as possible to seek to relieve me of this duty, as often as possible. Additionally, I welcome suggestions of topics that may be addressed. Please address all correspondences to abedon.1@osu.edu or to "Editorials," *Bacteriophage Ecology Group News*, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. Please send all submissions as Microsoft Word documents, if possible (I'll let you know if I have trouble converting other document formats), and in English.

Naming Bacteriophages

by Hans-Wolfgang Ackermann & Stephen Tobias Abedon

The first bacteriophage known to science was the *Bacteriophagum intestinale* described by Félix d'Hérelle (3), an enterobacterial phage or a mixture of phages that was considered by d'Hérelle as a single virus with many races. In 1961 Eisenstark published the first list of phages, which included 111 phages with tailed, cubic or filamentous morphology (4). A second phage list, published by Fraenkel-Conrat in 1974, included 411 bacterial viruses and the dimensions and physicochemical properties of many of them (5). Unfortunately, phage names with the Greek letter ϕ were reported without this letter. At present, over 5000 bacteriophages have been studied by electron microscopy and can be attributed to 11 virus families.

During 80 years, phage names have been constructed in the absence of any system and usually reflect little more than their author's imagination (or lack thereof). Phage nomenclature is therefore in a primitive and confusing state. Phage names may:

1. Be single letters or numerals in any combination, even names of individuals or cities.
2. Include the Greek letter ϕ or the Latin letter P to indicate *phage* status.
3. Include special types (^{superscript} or $_{infrascript}$ characters, dots, dashes).
4. Vary between authors, studies, even printer conventions.

As a result, (i) phage names do not reflect basic phage properties, (ii) synonyms and homonyms abound, and (iii) some designations are unduely complicated and a printer's nightmare. Certain synonyms of enterobacterial phages are even willful creations of investigators who published one and the same virus up to six times under different designations. Further ambiguities are created by the identity of some Roman letters and numerals (I, V), or are the product of odd printer conventions (witness, for the latter, the ambiguous numeral subscript status of the original T phages of *Escherichia coli* B; 2). However, one notes that quite numerous phage names have been constructed from host names and therefore reflect host ranges, and that names of temperate phages often comprise two elements, one for the phage and another for the host strain.

Eighty years after the discovery of phages, it it clearly too late to construct a nomenclature system that reflects basic phage properties such as nucleic acid or particle shape. The most that can be done is to limit the amount of synonyms and homonyms. The practice of constructing phage names from host names should be continued as it gives at least a clue to the phage. We suggest the following:

1. To use the first two letters of the host genus and the host species names, respectively (e.g., Esco for *Escherichia coli*).
2. To complement the above constructs with any letters or numerals (e.g., Esco1).
3. To avoid the over-used letters ϕ and P.
4. To avoid superscript or infrascript characters, parentheses, or dashes.
5. To check phage-name lists (e.g., "Bacteriophage Names 2000") for naming precedent.
6. To avoid the invention of new names for old phages.
7. To click here for a description of ICTV nomenclature rules.
8. To obtain rules on virus genera and families see Van Regenmortel, M.H.V., Fauquet, C.M., Bishop, D.H.L. (eds.-in-chief). 2000. *Virus Taxonomy. Classification and nomenclature of Viruses. Seventh Report of the International Committee on Taxonomy of Viruses.* Academic Press, San Diego, 1065-1069.

For reference, see our new web site, Bacteriophage Names 2000, which presents these names alphanumerically, by phage family, and by host genera. We have also compiled a "List of Phage Names" that we present below.

References

1. Ackermann, H.-W. 2001. Bacteriophage descriptions in the year 2000. Arch. Virol., in press.
2. Demerec, M., and Fano, U. 1945. Bacteriophage-resistant mutants in *Escherichia coli*. Genetics 30, 119-136.
3. D'Hérelle, F. 1918. Technique de la recherche du microbe filtrant bactériophage (*Bacteriophagum intestinale*). C.R. Soc. Biol. 81, 1160-1162.
4. Eisenstark, A. 1967. Bacteriophage techniques. In: Maramorosch, K., Koprowski, H. (eds.), Methods in Virology, vol. 1. Academic Press, New York, pp. 449-525.
5. Fraenkel-Conrat, H., 1974. Descriptive catalogue of viruses. In: Fraenkel-Conrat, H., Wagner, R.R. (eds.), Comprehensive Virology, vol. 1, Plenum Press, New York, pp. 121-156.

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New BEG Members

The BEG members list can be found at www.phage.org/beg_members.htm as well as on the BEG home page. As we add new members, these individuals will be introduced in this section. Note that, in fact, there are two ways of "joining" BEG. One, the "traditional" way, is to have your name listed on the web page and on the list server. The second, the "non-traditional" way, is to have your name only listed on the list server. The latter I refer to as "non-members" on that list. Members, e.g., individuals listed on the BEG home page, should be limited to individuals who are actively involved in science and who can serve as a phage ecology resource to interested individuals. If you have an interest in phage ecology but no real expertise in the area, then you should join as a non-member. To join as a member, please contact BEG using the following link: abedon.1@osu.edu. Include:

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

Note that it is preferable that you include the full reference, including the abstract, if the reference is not already present in the BEG bibliography. Responsibility of members includes keeping the information listed on the BEG members list up to date including supplying on a reasonably timely basis the full references of your new phage ecology publications. Reprints can also be sent to *The Bacteriophage Ecology Group*, care of Stephen Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. To join BEG as a non-member, please contact BEG using the following link: abedon.1@osu.edu and minimally include your name and e-mail address.

Please welcome our newest members

name (home page links)	status	e-mail	address
Christina Burch	---	cburch @princeton.edu	Department of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ 08540
	interests:	I have used the bacteriophage phi-6 as a model system to examine whether conceptual frameworks such as Fisher's geometric model of adaptation and Wright's adaptive landscape accurately predict the genetics of adaptation. (contents | BEG members | top of page)	
Sylvain Moineau	PI	Sylvain.Moineau @bcm.ulaval.ca	Professeur agrégé / Associate Professor, Department of Biochemistry and Microbiology, Faculté des sciences et de genie, Université Laval, Québec, Canada, G1K 7P4
	interests:	My research group focuses on phages of *Lactococcus lactis* and *Streptococcus thermophilus*. These dairy phages are investigated from several aspects such as classification, control, detection, ecology, evolution, genomic and proteomic. (contents | BEG members | top of page)	
David Prangishvili	PI	david.prangishvili @biologie.uni-r.de	Universität Regensburg, Lehrstuhl für Mikrobiologie, Univesitätsstrasse 31, 93053 Regensberg GERMANY
	interests:	Molecular biology of extremely thermophilic Archaea including genomics and the evolution of their viruses. (contents | BEG members | top of page)	
Jan Rybniker	---	jrybnike @smail.uni-koeln.de	Institut für medizinische Mikrobiologie, Immunologie und Hygiene; University of Cologne
	interests:	Mycobacteriophages as vectors (always interested in more vectors); general interest in phages - esp. mycobacteriophages (environmental isolation). (contents | BEG members | top of page)	
Steve Tucker	---	s.tucker @mailbox.gu.edu.au	19 Avocado Cres., Bli Bli, Griffith University, Queensland, Australia 4560
	interests:	Potential of phages to influence the number and species composition of bacterioplankton in aquatic ecosystems. (contents | BEG members | top of page)	

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New Links

Links relevant to The Bacteriophage Ecology Group fall into a number of categories (e.g., see Bacteriophage Ecology Links at www.phage.org/beg_links.htm). Listed below are new links found on that page. If you know of a link that should be included on this page, or the whereabouts of a now-dead link, please let me know.

New Bacteriophage Ecology (Etc.) Links

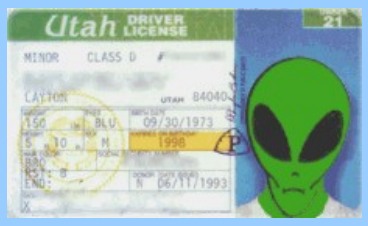
Have you ever wondered how I find new links? Well, as part of my apparently ongoing effort to avoid actually doing a new search for new links, I will tell you my little secrets. Note that these are useful for all sorts of on-line efforts such as finding images for lectures or for seminars. There is no time saver quite like borrowing an image rather than drawing one from scratch.

(Just remember to properly cite all images stolen. I usually do this by linking the image to its source page, though beware that the image may very well have been posted where you found it in violation of copyright. Also, make sure you ask permission before including online images in offline publications and theses.)

So we'll start with images. The hard (but still useful) way to find images is to open your favorite browser, do some sort of key word search, and then manually look for images. A shortcut is to do an altavista (www.altavista.com) image search. This requires that you seek out the "images" link on the altavista homepage (or, alternatively, just click here).

Want to find the image of a phage? Just type "phage" (without the quotation marks) into the altavista image search engine. This will result in the display of a variety of phage or phage-related images. By clicking the associated URL you can visit the page the phage image is found on and then download the image to your own computer by right-mouse clicking on the image and then saving it.

(beware, by the way, that it isn't altogether uncommon for authors to misspell "page" as "phage" or, blasphemy, for the suffix phage to be used to describe all sorts of things that have less to do with bacteria, e.g., "macrophage", etc. Note, for example, the following image:



which is found at the following URL: http://www.bayarea.net/~phage/peeve.htm.)

More interested in text than images? It is no secret that my favorite search engine is supplied by the people at google (www.google.com). This isn't just because a search for "phage" or "bacteriophage" has this site as its number one hit. It is, instead, because google simply works better than other search engines (even yahoo agrees: see: http://google.yahoo.com/bin/query?p=bacteriophage&hc=0&hs=0).

If you are looking for pages addressing, for example, phage ecology, you could try a phage ecology google search. That will yield over 3,000 hits. You can narrow this significantly by placing phage ecology in quotes in your google search: "phage ecology". Now there are "just" 77 web pages listed.

What now? Well, this is the painful part. Now one must walk through each page to confirm that the page really does deal with issues of phage ecology and, otherwise, is reasonably relevant to a phage ecologist. Then, for the sake of links-page maintenance, it is necessary to make sure that the page is not already listed (and, for that matter, it is also necessary to make sure that the links already listed still work... Yuck!).

Want another short cut? Go to the google advanced search page. Now we can get fancy. Want to find all the world's (known) web sites or pages with a link to BEG? Go down to "Page-Specific Search" and do a search under "Links" for www.phage.org. Press the "Search" button and google will display over 300 links presumably phage-ecology related links (see: link:www.phage.org).

Anyway, enough excuses. It's going to be a long, hot summer and with any luck (and sufficient motivation) by the next issue of BEG News I will have updated the BEG links library with new links.

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New Features

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

Bacteriophage Names 2000:

Hans Ackermann has assembled a list of 5000+ phage names (organized with my help). Check it out!

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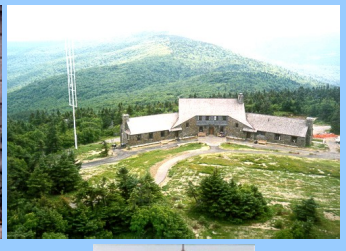
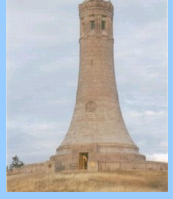
Upcoming Meetings

The BEG Meetings link will continue. Reminders of upcoming meetings will be placed in this section of *BEG News*. If you know of any meetings that might be of interest to BEG members, or would like to recap a meeting that you've attended, then please send this information for posting to abedon.1@osu.edu or to "BEG Meetings," *Bacteriophage Ecology Group News*, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906.

Microbial Population Biology Gordon Conference

This meeting will be held from July 29 through August 3, 2001. The web page for this meeting can be found at http://www.grc.uri.edu/programs/1999/micropop.htm. OK, there will only be one seminar specifically covering phages (by John Yin), but presumably there will be lots of related stuff (e.g., two sessions are titled "Viral Evolution"). Here are some pictures of Western Mass and Williams college:





Evergreen International Phage Meeting

There is still time (before July 1) to get in your abstract for this Summer's phage meeting, to be held August 8-13, 2001. The web page for this meeting can be found at http://www.evergreen.edu/user/T4/2001Meet.html. As always, this will be *the* meeting that brings together phage people with the widest possible array of interests - from the ecological to the molecular - in a setting of rain forest spender in the city that *Time Magazine* dubbed the "Hippest town in the West".

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Jobs

Looking for job? Looking to fill a position? Please send advertisement and information to abedon.1@osu.edu or to "Jobs", Bacteriophage Ecology Group News, care of Stephen T. Abedon, Department of Microbiology, The Ohio State University, 1680 University Dr., Mansfield, Ohio 44906. Please send all information as text (e.g., as an e-mail) or as Microsoft Word documents, if possible (I'll let you know if I have trouble converting any other document formats), and in English. I will update this section as I receive material, regardless of what date this issue of BEG News goes live.

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Submissions

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

A List of Phage Names

by Hans-Wolfgang Ackermann & Stephen Tobias Abedon

a , a , a , a , a , a , A , A , A , A , A , A005 , A006 , A020 , A1 , A1 , A-1 , A-1 , A-1 , A-1(L) , A10 , A10 , A10/45 , a10/J1 , a10/J2 , a10/J5 , a10/J9 , A101 , A11 , A-11 , A11/A79 , A118 , A12 , A12 , A-12 , A128 , A13 , A13 , A13 , A133 , A137 , A139 , A14 , A14 , A-14 , A15 , A155 , A16 , A17 , A182 , A19 , A19 , A1-Dat , A2 , A2 , A2 , A-2 , A20 , A20/415 , A21 , A-21 , A-22 , A23 , A-23 , A-24 , A25 , A29 , A2P , A3 , A3 , A3/2 , A31 , A31 , A33 , A34 , A342 , A36 , A37 , A4 , A4 , A-4(L) , A41 , A422 , A5 , A5 , A5/415 , A5/A6 , A500 , A502 , A511 , A511 , A56-1 , A6 , A6 , A6"C" , A620 , A64/A62 , A640 , A69-4 , A7 , A7 , A74/A3 , A8 , A8 , A856 , A86/A88 , A9 , A9 , A9"C" , Aaϕ23 , Aaϕ247 , Aaϕ76 , Aaϕ97 , Aaϕ99 , AA-1 , Ab-1 , AB48 , AC1 , AC-1 , AC1L16M , AC2 , AC201-S , AC23R-3 , AC28 , Ac3 , AC3 , AC30 , AC43 , AC50 , AC57 , AC6 , AC7 , AC81 , AC95 , Acm1 , Acm2 , Acm5 , Acm6 , Acm7 , $ad1_2$, AE2 , Aeh1 , Aeh2 , af , ag , AG1 , AGL1 , AGL11 , AGL12 , AGL13 , AGL16 , AGL17 , AGL2 , AGL3 , AGL4 , AGL5 , AGL6 , AGL8 , ai , AI-1 , AI-2 , AIO-1 , AIO-2 , *aiz*1 , AL_1 , AI-1 , *ale*1 , alfa , AI-K-I , AN-10 , AN-15 , AN-20 , AN-22 , AN-24 , AN25S1 , AN29R2 , AN31S-1 , AO-1 , AO-2 , AO-3 , *AP*SE-1 , AP-2863 , AP-3 , AP50 , AP50-04 , AP50-11 , AP50-23 , AP50-26 , AP50-27 , Ap85III , AR1 , AR13 , AR2 , AR3 , AR7 , AR9 ,

ARA3 , ARA8 , ARA9 , Arp , AS-1 , AS-1M , A-Saratov , asccϕ28 , ASP16 , ASP2 , ASP4 , ASP7 , AT , AT298 , ATCC 11759 , ATCC 25180 , AU , Av-1 , Av-2 , Av-3 , AV9/3 , b , b , b , B , B , B , B.A.O.R. , B.C$_3$, Bα , B$_{24}$, B$_9$GP , B$_9$PP , b^{581} , B012 , B021 , B024 , B025 , B035 , B051 , B053 , B054 , B055 , B056 , B1 , B1 , B-1 , B10 , B101 , B11 , B110 , B11-1 , B12 , B123BN , B17 , B17 , B1715V1 , B18 , b2 , B2 , B2 , B26 , B271 , B275 , B276 , B277 , B278 , B279 , B282 , B3 , B30 , B33 , B35 , B39 , B39-1 , B40-8 , B5 , B51 , B545 , b594n , b6 , B6 , B604 , B653 , B7 , B7 , B89 , B932a , BA , BA-4 , Bace-11 , BaF1 , Baf-44 , Baf-48B , Baf-64 , Bam35 , Bastille , Bat10 , BB1 , BB10 , BB12 , BB14 , BB4 , BB8 , BC , BC1 , BC2 , BCJA1 , BE/1 , Beccles , Berkeley , BF , Bf-1 , Bf145 , Bf203 , Bf209 , BF307 , Bf-41 , Bf42 , Bf-52 , Bf71 , BFK20 , BG2 , B-I , BI-1 , B-II , bIL67 , Bir , Bk , BK$_5$, BK1 , BK1 , BK1 , BK5 , BK5-T , BK5-T , BL1 , BL1 , BL2 , BL2 , BL3 , BL3 , BL4 , BL5 , BL6 , BL8 , BL9 , BLE , BLL1 , BM$_{29}$, BN1 , Bo1 , BO54 , BP1 , BP123 , BP124 , BP124 , BP128 , BP142 , BP142 , BP153 , BP153 , BP52 , BPP-10 , br , BS1 , BS101 , BS102 , BS104 , BS105 , BS106 , BS107 , BS11 , BS15 , BS16 , BS18 , BS2 , BS20 , BS21 , BS22 , BS23 , BS26 , BS28 , BS28 , BS3 , BS31 , BS32 , BS4 , BS46 , BS5 , BS6 , BS7 , BS8 , BS80 , BSL1 , BSL10 , BSL11 , BSL2 , BT , BT11 , BTB , BU77-B1 , butyricum , BW73 , c , c , c , C , C , C , C , C type , c1 , c1 , C1 , C1 , C1 , C1 , C1 , C-1 , c10I , c10II , c10III , c11 , c13 , C154 , C16 , C163 , C167 , c2 , C2 , C2 , C2 , C2 , C2 , C-2 , C-2 , c20-1 , c20-2 , c-203 Tox- , C2121 , C22 , C236 , C2F , c2t$_1$, c2t$_2$, c3 , c3 , C3 , C3 , c31 , C31 , C36-3 , c4 , C4 , c5 , c5 , C5 , C-5 , C557 , c5h , C5W9 , C60-2 , C625 , c6A , C707 , C966N , CA1 , CA1 , CA1 , CA-1 , CA2 , CA-2 , CA3 , CA-3 , CA-4 , CA5 , CA-5 , Ca7 , CAK1 , cap$_1$, CB3 , CC1 , CD , cd1 , CEβ , CEγ , Cf , Cflt , CFO103 , CG1 , CG2 , CG33 , CG5 , CGK1 (defective) , Ch , ch2 , ChMF-1-P , Chp1 , Cl-1 , Cl-1 , Cl-2 , CK-1 , CL31 , Clark , Cld1 , Clichy 12 , Clm11 , Clm8 , ClmX , ClmXC , CM , cM-ϕ1 , CM$_1$, CM$_2$, CM1 , CM2 , CM20 , CM21 , CM3 , cm4 , CM4 , cm4-9 , CM5 , CM6 , cm-68a , CM7 , CM8 , CM9 , cmf-1-F , CMF-1-F , CMP1 , CN11 , c-n71 , CN8 , Cog , Col 11 , Col 18 , Col 2 , Col 21 , Col1 , CON11 , CON8 , CONX , CONXC , Cor1 , Cp-1 , Cp-10 , Cp-5 , CP-51 , CP-53 , CP-54 , Cp-7 , CP75 , Cp-9 , CPC , CPT , CPT1 , CP-T1 , CPT4 , CRK , CS$_1$, CS-1 , CsI$_{x13}$a , CsI$_{x13}$b , CT , CT , Ct$_{kas}$, CT1 , CT1 , CT2 , CT3 , CT3 , CT4 , CT4 , CT5 , CT6 , CT6 , CT7 , CT8 , CTK , CTXΦ , CVX-5 , CW2 , CW3 , CW4 , CW5 , CWK , d , d , d , D , D , D , D , D , D , D , D , dϕ3 , dϕ4 , dϕ5 , D$_d$-Vi , D1 , D108 , D11 , D20 , D29 , D29 , D2A , D2c , D2d , D3 , D3112 , D37 , D4 , D40 , D441 , D5 , D-5 , D59-1 , D6 , D62 , D8 , DAFV , *dar*1 , DAV1 , DD-2 , DD7 , DDUP , DDVi , DDVI , DD-VI , DDVII , DEβ , *den*1 , DF$_{78}$, D'Hérelle , DLP10716 (defective) , DLP-11946 (defective) , DM-11 , DM-21 , DM-31 , DM-41 , DM-51 , DM-61 , DNAIII , DP-1 , Dp-4 , DP-7 , DPB12 (defective) , DPB21 (defective) , DPB22 (defective) , DPB23 (defective) , DPB5 (defective) , DRC$_2$, DRC$_3$, drc1 , drc2 , drc3 , drc3 , DS96 , DSP$_1$, DT1 , Dundee , e , e , e , E , E , E , EϕB , EΦ-y , e1 , E1 , E1 , e10 , E10-1 , E13 , E14 , E15 , E15P , E16-2 , E16B , E16P , e2 , E2 , E20 , E21 , E24 , E28 , E29 , e3 , E3 , e4 , E4 , E4 , E41 , e5 , E5 , E6 , E62 , E7 , E7 , E79 , e8 , E8 , E9 , eb4 , eb7 , eb9 , EC1 , EC2 , Ec9 , EJ-1 , *ent*1 , *ent*2 , EP1 , EPy-1 , EPy-2 , EPy-3 , EPy-4 , EPy-5 , Erh1 , ES , Esc-7-11 , ESV , ET25 , ET42 , Ev , EV , EW , f , F , F , F , F$_1$, F$_1$m , F$_1$U , F$_{10}$, F$_{10}$, F$_{11}$, F$_{12}$, f$_2$, F$_2$, F$_2$, F$_{20}$140/76 , F$_{25}$, F$_{25}$u , F$_{25}$U , F$_3$, F$_4$, F$_4$, F$_{44}$, F$_{45}$, F$_{48}$, F$_5$, F$_5$, F$_6$, F$_7$, F$_8$, F$_9$, F$_9$, F$_A$101 , F$_E$Ths , F$_K$, F$_K$11 , F$_{KK}$101 , F$_{KL}$10 , F$_{KP}$74 , F$_{LO}$Ths , F$_{LO}$Ths , F$_o$*lac* , F$_Y$101 , f1 , f1 , f-1 , F1 , F1 , F1 , F1 , F1 , F1 , F1 , F1 , F10 , F10 , F10 , F11 , F11 , F116 , F12 , F12-9 , F1m , F1U , f2 , F2 , F2 , F2 , f25 , F25 , F25U , F25V , F26S , F27S , F29-1 , F3 , F3 , F4 , F4 , F4 , F4/L425I , F4/L425II , F4-1 , F44 , F45 , F48 , F5 , F5 , F5 , F5/L422 , F5-4 , F6 , F6 , F7 , F7 , F7 , f7.8 , F8 , F8 , F9 , F9 , F9 , F9-11 , FC3-1 , FC3-10 , FC3-11 , FC3-2 , FC3-3 , FC3-4 , FC3-6 , FC3-7 , FC3-8 , FC3-9 , fd , FD2 , FE5-B2 , FE5-B3 , FE5-B4 , Fels 2 , FH5 , Fi , FI1 , FI-2 , FI3 , FI-4 , FI-5 , FIA , Fim , Firenze 75/13 , FiU , FK , F-K , FO$_1$, FO1 , fOg29 , fOg30 , fOg44 , FoP1 , FoS$_1$, FoS$_2$, FP$_2$, FP1 , FP10 , FP11 , FP2 , FP2 , FP22 , FP3 , FP4 , FP43 , FP5 , FP6 , FP7 , FP8 , FP9 , FPy-1 , FQ1 , fr , FRC1 , FRC2 , FRC3 , FRC4 , fri , fs , F-S , FSα , FS$_1$, FS$_1$, FS$_2$, FS$_2$, FS$_{2a}$, FS$_3$, FS$_4$, FS$_4$, FS$_5$, FS$_5$, FS$_6$, FS$_7$, FS$_8$, FS$_9$, FS$_9$, FS$_{D2b}$, FS$_{D2d}$, FS$_{D2E}$, FS$_{D8}$, fs1 , FS10 , fs2 , FS7 , Fsa , fv , fv2377 , fv2527 , fv83-554/3 , fv8501 , fv88-531/2 , Fyc , Fz , Fz75/13 , g , g , g , G , G , G , G , G$_{10}$, G101 , g12 , g13 , G13 , g14 , G14 , g15 , g16 , g17 , G173 , g18 , g21 , g23 , g24 , g29 , g3 , G3 , G3 , G35 , G36 , G4 , G4 , G4 , G4 , G5 , G5 , G6 , G69-1 , G72-1 , g8 , ga , GA-1 , GA-2 (defective) , *gal*1 , gamma , gamma , gamma 66 , gamma 66a , gb , gb2-80 , gb2t , gb4 , gb-4 , gb4-9 , gd , ge , GE1 , gf , GF-2 , gh-1 , GH8 , GI , GIII , GII , GII , GM , GP1 , GP1 , GP-10 , group I , Group I , group II , group II , group III , group IV , GS$_1$, GS$_4$E , GS$_7$, Gs1 , Gs2 , GS2 , Gs3 , GS4E , GS6 , GS7 , GS-7 , GT-1 , GT-2 , GT-234 , GT-3 , GT-4 , GT-4 , GT-5 , GT-6 , GT-7 , GT8 , GV , GV-1 , GV-2 , GV-3 , GV-5 , GV-6 , GVI , GVIII , GW6210 , h , h , H , H , H , H , HΦ , H$_{11}$/A$_1$, H$_{158}$/A$_1$, H$_{18}$/A$_1$, H$_{22}$/S$_{23}$, H00/1 , h1 , H1 , H-1 , H-1 , H103-1 , H105-1 , H106-1 , H107 , H108 , H108 , H110 , H114/2 , H118/1 , H120/1 , H163/84 , H17/1 , H19 , H19-J , H1OG , H2 , H-2 , H20 , H21 , H22 , H24 , H3 , H-3 , H312 , H340 , H387 , H39 , H391/73 , H3V , H-4 , H43 , H46 , H684/74 , H7/2 , H71/1 , H71/2 , H71/5 , H75 , H8 , H8/73 , H90 , H924A , hb , HB3 , HB-3 , HB-623 , HB-746 , HDC-2 , HF , HF1 , HF2 , Hgal , Hh-1 , Hh-3 , Hi , HI , HI8A , HI8B , HII , HIII , His1 , HIV , HIX , HK022 , HK139 , HK2 , HK243 , HK253 , HK256 , HK620 , HK97 , HM2 , HM3 , HM7 , HMT , hp , HP , HP1 , HP1 , HP1 , HP1 , HP2 , HP3 , HP4 , hq$_1$, hq$_2$, HR , Hr1 , Hs1 , H-Sh , HSO47 , HSV , HT-2 , hv , hv-1 , HVI , HVII , HVIII , hw , hw1 , Hw12 , HXI , HXII , HXX , Hyϕ1A , Hyϕ22a , Hyϕ30 , Hyϕ32a , Hy-11 , Hy-12 , Hy-39 , Hy-40 , Hy-41 , Hy-42 , Hy71 , Hyfa-1 , Hyfa-13 , Hyfa-14 , Hyfa-15 , Hyfa-16 , Hyfa-17 , Hyfa-18 , Hyfa-19 , Hyfa-2 , Hyfa-20 , Hyfa-21 , Hyfa-22 , Hyfa-23 , Hyfa-24 , Hyfa-25 , Hyfa-26 , Hyfa-27 , Hyfa-28 , Hyfa-29 , Hyfa-3 , Hyfa-30 , Hyfa-31 , Hyfa-32 , Hyfa-33 , Hyfa-34 , Hyfa-35 , Hyfa-36 , Hyfa-37 , Hyfa-4 , Hyfa-48 , Hyfa-5 , Hyfa-6 , Hyfa-7 , Hyza-38 , i , i , i , I , I , I , I , Iα , I$_1$, I$_1$/31 , I$_1$/H$_{33}$, I$_2$, I$_2$-2 , I10 , I119 , I129 , I16-1 , I-2 , I3 , I37-1 , I52 , I66 , I8 , I9 , Ia11 , If1 , IF2 , II , II , II , II , II-1 , II-2 , II-3 , II-5 , III , III , III , III , III-1 , IKe , Im , IPα , IP1 , IPy-1 , IRA , IS$_1$, IV , IV , IV , IV , IV , IVa , IVA , IX , IX , j , j , J , J , J , J , J$_1$, J1 , J-1 , J29-1 , J7W-1 , Ja1 , Ja-1 , Jb19 , JCL1032 , Jersey , jj18 , JRW3 , jw1 , jw12 , jw13 , jw14 , jw16B , jw2 , JW2040 , jw25 , jw27 , jw27A , jw31 , jw32 , jw4 , jw8 , jw9a , k , K , K , K , K , K , K , K , K , K , K$_1$, K$_2$/A$_1$, K$_{21}$/S$_{23}$, K$_5$, K$_6$, K^{tox-} , K1 , K10 , K104 , K109 , K139 , K166 , K170/11 , K18 , K19 , K1F , K2 , K2 , K267 , K29 , K3 , K31 , K328 , K4 , K7 , K9 , kappa , KC1 , *ken*1 , KF1 , KI , KII , KIX , KK-88 , KI$_1$, KI$_{106}$B , KI$_{106}$B , KI$_{11}$, KI$_{12}$, KI$_{13}$, KI$_{14}$, KI$_{15}$, KI$_{16}$, KI$_{165}$B , KI$_{17}$, KI$_{171}$B , KI$_{171}$B , KI$_{18}$, KI$_{181}$B , KI$_{181}$B , KI$_{19}$, KI$_2$, KI$_2$B , KI$_{20}$, KI$_{21}$, KI$_{22}$, KI$_{23}$, KI$_{24}$, KI$_{25}$, KI$_{26}$, KI$_{27}$, KI$_{28}$, KI$_{29}$, KI$_3$, KI$_{30}$, KI$_{31}$, KI$_{32}$, KI$_{328}$B ,

KI$_{33}$, KI$_{34}$, KI$_{35}$, KI$_{35}$, KI$_{4}$, KI$_{4}$B , KI$_{4}$B , KI$_{42}$B , KI$_{5}$, KI$_{6}$, KI$_{6}$B , KI$_{7}$, KI$_{765/1}$, KI$_{8}$, KI$_{8}$, KI$_{832}$B , KI$_{842}$B , KI$_{9}$, KI$_{937}$B , KI1 , KI181 , KI181B , KI2 , KI25 , KI27 , KI2B , KI3 , KI31 , KI4 , KI42 , KI42B , KI5 , KI6 , KI7 , KI765/1 , KI8 , KI832B , KI9 , KI9 , KI937B , KLXI , KM1 , Kotljarova , KSY1 , KSY2 , KT , Kum1 , KV , KVI , KVII , Kvp1 , KVP20 , KVP40 , KX , KXI , KXII , Kyu1 , l , L , L , L , L , L.228 , L.359 , lϕ1 , lϕ3 , lϕ7 , lϕ9 , L$_{1}$232 , L$_{2}$232 , L$_{7}$, L^{o} , L^{tox+} , L1 , L1 , L1 (Ia7) , L10(Bb4) , L11(Cb3) , L112 , l12 , L12(Fa6) , L13(Fb2) , L14(Ib10) , L15(Ib8) , L16(MLS4) , L17(Psu-1) , L172 , L172 , L18(1674) , L19(1890) , L2 , L2(Ia8) , L20(2119) , L3(Ea3) , L34 , L39x35 , L4(Aa1) , L412a , L419 , L422 , L422a , L425a , L426a , L431 , L432a , L434a , L439 , L441 , L449 , L5 , L5(Bb4) , L54a , L6(ML34) , L7 (ML34) , L8(1890) , L9(Aa1) , La$_{6}$k$_{1}$, Labol , lacticola , lambda , LB$_{1}$, LB2 , lb4 , lb5 , lb539 , lb6 , LB7 , LC1 , LC2 , LC3 , LC4 , LC5 , Lc-58 , LC6 , Lcg , LC-Nu , LE1 , LE3 , LE4 , Legendre , Leo , LHIIBNV6-2 , LHIIBV7-2 , LIIBNV6-1 , LIIBV7-1 , LI1 , LI2 , LI3 , ll-h , LL-H , LL-K , LL-Ku , LL-S , LP , LP52 , LP-52 , LP7 , LPP-1 , Lr-4 , LTH24P , LTH25P , LTH26P , LTH27P , LTH28P , LTH29P , LTH30P , LTH31P , LTH32P , LTH33P , LTH34P , Lucas 110 , Lucas 303 , Lucas 404 , lv , LV-1 , lvpf5 , m , M , M , M , M , M , M (defective) , M$_{L}$, M1 , M1 , M1 , M1 , M1 , M1 , M102 , M12 , M-12 , m12r , M13 , M-13 , M20 , M3 , M35 , M4 , M42 , M51 , m59 , M6 , M6a , M85 , MAC-1 , MAC-1' , MAC-2 , MAC-3 , MAC-4 , MAC-4' , MAC-5 , MAC-6 , MAC-7 , MB78 , MC/75 , MC-1 , MC-1 , MC-2 , MC-3 , MC-3 , MC-4 , MC-4 , Mex , Mex1 , MG40 , minetti , MJ-1 , MJ-4 , MJP1 , MJP20 , MJP25 , ml1 , ml3 , ML3 , ML34 , MLMa , MLSP1 , MLSP2 , MLSP3 , MM , MM$_{1}$, MM1C , MM1H , MMP1 , MNP1 , MNP2 , MNP7 , MNP8 , MOI , *mor*1 , *mor*2 , Mp1 , MP10 , MP12 , MP13 , MP14 , MP15 , MP20 , MP21 , MP23 , MP24 , MP27 , MP28 , MP29 , MP3 , MP30 , MP32 , MP34 , MP36 , MP37 , MP39 , MP40 , MP41 , MP43 , MP44 , MP45 , MP47 , MP49 , MP50 , MP-7 , MP9 , Ms , MS2 , MSP1 , MSP10 , MSP11 , MSP12 , MSP13 , MSP14 , MSP15 , MSP16 , MSP17 , MSP18 , MSP19 , MSP2 , MSP3 , MSP4 , MSP5 , MSP7 , MSP8 , MSP9 , MT , Mtc1 , MTPH11 , mu , Mu , Mu1 , Mu-1 , MU-1 , Mul , mv1 , Mv-1g1 , Mv-1g2 , mv4 , Mv8g1 , Mv8g2 , MVBr1 , MV-G51 , MV-L1 , MV-L172 , MVL2 , MV-L2 , MVL3 , MV-L3 , MVL51 , MVL52 , MV-L59 , MV-L60 , MV-Lg-L172 , MV-Lg-pS2-L172 , MV-M1 , MV-O1 , MVP4 , MVP5 , MX-1 , Mx4 , MX4 , MX41 , MX43 , Mx8 , Mx81 , Mx9 , MyF$_{3}$P/59a , N , N , N , N$_{2}$, N$_{4}$, N$_{5}$, N^{o}2 , N1 , N1 , N1 , N-1 , N-1 , N10 , N-10 , N11 , N11 , N12 , N13 , N14 , N15 , N16 , N17 , N-17 , N-18 , N19 , N2 , N2 , N2 , N2 , N20 , N-22 , N3 , N3 , N3 , N3 , N4 , N4 , N4 , N4 , N-4 , N40 , N5 , N5 , N5 , N5 , N5 , N-5 , N6 , N6P , N7 , N7 , N8 , N8 , N9 , NA1 , Na1^{tox+} , NA2^{tox-} , NB1^{tox+} , NCDO 01244 , NCMB384 , ND-1 , ND-2 , ND-3 , ND4 , ND-5 , ND6 , ND-7 , Neo1 , Nf , NF5 , NHc , NHs , NJ-L , NLP-1 , NM1 , NM2 , NM3 , NM4 , NM5 , NM6 , NM7 , NM8 , no. 3 , no. 9 , no. A , no. E , No.1 , No.1M (defective) , no.D , NP1 , NS-8 , NSV , nt-1 , NT1 , NT2 , NT3 , NT4 , nt-6 , NTc , NTCC12669 , NTCC12670 , NTCC12671 , NTCC12672 , NTCC12673 , NTCC12674 , NTCC12675 , NTCC12676 , NTCC12677 , NTCC12678 , NTCC12679 , NTCC12680 , NTCC12681 , NTCC12682 , NTCC12683 , NTCC12684 , Nu , O , O1 , O$_{1}$, O-1 , O-1 , O111 , O1205 , O1761 , O2 , O2 , O25 , O3 , o6 , O6N-12P , O6N-21P , O6N-22P , O6N-24P , O6N-25P , O6N-34P , O6N-52P , O6N-58P , O-I , ot , ov$_{1}$, ov$_{2}$, ov$_{3}$, Ox-1 , OX1 , OX1 , Ox2 , Ox-2 , OX2 , OX2 , Ox-3 , Ox-4 , Ox-5 , OX5 , Ox-6 , OXN-100P , OXN-32P , OXN-36P , OXN-52P , OXN-69P , OXN-72P , OXN-85P , OXN-86 , P , P , P , P , P , P.C. , P28 , P$_{22}$, P-$_{23}$, P$_{4}$, P-$_{46}$, P0 , P001 , P002 , P003 , P009 , P009S , P010 , P013 , P026 , P029 , P031 , P034 , P0362 (defective) , P039 , P047 , P053 , P059 , P087 , P096 , P1 , P1 , P1 , P1 , P1 , P1 , P10 , P10 , P10 , P107 , P108 , P109 , P111 , P112ag , P113 , P113G , P114-4BN , P11-M15 , P12 , P12 , P127 , P13 , P13 , P13 , P1-3a , P14 , P14 , P142 , P147 , P159 , P167 , P177 , P179 , P18 , P188 , P191 , P19402 , P1D , P1K , p2 , P2 , P2 , P2 , P2 , P204 , P219 , P22 , P220 , P22-1 , P22-11 , P22-12 , P221BN , P22-3 , P22-4 , P22-7 , P228 , P22a1 , P23 , P232 , P239 , P25 , P27 , P272 , P2-SO-S , P3 , P3 , P3 , P3 , P315 , P32 , P323 , P330 , P335 , P35 , P37-14 , P38 , P38 , P4 , P4 , P4 (defective) , P42 , P42D , P465 , P468II , P49 , P5 , P50 , P50 , P5046 , P51 , P517 , P52 , P52 , P52A , P53 , P53 , P54 , P55 , P56 , P57 , P5771 , P58 , P58I , P58II , P59 , P6 , P6 , P6 , P6 , P63 , P64 , P65 , P67 , P67 , P68 , P69 , P71 , P71 , P73 , P75 , P76 , P77 , P78 , P8 , P8 , P8 , P8 , P82 , P83 , P87 , P88 , P9 , P9 , P9 , P9 , P9 , P90 , P9a , P9c , pA1 , P-a-1 , PA1350e , P-a-2 , PA-2 , P-a-3 , P-a-4 , pa40 , pa42 , P-a-5 , P-a-6 , PA6 , P-a-7 , P-a-8 , P-a-9 , pa97 , PAA17 , PAA23 , PAA24 , PAA84 , pAg-1 , PAU , PB , PB$_{2}$A , PB1 , PB-1 , PB-1 , PB2 , PB2 , PB2A , PB6 , PB-6 , PBA12 , PBC1 , PBL0.5c , PBL1 , PBLA , PBLB (defective) , PBP1 , PBS1 , PBSH (defective) , PBSV (defective) , PBSW (defective) , PBSX (defective) , PBSY (defective) , PBSZ (defective) , PC , PC13-1 , PC35-1 , PCan , PCH-1 , PE1 , PE5 , PE69 , PEa7 , PEal(h) , Pf , Pfö , Pf1 , Pf-1 , PF1 , pf16 , Pf2 , Pf2 , Pf3 , Pf3 , Pf4 , PG , PG60 , PH , Ph-1 , Ph10 , Ph12 , Ph13 , PH132 , Ph14 , PH2 , Ph5 , PH51 , Ph6 , Ph9 , PH93 , phi (defective) , Phl-1 , Phl-5 , phlei , phlei 1 , phlei 4 , PIIBNV6 , PIIBNV6-C , pilHα , Pk , PK1 , pKA-1 , pKG-1 , pKG-2 , pKG-3 , pKG-4 , PL-1 , PL163/10 , PL-2 , PL25 , PL26 , PL37 , PL73 , PL78 , PL81 , PLgY no. 4 , PLgY no.16 , PLgY no.22 , PLgY no.7 , PLS-1 , PLT$_{22}$, PLT22 , Pm1 , PM1 , Pm10 , PM105 , Pm11 , PM113 , PM13 , PM2 , PM2 , Pm3 , PM3 , Pm4 , PM4 , Pm5 , PM5 , PM57 , Pm6 , PM6 , PM61 , PM62 , PM63 , PM681 , PM682 , PM69 , Pm7 , Pm8 , Pm9 , PMB1 , PMB12 , PMJ1 , PMN17 , PMW , PO4 , pOA-1 , POF025 , Polonus I , Polonus II , PP1 , PP1 , PP114 , PP2 , PP206 , PP207 , PP3 , PP306 , PP4 , PP4 , PP401 , PP5 , PP5 , PP56 , PP6 , PP6 , PP64 , PP65 , PP651 , PP66 , PP7 , PP7 , PP71 , PP711 , PP8 , PP8 , PP86 , PP87 , PP88 , PP891 , PP92 , PPN25 , PPN35 , PPN89 , PPN91 , PR10 , PR-1001 , PR3 , PR4 , PR5 , PR-590a , PR64FS , PR772 , PRD1 , pro , PRR1 , ps$_{1}$, PS-10 , PS17 , PS-192 , PS20 , PS3 , PS4 , PS8 , PS-8 , PSA , Psa1 , PSA68 , Psael , PsP1 , PsP2 , Psp231a , PsP3 , PSP3 , PsP4 , PsP5 , PsR-1012 , Pssy15 , Pssy401 , Pssy403 , Pssy404 , Pssy41 , Pssy42 , Pssy420 , Pssy4210 , Pssy4220 , Pssy9220 , Pssy923 , PST , PST , PSU$_{1}$, PT11 , PTB , PTB2 , PTB20 , PTB42 , PTB80 , PV-1 , Pv2 , PWH2 , PX1 , PX10 , PX12 , PX14 , PX2 , PX3 , PX4 , PX5 , PX7 , PYO1 , PYO10 , PYO103 , PYO12 , PYO13 , PYO14 , PYO16 , PYO18 , PYO19 , PYO2 , PYO20 , PYO200 , PYO29 , PYO32 , PYO33 , PYO34 , PYO35 , PYO36 , PYO37 , PYO38 , PYO39 , PYO41 , PYO42 , PYO45 , PYO47 , PYO48 , PYO49 , PYO5 , PYO50 , PYO51 , PYO52 , PYO53 , PYO57 , PYO59 , PYO6 , PYO64 , PYO69 , PYO70 , PYO71 , PYO9 , Pz , q , Q , Qβ , Q-$_{05}$, Q-$_{06}$, Q-$_{16}$, Q-$_{21}$, Q-$_{26}$, Q-$_{40}$, Q-$_{46}$, R , R , R , R , Rϕ-1 , Rϕ6 , Rϕ6P , R$_{1}$, R$_{1}$, R$_{1}$, r$_{1}$t , R$_{1}$-T , R$_{2}$, R$_{S}$29 , R1 , R1 , R17 , R-17 , R1Myb , R1-T , r1v , R2V , R4 , R4 , r6 , rabinovitschi , RB42 , RB43 , RB49 , RB69 , RC1 , RC2 , RC3 , RC5 , RG , R-I , RL1 , RL4 , Roy , rp-1 , Rp1.Rp1 , RP10 , RP2 , RP3 , RP6 , RR68 , RS1 , RS1 , RS2 , RZ1 , RZh , S , S , S , S , S , S$_{111}$, S$_{2}$, S$_{41}$/A$_{1}$, S$_{44}$/S$_{23}$, S$_{9}$/S$_{3}$, S$_{B-1}$, s$_{d}$, S$_{d}$, S$_{D}$, S$_{I}$, S$_{II}$, S$_{IVa}$, S$_{IVAa}$, S$_{IVab}$, S$_{IVb}$, S$_{IX}$, S$_{VI}$, S$_{VII}$, S$_{VIII}$, S$_{VIII}$A , S$_{XI}$, S$_{XII}$, S1 , S1 , S1 , S1 , S-1 , S13 , S-13 , S171 , S1BL , S2 , S2 , S2 , S2 , S2 , S206 , s265 , S-2L , S-2L , S-2L(L) , S3 , S3 , S-3(L) , S3K , S4 , S45 , S-4L(L) , S5 , S-5(L) , S5-L , S6 , S-6(L) , S66 , S-6L , S-7(L) , S70 , S708 , S-7L , S-9 , S-a , SA$_{02}$, Sa1 , SA1 , SA2 , SA3 , SA4 , SA5 , SA6 , SA7 , Sab1 , Sab2 , Sab2 , Sab3 , Sab4 , Sab5 , Sal-1 , Sal-2 , Sal-3 , Sal-4 , Sal-5 , Sal-6 , San1 , San13 , San14 , San15 , San16 , San17 , San18 , San19 , San2 , San20 , San21 , San22 , San23 , San24 , San25 , San26 , San3 , San4 ,

San6 , San7 , San8 , San9 , SAP1 , SAP2 , SAP3 , Sa-S , SasL1 , SasL2 , SasL3 , SasL4 , SasL5 , SasL6 , SAt1 , SAV1 , Sb-1 , SB101 , SB24 , S-BBP1 , S-BBS1 , S-BM1 , S-BS1 , SBX-1 , sc , SC1 , sch , sd , Sd , SD , SD1 , SE3 , sf , SF , SF_6 , SF2 , SF5 , Sf6 , SF6 , Sfi11 , SFi11 , sfi19 , SFi19 , Sfi21 , SFi21 , SfII , SG_{3201} , SG_{3203} , SG_{3204} , SG_{3244} , SG_{35} , SG_{36} , SG_{42} , SG_{55} , sg1 , Sh , SH_{I} , SH_{II} , SH_{III} , SH_{III} , SH_{IV} , SH_{IX} , SH_{V} , SH_{VI} , SH_{VII} , SH_{X} , SH_{XI} , SH_{XI} , SH_{XII} , SH10 , SH133 , SH6 , Sha1 , SHV , SHV_{VIII} , SHX , SI , SIFV , SII , SIIIb , SiI1 , SIO1 , SIRV , SIRV-2 , $SK\gamma66$, SK_{F12} , SK_{II} , SK_{III} , SK_{IV} , SK_{IV} , SK_{IVa} , SK_{IVa} , SK_{V} , SK_{VI} , SK_{VIII} , SK_{VIIIA} , SK_{X} , SK_{XI} , sk1 , SK1 , SKI , SKIX , SKVII , SKXII , SL1 , SL1 , sl122 , sl123 , SL2 , sl23 , SL3 , SL4 , SL4 , SL5 , SL6 , SL7 , SLE111 , SLP , SLP1 , SM , SM-1 , SM2 , SM-2 , sm26 , SM4 , sm59 , SMB1 , SMB2 , SMB3 , smegmatis , SMP , SMP2 , SMP5 , SMPA , SN_1 , SN45 , SNDV , SNT-1 , SNT-2 , SNT-3 , SO-3201/G , SO-3203/G , SO-3204/G , SO-3244/G , SO-35/G , SO-36/G , SO-42/G , SO-55/G , Sp , SP , SPα (defective) , SPβ , SP1 , SP10 , SP-15 , SP3 , SP5 , SP50 , SP-50 , SP6 , SP6 , SP7 , SP8 , SP82 , SP9 , SPI , S-PM1 , S-PMW4 , SPO1 , SPO2 , S-PS1 , SpV4 , S-PWM , S-PWM1 , S-PWM2 , S-PWP1 , SPy-1 , SPy-2 , SPy-3 , SR , $Ss\gamma66$, SsF_{12} , SsI , SsII , SsIV , SsIVa , SsIX , SST , SsV , SSV1 , SSV2 , SSV3 , SsVII , SSVx , SsX , SsXI , SsXII , St/1 , ST_1 , ST_2 , ST_4 , ST_G , ST_{I} , ST_{II} , ST_{III} , ST_{IV} , ST_{IX} , ST_{V} , ST_{VI} , ST_{VI} , ST_{VII} , ST_{VIII} , ST_{XI} , ST_{XII} , St-1 , ST1 , ST-1 , st2 , stc1 , STC1 , stc2 , STC2 , STI , STI1 , StI3 , StI5 , STX , SU-11 , *sub*1 , SV , SV1/KC3·VC3 , SV2 , SV-C1 , SV-C2 , SVC3 , SV-C3 , SVC3/608 , SVC3/SMCA , SW , SW12 , SW14 , SW7 , S-WHM1 , SX , t , t , T , T , Tϕ3 , T-ϕD1B , T-ϕDO , T_1 , T_2 , T_{24} , T_3 , T_4 , T_5 , T_7 , T1 , T-1 , T104 , T2 , T-2 , T3 , T-3 , T35 , T35 , T3C , T4 , T-4 , T5 , T-5 , T6 , T7 , T-7 , T8345 , Ta_1 , Taunton , Tb , TB , Tb1 , Tb1 , Tb10 , Tb2 , Tb26 , Tb5 , Tb51 , Tb53 , Tb55 , Tb560 , Tb595 , Tb77 , Tb97 , Tb99 , Tbilisi , TC23 , TC45 , Td15 , Td6 , Td8 , tf , tf-1 , Tf2 , Tf3 , Tf4 , Tg1 , TG1 , Tg10 , Tg11 , Tg12 , Tg13 , Tg13 , Tg14 , Tg15 , Tg18 , Tg21 , Tg4 , Tg6 , Tg7 , Tg8 , Tg9 , Thf2 , Thf3 , *thu*1 , *thu*2 , *thu*3 , *thu*4 , *thu*5 , Tin1 , Tin13 , Tin23 , Tin4 , Tin7 , Tin8 , TKc , TL110B7 , Tm1 , Tm1 , TM10 , Tm2 , TM20 , Tm3 , TM4 , TM9 , TMc , TN1 , Toc1 , Tog1 , *tol*1 , TP1 , TP-1 , TP-1 , $TP\text{-}10_{vir}$, TP-11-13 , TP-13 , TP-15c , TP-16c , TP-17c , TP-19 , TP-20 , TP21 , TP-21-2 , TP3106 , TP3107 , TP33 , TP35 , TP-40-3 , TP446 , TP50 , TP51 , TP52 , TP-712 , TP-84 , TP-901-1 , TP-918 , TP-936-1 , TP-938-2 , TP-951-1 , TP-Bu2-K5 , TP-Bus3018 , TP-Bus3021 , TP-C10 , TP-J34 , TP-P2/1-3 , TPW22 , TP-Wis3-1 , TP-Wis98.1 , TSP-1 , Tsp10 , Tsp38 , Tsp8 , Tt4 , Tt6 , TTV1 , TTV2 , TTV3 , TTV4 , Tuc2009 , Tull* , Tull*-24 , Tull*46 , Tull*-6 , Tull*-60 , Twort , TX , type 1 (defective) , type A , type B , type C , type D , type E , type F , type G , type I , type Ia , type Ia , type II , type III , type IV , type IV , type IV , type V , type V , type VI , TZc , U , U15 , U153 , U2-SO-S , U3 , U4 , UB_1 , ub_2 , UC-1 , uc1001 , uc1002 , uc1003 , UC-18 , uc311a , uc311b , uc311c , uc311d , uc311e , uc311f , uc411a , uc411b , uc411c , uc411d , uc411e , uc411f , uc412a , uc412b , uc412c , uc412d , uc412e , uc412f , uc450a , uc450b , uc450c , uc450d , UH_1 , uh_3 , UH_3 , uh_5 , uh_6 , UL1 , UL10 , UL11 , UL12 , UL13 , UL14 , UL15 , UL16 , UL17 , UL19 , UL2 , UL21 , UL22 , UL23 , UL24 , UL25 , UL26 , UL28 , UL29 , UL3 , Ul30 , UL31 , UL35 , ul36 , UL36 , ul37 , UL38 , UL4 , UL6 , UL7 , UL9 , U-mole , UNL-1 , UTAK , UZ , V , V , V , V.43 , V16 , V19 , V19 , V2 , V20(V45) , V3 , V40 , V45 , V-45 , V56 , v6 , V8 , Va , VA-1 , VA-9 , VC11 , VcA-1 , VcA-2 , VcA-3 , VD13 , Versailles , Vf12 , Vf33 , Vfi-1 , Vfi-6 , Vfv-3 , VI , VI , VI , VI , Vi1 , ViI , VII , VII , ViII , VIII , VIII , VIIIA , ViIII , ViIV , ViV , ViVI , ViVII , VL , VL-1 , VP1 , VP1 , VP10 , VP11 , VP11 , VP12 , VP13 , VP15 , VP16 , VP17 , VP18 , VP19 , VP2 , VP3 , VP4 , VP5 , VP5 , VP6 , VP7 , VP7 , VP8 , VP9 , VPIΦ , VSH-1 , VSK , VW3 , VWB , Vx , w , W , W , W , Wϕ , W_1 , W_{111} , W_2 , W_2a , W_2B , W_2d , W_2e , W_{523} , W1 , W11 , W2 , W31 , W4 , w401c , w401t , w401x1 , w406 , w407c , w407t , w407x1 , w411c , w411t , w501 , w502 , w503c , w503t , W7 , WA , WA/1 , WA_{01} , WA_{03} , Wb , Weybridge , WF/1 , Worksop , WPK , WS-EO20 , WS-EP13 , WS-EP19 , WS-EP26 , WS-EP28 , WS-EP32 , WS-EP57 , WS-EP94 , WS-EP96 , WSP1 , WSP3 , WSP4 , WSP5 , WSV , WT1 , WW/1 , wx23 , wx26 , wy , X , X , X , X , X , X , X2 , X2 , X-2 , X29 , X6 , $XCVP_1$, xf , Xf , Xf2 , XI , XO1 , XO3 , XO4 , XO5 , Xp12 , XP12 , XP-12 , XP5 , XPL , XTP1 , Y , Y10 , Y46/(CE2) , y5 , Y7 , Ya_1 , Ya_{11} , Ya_4 , Ya_5 , Ya_7 , Yer2AT , YerA20 , YerA3 , YerA41 , YerA41 , YerA7 , Yun1 , Z_1 , Z_4 , Z-1/H-16 , Z63-B2 , z8 , ZD13 , ZG/1 , ZG/2 , ZG/3A , ZIK/1 , ZJ/1 , ZJ2 , ZL/3 , ZS/3 , ZV-260 , ZV-580 , ZV-622 , α , α , α , α1 , α1 , α1 , α10 , α15 , α2 , α2 , α3 , α3a , α3b , β , β , β^{hv64} , β^{tox+} , β1 , β22 , β4 , βvir , χ , χ_1 , δ , Δ^H , δ^{tox+} , δ1 , δA , ε_{15} , ε_{34} , ϕ03 , ϕ04 , Φ04-CF , ϕ05 , Φ05 , ϕ06 , Φ06 , Φ06 , Φ07 , ϕ1 , ϕ1 , ϕ1 , Φ1 , ϕ1.2 , ϕ1[40] , ϕ10 , Φ10 , ϕ100 , ϕ1002 , Φ1002 , ϕ101 , ϕ101 , ϕ102 , ϕ102 , ϕ1033 , ϕ1034 , ϕ105 , ϕ105 , ϕ1050 , ϕ105-10 , ϕ105-5 , ϕ1076 , ϕ108 , ϕ109 , ϕ1090 , ϕ1092 , ϕ1094 , ϕ1095 , ϕ1097 , ϕ11 , ϕ11 , ϕ11 , ϕ110 , ϕ1100 , ϕ111 , ϕ112 , ϕ112 , ϕ113 , ϕ-115A , ϕ1178 , ϕ118 , ϕ1190 , ϕ1199 , ϕ1256 , Φ1261M , Φ1261V , ϕ1280 , $\Phi 12S_v$, ϕ13 , ϕ138 , $\Phi 13S_v$, ϕ14 , ϕ149 , ϕ15 , ϕ-150A , ϕ151 , ϕ152 , Φ16 , ϕ17 , Φ17 , Φ17 , ϕ172 , ϕ18 , ϕ18 , $\Phi 1S_v$, ϕ2 , ϕ2 , ϕ2 , ϕ2 , ϕ-2 , Φ2 , ϕ20 , Φ2011 , ϕ2037/1 , ϕ2037/2 , ϕ2037/3 , ϕ2037/4 , ϕ2037/5 , ϕ2037/6 , ϕ2037/7 , Φ204 , ϕ2042 , ϕ2048 , ϕ218 , ϕ219 , ϕ2193/1 , ϕ2193/2 , ϕ2193/2 , ϕ2200 , ϕ2205 , ϕ227 , ϕ240 , ϕ25 , ϕ263 , ϕ28 , ϕ29 , $\Phi 2S_v$, ϕ3 , Φ3 , ϕ3001 , ϕ31 , ϕ31C , ϕ335 , ϕ336 , ϕ336-11 , ϕ368 , ϕ392-A2 , ϕ393 , ϕ399 , $\Phi 3S_v$, ϕ3T , Φ4 , ϕ400 , ϕ4002 , ϕ404 , ϕ41k , ϕ42 , ϕ48 , $\Phi 4S_t$, ϕ5 , ϕ5 , Φ5 , ϕ50 , ϕ5114 , ϕ56 , Φ57 , ϕ6 , ϕ6 , Φ6 , ϕ624 , ϕ63 , ϕ630 , ϕ630 , ϕ643 , ϕ643 , ϕ66t , ϕ66t- , $\Phi 6S_t$, ϕ7 , ϕ7 , Φ7 , ϕ7116 , Φ7201 , ϕ75 , ϕ779 , Φ779 , ϕ783 , ϕ786 , ϕ8 , Φ8 , ϕ80 , ϕ80 , ϕ806 , ϕ81 , ϕ812 , ϕ815 , ϕ82 , ϕ825 , ϕ83 , ϕ84 , ϕ85 , ϕ852 , ϕ853 , ϕ86 , ϕ87 , ϕ876 , ϕ878 , ϕ88 , ϕ886 , ϕ89 , ϕ897 , ϕ899 , ϕ9 , ϕ9 , Φ9 , ϕ90 , ϕ91 , ϕ92 , ϕ92 , ϕ92 , ϕ923 , ϕ924 , ϕ927 , ϕ93 , ϕ936 , ϕ939 , ϕ94 , Φ943 , ϕ949 , ϕ95 , ϕ95 , ϕ956 , ϕ957 , ϕ958 , ϕ96 , ϕ97 , ϕ98 , ϕ984 , ϕ99 , ϕa , ϕA , ϕA1 , ϕA1 , ΦA161 , ϕA2 , ϕA3 , ϕA4 , ϕA5 , ϕA6 , ϕA7 , ϕA8 , ϕA9 , ϕAa17 , ϕAAU2 , ϕAC1 , ΦAc-1 , ϕAc11 , ϕAc12 , ϕAc13 , ϕAc14 , ϕAc15 , ϕAC2 , ϕAc20 , ϕAC3 , ϕAc31 , ϕAc33 , ϕAc35 , ϕAc36 , ϕAc37 , ϕAc38 , ϕAc39 , ϕAc41 , ϕAc45 , ϕAc46 , ϕAc57 , ϕAc59 , ϕAcM_2 , ϕAcM_3 , ϕAcM_4 , ϕAcM_5 , ϕAcS_1 , ϕAcS_2 , ϕadh , ΦAE5 , ϕAg8010 , ϕb , ϕB , ϕB5-2 , ϕBa1 , ϕBA1 , ϕBE , ϕBHG1 , ϕBP1 , ϕBP2 , ϕbr , ϕBr01 , ϕBr02 , ϕBS , ϕC , ϕC11 , ϕC11-1 , ϕC13 , ϕC15 , ϕC17 , ϕc31 , ϕC31 , ϕC3888 , ϕC43 , ϕC5 , ϕC69 , ϕCb12r , ϕCb13 , ϕCb23r , ϕCb3 , ϕCB38 , ϕCb5 , ϕCb6 , ϕCb8r , ϕCbK , ϕcc2b , ϕcc59a , ϕcc59b , ϕcc5a , ϕcc62 , ϕCC814/1 , ϕCC814/2 , ϕCC814/3 , ϕCC814/4 , ϕCd1 , ΦCh1 , ΦCh38 , ϕCj1 , ϕCj10 , ϕCj11 , ϕCj12 , ϕCj13 , ϕCj14 , ϕCj15 , ϕCj16 , ϕCj2 , ϕCj20 , ϕCj23 , ϕCj24 , ϕCj25 , ϕCj26 , ϕCj27 , ϕCj28 , ϕCj29 , ϕCj30 , ϕCj31 , ϕCj32 , ϕCj33 , ϕCj34 , ϕCj35 , ϕCj36 , ϕCj5 , ϕCj7 , ϕCj8 , ϕCj9 , ϕCN11 , ϕCN8 , ϕCp14 , ϕCp2 , ΦCP-3 , ϕCp34 , ΦCP-6 , ΦCP6-1 , ΦCP6-2 , ΦCP6-4 , ΦCP6-5 , ϕCr1 , ϕCr10 , ϕCr11 , ϕCr12 , ϕCr13 , ϕCr14 ,

ϕCr15 , ϕCr2 , ϕCr20 , ϕCr21 , ϕCr22 , ϕCr23 , ϕCr24 , ϕCr25 , ϕCr26 , ϕCr27 , ϕCr28 , ϕCr29 , ϕCr30 , ϕCr31 , ϕCr32 , ϕCr33 , ϕCr34 , ϕCr35 , ϕCr36 , ϕCr37 , ϕCr38 , ϕCr39 , ϕCr4 , ϕCr40 , ϕCr41 , ϕCr42 , ϕCr43 , ϕCr5 , ϕCr6 , ϕCr7 , ϕCr8 , ϕCr9 , ϕCTX , ϕCVL-29 , ϕCW1 , ϕD , ϕD , ϕD-10 , ΦD326 , ϕDM1 , ϕe , ϕEC , ΦF1 , ϕF3 , ΦFM1 , ϕFR113 , ϕFR114 , ϕFR13 , ϕFR371 , ϕFR747 , ϕFR755R , ϕFRa-A , ϕFRa-C , ϕFRa-E , ϕFRb-B , ϕFRb-D , ϕFRb-M , ϕFRb-O , ϕFRb-P , ϕFRG9 , ϕFrv-J , ϕFrv-N , ϕFrv-S , ϕFrv-T , ϕFSV , ϕFSW , ϕg1e , ϕG3a1 , ϕGA1 , ϕgal1/OW , ϕgal1/R , ϕgal1261/M , ϕgal3/OW , ϕgal3/R , Φgor3V , ϕH , ϕHAU3 , ϕHAWI-1 , ΦHAWI-10 , ΦHAWI-2 , ΦHAWI-3 , ΦHAWI-4 , ΦHAWI-5 , ΦHAWI-6 , ΦHAWI-7 , ΦHAWI-8 , ΦHAWI-9 , ΦHC1-1 , ΦHC1-2 , ΦHC1-3 , ΦHC1-4 , ΦHC2-1 , ΦHC2-2 , ΦHC2-3 , ΦHC2-4 , ΦHC3-1 , ΦHC3-2 , ΦHC3-3 , ΦHD1S-1 , ΦHD1S-2 , ΦHD2S-1 , ΦHD2S-2 , ΦHD2S-3 , ΦHD2S-4 , ΦHD2S-5 , ΦHDO-1 , ΦHDO-2 , ΦHDO-3 , ΦHDO-4 , ΦHDO-5 , ΦHDO-6 , ΦHK97 , ϕI , ϕI , ϕI , ϕIV_1 , ϕK12 , ϕK13 , ϕK27 , ϕK3 , ϕK7 , ϕK70 , ΦKf77 , ϕKISR1 , ΦKL-33 , ΦKL-34 , ΦKL-35 , ΦKL-36 , ΦKWH-2 , ΦKWH-3 , ΦKWH-4 , ϕKZ , ΦKZ , ΦL-5 , ϕLC3 , ϕLC3 , ΦLco23 , ϕLf , Φlh60 , ϕLig , ϕLiv , ϕLL-H , ϕLo22a , ϕLo27a , ϕLo27b , ΦLP1-A , ΦLP1-B , ΦLP2 , ΦLP571 , ΦLP65 , ΦLP651 , ΦLS5B , ϕ-LT , ϕm , ϕm , ϕM1 , ΦM11S , ϕM12 , ϕm12r , ΦM14S , ΦM20S , ΦM23S , ΦM26S , ΦM27S , ΦM5N1 , ΦMARQ-1 , ΦMARQ-2 , ΦMARQ-3 , ϕ-MC , ϕmed-2 , ΦMl-5 , ϕMLUP5 , ΦmnF82 , ϕMO , ΦMOAT-1 , ϕmp , ΦMT1 , ΦMT2 , ΦMT3 , ΦMT4 , ΦMT5 , ϕMu1 , Φmu78 , ΦN , ϕNR2 , ϕNS11 , ϕNZ , ϕO1205 , ΦO139 , ϕot , ΦPEL13A-1 , ΦPEL13B-1 , ΦPEL13B-10 , ΦPEL13B-2 , ΦPEL13B-3 , ΦPEL13B-4 , ΦPEL13B-5 , ΦPEL13B-6 , ΦPEL13B-7 , ΦPEL13B-8 , ΦPEL13B-9 , ΦPEL1A-1 , ΦPEL1A-2 , ΦPEL8A-1 , ΦPEL8A-2 , ΦPEL8A-3 , ΦPEL8C-1 , ΦPEL8C-2 , ϕPhA1 , ϕPhA1 , ϕPLS-1 , ϕPLS27 , ϕPLS743 , ϕPS , ϕQ13 , ϕQ30 , ϕQ38 , ϕR , Φr1t , ϕR73 (defective) , ϕRE , ϕRS , ϕRsA , ϕRsD , ϕRsG1 , ΦRsG1 , ϕRsV , ϕS-1 , ϕS3 , ϕSaC1 , ϕSaG1 , ϕSaV1 , ϕSD , ϕSE6 , ϕSF1 , ϕSfi11 , ϕSFi11 , ΦSfi11 , ϕSfi19 , ϕSFi19 , ϕSfi21 , ϕSFi21 , ϕsg1 , Φsk1 , ϕSK311 , ϕSL , ϕSPK1 , ΦSPP1 , ϕST-1 , ϕT , ΦTBK5 , ϕTl87 , ΦTP901-1 , ϕTP-J34 , ΦTP-J34 , ϕUS3 , ϕUW21 , ϕUW51 , ϕv , ϕV-1 , ϕVP143 , ϕVP253 , ϕW , ϕW-14 , ϕX , ϕX , ϕX174 , ϕX-174 , ΦX174 , ϕXo , ϕXv , ϕy8 , ϕYerO3-12 , ϕYS40 , ϕχ , ϕ$χ_1$, ϕχ7 , ϕγ , Φλ , ϕμ-4 , γ , γ , γ , $γ^{tox-}$, γ19 , γ2 , γ66 , γ66 , γ66b , η , η8 , κ , λ , μ , μ (defective) , $μ_2$, μ2 , π1 , π2600 , θc , ρ , $ρ^{tox-}$, ρ11, , σ , ω , ω , ω , Ω , ω1 , ω10 , ω2 , ω3 , ω4 , ω5 , ω6 , ω8 , Ω8 , ψ , ψ (defective) , ψM1 , ζ3 , $^{24}/_{25}$14 , 00241 , 00611 , 010 , 01013 , 01014 , 011 , 01117 , 011clr , 01243 , 0237 , 0240 , 0241 , 0243 , 0244 , 0252 , 02971A , 02971C , 0303 , 032 , 034 , 035 , 03cl , 0448 , 0449 , 0465 , 0494 , 05 , 050E (defective) , 050R (defective) , 056 (defective) , 06 , 065 , 0762 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1 , 1(40) , 1,37; , 1/1 , 1/1004 , 1/1180 , 1/72 , 1/F2852-76 , 1/M6176 , 10 , 10 , 10 , 10 , 10 , 10 , 10/1 , 10/1 , 10/1a , 10/502 , 10/9253 , 10041/2815 , 1007 , 10072 , 1009 , 101 , 101 , 101/8900 , 1010 , 1011 , 102 , 102 , 102 , 103 , 103/39 , 103/40 , 10-33b , 1035 , 1039 , 103a , 103b , 104 , 1045 , 1046 , 105 , 1051 , 1056 , 1057 , 106 , 106 , 106 , 1061 , 1064 , 107 , 107/69 , 1070 , 1072 , 1075 , 10-77a , 108 , 108 , 108/106 , 108A-10 , 108A-3 , 109 , 1090 , 10-94a , 1097-B12 , 1097-B14 , 109A-6 , 109A-8 , 109-B1 , 10A/31 , 10F , 10n , 10p , 10tur , 10w , 11 , 11 , 11 , 11 , 11 , 11 , 11 , 11 , 11 , 11 , 11 , 11/DE , 110 , 110A-1 , 110A-2 , 110A-4 , 110A-5 , 110A-7 , 111 , 1-11 , 111c , 112 , 112/S_{23} , 1123 , 1124 , 11355C , 1139 , 114 , 1143 , 1146 , 115 , 115 , 115 , 115/10 , 1154A , 11-68c , 11711A , 1174 , 1175 , 1176 , 1177 , 1178 , 119 , 119 , 119x , 11F , 12 , 12 , 12 , 12 , 12 , 12 , 12/100 , 12/12 , 12/55 , 12029 , 1204 , 121 , 121 , 121/41 , 121/42 , 12100 , 12-13a , 12-13b , 1214 , 1214 , 123/43 , 123/44 , 124/44 , 12-41b , 1250 , 1259 , 1277 , 128 , 1280 , 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1921/11500 , 1921/11566 , 1921/12460 , 1921/12582 , 1921/959 , 1931 , 1932 , 196 , 1967 , 1-97 , 1-97A , 1-97B , 198 , 19A/653 , 19S , 1A , 1A , 1A , 1B , 1B , 1C , $1C^{tox+}$, 1D , $1D^{tox+}$, 1F , 1H , $1P^{+}$f , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2 , 2.5 , 2/1180 , 2/44 , 2/79 , 20 , 20 , 20 , 20 , 20 , 20 , 20.2 , 20/826 , 200 , 200 , 204 , 205 , 206 , 206 , 208 (defective) , 20A , 20E , 21 , 21 , 21 , 21 , 21 , 21/9253 , 21096C , 212 , 212/XV , 214/S_{23} , 2148 , 218 , 21EL , 22 , 22 , 22 , 22 , 22 , 22/608 , 222 , 222a , 223 , 223-B2 , 223-B3 , 224D1 , 224D2 , 225 , 226 , 227 , 227 , 227 , 228 , 229F , 23 , 23 , 23 , 23/532 , 231 , 233/A_1 , 234/S_{23} , 235 , 235 , 235/S_{23} , 236 , 2389 , 24 , 24 , 24 , 24 , 24 , 24 , 24 , 24/860 , 24/II , 242 , 2425 , 246 , 2460 , 249 , 249E (defective) , 249R (defective) , 25 , 25 , 25 , 25 , 25/909 , 258 , 25F , 26 , 26 , 26/219 , 2600/D52 , 26-2 , 2638A , 2638B , 2638C , 264 , 265 , 267 , 2671 , 2685 , 269 , 27 , 27 , 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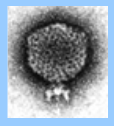

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- Phage T4 (art) - Francis S. Lin
- Phage T4 on the pedestal outside of Barker Hall at Berkeley
- Electron micrograph of phage P22

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. Bacteriological and virological quality of seawater bathing areas along the Tyrrhenian coast. Aulicino, F. A., Orsini, P., Carere, M., Mastrantonio, A. (2001). *International Journal of Environmental Health Research* 11:5-11. [PRESS FOR ABSTRACT]

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122. Advance in bacterial typing methods (a review). Milch, Hedda (1998). *Acta Microbiologica et Immunologica Hungarica* 45:401-408. [PRESS FOR ABSTRACT]

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125. Biochemical and phylogenetic characterization of the dUTPase from the archaeal virus SIRV. Prangishvili, D., Klenk, H. P., Jakobs, G., Schmiechen, A., Hanselmann, C., Holz, I, Zillig, W. (1998). *Journal of Biological Chemistry* 273:6024-6029. [PRESS FOR ABSTRACT]

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127. Yeast positive-stranded virus-like RNA replicons: 20 S and 23 S RNA terminal nucleotide sequences and 3' end secondary structures resemble those of RNA coliphages. Rodriguez-Cousino, Nieves, Solorzano, Alicia, Fujimura, Tsutomu, Esteban, Rosa (1998). *Journal of Biological Chemistry* 273:20363-20371. [PRESS FOR ABSTRACT]

128. Isolation of three different bacteriophage from mesophilic *Aeromonas* sp. that use different types of monopolar flagella as their primary receptor. Rubires, X, Merino, Susana, Aguilar, Alicia, Nogueras, Maria Merce, Tomas, Juan M. (1998). *FEMS Microbiology Letters* 161:53-57. [PRESS FOR ABSTRACT]

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130. A comparative study on the frequency of prophages among natural isolates of *Salmonella* and *Escherichia coli* with emphasis on generalized transducers. Schicklmaier, P., Moser, E., Wieland, T., Rabsch, W., Schmieger, H. (1998). *Antonie van Leeuwenhoek* 73:49-54. [PRESS FOR ABSTRACT]

131. A new bacteriophage typing scheme for *Proteus mirabilis* and *Proteus vulgaris* strains: 3. Analysis of lytic properties. Sekaninova, G., Rychlik, I, Kolarova, M., Pillich, J., Semenka, J., Zajicova, V (1998). *Folia Microbiologica* 43:136-140. [PRESS FOR ABSTRACT]

132. Bacterioplankton dynamics in Lake Constance (Bodensee): Substrate utilization, growth control, and long-term trends. Simon, M., Bunte, C., Schulz, M., Weiss, M., Wuensch, C. (1998). *Ergebnisse der Limnologie* 195-221. [PRESS FOR ABSTRACT]

133. RT-PCR amplification detects inactivated viruses in water and wastewater. Sobsey, M. D., Battigelli, D. A., Shin, G. A., Newland, S. (1998). *Water Science and Technology* 38:91-94. [PRESS FOR ABSTRACT]

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135. DNA analysis of temperate bacteriophage Aavariant phi23 isolated from *Actinobacillus actinomycetemcomitans*. Willi, K., Meyer, J. (1998). *Molecular & General Genetics* 258:323-325. [PRESS FOR ABSTRACT]

136. The effect of storage and ozonation on the physical, chemical, and biological characteristics of swine manure slurries. Wu, J. J., Park, S. H., Hengemuehle, S. M., Yokoyama, M. T., Person, H. L., Masten, S. J. (1998). *Ozone Science & Engineering* 20:35-50. [PRESS FOR ABSTRACT]

137. Properties of mycobacteriophage MTPH11. Zhilenkov, E. L., Shemyakin, I. G., Stepanshina, V. N., Korobova, O. V., Oborotov, M. V., Dorozhkova, I. R. (1998). *Mikrobiologiya* 67:660-665. [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. **Bacteriological and virological quality of seawater bathing areas along the Tyrrhenian coast. Aulicino, F. A., Orsini, P., Carere, M., Mastrantonio, A. (2001). *International Journal of Environmental Health Research* 11:5-11.** Monitoring was carried out during summer 1997 along a selected area of the Tyrrhenian coast near the Tiber river mouth. Fifty-eight seawater samples, collected from 19 stations, were examined for coliforms, streptococci, *Enteroviruses*, *Salmonellae*, coliphages, *Bacteroides fragilis* phages, *Pseudomonas*, alophilic Vibrios, *Aeromonas* and yeasts. Salmonellae and coliphages were isolated in 3 and 12 out of 58 samples, respectively. Enteroviruses and *Bacteroides fragilis* phages were not isolated. Reoviruses were isolated only from 2 out of 58 samples. A limited number of samples of the northern stations located near the Tiber and other river mouths exceeded the guide values for bathing water by the EU Directive. All the southern stations, located near canals, were of very good microbiological quality. *Pseudomonas*, *Vibrio*, *Aeromonas* and yeasts were isolated from all stations and their values in 100 ml of seawater were $10\text{-}10^6$, $10\text{-}10^6$, $0\text{-}10^6$ and $1\text{-}10^3$, respectively. An extensive disinfection practice carried out on domestic wastes, which are discharged in rivers and canals, probably brought pollution levels of most stations to values within the bacterial standards. The spread of Pseudomonas, Aeromonas, etc. showed that all the coastal area studied was characterized by the presence of organic matter coming from land that can support the presence of opportunistic pathogens and other microbial flora

2. **The genome of the archael virus SIRV1 has features in common with genomes of eukaryal viruses. Blum, H., Zillig, W., Mallock, S., Domdey, H., Prangishvili, D. (2001). *Virology* 281:6-9.** The virus SIRV1 of the extremely thermophilic archaeon *Sulfolobus* has a double-stranded DNA genome similar in architecture to the genomes of eukaryal viruses of the families Poxviridae, Pycodnaviridae, and Asfarviridae: the two strands of the 32,301 bp long linear genome are covalently connected forming a continuous polynucleotide chain and 2029 kb long inverted repeats are present at the termini. Very likely it also shares with these viruses mechanisms of initiation of replication and resolution of replicative intermediates

3. **Phylogeny, genome evolution, and host specificity of single-stranded RNA bacteriophage (family Leviviridae). Bollback, J. P., Huelsenbeck, J. P. (2001). *Journal of Molecular Evolution* 52:117-128.** Bacteriophage of the family Leviviridae have played an important role in molecular biology where representative species, such as Qbeta and MS2, have been studied as model systems for replication, translation, and the role of secondary structure in gene regulation. Using nucleotide sequences from the coat and replicase genes we present the first statistical estimate of phylogeny for the family Leviviridae using maximum-likelihood and Bayesian estimation. Our analyses reveal that the coliphage species are a monophyletic group consisting of two clades representing the genera Levivirus and Allolevivirus. The *Pseudomonas* species PP7 diverged from its common ancestor with the coliphage prior to the ancient split between these genera and their subsequent diversification. Differences in genome size, gene composition, and gene expression are shown with a high probability to have changed along the lineage leading to the Allolevivirus through gene expansion. The change in genome size of the Allolevivirus ancestor may have catalyzed subsequent changes that led to their current genome organization and gene expression

4. **Phage-related DNA polymorphism in dairy and probiotic *Lactobacillus*. Brandt, K., Tilsala-Timisjarvi, A., Alatossava, T. (2001). *Micron* 32:59-65.** Various DNA-based methods are presently being applied for identification of industrial bacterial cultures including dairy starter and probiotic strains of *Lactobacillus*. The success of strain-specific identification depends on the power of the DNA-based methods to reveal intraspecies DNA polymorphism. This study reveals that all eleven arbitrarily chosen *Lactobacillus rhamnosus* starter, laboratory and probiotic strains contain *Lb. rhamnosus* phage Lc-Nu related nucleotide sequences. One of these highly homologous regions in the genome of phage Lc-Nu was the 2.4 kb HindIII fragment, which has been sequenced. Nucleotide sequence analysis suggested that one side of the 2.4 kb HindIII fragment encodes a phage Lc-Nu helicase and accordingly represents an early gene region of phage Lc-Nu genome. Five forward and five reverse primers were derived from the nucleotide sequence of the 2.4 kb HindIII fragment of phage Lc-Nu DNA for PCR-based identification of the eleven *Lb. rhamnosus* strains included in this study. Six different types of PCR product patterns were obtained. Among the patterns three were unique to particular *Lb. rhamnosus* strains. The results suggest that phage-related DNA sequences are, surprisingly, distributed widely among the *Lb. rhamnosus* strains, and that these sequences could also be a source of DNA polymorphism to apply for DNA-based identification of bacterial strains. Phage Lc-Nu related DNA homology was also found in the chromosome of *Lb. casei*, the species closely related to *Lb. rhamnosus*

5. **Analysis of the complete DNA sequence of the temperate bacteriophage TP901-1: Evolution, structure, and genome organization of lactococcal bacteriophages. Brondsted, L., Ostergaard, S., Pedersen, M., Hammer, K., Vogensen, F. K. (2001). *Virology* 283:93-109.** A complete analysis of the entire genome of the temperate lactococcal bacteriophage TP901-1 has been performed and the function of 21 of 56 TP901-1-encoded ORFs has been assigned. This knowledge has been used to propose 10 functional modules each responsible for specific functions during bacteriophage TP901-1 proliferation. Short regions of microhomology in intergenic regions present in several lactococcal bacteriophages and chromosomal fragments of *Lactococcus lactis* are suggested to be points of exchange of genetic material through homologous recombination. Our results indicate that TP901-1 may have evolved by homologous recombination between the host chromosome and a mother phage and support the observation that phage remnants as well as prophages located in the Lactococcus chromosome contribute

significantly to bacteriophage evolution. Some proteins encoded in the early transcribed region of the TP901-1 genome were more homologous to proteins encoded by phages infecting gram-positive hosts other than L. lactis. This protein homology argues for the occurrence of horizontal genetic exchange among these bacteriophages and indicates that they have access to a common gene pool

6. **Induction of lysogenic bacteriophage and phage-associated toxin from group A streptococci during coculture with human pharyngeal cells. Broudy, T. B., Pancholi, V, Fischetti, V. A. (2001). *Infection and Immunity* 69:1440-1443.** We found that when group A streptococci are cocultured with human pharyngeal cells, they upregulate and secrete a 25-kDa toxin, determined to be the bacteriophage-encoded streptococcal pyrogenic exotoxin C (SpeC). This prompted us to determine if the bacteriophage themselves are induced during coculture conditions. We found that bacteriophage induction does occur, resulting in the release of apprx10^5 phage particles during the 3-h coculture. Furthermore, we show that the bacteriophage induction event is mediated by a pharyngeal cell soluble factor for which we provide an initial characterization

7. **Analysis of six prophages in *Lactococcus lactis* IL1403: Different genetic structure of temperate and virulent phage populations. Chopin, A., Bolotin, A., Sorokin, A., Ehrlich, S. D., Chopin, M. C. (2001). *Nucleic Acids Research* 29:644-651.** We report the genetic organisation of six prophages present in the genome of *Lactococcus lactis* IL1403. The three larger prophages (36-42 kb), belong to the already described P335 group of temperate phages, whereas the three smaller ones (13-15 kb) are most probably satellites relying on helper phage(s) for multiplication. These data give a new insight into the genetic structure of lactococcal phage populations. P335 temperate phages have variable genomes, sharing homology over only 10-33% of their length. In contrast, virulent phages have highly similar genomes sharing homology over >90% of their length. Further analysis of genetic structure in all known groups of phages active on other bacterial hosts such as *Escherichia coli*, *Bacillus subtilis*, *Mycobacterium* and *Streptococcus thermophilus* confirmed the existence of two types of genetic structure related to the phage way of life. This might reflect different intensities of horizontal DNA exchange: low among purely virulent phages and high among temperate phages and their lytic homologues. We suggest that the constraints on genetic exchange among purely virulent phages reflect their optimal genetic organisation, adapted to a more specialised and extreme form of parasitism than temperate/lytic phages

8. **H-mutant bacteriophages as a potential biocontrol of bacterial blight of geranium. Flaherty, J. E., Harbaugh, B. K., Jones, J. B., Somodi, G. C., Jackson, L. E. (2001). *Hortscience* 36:98-100.** Bacteriophages specific to *Xanthomonas campestris* pv. pelargonii (Xcp), the causal agent of bacterial blight of geranium, *Pelargonium Xhortorum* L.H. Bailey, were isolated from soil and sludge samples from Florida, California, Minnesota, and Utah. Sixteen phages were evaluated for their potential to lyse 21 Xcp strains collected from around the world. The Xcp strains varied in their susceptibility to the phage isolates with 4 to 14 phages producing a lytic or highly virulent reaction. A mixture of five h-mutants was developed from phages that exhibited the broadest host-ranges and tested against the same Xcp strains. The h-mutant phage mixture lysed all 21 Xcp strains. Three experiments were designed to determine the efficacy of using a mixture of four h-mutant phages to control the spread of the bacterial blight pathogen on potted and seedling geraniums under greenhouse conditions. Plants surrounding diseased inoculated plants were treated with a phage mixture at 5 X 108 pfu/mL daily, biweekly, or triweekly, or treated with Phyton-27(R), at 2.0 mLcntdotL-1 every 10 or 14 days. In potted geraniums, daily foliar sprays of the phage mixture had reduced disease incidence and severity by 50% and 75%, respectively, relative to control plants after 6 weeks. In two plug experiments, the phage mixture applied daily also had reduced disease incidence and severity by 69% and 86%, and 85% and 92%, respectively, when compared with controls after 5 weeks. In all three experiments, disease incidence and severity were less for plants treated daily with phages than for those treated less frequently with phages or with Phyton-27(R). Chemical name used: copper sulfate pentahydrate (Phyton-27(R))

9. **Bacteriophage lambda: Alive and well and still doing its thing. Friedman, D. I., Court, D. L. (2001). *Current Opinion in Microbiology* 4:201-207.** The lambda (lambda) family of bacteriophages continues to provide significant insights into the understanding of basic biological processes, as well as useful technological innovations. Areas in which recent advances have occurred include transcription elongation, repressor interactions, genomics and post-transcriptional regulation. The homologous lambda recombination functions have been exploited as an efficient in vivo recombinant engineering system for functional genomic studies. The virulence of some pathogenic strains of *Escherichia coli* is enhanced by the expression of Shiga toxin (stx) genes encoded on a resident lambdoid prophage. Recent work suggests that the phage regulatory network may be a significant contributor to toxin production and release by these pathogenic *E. coli*

10. **Bacteriophage therapy for bacterial infections: Rekindling a memory from the pre-antibiotics era. Ho, K. (2001). *Perspectives in Biology and Medicine* 44:1-16.**

11. **Practical evaluation of molecular subtyping and phage typing in outbreaks of infection due to *Salmonella enterica* serotype typhimurium. Jeoffreys, N. J., James, G. S., Chiew, R., Gilbert, G. L. (2001). *Pathology* 33:66-72.** Identification and control of food-poisoning outbreaks due to salmonellosis depend on prompt microbiological diagnosis and subtyping to identify the causative strain. In Australia, *Salmonella enterica* subspecies enterica serotype typhimurium (*S. typhimurium*) is responsible for 40-70% of cases of human salmonellosis. Phage typing is the usual method of subtyping *S. typhimurium*, but on its own, has limitations. We compared it with three molecular subtyping methods using 100 isolates of *S. typhimurium*, representing four different phage types (PT 1, 9, 126 and 135) and comprising 74 isolates from three presumed outbreaks, 25 isolates from sporadic cases of salmonellosis and *S. typhimurium* ATCC 10428 (phage type 126). The isolates were divided into 11 subtypes by IS200 restriction fragment length polymorphism (RFLP) typing, four each by ribotyping and pulsed-field gel electrophoresis (PFGE) and 17 distinct strains using a combination of phage and molecular typing. Isolates from two presumed outbreaks were resolved into multiple strains, possibly explaining the failure to identify a common source for either during the original investigations. IS200 RFLP analysis was the most discriminatory and reproducible typing method. Several strains were identifiable within and shared between phage types 1, 9 and 126. Phage and IS200 RFLP typing together, would provide improved definition of *S. typhimurium* outbreaks

12. **Mechanism of the photocatalytic inactivation of *Lactobacillus casei* phage PL-1 by titania thin film. Kashige, N., Kakita, Y., Nakashima, Y., Miake, F., Watanabe, K. (2001). *Current Microbiology* 42:184-189.** The mechanism of the inactivation of *Lactobacillus casei* phage PL-1 suspended in a phosphate buffer by black-light (BL)-catalytic titanium dioxide (TiO_2) thin film was studied. Generation of both superoxide anions (O^{2-}) and hydroxyl radicals (•OH) was confirmed in the aqueous medium in which TiO_2 film was settled with BL irradiation under gentle shaking. With BL-irradiation alone without TiO_2 film, only O_2- was generated to some extent. The genome DNA inside the phage particles was found to be fragmented by the

treatment of PL-1 phages with BL-catalytic TiO_2 film. The phage inactivation by BL-catalytic TiO_2 film was inhibited by the addition of albumin in a concentration-dependent manner. BL-catalytic TiO_2 film was considered to cause primarily the damage to the capsid protein through the generation of active oxygen species such as •OH, followed by damage to the genome DNA inside the phage particles

13. **Cloning of genomic DNA of *Lactococcus lactis* that restores phage sensitivity to an unusual bacteriophage sk1-resistant mutant. Kraus, J., Geller, B. L. (2001). *Applied and Environmental Microbiology* 67:791-798.** An unusual, spontaneous, phage sk1-resistant mutant (RMSK1/1) of *Lactococcus lactis* C2 apparently blocks phage DNA entry into the host. Although no visible plaques formed on RMSK1/1, this host propagated phage at a reduced efficiency. This was evident from center-of-infection experiments, which showed that 21% of infected RMSK1/1 formed plaques when plated on its phage-sensitive parental strain, C2. Moreover, viable cell counts 0 and 4 h after infection were not significantly different from those of an uninfected culture. Further characterization showed that phage adsorption was normal, but burst size was reduced fivefold and the latent period was increased from 28.5 to 36 min. RMSK1/1 was resistant to other, but not all, similar phages. Phage sensitivity was restored to RMSK1/1 by transformation with a cloned DNA fragment from a genomic library of a phage-sensitive strain. Characterization of the DNA that restored phage sensitivity revealed an open reading frame with similarity to sequences encoding lysozymes (beta-1,4-N-acetylmuramidase) and lysins from various bacteria, a fungus, and phages of *Lactobacillus* and *Streptococcus* and also revealed DNA homologous to noncoding sequences of temperate phage of *L. lactis*, DNA similar to a region of phage sk1, a gene with similarity to tRNA genes, a prophage attachment site, and open reading frames with similarities to sun and to sequences encoding phosphoprotein phosphatases and protein kinases. Mutational analyses of the cloned DNA showed that the region of homology with lactococcal temperate phage was responsible for restoring the phage-sensitive phenotype. The region of homology with DNA of lactococcal temperate phage was similar to DNA from a previously characterized lactococcal phage that suppresses an abortive infection mechanism of phage resistance. The region of homology with lactococcal temperate phage was deleted from a phage-sensitive strain, but the strain was not phage resistant. The results suggest that the cloned DNA with homology to lactococcal temperate phage was not mutated in the phage-resistant strain. The cloned DNA apparently suppressed the mechanism of resistance, and it may do so by mimicking a region of phage DNA that interacts with components of the resistance mechanism

14. **A novel virus (HaNIV) causes lysis of the toxic bloom-forming alga *Heterosigma akashiwo* (Raphidophyceae). Lawrence, J. E., Chan, A. M., Suttle, C. A. (2001). *Journal of Phycology* 37:216-222.** We describe a previously unknown virus that causes lysis of the toxic blopm-forming alga *Heterosigma akashiwo* (Hada) Hara et Chihara (Raphidophyceae). Heterosigma akashiwo nuclear inclusion virus (HaNIV) does not resemble other algal viruses described to date. HaNIV is small (ca. 30 nm diameter), is assembled in the nucleus, and forms crystalline arrays. We estimate that approximately 10^5 HaNIV particles are released during lysis of a cell. During a time-course experiment, TEM revealed the first signs of HaNIV infection 24 h after viral addition, and by 74 h 98% of observed cells were visibly infected. The onset of cell lysis, as indicated by a decrease in the relative fluorescence of the cultures, was apparent by 42 h postinfection. The heterochromatin of infected cells is frequently found at the margin of the nucleoplasm, which is consistent with virus-mediated programmed cell death, or apoptosis. HaNIV is clearly different from other described viruses that infect alg ae, including other viral pathogens of *H, akashiwo*. These results indicate that viruses other than Phycodnaviridae are pathogens and cause mortality of microalgae in marine systems. It is Likely that HaNIV plays an integral role in the population dynamics of *H. akashiwo*.

15. **Efficacy of bacteriophage use in complex treatment of the patients with burn wounds. Lazareva, E. B., Smirnov, S. V., Khvatov, V. B., Spiridonova, T. G., Bitkova, E. E., Darbeeva, O. S., Mayskaya, L. M., Parphenyuk, R. L., Menshikov, D. D. (2001). *Antibiotiki i Khimioterapiya* 46:10-14.** Results of clinical and laboratory evaluation of the treatment with pyobacteriophage in tablets of the patients with burn wounds are presented. It was shown that phagotherapy provided more rapid cure of pyoseptic complications, temperature normalization, wounds purification and lower lethality Bacteriological analysis of wound secretions revealed that after the treatment staphylococci and streptococci were cultured 2 times rarely, *Proteus* spp. Were isolated 1.5 times rarely, *E. coli* was not isolated. The amount of positive haemocultures also diminished. Investigation of immunologic status demonstrated statistically significant normalization of immunity on cell level. Phagocytosis level didn't change while in control group (without bacteriophage use) it became lower. Antibody level enhanced but less extensively than in control group. The results of trial demonstrates positive effect of phagotherapy use at the patients with burns

16. **Mechanism of host cell death induced by infection of *Escherichia coli* with the c2 clear-plaque mutant of phage f1. Lin, S. H., Chen, W. P., Kuo, T. T. (2001). *Botanical Bulletin of Academia Sinica (Taipei)* 42:45-52.** The c2 clear-plaque mutant arose spontaneously from the turbid plaque-inducing wild-type strain of bacteriophage f1. The mechanism of host cell death induced by infection of *Escherichia coli* with c2 has now been investigated. A marked decrease in cell membrane potential was apparent as early as 30 min after infection with c2, and leakage of cell contents was apparent after 4 h. Transmission electron microscopy also revealed the accumulation of granular membrane-like structures within cells at early stages of c2 infection. Electrophoretic analysis showed that the abundance of several bacterial outer membrane proteins was markedly reduced 2 h after infection with c2. Furthermore, substantial amounts of the phage coat protein (gpVIII) and single-stranded DNA-binding protein (gpV) were apparent in the inner membrane of c2-infected cells 2 h after infection. These data support the hypothesis that the death of c2-infected cells results from phage-induced damage to the bacterial cell membrane

17. **Analysis of the genetic switch and replication region of a P335-type bacteriophage with an obligate lytic lifestyle on *Lactococcus lactis*. Madsen, S. M., Mills, D., Djordjevic, G., Israelsen, H., Klaenhammer, T. R. (2001). *Applied and Environmental Microbiology* 67:1128-1139.** The DNA sequence of the replication module, part of the lysis module, and remnants of a lysogenic module from the lytic P335 species lactococcal bacteriophage variant phi31 was determined, and its regulatory elements were investigated. The identification of a characteristic genetic switch including two divergent promoters and two cognate repressor genes strongly indicates that variant phi31 was derived from a temperate bacteriophage. Regulation of the two early promoters was analyzed by primer extension and transcriptional promoter fusions to a lacLM reporter. The regulatory behavior of the promoter region differed significantly from the genetic responses of temperate *Lactococcus lactis* phages. The cro gene homologue regulates its own production and is an efficient repressor of cI gene expression. No detectable cI gene expression could be measured in the presence of cro. cI gene expression in the absence of cro exerted minor influences on the regulation of the two promoters within the genetic switch. Homology comparisons revealed a replication module which is most likely expressed from the promoter located upstream of the cro gene homologue. The replication module encoded genes with strong homology to helicases and primases found in several *Streptococcus thermophilus* phages. Downstream of the primase homologue, an AT-rich noncoding origin region was identified. The characteristics and location of this region and its ability to reduce the efficiency of plaquing of variant phi31 106-fold when present at high copy number in trans provide evidence for identification of the phage origin of replication. Phage variant phi31 is an obligately lytic phage that was isolated from

commercial dairy fermentation environments. Neither a phage attachment site nor an integrase gene, required to establish lysogeny, was identified, explaining its lytic lifestyle and suggesting its origin from a temperate phage ancestor. Several regions showing extensive DNA and protein homologies to different temperate phages of *Lactococcus, Lactobacillus*, and *Streptococcus* were also discovered, indicating the likely exchange of DNA cassettes through horizontal gene transfer in the dynamic ecological environment of dairy fermentations

18. **Mu-like prophage in serogroup B *Neisseria meningitidis* coding for surface-exposed antigens. Masignani, V, Giuliani, Marzia Monica, Tettelin, Herve, Comanducci, Maurizio, Rappuoli, Rino, Scarlato, V (2001). *Infection and Immunity* 69:2580-2588.** Sequence analysis of the genome of *Neisseria meningititdis* serogroup B revealed the presence of an apprx35-kb region inserted within a putative gene coding for an ABC-type transporter. The region contains 46 open reading frames, 29 of which are colinear and homologous to the genes of *Escherichia coli* Mu phage. Two prophages with similar organizations were also found in serogroup A meningococcus, and one was found in Haemophilus influenzae. Early and late phage functions are well preserved in this family of Mu-like prophages. Several regions of atypical nucleotide content were identified. These likely represent genes acquired by horizontal transfer. Three of the acquired genes are shown to code for surface-associated antigens, and the encoded proteins are able to induce bactericidal antibodies

19. **Improvement and optimization of two engineered phage resistance mechanisms in *Lactococcus lactis*. McGrath, S., Fitzgerald, G. F., van Sinderen, D. (2001). *Applied and Environmental Microbiology* 67:608-616.** Homologous replication module genes were identified for four P335 type phages. DNA sequence analysis revealed that all four phages exhibited more than 90% DNA homology for at least two genes, designated rep2009 and orf17. One of these genes, rep2009, codes for a putative replisome organizer protein and contains an assumed origin of phage DNA replication (ori2009), which was identical for all four phages. DNA fragments representing the ori2009 sequence confer a phage-encoded resistance (Per) phenotype on lactococcal hosts when they are supplied on a high-copy-number vector. Furthermore, cloning multiple copies of the ori2009 sequence was found to increase the effectiveness of the Per phenotype conferred. A number of antisense plasmids targeting specific genes of the replication module were constructed. Two separate plasmids targeting rep2009 and orf17 were found to efficiently inhibit proliferation of all four phages by interfering with intracellular phage DNA replication. These results represent two highly effective strategies for inhibiting bacteriophage proliferation, and they also identify a novel gene, orf17, which appears to be important for phage DNA replication. Furthermore, these results indicate that although the actual mechanisms of DNA replication are very similar, if not identical, for all four phages, expression of the replication genes is significantly different in each case

20. **Prevention and elimination of upper respiratory colonization of mice by group A streptococci by using a bacteriophage lytic enzyme. Nelson, D., Loomis, L., Fischetti, V. A. (2001). *Proceedings of the National Academy of Sciences of the United States of America* 98:4107-4112.** Bacteriophage lytic enzymes quickly destroy the cell wall of the host bacterium to release progeny phage. Because such lytic enzymes specifically kill the species in which they were produced, they may represent an effective way to control pathogenic bacteria without disturbing normal microflora. In this report, we studied a murein hydrolase from the streptococcal bacteriophage C1 termed lysin. This enzyme is specific for groups A, C, and E streptococci, with little or no activity toward several oral streptococci or other commensal organisms tested. Using purified lysin in vitro, we show that 1,000 units (10 ng) of enzyme is sufficient to sterilize a culture of apprxeq10^7 group A streptococci within 5 seconds. When a single dose of lysin (250 units) is first added to the oral cavity of mice, followed by 10^7 live group A streptococci, it provides protection from colonization (28.5% infected, n = 21) compared with controls without lysin (70.5% infected, n = 17) ($P < 0.03$). Furthermore, when lysin (500 units) was given orally to 9 heavily colonized mice, no detectable streptococci were observed 2 h after lysin treatment. In all, these studies show that lysin represents a unique murein hydrolase that has a rapid lethal effect both in vitro and in vivo on group A streptococci, without affecting other indigenous microorganisms analyzed. This general approach may be used to either eliminate or reduce streptococci from the upper respiratory mucosal epithelium of either carriers or infected individuals, thus reducing associated disease

21. **Three-component-mediated serotype conversion in *Pseudomonas aeruginosa* by bacteriophage D3. Newton, G. J., Daniels, C., Burrows, L. L., Kropinski, A. M., Clarke, A. J., Lam, J. S. (2001). *Molecular Microbiology* 39:1237-1247.** Bacteriophage D3 is capable of lysogenizing *Pseudomonas aeruginosa* PAO1 (serotype O5), converting the O-antigen from O5 to O16 and O-acetylating the N-acetylfucosamine moiety. To investigate the mechanism of lysogenic conversion, a 3.6 kb fragment from the D3 genome was isolated capable of mediating serotypic conversion identical to the D3 lysogen strain (AK1380). The PAO1 transformants containing this 3.6 kb of D3 DNA exhibited identical lipopolysaccharide (LPS) banding patterns to serotype O16 in silver-stained SDS-PAGE gels and displayed reactivity to an antibody specific for O-acetyl groups. Further analysis led to the identification of three open reading frames (ORFs) required for serotype conversion: an alpha-polymerase inhibitor (iap); an O-acetylase (oac); and a beta-polymerase (wzybeta). The alpha-polymerase inhibitor (Iap) is capable of inhibiting the assembly of the serotype-specific O5 B-band LPS and allows the phage-encoded beta-polymerase (Wzybeta) to form new beta-linked B-band LPS. The D3 phage also alters the LPS by the addition of O-acetyl groups to the FucNAc residue in the O-antigen repeat unit by the action of the D3 O-acetylase (Oac). These three components form a simple yet elegant system by which bacteriophage D3 is capable of altering the surface of *P. aeruginosa* PAO1

22. **Complete genomic sequence of the lytic bacteriophage fYeO3-12 of *Yersinia enterocolitica* serotype O:3. Pajunen, M. I., Kiljunen, S. J., Soderholm, M. E. L., Skurnik, M. (2001). *Journal of Bacteriology* 183:1928-1937.** fYeO3-12 is a T3-related lytic bacteriophage of *Yersinia enterocolitica* serotype O:3. The nucleotide sequence of the 39,600-bp linear double-stranded DNA (dsDNA) genome was determined. The phage genome has direct terminal repeats of 232 bp, a GC content of 50.6%, and 54 putative genes, which are all transcribed from the same DNA strand. Functions were assigned to 30 genes based on the similarity of the predicted products to known proteins. A striking feature of the phiYeO3-12 genome is its extensive similarity to the coliphage T3 and T7 genomes; most of the predicted fYeO3-12 gene products were >70% identical to those of T3, and the overall organizations of the genomes were similar. In addition to an identical promoter specificity, fYeO3-12 shares several common features with T3, nonsubjectibility to F exclusion and growth on *Shigella sonnei* D2371-48 (M. Pajunen, S. Kiljunen, and M. Skurnik, J. Bacteriol. 182:5114-5120, 2000). These findings indicate that phiYeO3-12 is a T3-like phage that has adapted to *Y. enterocolitica* O:3 or vice versa. This is the first dsDNA yersiniophage genome sequence to be reported

23. **Viruses of the extremely therophilic archaeon *Sulfolobus*. Prangishvili, D., Stedman, K., Zillig, W. (2001). *Trends Microbiol.* 9:39-42.** Viruses of *Sulfolobus* are highly unusual in their morphology, and genome structure and sequence. Certain characteristics of the replication strategies of these viruses and the virus-host interactions suggest relationships with eukaryal and bacterial viruses. Moreover, studying these viruses led to the discovery of archaeal promoters and has provided tools for the development of the molecular genetics of these organisms. The *Sulfolobus* viruses contain unique regulatory features and

structures that undoubtedly hold surprises for researchers in the future.

24. **Seasonal variations in the microbial population density present in biological sludge. Saleem, M., Al-Malack, M. H., Bukhari, A. A. (2001). *Environmental Technology* 22:255-259.** Sludge produced during the treatment of wastewater is being used as fertilizer in several Gulf countries. The Water and Sewage Authority of Saudi Arabia has targeted the reuse of the total amount of sludge in the future. However, these sludges should be properly treated before reuse as they contain a large number of pathogens and parasites. Little information is available on the microbial characteristics of sludge produced in wastewater treatment plants operating in this region. Variations in the population densities measured by Standard Plate Count, total coliform, fecal coliform, coliphage, and *Clostridium perfringens* present in the sludge, were monitored during a one year study at Al-Khobar wastewater treatment plant so that the effect of seasonal variations on the fate of these five indicator microorganisms could be investigated. This paper covers an evaluation of the fate of indicator microorganisms in the drying sludge. Insight gained in this study will be helpful in establishing guidelines for the use of sludge as fertilizer for agriculture purposes

25. **Bacteriophage K1-5 encodes two different tail fiber proteins, allowing it to infect and replicate on both K1 and K5 strains of Escherichia coli. Scholl, D., Rogers, S., Adhya, S., Merril, C. R. (2001). *Journal of Virology* 75:2509-2515.** A virulent double-stranded DNA bacteriophage, PHIK1-5, has been isolated and found to be capable of infecting *Escherichia coli* strains that possess either the K1 or the K5 polysaccharide capsule. Electron micrographs show that the virion consists of a small icosohedral head with short tail spikes, similar to members of the Podoviridae family. DNA sequence analysis of the region encoding the tail fiber protein showed two open reading frames encoding previously characterized hydrolytic phage tail fiber proteins. The first is the K5 lyase protein gene of PHIK5, which allows this phage to specifically infect K5 *E. coli* strains. A second open reading frame encodes a protein almost identical in amino acid sequence to the N-acetylneuraminidase (endosialidase) protein of PHIK1E, which allows this phage to specifically infect K1 strains of E. coli. We provide experimental evidence that mature phage particles contain both tail fiber proteins, and mutational analysis indicates that each protein can be independently inactivated. A comparison of the tail gene regions of PHIK5, PHIK1E, and PHIK1-5 shows that the genes are arranged in a modular or cassette configuration and suggests that this family of phages can broaden host range by horizontal gene transfer

26. **Reaction kinetics of protease with substrate phage: Kinetic model developed using stromelysin. Sharkov, N. A., Davis, R. M., Reidhaar-Olson, J. F., Navre, M., Cai, D. (2001). *Journal of Biological Chemistry* 276:10788-10793.** Peptide libraries generated using phage display have been widely applied to proteolytic enzymes for substrate selection and optimization, but the reaction kinetics between the enzyme and substrate phage are not well understood. Using a quantitative ELISA assay to monitor the disappearance of substrate, we have been able to follow the course of reaction between stromelysin, a metalloprotease, and its substrate phage. We found that under the proteolytic conditions where the enzyme was present in nanomolar concentration or higher, in excess over the substrate, the proteolysis of substrate phage was a single exponential event and the observed rate linear with respect to enzyme concentration. The enzyme concentration dependence could be described by pseudo first-order kinetic equations. Our data suggest that substrate binding is slow relative to the subsequent hydrolysis step, implying that the phage display selection process enriches clones that have high binding affinity to the protease, and the selection may not discriminate those of different chemical reactivity toward the enzyme. Considering that multiple substrate molecules may be present on a single phage particle, we regard the substrate phage reaction kinetic model as empirical. The validity of the model was ascertained when we successfully applied it to determine the binding affinity of a competitive inhibitor of stromelysin

27. **The place of viruses in the "tree of life". Sinkovics, J. G. (2001). *Acta Microbiologica et Immunologica Hungarica* 48:115-127.** Ribozymal entry into vesicle containing autocatalytically replicating oligopeptides engendered RNA proliferation and enzyme synthesis within units whose RNA genomes derived from ancestors of viroids. There is good reason to consider the coexistence of proto- or spheroplastic forms of ancient prokaryotes and archaeons. Predecessors of extant mycoplasmavirus L3 or archaeal fuselloviruses could induce cell fusions among these entities. The possibility that the first eukaryotic cells arose consequentially to virally mediated fusions of prokaryotic and archaeal proto- or spheroplasts is presented. Retrotransposons and endogenous retroviruses might have emerged in theropod dinosaurs when Aves evolved; and directed the development of syncytiotrophoblasts in the placentae of the first mammals. As viruses co-evolved with their hosts descendants of ancient viruses diverged from one another. Certain phenotypical features could connect extant phages and eukaryotic viruses to common ancestors

28. **Bacteriophage therapy. Sulakvelidze, A., Alavidze, Z., Morris, J. G. (2001). *Antimicrobial Agents and Chemotherapy* 45:649-659.**

29. **Fate of indicator microorganisms, *Giardia* and *Cryptosporidium* in subsurface flow constructed wetlands. Thurston, J. A., Gerba, C. P., Foster, K. E., Karpiscak, M. M. (2001). *Water Research* 35:1547-1551.** Limited information is available on the ability of subsurface flow wetlands to remove enteric pathogens. Two multi-species wetlands, one receiving secondary sewage effluent and the other potable (disinfected) groundwater were studied from February 1995 to August 1996, at the Pima County Constructed Ecosystems Research Facility in Tucson, Arizona. Each wetland had a retention time of approximately 4 days. The objectives of this study were (1) to evaluate the ability of multi-species subsurface wetlands to physically remove *Giardia* cysts; *Cryptosporidium* oocysts, total and fecal coliforms, and coliphages; and (2) to determine the likely impact of local wildlife on the occurrence of these indicators and pathogens. In the wetland receiving secondary sewage effluent, total coliforms were reduced by an average of 98.8% and fecal coliforms by 98.2%. Coliphage were reduced by an average of 95.2%. Both *Giardia* cysts and *Cryptosporidium* oocysts were reduced by an average of 87.8 and 64.2%, respectively. In the wetland receiving disinfected groundwater, an average of 1.3×10^2 total coliforms/100 mL and 22.3 fecal coliforms/100 mL were most likely contributed by both flora and fauna. No parasites or coliphages were detected

30. **Complete nucleotide sequence of the mycoplasma virus P1 genome. Tu, A. H., Voelker, L. L., Shen, X, Dybvig, K. (2001). *Plasmid* 45:122-126.** *Mycoplasma* virus P1 is one of only four viruses isolated from the genus *Mycoplasma*. The host for P1, *Mycoplasma pulmonis*, possesses complex, phase-variable restriction and modification enzymes and the Vsa family of phase-variable surface proteins. The ability of P1 virus to infect host cells is influenced by these phase-variable systems, rendering P1 a valuable tool for assessing host properties. The double-stranded P1 DNA genome was sequenced (11,660 bp) and 11 ORFs were identified. The predicted P1 DNA polymerase is similar to that of phages that are known to have terminal protein (TP) attached to the 5' end of their genome, consistent with previous studies indicating that P1 DNA has covalently attached TP. Most of the other predicted P1 proteins have little sequence similarity to known proteins, and P1 virus is unrelated to the other mycoplasma virus, MAV1, for which the genome sequence is known. One of the predicted P1 proteins, the ORF 8

gene product, contains a repetitive collagen-like motif characteristic of some bacteriophage tail fiber proteins and is a candidate for interacting with the Vsa proteins

31. **The clc element of *Pseudomonas* sp. strain B13 and other mobile degradative elements employing phage-like integrases. van der Meer, J. R., Ravatn, R., Sentchilo, V (2001). *Archives of Microbiology* 175:79-85.** Genes for metabolic pathways in bacteria that degrade aromatic or aliphatic pollutants have mostly been confined to either plasmid DNAs or to the chromosome. For a few pathways, including classical pathways for chlorocatechol and biphenyl degradation, recent evidence has been obtained for location of the pathway genes on mobile DNA elements which employ phage-like integrases. This enables the DNA elements to integrate into specific sites on the chromosome and yet to excise and transfer to other host bacteria. This mini-review gives an overview of those elements and their relationship to an increasing number of phage-like elements associated with bacterial virulence

32. **Characterization of a lytic *Lactobacillus plantarum* bacteriophage and molecular cloning of a lysin gene in *Escherichia coli*. Yoon, S. S., Kim, J. W., Breidt, F., Fleming, H. P. (2001). *International Journal of Food Microbiology* 65:63-74.** Bacteriophage SC921, which can infect *Lactobacillus plantarum* specifically, was isolated from a fermented vegetable source, Kimchi. This phage is active against six of 11 strains of *L. plantarum* tested as hosts. Morphologically, it has an isometric head (60 nm in diameter) and a non-contractile tail (260 nm long and 9-11 nm wide), indicating that it belongs to Bradley's group B or the Siphoviridae family according to the International Committee on Taxonomy of Viruses (ICTV). The bouyant density was 1.58 g/cm3. SDS-PAGE experimentation indicated that the phage particle contains two major structural proteins and several minor proteins. The genome was a double stranded linear DNA molecule with cohesive ends and 66.5 kb long by mapping genomic DNA digested with the restriction endonucleases: KpnI, SmaI, and XbaI. The (G + C) content of the phage DNA is 39.4%. For this lysin gene study, 9.4 kb of KpnI-digested DNA fragment was cloned into pUC19 and expressed in Escherichia coli. The KpnI fragment was considered as the genetic element responsible for the lysis gene of *L. plantarum* bacteriophage. The cloned fragment in pUC19 was hybridized to a 9.4-kb fragment generated by KpnI digestion of SC 921 as a probe. This confirmed that the fragment in pUC19 originated from phage DNA. The lysin gene was near the middle of the phage genome

33. **Application of wild starter cultures for flavour development in pilot plant cheese making. Ayad, E. H. E., Verheul, A., Wouters, Jan T. M., Smit, G. (2000). *International Dairy Journal* 10:169-179.** A number of wild lactococci of dairy and non-dairy origin which have the ability to produce unusual new flavours in model systems were studied with regard to various characteristics important for cheese making. All strains were found to be non-lysogenic and resistant to phages affecting strains present in commercial starters. Since the overall acidifying activity of many potentially interesting strains is rather low, they were used in combination with commercial starters. Defined-strain starter cultures (DSS) were prepared, composed of a combination of wild strains together with industrial strains, and tested in real cheese making (Gouda-type) experiments. The population dynamics of DSS were studied to understand the behaviour of the selected wild strains in the cheese environment. Wild strains showed various interactions with industrial strains in a defined-strain starter culture. Some wild strains, which were able to grow well together with industrial strains could be used relatively easily for practical applications. Other strains appeared to inhibit the growth of the industrial strains, due to the production of bacteriocins. In many cases the bacteriocin appeared to be nisin. Sensory evaluation revealed that the selected wild strains also produced typical flavours in a real cheese environment which corroborated the results obtained in model systems. GC/MS data confirmed the results of sensory evaluations

34. **Light scattering by viral suspensions. Balch, W. M., Vaughn, J., Novotny, J., Drapeau, D. T., Vaillancourt, R., Lapierre, J., Ashe, A. (2000). *Limnology and Oceanography.* 45:492-498.** Viruses represent one of the most abundant, ocean-borne particle types and have significant potential for affecting optical backscattering. Experiments addressing the light-scattering properties of viruses have heretofore not been conducted. Here we report the results of laboratory experiments in which the volume-scattering functions of several bacterial viruses (bacteriophages) were measured at varying concentrations with a laser light-scattering photometer using a He-Ne and/or Argon ion laser (632.8 and 514.0 nm, respectively). Four bacterial viruses of varying size were examined, including the coliphages MS-2 (capsid size 25-30 nm) and T-4 (capsid size apprx100 nm), and marine phages isolated from Saco Bay, Maine (designation Y-1, capsid size 50-80 nm) and Boothbay Harbor, Maine (designation C-2, capsid size apprx110 nm). Volume-scattering functions (VSFs) were fitted with the Beardsley-Zaneveld function and then integrated in the backward direction to calculate backscattering cross section. This was compared to the virus geometric cross section as determined by transmission electron microscopy and flow-field fractionation. Typical backscattering efficiencies varied from 20 X 10^{-6} to 1,000 X 10^{-6}. Data on particle size and backscattering efficiencies were incorporated into Mie scattering calculations to estimate refractive index of viruses. The median relative refractive index of the four viruses was apprx1.06. Results presented here suggest that viruses, while highly abundant in the sea, are not a major source of backscattering

35. **Low-frequency transduction of imipenem resistance and high-frequency transduction of ceftazidime and aztreonam resistance by the bacteriophage AP-151 isolated from a *Pseudomonas aeruginosa* strain. Blahova, J., Kralikova, K., Krcmery, V., Sr., Jezek, P. (2000). *JOURNAL OF CHEMOTHERAPY* 12:482-486.** Bacteriophage AP-151, isolated from a multidrug resistant *Pseudomonas aeruginosa* strain, was found to transduce antibiotic resistance determinants to recipient strains of *P. aeruginosa*. Resistance to cefotaxime, ceftazidime, aztreonam, imipenem and meropenem was transduced as a block, at different frequencies, to two *P. aeruginosa* strains. Resistance was two logarithms higher (in the range 10^{-5}) for cefotaxime, ceftazidime or aztreonam than for imipenem in recipient strain PAO-1670. The frequency of transduced imipenem resistance was also lower in recipient strain ML-1009. This phenomenon reflects the difference in the lytic activity of AP-151 in both strains, as the titer of the AP-151 phage in the PAO strain was found to be restricted to 10^{-4}-10^{-5} in contrast to the titer of the same phage in the ML strain which was 10^{-10}. The limited lytic activity in the PAO recipient strain was correlated with higher transducing activity. It can be concluded that some wild-type bacteriophages of *P. aeruginosa* might have highly individual relations between lytic and transducting activity in various potential recipient nosocomial strains of *P. aeruginosa*. The nature of resistance to ceftazidime and imipenem was studied using clavulanate and EDTA as inhibitors of individual class of beta-lactamases, indicating the presence of extended-spectrum beta-lactamase and a metallo-beta-lactamase in this isolate

36. **Mathematical analysis of growth and interaction dynamics of streptomycetes and a bacteriophage in soil. Burroughs, N. J., Marsh, P., Wellington, E. M. H. (2000). *Applied and Environmental Microbiology* 66:3868-3877.** We observed the infection cycle of the temperate actinophage KC301 in relation to the growth of its host *Streptomyces lividans* TK24 in sterile soil microcosms. Despite a large increase in phage population following germination of host spores, there was no observable impact on host population numbers as measured by direct plate counts. The only change in the host population following infection was the establishment of a small subpopulation of KC301 lysogens. The interaction of S. lividans and KC301

in soil was analyzed with a population-dynamic mathematical model to determine the underlying mechanisms of this low susceptibility to phage attack relative to aquatic environments. This analysis suggests that the soil environment is a highly significant component of the phage-host interaction, an idea consistent with earlier observations on the importance of the environment in determining host growth and phage-host dynamics. Our results demonstrate that the accepted phage-host interaction and host life cycle, as determined from agar plate studies and liquid culture, is sufficient for quantitative agreement with observations in soil, using soil-determined rates. There are four significant effects of the soil environment: (i) newly germinated spores are more susceptible to phage lysis than are hyphae of developed mycelia, (ii) substrate mycelia in mature colonies adsorb about 98% of the total phage protecting susceptible young hyphae from infection, (iii) the burst size of KC301 is large in soil (> 150, 90% confidence) relative to that observed in liquid culture (120, standard error of the mean (SEM), 6), and (iv) there is no measurable impact on the host in terms of reduced growth by the phage. We hypothesize that spatial heterogeneity is the principal cause of these effects and is the primary determinant in bacterial escape of phage lysis in soil

37. **Transport and retention of bacteriophages in two types of willow-cropped lysimeters. Carlander, A., Aronsson, P., Allestam, G., Stenstrom, T. A., Perttu, K. (2000). *Journal of Environmental Science and Health Part A Toxic-Hazardous Substances & Environmental Engineering* A35:1477-1492.** Irrigation and fertilization of short-rotation willow coppice with wastewater is a new way of reusing wastewater in Sweden. To evaluate the possible impact of viruses on groundwater quality, the transport and retention of the bacteriophage Salmonella Typhimurium type 28B were studied in two types of willow-cropped field lysimeters containing clay or sand soil. Phages were applied to the soil surface and moderate irrigation was done daily under field-like conditions. In the clay, soil rapid transport of bacteriophages was recorded with breakthrough at 1.2-m depth after 2-24 hours indicating macropore flow through the soil. Phage transport through the sand oil varied considerably, but was in general much slower and the phage retention much higher compared with the clay soil. The willow plants were not found to facilitate phage leaching. Instead, the results indicate the presence of phage retaining processes in the rhizosphere

38. **Genome organization and the evolution of the virulence gene locus in *Listeria* species. Chakraborty, T., Hain, T., Domann, E. (2000). *IJMM International Journal of Medical Microbiology* 290:167-174.** The chromosomal region of *Listeria monocytogenes* harboring the gene cluster prfA-plcA-hly-mpl-actA-plcB (virulence gene cluster; vgc) harbors virulence genes critical for the survival of the bacteria following infection. Previous studies have implicated it as an ancestral pathogenicity island, derivatives of which are present in the species *L. ivanovii* and *L. seeligeri*, but absent in non-pathogenic species such as *L. innocua*. We cloned the corresponding region from *L. innocua* and *L. welshimeri* and compared its sequences to those from *L. monocytogenes*, *L. ivanovii* and *L. seeligeri*. The analysis allowed exact determination of delineation and size of the vgc and suggests that these genes may have been acquired by bacteriophage transduction. Thus, here we present an alternative view of the evolution of *Listeria* spp. and suggest that *L. monocytogenes* may be the primordial species of this genus

39. **Emmental cheese: A complex microbial ecosystem. Consequences on selection and use of starters. Chamba, J. F. (2000). *Sciences des Aliments* 20:37-54.** Two fermentations usually take place in emmental cheese, lactic acid fermentation, followed by propionic acid fermentation. Unfortunately, an undesirable fermentation sometimes occurs during cheese ripening: the butyric acid fermentation. Numerous microorganisms cooperate and interact in these fermentations: lactococci, thermophilic streptococci and lactobacilli, heterofermentative lactobacilli and pediococci, propionic acid bacteria. Thus, the cheese is a microbial ecosystem which, in addition to bacteriophages, has other parasites. The properties and the role of each species, the effects of various strains (and the interactions between them) on curd acidification, proteolysis during ripening, eye formation and sensorial characteristics of emmental cheese is demonstrated using examples. Such properties should be taken into account during the selection of lactic and propionic acid bacteria for use as starters

40. **Evolution of virulence in parasites: making hard and soft choices. Chao, L, Hanley, K. A., Burch, C. L., Dahlberg, C., Turner, P. E. (2000). *Quarterly Review of Biology* 75:261-275.**

41. **Forces dictating colloidal interactions between viruses and soil. Chattopadhyay, D., Puls, R. W. (2000). *Chemosphere* 41:1279-1286.**

42. **Comparative genomics of the late gene cluster from *Lactobacillus* phages. Desiere, F., Pridmore, R. D., Brossow, H. (2000). *Virology* 275:294-305.** Three prophage sequences were identified in the *Lactobacillus johnsoni* strain NCC533. Prophage Lj965 predicted a gene map very similar to those of pac-site *Streptococcus thermophilus* phages over its DNA packaging and head and tail morphogenesis modules. Sequence similarity linked the putative DNA packaging and head morphogenesis genes at the protein level. Prophage Lj965/*S. thermophilus* phage Sfi 11/*Lactococcus lactis* phage TP901-1 on one band and *Lactobacillus delbrueckii* phage LL-H/*Lactbacillus plantarum* phage phig 1e/*Listeria monocytogenes* phage A118 on the other hand defined two sublines of structural gene clusters in pac-site Siphoviridae from low-GC Gram-positive bacteria. Bacillus subtilis phage SPP1 linked both sublines. The putative major head and tail proteins from Lj965 shared weak sequence similarity with phages from Gram-negative bacteria. A clearly independent line of structural genes in Siphoviridae from low-GC Grampositive bacteria is defined by temperate cos-site phages including *Lactobacillus gasserl* phage adh, which also shared sequence similarity with phage D3 infecting a Gram-negative bacterium. A phylogenetic tree analysis demonstrated that the ClpP-like protein identified in four cos-site Siphoviridae from *Lactobacillus*, *Lactococcus*, *Streptococcus*, and *Pseudomonas* showed graded sequence relationships The tree suggested that the ClpP-like proteins from the phages were not acquired by horizontal gene transfer from their corresponding bacterial hosts.

43. **Elimination of enteroviruses, other enteric viruses, F-specific coliphages, somatic coliphages and *E. coli* in four sewage treatment plants of southern Germany. Fleischer, J., Schlafmann, K., Otchwemah, R., Botzenhart, K. (2000). *Journal of Water Supply Research and Technology - AQUA* 49:127-138.** The reduction processes at four advanced sewage treatment plants in Baden-Wuerttemberg were evaluated with regard to virus elimination and the elimination of indicator organisms from wastewater. The results of virus elimination were compared with the reduction of somatic and male specific bacteriophages and of *E. coli*. In total, 222 water samples were examined. The results obtained for the different treatment plants show reduction rates from 80.0% to 99.9% for enteroviruses, enumerated as PFU l^{-1} on BGM cell line, and reduction rates from 59.4% to 99.9% for other enteric viruses, enumerated as MPN l-1 on MA-104 cell line. Identification of the isolated enteroviruses yielded 88.3% for Coxsackie virus B (1-5), 18.3% were positive for Polio (1-3) and 8.3% for Echo virus (1+11). The reduction rates of somatic bacteriophages ranged from 76.4% to 99.90%, for male specific bacteriophages from 87.5% to 99.9% and for E. coli from 75.0% to 99.9% respectively. Two of the plants use standard chemical precipitation and the other two employ combinations of chemical and biological elimination techniques to reduce the concentrations of phosphorus and nitrogen. A correlation between the amount of precipitators and the elimination rates of the tested microorganisms could not be demonstrated, perhaps due to the fact that the treatment conditions could not be modified by the investigators. It is concluded

that the tested treatment plants using combinations of chemical and biological techniques for P and N removal show equal or higher elimination rates than conventional treatment processes using chemical elimination techniques

44. **Occurrence and distribution of microbiological indicators in groundwater and stream water. Francy, D. S., Helsel, D. R., Nally, R. A. (2000). *Water Environment Research* 72:152-161.** A total of 136 stream water and 143 groundwater samples collected in five important hydrologic systems of the United States were analyzed for microbiological indicators to test monitoring concepts in a nationally consistent program. Total coliforms were found in 99%, *Escherichia coli* in 97%, and *Clostridium perfringens* in 73% of stream water samples analyzed for each bacterium. Total coliforms were found in 20%, *E. coli* in less than 1%, and *C. perfringens* in none of the groundwater samples analyzed for each bacterium. Although coliphage analyses were performed on many of the samples, contamination in the laboratory and problems discerning discrete plaques precluded quantification. Land use was found to have the most significant effect on concentrations of bacterial indicators in stream water. Presence of septic systems on the property near the sampling site and well depth were found to be related to detection of coliforms in groundwater, although these relationships were not statistically significant. A greater diversity of sites, more detailed information about some factors, and a larger dataset may provide further insight to factors that affect microbiological indicators

45. **Effect of host bacteria genotype on spontaneous reversions of *Bacillus subtilis* bacteriophage PHI29 sus17 nonsense codon. Fucik, V, Beran, Jaroslav, Krasny, Libor, Jonak, Jiri (2000). *FEMS Microbiology Letters* 183:143-146.** Gene 17 of *Bacillus subtilis* bacteriophage PHI29 is an early gene playing a role in DNA replication. Its mutant sus17(112) carries the TAA nonsense triplet at the fifth codon of the gene. We isolated and sequenced 73 spontaneous revertants producing normal-size plaques on bacteria without an informational suppressor gene. In all revertants, the TAA triplet was changed by a one-base substitution and the sequences CAA, AAA, TTA, TAC and TAT were recovered at its place. The spectrum of these mutations was markedly influenced by the genotype of the bacteria in which the revertants arose. In agreement with the results described in *Escherichia coli*, the ratio of transversions to transitions (CAA being the only transition acceptable) was higher in strains harboring the functional allele recA+ than in those with recA4. Our results support the idea that also in the Gram-positive *B. subtilis*, the spectra of spontaneous mutations are specifically modified by an SOS function. It is assumed that the single-stranded DNA chains generated in the course of phage DNA replication might act as an inducing factor

46. **Sensitivity of microorganisms to different wavelengths of UV light: Implications on modeling of medium pressure UV systems. Giese, N., Darby, J. (2000). *Water Research* 34:4007-4013.** The responses of three species of coliform bacteria (*Citrobacter diversus*, *Citrobacter freundii* and *Klebsiella pneumoniae*) and the bacteriophage (virus) variant phiX-174 to three wavelengths of UV light (254, 280 and 301 nm) were measured. The values of germicidal efficiency at 280 nm determined for each of the microorganisms were not significantly different. At 301 nm, the values of germicidal efficiency were significantly different, but all values were too small (< 0.06) to warrant consideration in the modeling of the germicidal intensity delivered by a medium pressure UV system. The data from this study provide some evidence that the values of germicidal efficiency determined for one species of bacteria or virus may be used to represent the relative responses of all bacteria and viruses to medium pressure UV irradiation

47. **Phage-displayed peptides as biosensor reagents. Goldman, E. R., Pazirandeh, M. P., Mauro, J. M., King, K. D., Frey, J. C., Anderson, G. P. (2000). *Journal of Molecular Recognition* 13:382-387.** This study investigated the potential to utilize phage-displayed peptides as reagents in sensor applications. A library of random 12-mers displayed on phage was panned against staphylococcal enterotoxin B (SEB), a causative agent of food poisoning. Nine SEB binding phage clones were isolated, all of which share the consensus sequence Trp His Lys at their amino terminus. Binding of several of these phage was shown to be inhibited when they were assayed in a competitive enzyme-linked immunosorbent assay (ELISA) format with synthesized peptide corresponding to the peptide-encoding region of one of the clones. Whole phage were labeled with the dye Cy5, and incorporated into fluoroimmunoassays. Labeled phage were able to detect SEB down to a concentration of 1.4 ng/well in a fluorescence-based immunoassay. When incorporated into an automated fluorescence-based sensing assay, Cy5-labeled phage bound to probes coated with SEB generated a robust signal of about 10,000 pA, vs a signal of 1000 pA using a control fiber coated with streptavidin. These results demonstrate the potential for development of phage-based sensor reagents

48. **Bacterial indicator occurrence and the use of an F+ specific RNA coliphage assay to identify fecal sources in Homosassa Springs, Florida. Griffin, D. W., Stokes, R., Rose, J. B., Paul, J. H., III (2000). *Microbial Ecology* 39:56-64.** A microbiological water quality study of Homosassa Springs State Wildlife Park (HSSWP) and surrounding areas was undertaken. Samples were collected in November of 1997 (seven sites) and again in November of 1998 (nine sites). Fecal bacterial concentrations (total and fecal coliforms, *Clostridium perfringens*, and enterococci) were measured as relative indicators of fecal contamination. F^+-specific coliphage genotyping was performed to determine the source of fecal contamination at the study sites. Bacterial levels were considerably higher at most sites in the 1997 sampling compared to the 1998 sampling, probably because of the greater rainfall that year. In November of 1997, 2 of the 7 sites were in violation of all indicator standards and guidance levels. In November of 1998, 1 of 9 sites was in violation of all indicator standard and guidance levels. The highest concentrations of all fecal indicators were found at a station downstream of the animal holding pens in HSSWP. The lowest levels of indicators were found at the Homosassa Main Spring vent. Levels of fecal indicators downstream of HSSWP (near the point of confluence with the river) were equivalent to those found in the Southeastern Fork and areas upstream of the park influences. F^+ specific RNA coliphage analysis indicated that fecal contamination at all sites that tested positive was from animal sources (mammals and birds). These results suggest that animal (indigenous and those in HSSWP) and not human sources influenced microbial water quality in the area of Homosassa River covered by this study

49. **Characterization of PHI8, a bacteriophage containing three double-stranded RNA genomic segments and distantly related to PHI6. Hoogstraten, D., Qiao, X, Sun, Y., Hu, A., Onodera, S., Mindich, L. (2000). *Virology* 272:218-224.** The three double-stranded RNA genomic segments of bacteriophage PHI8 were copied as cDNA, and their nucleotide sequences were determined. Although the organization of the genome is similar to that of PHI6, there is no similarity in either the nucleotide sequences or the amino acid sequences, with the exception of the motifs characteristic of viral RNA polymerases that are found in the presumptive polymerase sequence. Several features of the viral proteins differ markedly from those of PHI6. Although both phages are covered by a lipid-containing membrane, the protein compositions are very different. The most striking difference is that protein P8, which constitutes a shell around the procapsid in PHI6, is part of the membrane in PHI8. The host attachment protein consists of two peptides rather than one and the phage attaches directly to the lipopolysaccharide of the host rather than to a type IV pilus. The host range of PHI8 includes rough strains of *Salmonella typhimurium* and of pseudomonads

50. **Protocol for the manufacture of miniature washed-curd cheeses under controlled microbiological conditions. Hynes, E., Ogier, J. C., Delacroix-Buchet, A. (2000). *International Dairy Journal* 10:733-737.** A protocol for the preparation of

miniature washed-curd cheeses under controlled bacteriological conditions was designed and tested for reproducibility. The process was adapted from "Saint-Paulin" technology, and involves inoculation and renneting in autoclaved bottles, and cutting, stirring, curd washing and removal of whey by centrifugation. Pressing was simulated by low-speed centrifugation. All operations were performed using sterile techniques and autoclaved equipment. Forty miniature cheeses (approximately 40 g) were produced over 10 working days, and ripened for 28 days. Gross composition (dry matter, salt-in-moisture and pH) of the one-day-old cheeses did not differ significantly between cheesemaking days, and average values were 45.16, 2.46 and 5.15%, respectively. Adventitious *Lactobacillus* population remained less than 200 CFU g^{-1} all during ripening, and phages were absent. Nitrogen soluble at pH 4.4 and in phosphotungstic acid attained 21 and 3% of total nitrogen, respectively, in 28-day-old cheeses. The proposed model was shown to be suitable for the preparation of miniature cheese specimens for use in microbiological studies of cheese manufacture and ripening

51. **Virus removal and transport in saturated and unsaturated sand columns. Jin, Y., Chu, Y., Li, Y. (2000). *Journal of Contaminant Hydrology* 43:111-128.** The purpose of this research was to determine the role that unsaturated flow conditions play in virus sorption and inactivation during transport through sand columns. Column flow experiments were conducted in Ottawa sand under both saturated and unsaturated flow conditions using two bacteriophages, MS2 and phiX174. Input solution containing bromide (Br-) tracer and the viruses was applied to the column as a step function and samples were collected at the effluent end using a fraction collector. The convection-dispersion equation, partially calibrated with the transport parameters measured from the Br- signal, was used to evaluate the sorption and inactivation characteristics of the viruses. We found that, while removal of both MS2 and phiX174 increased significantly under unsaturated flow conditions, the mechanisms responsible for removing the two viruses seemed to be different. The results from elution experiments using beef extract solution revealed that the increased removal of phiX174 in the Ottawa sand under unsaturated conditions appeared to be caused by increased sorption whereas the increased removal of MS2 was due to inactivation. The difference in virus removal and transport behavior between saturated and unsaturated conditions was likely caused by additional sorption at the solid surfaces and the presence of the air-water interface (AWI) in the unsaturated system

52. **Photocatalytic inactivation of *Lactobacillus* PL-1 phages by a thin film of titania. Kakita, Y., Obuchi, E., Nakano, K., Murata, K., Kuroiwa, A., Miake, F., Watanabe, K. (2000). *Biocontrol Science* 5:73-79.** A thin film of titanium dioxide (TiO_2, anatase crystalline form) coated on a glass plate inactivated *Lactobacillus casei* PL-1 phages suspended in a buffer solution, when the reaction mixture was illuminated with a black-light lamp (maximum wave length, 365 nm) and shaken gently. When the reaction mixture was not illuminated, the TiO_2 film exhibited no phage-inactivating activity. TiO_2 was not photoexcited by white (fluorescent)-light lamp. The degree of phage inactivation was directly proportional to the surface area of the TiO_2 film. The phage inactivation approximately followed first-order reaction kinetics. The phage inactivation by photoexcited TiO_2 film was inhibited by superoxide dismutase and D-mannitol, and accelerated by hydrogen peroxide, indicating that the phage inactivation is due to the active oxygen species generated on the surface of TiO2 film under the black-light illumination. Electron microscopic observation of the negatively-stained preparation revealed that about 43% of the phages treated with photoexcited TiO_2 film were converted into ghost-particles with empty heads

53. **Sequence of the genome of the temperate, serotype-converting, *Pseudomonas aeruginosa* bacteriophage D3. Kropinski, A. M. (2000). *Journal of Bacteriology* 182:6066-6074.** Temperate bacteriophage D3, a member of the virus family Siphoviridae, is responsible for serotype conversion in its host, *Pseudomonas aeruginosa*. The complete sequence of the double-stranded DNA genome has been determined. The 56,426 bp contains 90 putative open reading frames (ORFs) and four genes specifying tRNAs. The latter are specific for methionine (AUG), glycine (GGA), asparagine (AAC), and threonine (ACA). The tRNAs may function in the translation of certain highly expressed proteins from this relatively AT-rich genome. D3 proteins which exhibited a high degree of sequence similarity to previously characterized phage proteins included the portal, major head, tail, and tail tape measure proteins, endolysin, integrase, helicase, and NinG. The layout of genes was reminiscent of lambdoid phages, with the exception of the placement of the endolysin gene, which parenthetically also lacked a cognate holin. The greatest sequence similarity was found in the morphogenesis genes to coliphages HK022 and HK97. Among the ORFs was discovered the gene encoding the fucosamine O-acetylase, which is in part responsible for the serotype conversion events

54. ***Vibrio cholerae* O139 bacteriophages. Kudryakova, T. A., Makedonova, L. D., Kachkia, G. V., Sayamov, S. R. (2000). *Zhurnal Mikrobiologii Epidemiologii i Immunobiologii* 28-30.** Cholera bacteriophages have been isolated from 27 lesogenic cultures of *V. cholerae* O139. As shown the pages under study belog to two morphological groups A1 and F1 and serological types II and XII. The use of prophage typing and the sensitivity test to specific phage made it possible to differetiate *V. cholerae* strains, serogroup O139

55. **Biological significance of lysogenic conversion. Masuda, S. (2000). *Jikeikai Medical Journal* 47:129-130.**

56. **Characterization of a novel *Vibrio parahaemolyticus* phage, KVP241, and its relatives frequently isolated from seawater. Matsuzaki, S., Inoue, T., Tanaka, S., Koga, T., Kuroda, M., Kimura, S., Imai, S. (2000). *Microbiology and Immunology* 44:953-956.** A vibriophage, KVP241, and six of its relatives were isolated independently from seawater using *Vibrio parahaemolyticus* as the host. All of the phages had the same morphology (a hexagonal head and a tail with a contractile sheath) and the same host range (specific for some *V. parahaemolyticus* strains). DNA-DNA hybridization experiments elucidated that their genomes are highly homologous to each other. Analyses of amino acid sequences of putative major capsid proteins indicated that KVP241 may be weakly related to T4-type phages having a more elongated head

57. **Evolution of microbial pathogens. Morschhaeuser, J., Koehler, G., Ziebuhr, W., Blum-Oehler, G., Dobrindt, U., Hacker, J. (2000). *Philosophical Transactions of the Royal Society of London B Biological Sciences* 355:695-704.** Various genetic mechanisms including point mutations, genetic rearrangements and lateral gene transfer processes contribute to the evolution of microbes. Long-term processes leading to the development of new species or subspecies are termed macroevolution, and short-term developments, which occur during days or weeks, are considered as microevolution. Both processes, macro- and microevolution need horizontal gene transfer, which is particularly important for the development of pathogenic microorganisms. Plasmids, bacteriophages and so-called pathogenicity islands (PAIs) play a crucial role in the evolution of pathogens. During microevolution, genome variability of pathogenic microbes leads to new phenotypes, which play an important role in the acute development of an infectious disease. Infections due to *Staphylococcus epidermidis*, *Candida albicans* and *Escherichia coli* will be described with special emphasis on processes of microevolution. In contrast, the development of PAIs is a process involved in macroevolution. PAIs are especially important in processes leading to new

pathotypes or even species. In this review, particular attention will be given to the fact that the evolution of pathogenic microbes can be considered as a specific example for microbial evolution in general

58. **Molecular characterization and allelic distribution of the phage-mediated hyaluronidase genes hylP and hylP2 among Group A streptococci from western Norway. Mylvaganam, H., Bjorvatn, B., Hofstad, T., Osland, A. (2000). *Microbial Pathogenesis* 29:145-153.** Forty-two isolates of group A streptococcus from patients with invasive and non-invasive diseases in western Norway, belonging to the emm sequence types emml, emm3, emm6, emm22, emm28, emm75 and emm78 were screened by PCR for the phage-mediated hyaluronidase genes hylP and hylP2. The amplified genes were characterized by nucleotide sequencing and/or by PCR-RFLP, with the objective of looking for possible associations between alleles of these two genes and invasiveness. The hylP was amplified from all isolates and two main alleles were found: hylP-emm3 in all emm3 isolates and hylP-emm6A in all emm6 isolates, the latter possibly generated by an intergenic recombination between hylP and hylP2. The isolates of the other sequence types had either of these two alleles, or both. Only 27 isolates gave amplicons of the appropriate size with the primers targeting hylP2. Sequencing of these amplicons showed two main types: one was similar to the published hylP2 and the other (hylP-emm6B) was probably a variant of hylP. PCR-RFLP revealed the presence of both hylP-emm6B and hylP2 in at least six of the emm6 isolates. The alleles of both hylP and hylP2 seemed to have emm sequence type preferences. No association between invasiveness and specific phage-mediated hyaluronidase genes/alleles or the production of extracellular hyaluronidase was observed

59. **Microbiological survey of shellfish. Nanni, H., Bronzetti, L., Fabio, G., Pupillo, M., Quaglio, P. (2000). *Igiene Moderna* 114:113-127.** Raw and partially cooked molluscan shellfish appear to be a common vehicle for trasmission of foodborne bacterial and viral infections. Coliphages have been proposed as indicators of viral contamination owing to their biological characteristics which are similar to those of enteroviruses. The presence of standard indicators of faecal pollution (faecal coliforms, *Escherichia coli*, *Salmonella*), *Vibrio parahaemolyticus* and coliphages was tested in 264 shellfish samples (87 *Mytilus galloprovincialis*, 177 *Tapes philippinarum*) harvested in sea water. The search for coliphages was carried out with "the plaque count agar" method. *V. parahaemolyticus* was never detected. Two strains belonging to *Salmonella* (*S. typhimurium* and *S. napoli*) were isolated from clams; two strains of *S. tennessee* were isolated from mussels. We found high levels of coliphages during winter and autumn but much lower levels during dry weather. Clam samples appeared the most contaminated ones. Furthemore, we did not observe any relationship between the presence of enterobacteria commonly considered as faecal contamination and coliphages

60. **Rapid movement of wastewater from on-site disposal systems into surface waters in the Lower Florida Keys. Paul, J. H., McLaughlin, M. R., Griffin, D. W., Lipp, E. K., Stokes, R., Rose, J. B. (2000). *Estuaries* 23:662-668.** Viral tracer studies have been used previously to study the potential for wastewater contamination of surface marine waters in the Upper and Middle Florida Keys. Two bacteriophages, the marine bacteriophage phiHSIC and the *Salmonella* phage PRD1, were used as tracers in injection well and septic tank studies in Saddlebunch Keys of the Lower Florida Keys and in septic tank studies in Boot Key Harbor, Marathon, of the Middle Keys. In Boot Key Harbor, both phages were detected in a canal adjacent to the seeded septic tank within 3 h 15 min of the end of the seed period. The tracer was then detected at all sampling sites in Boot Key Harbor, including one on the opposite side of U.S. Highway 1 in Florida Bay, and at an Atlantic Ocean beach outside Boot Key Harbor. Rates of migration based on first appearance of the phage ranged from 1.7 to 57.5 m h-1. In Saddlebunch Keys, phiHSIC and PRD1 were used to seed a residential septic tank and a commercial injection well. The septic tank tracer was not found in any surface water samples. The injection well tracer was first detected at a site most distant from the seed site, a channel that connected Sugarloaf Sound with the Atlantic Ocean. The rate of tracer migration from the injection well to this channel ranged from 66.8 to 141 m h-1. Both tracer studies showed a rapid movement of wastewater from on-site sewage treatment and disposal systems in a southeasterly direction toward the reef tract and Atlantic Ocean, with preferential movement through tidal channels. These studies indicate that wastewater disposal systems currently in widespread use in the Florida Keys can rapidly contaminate the marine environment

61. **Bacterial plasmids: Parasitic organisms? Permaul, K., Pillay, B., Pillay, D. (2000). *South African Journal of Science* 96:555-556.** The presence of plasmids in bacteria raises the question whether these plasmids constitute a stable characteristic of the host cell or whether they are parasitic genetic nomads whose stay in any bacterial population is incidental and transient. While it is still largely true that specific plasmids are associated with certain host bacteria, the existence of broad-host-range conjugative plasmids lifts this restriction on their lifestyle. It is becoming apparent from analyses of DNA sequences of plasmids that they comprise DNA segments from various sources. This apparent sequestering of DNA by plasmids and the presence of separate evolutionary lineages by the various subgroups of plasmids suggests that they could be regarded as bacterial parasites, a concept that is the focus of this article

62. **Efficacy of four conjugal lactococcal phage resistance plasmids against phage in commercial *Lactococcus lactis* subsp. cremoris cheese starter strains. Pillidge, C. J., Collins, L. J., Ward, L. J. H., Cantillon, B. M., Shaw, B. D., Timmins, M. J., Heap, H. A., Polzin, K. M. (2000). *International Dairy Journal* 10:617-625.** The efficacy of four lactococcal phage resistance plasmids (pNP40, pMU1311, pDI60 and pKP100) against phage was assessed after their conjugal transfer to four commercial *Lactococcus lactis* subsp. cremoris cheese starter strains and to the plasmid-free strain *L. lactis* subsp. cremoris MG1363. In MG1363, only pNP40 conferred resistance to prolate phages c2 and 643. Highest levels of resistance to small isometric phages in MG1363 occurred when pNP40 was stacked together with pMU1311 or pDI60. In the four starter strains, the plasmids conferred varying levels of resistance to small isometric phages. Growth and acidification rates in milk of most transconjugants derived from the starter strains decreased, but this was not always due to loss of plasmid-encoded cell wall proteinase (lactocepin) activity. Only one transconjugant grew during repeated subculture in milk with addition of factory wheys containing phages. This and the presence of bacteriocins encoded on pMU1311 and pDI60 limited application of the plasmids to protect *L. lactis* subsp. cremoris starters against phages in industry. However, some of the plasmids could be useful in extending the industry life of starters where fast acid production is not required or where bacteriocin production is acceptable

63. **Comparative study of temperate bacteriophages isolated from *Yersinia*. Popp, A., Hertwig, S., Lurz, R., Appel, B. (2000). *Systematic and Applied Microbiology* 23:469-478.** 170 *Yersinia* strains belonging to various species were investigated for the presence of temperate bacteriophages. By induction with mitomycin C seven phages were isolated from *Y. enterocolitica* strains and one phage from a *Y. frederiksenii* strain. The phages were characterized on the basis of their morphology, host range, genome size, DNA homology, and protein composition. They belong to different phage families and reveal narrow to moderate wide host ranges. Some of the isolated phages were able to infect pathogenic as well as nonpathogenic strains of *Y. enterocolitica*. The genomes of all isolated phages were found to be composed of double stranded DNA ranging from about 40 to 60 kb. In addition to the analysed phages, a number of putative phages were induced in strains of

Y. frederiksenii, *Y. kristensenii*, *Y. intermedia*, and *Y. mollaretii*. The putative phages were identified by isolation of phage DNA from cell free lysates but could not be propagated on indicator strains. Southern hybridization experiments revealed relationships between phages belonging to different families. Moreover, DNA homologies were observed between phages isolated from nonpathogenic *Yersinia* strains and a phage which was isolated from a pathogenic *Y. enterocolitica* serogroup O:3 strain

64. **Occurrence of coliphages in fish and aquaculture farms. Rao, B. M., Surendran, P. K. (2000). *Fishery Technology* 37:146-149.** Coliphages were detected in water samples collected from brackish water and fresh water fish farms. Coliphages were also detected in the farmed fresh water fish, common carp and marine fish, oil sardine, from local market. Coliphage levels obtained were as follows:- water from brackish water fish farm 3 pfu.ml-1, water from fresh water fish farm 23 pfu.ml-1, fresh water fish 240 $pfu.g^{-1}$ and marine fish 3500 $pfu.g^{-1}$

65. **Food and water contamination by human pathogenic viruses. Scipioni, A., Daube, G., Thiry, E. (2000). *Annales de Medecine Veterinaire* 144:207-221.** Food and water contamination by human viruses is a great health problem. These viruses are shed in stools. Norwalk-like viruses, hepatitis E virus, poliovirus, echovirus, hepatitis A virus, rotavirus, astrovirus, enteric adenovirus and parvovirus B19 have been described. The most important ones are Norwalk-like viruses, rotavirus and hepatitis A virus as reported in epidemiological surveys. The most frequently implicated foods are shellfish (bivalve mollusks) harvested from waters contaminated with human sewage, as well as water itself. The other source of infection is the handling of food in poor hygienic conditions. In this case contaminated foods are vegetables, sandwiches, fruits, pastries that are soiled. The detection of viruses in foods is difficult for several reasons: Virus-food interactions make difficult the concentration and the purification of viruses, several virus species are difficult or unable to grow in cell culture, furthermore viruses are present in the sample in very low amounts. Molecular techniques are therefore the methods of choice for detecting these viruses, especially the polymerase chain reaction which is often described. Another possibility consists in a fecal viral indicator. Bacteriophages seem to be the most promising in this respect

66. **Denaturing gradient gel electrophoresis resolves virus sequences amplified with degenerate primers. Short, S. M., Suttle, C. A. (2000). *BioTechniques* 28:20.**

67. **The ecology, evolutionary and geochemical consequences of viral infection of cyanobacteria and eukaryotic algae. Suttle, C. A. (2000). pp. 248-286 in Hurst, C. J. (ed.) *Viral Ecology*. Academic Press, New York.**

68. **Cyanophages and their role in the ecology of cyanobacteria. Suttle, C. A. (2000). pp. 563-589 in Whitton, B. A., Potts, M. (eds.) *The Ecology of Cyanobacteria: Their Diversity in Time and Space*. Kluwer Academic Publishers, Boston.**

69. **Use of the bacteriophage F44 for the search of the *Erwinia horticola* external suppressors. Tovkach, F. I., Gorb, T. E. (2000). *Biopolimery i Kletka* 16:64-68.** Earlier we have separated from *E. horticola* the phage F44 which has the wide area of the host bacteria. The hydroxylamine has been used to obtain the F44 nonsense mutants. The selection of F44 nonsense mutants has been carried out on *Escherichia coli* having the definite suppressor (supE44/su2+). We have isolated spontaneous revertants His+ from the auxotrophic mutants of the *E. horticola* His- which have been obtained by the treatment of 2-aminopurine and hydroxylamine. The selection of the *E. horticola* suppressor strains has been based on the sensitivity of the revertants to the F44 and to its nonsense mutants. We have concluded that the use of the F44 as the test system for the search of the *E. horticola* external suppressors is sufficiently effective for such poorly investigated bacteria as *Erwinia*

70. **Targeting of phage display vectors to mammalian cells. Uppala, A., Koivunen, E. (2000). *Combinatorial Chemistry & High Throughput Screening* 3:373-392.** Phage display libraries offer a strategy to isolate peptide ligands to target proteins and to define potential interaction sites between proteins. Recent studies have indicated a novel utility for phage display in that bacteriophage engineered to express peptide ligands to specific cell surface receptors are internalized by mammalian cells. Thus, reporter genes such as green fluorescent protein and lacZ harbored in the phage genome can be delivered to mammalian cells using targeting peptides displayed on the surface of phage. There is also the possibility to generate novel types of peptide libraries expressed intracellularly using a phage capable of inducing expression of its coding genes in human cells

71. **Bacteriophage therapy of bacterial infections: An update of our institute's experience. Weber-Dabrowska, B., Mulczyk, M., Gorski, A. (2000). *Archivum Immunologiae et Therapiae Experimentalis* 48:547-551.** 1307 patients with suppurative bacterial infections caused by multidrug-resistant bacteria of different species were treated with specific bacteriophages (BP). BP therapy was highly effective; full recovery was noted in 1123 cases (85.9%). In 134 cases (10.9%) transient improvement was observed and only in 50 cases (3.8%) was BP treatment found to be ineffective. The results confirm the high effectiveness of BP therapy in combating bacterial infections which do not respond to treatment with the available antibiotics

72. **Characterization of the distal tail fiber locus and determination of the receptor for phage AR1, which specifically infects *Escherichia coli* O157:H7. Yu, S. L., Ko, K. L., Chen, C. S., Chang, Y. C., Syu, W. Jr (2000). *Journal of Bacteriology* 182:5962-5968.** Phage AR1 is similar to phage T4 in several essential genes but differs in host range. AR1 infects various isolates of *Escherichia coli* O157:H7 but does not infect K-12 strains that are commonly infected by T4. We report here the determinants that confer this infection specificity. In T-even phages, gp37 and gp38 are components of the tail fiber that are critical for phage-host interaction. The counterparts in AR1 may be similarly important and, therefore, were characterized. The AR1 gp37 has a sequence that differs totally from those of T2 and T4, except for a short stretch at the N terminus. The gp38 sequence, however, has some conservation between AR1 and T2 but not between AR1 and T4. The sequences that are most closely related to the AR1 gp37 and gp38 are those of phage Ac3 in the T2 family. To identify the AR1-specific receptor, E. coli O157:H7 was mutated by Tn10 insertion and selected for an AR1-resistant phenotype. A mutant so obtained has an insertion occurring at ompC that encodes an outer membrane porin. To confirm the role of OmpC in the AR1 infection, homologous replacement was used to create an ompC disruption mutant (RM). When RM was complemented with OmpC originated from an O157:H7 strain, but not from K-12, its AR1 susceptibility was fully restored. Our results suggest that the host specificity of AR1 is mediated at least in part through the OmpC molecule

73. **Interspecies lysogenization in staphylococci: Transfer of enterotoxin a converting bacteriophage from clinical strain of *Staphylococcus aureus* to *Staphylococcus intermedius*. Zabicka, D., Mlynarczyk, G., Luczak, M. (2000). *Medycyna Doswiadczalna i Mikrobiologia* 52:317-326.** The ability of lysogenization was examined of 50 S. intermedius strains and of 77 strains belonging to 14 different species of coagulase-negative staphylococci using 8 enterotoxin A converting bacteriophages

isolated from S. aureus. All the examined bacteriophages showed lytic activity against at least 1 of 11 susceptible strains of *S. intermedius* to them. Lytic activity towards coagulase-negative staphylococci was observed for 6 of 8 examined bacteriophages. Two bacteriophages were active against 1 of 9 examined *S. capitis* strains, one against 1 of 11 examined *S. haemolyticus* strains, four against 1 of 6 examined S. lugdunensis strains, three against 1 of 6 examined *S. warneri* strains and one against 1 of 5 examined *S. xylosus* strains. Lysogenization with bacteriophage f421-1 able to convert positively enterotoxin A and staphylokinase and negatively beta-haemolysin of one S. intermedius strain was successful. *S. intermedius* lysogenized with variant phi421-1 was able to produce both enterotoxin A and staphylokinase and lost ability to produce beta-haemolysin. Our results showed a broad lytic spectrum and interspecies host range of some *S. aureus* bacteriophages and the ability of interspecies transfer of bacteriophages between *S. aureus* and *S. intermedius*

74. **Antirestriction. Zavilgelsky, G. B. (2000). *Molekulyarnaya Biologiya (Moscow)* 34:854-862.** A review was made of the analysis of current data on the molecular mechanisms of antirestriction. Systems of inhibition of the enzymes of restriction-modification type 1 in bacteriophages and conjugative plasmids were examined, as well as the phenomenon of "DNA restriction weakening" and its mechanism in the bacteria of *Escherichia coli*. The principle of "protein mimicry of nucleic acids" as a new mechanism of regulating biological processes in the cell in its application to Ard proteins-antirestrictors was discussed

75. **Primary structure and features of the genome of the *Lactobacillus gasseri* temperate bacteriophage phiadh. Altermann, E., Klein, J. R., Henrich, B. (1999). *Gene (Amsterdam)* 236:333-346.** The complete DNA sequence of the *Lactobacillus* (Lb.) *gasseri* temperate phage phiadh was determined. The linear and double-stranded genome consists of 43.785 bp with a G+C content of 35.3% and 3' protruding cohesive ends of 12 nt. Sixty-two possible ORFs were identified. On the basis of homology comparisons, some of them could be assigned to possible functions, such as a helicase, a nucleic acid polymerase and a protease. In a non-coding area of the phiadh genome, structural features of a potential replication origin were detected. After subcloning, this region was functional as a replicon in Lb. gasseri and Lactococcus lactis. N-terminal aa sequencing and electron microscopic analysis of intact and defective phage particles enabled the identification of two capsid protein genes. One of their products, the major head protein, seems to be processed on the posttranslational level

76. **Stable expression of the *Lactobacillus casei* bacteriophage A2 repressor blocks phage propagation during milk fermentation. Alvarez, M. A., Rodriguez, A., Suarez, J. E. (1999). *Journal of Applied Microbiology* 86:812-816.** A general strategy was applied to implement resistance against temperate bacteriophages that infect food fermentation starters through cloning and expression of the phage repressor. *Lactobacillus casei* ATCC 393 and phage A2 were used to demonstrate its feasibility as milk fermentation is drastically inhibited when the strain is infected by this phage. The engineered strain *Lact. casei* EM40::cI, which has the A2 repressor gene (cI) integrated into the genome, was completely resistant and able to ferment milk whether phage was present or not. In addition, viable phages were eliminated from the milk, probably through adsorption to the cell wall. Finally, the integration of cI in the genome resulted in a stable resistance phenotype, being unnecessary selective pressure during milk fermentation

77. **The genetic element pSSVx of the extremely thermophilic crenarchaeon *Sulfolobus* is a hybrid between a plasmid and a virus. Arnold, H. P., She, Q., Phan, H., Stedman, K., Prangishvili, D., Holz, I, Kristjansson, J. K., Garrett, R., Zillig, W. (1999). *Molecular Microbiology* 34:217-226.** A new *Sulfolobus islandicus* strain, REY15/4, harboured both a novel fusellovirus, SSV2, and a small plasmid, pSSVx. The plasmid spread in *S. solfataricus* P1 together with the virus after infection with either the supernatant of a culture of REY15/4 or purified virus. Spreading of the plasmid required co-transfection with either SSV2 or the related SSV1 as helpers. Virus purified from REY15/4 constituted a mixture of two sizes of particles, one with the dimensions of a normal fusellovirus and the other smaller. Cloned SSV2 produced only the larger particles and only SSV2 DNA, indicating that the smaller particles contained pSSVx packaged into capsids made up of SSV2 components. The 5.7 kb genome of pSSVx revealed regions of high sequence similarity to the cryptic Sulfolobales plasmids pRN1, pRN2 and pDL10. Thus, pSSVx belongs to the family of pRN plasmids that share a highly conserved region, which probably constitutes the minimal replicon. They also contain a variable region showing no sequence similarity. In pSSVx, this region contains three open reading frames (ORFs), two of which are juxtapositioned and show high sequence similarity to a tandem of ORFs in fusellovirus genomes. Neither pRN1 nor pRN2, which lack this tandem, spread in the presence of the fuselloviruses, which implies that the sequences of these ORFs enable pSSVx to use the packaging system of the viral helpers for spreading

78. **Use of plaque assay to detect enteric viruses in a rural watershed. Brenner, F. J., Brenner, E. K., Schwartz, T. E. (1999). *Journal of Environmental Quality* 28:845-849.** Water samples were collected from four locations within the Munnell Run Watershed in Mercer County, Pennsylvania, and analyzed for fecal coliforms by MPN and enteric phages by plaque assay using *Salmonella typhimurium* WG 49 and *Bacteroides fragilis* HSP 40 as hosts. Fecal coliform concentrations and the number of phages varied seasonally ($P < 0.001$), as well as among the different sampling stations ($P < 0.001$). At all sampling stations positive for phages, *S. typhimurium* WG 49 PFUs outnumbered *B. fragilis* HSP 40 PFUs. Phages also were isolated from a septic discharge pipe and a wetland receiving septic drainage, but not from three avian species, 12 mammalian species, two streams without human wastes or from natural wetland, indicating that these viruses were of human origin. MPNs of fecal coliforms and *S. typhimurium* and *B. fragilis* PFUs were correlated with stream temperature ($P < 0.001$) and rainfall ($P < 0.01$). Only fecal coliforms and *S. typhimurium* WG 49 phages were correlated with suspended solids concentrations ($P < 0.01$). Likewise, there was a significant interaction among these parameters and MPNs of fecal coliform and HSP 40 and WG 49 PFUs ($P < 0.001$). The presence of host specific phages indicate the existence of septic discharges in the watershed, but both fecal coliforms and enteric viruses persist in stream systems, especially during the summer months

79. **Iodine disinfection of a model bacteriophage, MS2, demonstrating apparent rebound. Brion, Gail M., Silverstein, Joann (1999). *Water Research* 33:169-179.** MS2 coliphage viruses suspended in buffered distilled water were rapidly inactivated by < 5 mg/L iodine doses, losing 6 logs (99.9999%) of infectivity within less than 3 min contact time. The effect of pH on MS2 inactivation within the range of 6 to 8 was not statistically significant. However, in the presence of dissolved organic substances, such as detergents and proteins, the inactivation of MS2 viruses decreased significantly to less than 4 logs (99.99%). Of special interest was that in the presence of beef extract proteins, an apparent reversal of MS2 inactivation, dubbed rebound, was observed. It was observed that after an initial 5 to 6 log reduction in infectivity, a consistent and statistically significant increase in the number of plaque forming units (PFU), as much as 2 logs, was measured. MS2 rebound occurred only when the oxidized iodine residual had been quickly consumed by beef extract proteins in solution. Neither virus particle aggregation nor water salinity were found to account for the increase in PFU values. Based on other investigators' suggestions that iodine disinfection caused changes to viral protein coats, it was hypothesized that conformational changes in MS2's protein coat caused by iodine would result in a change in the isoelectric focusing point of whole MS2 virions. A shift in isoelectric focusing point from an acidic pH value of 3.9 to more basic values, and a dispersion of the virus band after exposure to high

levels of iodine was observed, supporting the hypothesis that iodine caused changes in the charge distribution characteristics of the protein coat

80. **Comparative sequence analysis of the DNA packaging, head, and tail morphogenesis modules in the temperate cos-site *Streptococcus thermophilus* bacteriophage Sfi21. Desiere, F., Lucchini S, Brussow H (1999). *Virology* 260:244-253.** The temperate *Streptococcus thermophilus bacteriophage* Sfi21 possesses 15-nucleotide-long cohesive ends with a 3' overhang that reconstitutes a cos-site with twofold hyphenated rotational symmetry, Over the DNA packaging, head and tail morphogenesis modules, the Sfi21 sequence predicts a gene map that is strikingly similar to that of lambdoid coliphages in the absence of any sequence similarity. A nearly one to one gene correlation was found with the phage lambda genes Nul to H, except for gene B-to-E complex, where the Sfi21 map resembled that of coliphage HK97. The similarity between Sfi21 and HK97 was striking: both major head proteins showed an N-terminal coiled-coil structure, the mature major head proteins started at amino acid positions 105 and 104, respectively, and both major head genes were preceded by genes encoding a possible protease and portal protein. The purported Sfi21 protease is the first viral member of the CipP protease family The prediction of Sfi21 gene functions by reference to the gene map of intensively investigated coliphages was experimentally confirmed for the major head and tail gene. Phage Sfi21 shows nucleotide sequence similarity with *Lactococcus* phage BK5-T and a lactococcal prophage and amino acid sequence similarity with the Lactobacillus phage A2 and the *Staphylococcus* phage PVL. PVL is a missing link that connects the portal proteins from Sfi21 and HK97 with respect to sequence similarity. These observations and database searches, which demonstrate sequence similarity between proteins of phage from gram-positive bacteria, proteobacteria, and Archaea, constrain models of phage evolution.

81. **The microbial quality of a Wetland Reclamation Facility used to produce an effluent for unrestricted non-potable reuse. Fujioka, R. S., Bonilla, A. J., Rijal, G. K. (1999). *Water Science and Technology* 40:369-374.** An auxiliary Wetland Reclamation Facility (WRF) was constructed to receive stabilization pond treated sewage and further treat it with water hyacinth ponds, chemical flocculation, filtration and ultraviolet light disinfection. This was the first facility in Hawaii which was approved to produce the highest quality reclaimed water using alternative treatment schemes. We assessed the effectiveness of the WRF by monitoring water samples after each of the WRF treatment schemes for five genetically different groups of sewage borne microorganisms (fecal coliform, enterococci, C. perfringens, FRNA phage, total heterotrophic bacteria). The concentrations of all fecal indicator microorganisms, especially FRNA phage were low in the influent water to the WRF indicating that extended pond treatment may be especially effective in removing human viruses from sewage. The WRF treatment scheme was calculated to be able to reduce >99.99% of fecal coliform and therefore was able to produce an effluent meeting the non-potable, unrestricted reuse standard of a geometric mean of <1 fecal coliform/100 ml

82. **Optimization of artificial wetland design for removal of indicator microorganisms and pathogenic protozoa. Gerba, C. P., Thurston, J. A., Falabi, J. A., Watt, P. M., Karpiscak, M. M. (1999). *Water Science and Technology* 40:363-368.** The enhancement of water quality by artificial wetland systems is increasingly being employed throughout the world. Three wetlands were studied in Tucson, AZ to evaluate their individual performance in the removal of indicator bacteria (coliforms), coliphage, and enteric pathogens (*Giardia* and *Cryptosporidium*). A duckweed-covered pond, a multi-species subsurface flow (SSF) and a multi-species surface flow (SF) wetland were studied. Removal of the larger microorganisms, *Giardia* and *Cryptosporidium*, was the greatest in the duckweed pond at 98 and 89 percent, respectively. The lowest removal occurred in the SF wetland, 73 percent for Giardia and 58 percent removal for *Cryptosporidium*. In contrast, the greatest removal of coliphage, total and fecal coliforms occurred in the SSF wetland, 95, 99, and 98 percent respectively, whereas the pond had the lowest removals (40, 62, and 61 percent, respectively). Sedimentation may be the primary removal mechanism within the duckweed pond since the removal was related to size, removal of the largest organisms being the greatest. However, the smaller microorganisms were removed more efficiently in the SSF wetland, which may be related to the large surface area available for adsorption and filtration. This study suggests that in order to achieve the highest treatment level of secondary unchlorinated wastewater, a combination of aquatic ponds and subsurface flow wetlands may be necessary

83. **Bacteriophage lambda: The untold story. Gottesman, M. (1999). *Journal of Molecular Biology* 293:177-180.** The study of bacteriophage lambda has provided key insights into fundamental biological processes. This review recalls some highlights in the history of lambda research, and relates how simple (but elegant) experiments yielded major scientific breakthroughs. What we know about recombination, gene regulation, and protein folding, for example, derives in large part from bacteriophage lambda genetics. Lambda not only represents a model system of scientific logic in a technology-driven age, but continues to reveal new principles of molecular biology

84. **Removal of MS-2 and PRD-1 bacteriophages from an ultrapure water system. Governal, R. A., Gerba, C. P. (1999). *Journal of Industrial Microbiology & Biotechnology* 23:166-172.** Viruses must be removed from the ultrapure water environment, as they have the potential to deposit on microelectronic devices and generate killer defects. Controlled and well-defined challenges by MS-2 and PRD-1 bacteriophages were treated in a pilot-scale ultrapure water system using ultraviolet radiation (UV), ozone, mixed bed ion exchange adsorption, and reverse osmosis filtration technologies typical of those used in industrial systems. Applying a first order kinetic model to the data generated rate constants for MS-2 removal by UV-185, 50 mg L^{-1} ozone, mixed bed ion exchange or reverse osmosis filtration of 15.5, 12.9, 3.9, and 10.4 min^{-1}, respectively, and PRD-1 removal of 13.8, 15.5, 8.2, and 11.9 min^{-1}, respectively. In all cases, removal of viruses by oxidative mechanisms such as ozone and UV were far superior to adsorption and filtration mechanisms. A theoretical viral population balance was generated to model the removal of the bacteriophages by these unit operations.This model relates the inlet time-dependent profile of viruses to the output, destruction, and accumulation profiles; it also relates these profiles to the unit operation's treatment mechanisms including oxidation, adsorption, and filtration. This model is the first step in generating a site-independent theoretical model to project the persistence of viruses in ultrapure water systems

85. **Bacteriocin-like inhibitory activities among various species of *Listeria*. Kalmokoff, M. L., Daley, E., Austin, J. W., Farber, J. M. (1999). *International Journal of Food Microbiology* 50:191-201.** Three hundred Listeria isolates were examined for inhibitory activities using a deferred antagonism plating assay. Approximately 75% of the surveyed isolates produced inhibitory activity, the majority of which (71%) resulted from the production of bacteriophage or defective bacteriophage particles. Twenty-three isolates (8%) produced inhibitory activities distinct from those resulting from bacteriophage. Four of these isolates (*Listeria innocua* 743, *L. innocua* 755, *L. innocua* 228, *L. monocytogenes* 538) produced heat-stable, protease sensitive peptides, which demonstrated broad-spectrum inhibitory activities against all *L. monocytogenes* serotypes tested

86. **An extrachromosomal prophage naturally associated with *Bacillus thuringiensis* serovar israelensis. Kanda, K., Ohderaotoshi, T., Shimojyo, A., Kato, F., Murata, A. (1999). *Letters in Applied Microbiology* 28:305-308.** *Bacillus*

thuringiensis serovar israelensis, an entomopathogen for mosquito larvae, was demonstrated to be lysogenized by temperate phage SU-11 whose genome was located extrachromosomally in the cell. The prophage SU-11 was cured at high frequency from the parental strain by continuous sub-culture at high temperature, but the ability to produce delta-endotoxin remained in the prophage cured strain. Moreover, phage induction was found to occur after mating of serovar israelensis with its prophage cured strain, as well as with *B. thuringiensis* serovar thuringiensis, *B. cereus* and *B. subtilis*

87. **The R-type pyocin of *Pseudomonas aeruginosa* C is a bacteriophage tail-like particle that contains single-stranded DNA. Lee, Frank K. N., Dudas, Kathleen C., Hanson, Julie A., Nelson, M. B., Loverde, Philip T., Apicella, Michael A. (1999). *Infection and Immunity* 67:717-725.** *Pseudomonas aeruginosa* R-type pyocin particles have been described as bacteriocins that resemble bacteriophage tail-like structures. Because of their unusual structure, we reexamined whether they contained nucleic acids. Our data indicated that pyocin particles isolated from *P. aeruginosa* C (pyocin C) contain DNA. Probes generated from this DNA by the random-primer extension method hybridized to distinct bands in restriction endonuclease-digested *P. aeruginosa* C genomic DNA. These probes also hybridized to genomic DNA from 6 of 18 *P. aeruginosa* strains that produced R-type pyocins. Asymmetric PCR, complementary oligonucleotide hybridization, and electron microscopy indicated that pyocin C particles contained closed circular single-stranded DNA, approximately 4.0 kb in length. Examination of total intracellular DNA from mitomycin C-induced cultures revealed the presence of two extrachromosomal DNA molecules, a double-stranded molecule and a single-stranded molecule, which hybridized to pyocin DNA. Sequence analysis of 7,480 nucleotides of *P. aeruginosa* C chromosomal DNA containing the pyocin DNA indicated the presence of pyocin open reading frames with similarities to open reading frames from filamentous phages and cryptic phage elements. We did not observe any similarities to known phage structural proteins or previously characterized pseudomonal prt genes expressing R-type pyocin structural proteins. These studies demonstrate that pyocin particles from *P. aeruginosa* C are defective phages that contain a novel closed circular single-stranded DNA and that this DNA was derived from the chromosome of *P. aeruginosa* C

88. **Identification of a *Vibrio cholerae* RTX toxin gene cluster that is tightly linked to the cholera toxin prophage. Lin, W., Fullner, K. J., Clayton, R., Sexton, J. A., Rogers, M. B., Calia, K. E., Calderwood, S. B., Fraser, C., Mekalanos, J. J. (1999). *Proceedings of the National Academy of Sciences of the United States of America* 96:1071-1076.** We identify and characterize a gene cluster in El Tor *Vibrio cholerae* that encodes a cytotoxic activity for HEp-2 cells in vitro. This gene cluster contains four genes and is physically linked to the cholera toxin (CTX) element in the *V. cholerae* genome. We demonstrate by using insertional mutagenesis that this gene cluster is required for the cytotoxic activity. The toxin, RtxA, resembles members of the RTX (repeats in toxin) toxin family in that it contains a GD-rich repeated motif. Like other RTX toxins, its activity depends on an activator, RtxC, and an associated ABC transporter system, RtxB and RtxD. In *V. cholerae* strains of the classical biotype, a deletion within the gene cluster removes rtxC and eliminates cytotoxic activity. Other strains, including those of the current cholera pandemic, contain a functional gene cluster and display cytotoxic activity. Thus, the RTX gene cluster in El Tor O1 and O139 strains might have contributed significantly to their emergence. Furthermore, the RTX toxin of V. cholerae may be associated with residual adverse properties displayed by certain live, attenuated cholera vaccines

89. **Similarly organized lysogeny modules in temperate Siphoviridae from low GC content gram-positive bacteria. Lucchini, S., Desiere, F., Brussow H (1999). *Virology* 263:427-435.** Temperate Siphoviridae from an evolutionarily related branch of low GC content gram-positive bacteria share a common genetic organization of lysogeny-related genes and the predicted proteins are linked by many sequence similarities. Their compact lysogeny modules [integrase/1-2 orfs (phage exclusion? and metalloproteinase motif proteins)/cI-like repressor/cro-like repressor/antirepressor (optional)] differ clearly from that of h-like and L5-like viruses, the two currently established genera of temperate Siphoviridae, while they resemble those of the P2-like genus of Myoviridae. In all known temperate Siphoviridae from low GC content gram-positive bacteria the lysogeny module is flanked by the lysis module and the DNA replication module. This modular organization is again distinct from that of the known genera of temperate Siphoviridae. On the basis of comparative sequence analysis we propose a new genus of Siphoviridae: "Sfi21-like" phages. With a larger database of phage sequences it might be possible to establish a genomics-based phage taxonomy and to retrace the evolutionary history of selected phage modules or individual phage genes. The antirepressor of Sfi21-like phages has an unusual widespread distribution since proteins with high aa similarity (40%) were found not only in phages from gramnegative bacteria, but also in insect viruses.

90. **Removal of microorganisms from water by columns containing sand coated with ferric and aluminum hydroxides. Lukasik, Jerzy, Cheng, Yueh Fung, Lu, Fuhua, Tamplin, Mark, Farrah, Samuel R. (1999). *Water Research* 33:769-777.** Tap water seeded with different microorganisms or untreated waste water was passed through columns containing sand modified by the in situ precipitation of metallic hydroxides or unmodified sand. Columns (35.5 X 5.0 cm) packed with 1 kg of sand modified with a combination of ferric and aluminum hydroxide removed greater than 99% of *Escherichia coli*, *Vibrio cholerae*, poliovirus 1 and coliphage MS-2 from dechlorinated tap water. This removal efficiency was consistent throughout the passage of 1201 of water during a 30 day test. After the passage of 1921 of tap water, these columns were still able to remove 99.9% MS-2, 80% E. coli and 90% of poliovirus 1. Columns containing modified sand efficiently removed microorganism from water samples at the various pH and temperature values tested while columns containing unmodified sand did not. In addition, these modified sand filters were able to remove coliform bacteria and coliphage from raw sewage. More than a 4 log10 reduction in the numbers of these microorganisms was achieved at room temperature. The modified sand seems to better remove microorganisms due to increased electrostatic interactions. Neither *E. coli* nor MS-2 were inactivated by the modified sand column effluents. The metal used for coating the sand could not be detected in the column effluents, indicating that the coatings were stable

91. **Induction of prophages of enterohemorrhagic *Escherichia coli* O157:H7 with norfloxacin. Matsushiro, A., Sato, K., Miyamoto, H., Yamamura, T., Honda, T. (1999). *Journal of Bacteriology* 181:2257-2260.** Norfloxacin (NFLX) caused induction of prophages VT1 and VT2 of enterohemorrhagic *Escherichia coli* O157 at subinhibitory concentrations. In time course experiments, we observed the following sequential events: upon induction, the phage genomes underwent multiplication; the amount of stx genes increased; and subsequently, large quantities of toxins VT1 and VT2 were produced. Further studies showed that the molecular mechanism of prophage induction is closely related to the RecA system since the prophage VT2 was not induced with NFLX in a recA mutant strain

92. **Isolation of a temperate bacteriophage encoding the type III effector protein SopE from an epidemic *Salmonella typhimurium* strain. Mirold, S., Rabsch, W., Rohde, M., Stender, S., Tschaepe, H., Ruessmann, H., Igwe, E., Hardt, W. D. (1999). *Proceedings of the National Academy of Sciences of the United States of America* 96:9845-9850.** *Salmonella typhimurium* employs the specialized type III secretion system encoded in pathogenicity island 1 (SPI1) to translocate effector proteins into host cells and to modulate host cell signal transduction. The SPI1 type III system and the effector proteins are

conserved among all salmonellae and are thought to be acquired by horizontal gene transfer. The genetic mechanisms mediating this horizontal transfer are unknown. Here, we describe that SopE, a SPI1-dependent translocated effector protein, is present in relatively few *S. typhimurium* isolates. We have isolated a temperate phage that encodes SopE. Phage morphology and DNA hybridization, as well as partial sequence information, suggest that this phage (SopEPHI) is a new member of the P2 family of bacteriophages. By lysogenic conversion this phage can horizontally transfer genes between different *S. typhimurium* strains. Strikingly, most of the isolates harboring SopEPHI belong to the small group of epidemic strains of *S. typhimurium* that have been responsible for a large percentage of human and animal salmonellosis and have persisted for a long period of time. Our data suggest that horizontal transfer of type III dependent effector proteins by lysogenic infection with bacteriophages (lysogenic conversion) may provide an efficient mechanism for fine-tuning the interaction of *Salmonella* spp. with their hosts

93. **Transmission of the methicillin resistance from *Staphylococcus epidermidis* to *Staphylococcus aureus* in mixed cultures. Mlynarczyk, A., Mlynarczyk, G., Jeljaszewicz, J. (1999). *Medycyna Doswiadczalna i Mikrobiologia* 51:199-205.** In mixed cultures of staphylococci a transfer of the resistance to methicillin and penicillinase plasmids as well as tetracycline and chloramphenicol plasmids was investigated. It was shown that the resistance to methicillin was transferred in mixed cultures from one strain of *S. aureus* to another and from *S. epidermidis* to *S. aureus*. In both cases transfer of methicillin resistance required, the presence of penicillinase plasmid in recipient or donor strain. In the case of other markers transmission was independent. Moreover it was shown that the transfer of resistance genes in mixed cultures was mediated by bacteriophage of the serologic group A

94. **Study of the potential relationship between the morphology of infectious somatic coliphages and their persistence in the environment. Muniesa, M., Lucena, F., Jofre, J. (1999). *Journal of Applied Microbiology* 87:402-409.** The proportions of different morphological types of infectious somatic coliphages were determined in faecally polluted freshwaters. Myoviridae, followed by Siphoviridae, were the most frequently isolated morphological types in raw sewage, treated sewage and river water collected a few metres downstreams from a sewage outfall. However, in river water collected further downstream from the pollution point, in river water after 'in situ' inactivation experiments and in chlorinated raw and treated sewage significant changes in the proportions of the different somatic coliphage morphological types occurred. In all cases, Siphoviridae, especially those with flexible and curled tails, became more abundant to the detriment of Myoviridae

95. **Bacterial and chemical quality of water supply in the Dertig village settlement. Nevondo, T. S., Cloete, T. E. (1999). *Water S A (Pretoria)* 25:215-220.** Water contaminated with microbiological and chemical constituents can cause a variety of diseases. Water intended for human consumption should be safe, palatable and aesthetically pleasing. Water sources have different qualities influenced by natural or anthropological pollution. In South Africa, the availability of safe and clean water is a serious problem, especially in rural areas. Most people in such areas use water directly from available sources without any treatment and therefore are exposed to a variety of water-related diseases. The objective of this study was to determine the chemical and microbiological quality of drinking water supply to a rural community in order to estimate the health implications thereof. Water samples were collected weekly from five water sources, that is, Lefatlheng Well, Tlhaloganyo groundwater, Tlhaloganyo rain water, Matlaisane groundwater and Tshwane River in the Dertig/Lefatlheng village settlement which is in Hammanskraal, about 55 km north of Pretoria. To provide an indication of the microbiological quality of the water resources, indicator organisms including heterotrophic bacteria, faecal coliform, total coliform, *Salmonella* and coliphages were used. In order to support the results, bacterial isolates were identified using both the 20E and 20NE API systems to confirm their isolation. For the chemical quality analyses, different chemical quality variables including temperature, pH, dissolved oxygen (DO), aluminium (A1), iron (Fe), manganese (Mn), fluoride (F), nitrate (NO3), nitrite (NO2) and colour were determined. The chemical quality of all the water sources analysed was acceptable. In contrast, however, the microbiological quality of all the water sources exceeded the standard for potable water and the sources pose a serious health risk to consumers

96. **Dependence of phage infection efficiency on the *Staphylococcus* cells energetic status. Polishko, T. N., Vinnikov, A. I. (1999). *Ukrainskii Biokhimicheskii Zhurnal* 71:28-32.** Studies of phage infection efficiency in *Staphylococcus aureus* showed its dependence on the energy processes. Addition of KCN, dycyclohexylcarbodiimide and chlorocarbonylcyanide-phenylhydrazone at the moment of cells contact with bacteriophages lowered phagolysis efficiency to 49,5-68,0%. These inhibitors influenced on cell specifically leading to suppressing generators of protonmotive force and to dissipating membrane potential. Adding phages to the suspension of bacterial led to the dissipation of membrane potential

97. **A novel virus family, the Rudiviridae: Structure, virus-host interactions and genome variability of the sulfolobus viruses SIRV1 and SIRV2. Prangishvili, D., Arnold, H. P., Gotz, D., Ziese, U., Holz, I, Kristjansson, J. K., Zillig, W. (1999). *Genetics* 152:1387-1396.** The unenveloped, stiff-rod-shaped, linear double-stranded DNA viruses SIRV1 and SIRV2 from Icelandic *Sulfolobus* isolates form a novel virus family, the Rudiviridae. The sizes of the genomes are 32. 3 kbp for SIRV1 and 35.8 kbp for SIRV2. The virions consist of a tube-like superhelix formed by the DNA and a single basic 15.8-kD DNA-binding protein. The tube carries a plug and three tail fibers at each end. One turn of the DNA-protein superhelix measures 4.3 nm and comprises 16.5 turns of B DNA. The linear DNA molecules appear to have covalently closed hairpin ends. The viruses are not lytic and are present in their original hosts in carrier states. Both viruses are quite stable in these carrier states. In several laboratory hosts SIRV2 was invariant, but SIRV1 formed many different variants that completely replaced the wild-type virus. Some of these variants were still variable, whereas others were stable. Up to 10% nucleotide substitution was found between corresponding genome fragments of three variants. Some variants showed deletions. Wild-type SIRV1, but not SIRV2, induces an SOS-like response in *Sulfolobus*. We propose that wild-type SIRV1 is unable to propagate in some hosts but surmounts this host range barrier by inducing a host response effecting extensive variation of the viral genome

98. **Phages for methicillin-resistant *Staphylococcus aureus*: An international trial. Richardson, J. F., Rosdahl, V. T., Van Leeuwen, W. J., Vickery, A. M., Vindel, A., Witte, W. (1999). *Epidemiology and Infection* 122:227-233.** An internationally agreed and validated set of phages is used worldwide for the typing of strains of *Staphylococcus aureus* of human origin. However, because of the sometimes reduced susceptibility of methicillin-resistant strains (MRSA) to these phages, some of the national typing centres use locally isolated and characterized sets of experimental phages. In this trial, 42 such phages were distributed to 6 centres and tested against 744 isolates of MRSA with the intention of defining a phage set to augment the international set. The use of these experimental phages increased the percentage typability from 75% with the international set to 93% and the number of identifiable lytic patterns from 192 to 424. A subset of 10 experimental phages was selected. When this subset was compared with the experimental panel, the typability rate was 91% and 370 distinct patterns were obtained. This subset of phages has been distributed for international trial

99. **Lethal toxicity of *Vibrio harveyi* to cultivated *Penaeus monodon* induced by a bacteriophage. Ruangpan, L.,**

Danayadol, Y., Direkbusarakom, S., Siurairatana, S., Flegel, T. W. (1999). *Diseases of Aquatic Organisms* 35:195-201. In Southern Thailand in 1996, intense luminescence in many shrimp rearing ponds was accompanied by massive mortality resulting in total crop loss within 3 or 4 d. Mortality was correlated with gross signs which shrimp farmers called (English translation) tea-brown gill syndrome (TBGS). Histological examination of moribund shrimp revealed massive lesions of the hepatopancreas characterized by hemocytic infiltration and the presence of bacterial cells. Bacterial isolation yielded several strains tentatively identified as *Vibrio harveyi* on the basis of luminescence and growth on BTB Teepol agar. Representative isolate VH1039 was selected and identified by biochemical tests as *V. harveyi*. When strain VH1039 and the other luminescent isolates were injected into normal shrimp (1 X 10^7 cells shrimp-1), no significant mortality was observed in comparison with control shrimp injected without bacteria. Nor was any significant mortality observed after injection of supernatant fluids fromnormal or sonicated bacterial cultures of VH1039 (1 X 10^8 cells ml^{-1}). Transmission electron microscopy (TEM) of hepatopancreatic tissue from farmed TBGS shrimp revealed bacterial cells of *Vibrio* morphology together with large numbers of bacteriophage particles that had round to hexagonal heads of approximately 60 nm diameter and tails of approximately 100 nm length. These were either free, attached to cell walls of intact bacteria or in various stages of replication within bacterial cells. Gills of farmed TBGS shrimp were subsequently homogenized in lobster haemolymph buffer (LHB) and membrane filtered (0.22 mum). Compared to control shrimp injected with LHB, shrimp injected with the 1000X diluted gill filtrate (DGF) showed no significant mortality. However, when DGF was injected together with 1 X 10^7 cells of strain VH1039, there was total mortality within 48 h. High and rapid mortality concurrent with brown gills was seen only in the mixed injection group. TEM of the artificially infected shrimp tissues did show the presence of bacterial cells, but no mature bacteriophage particles or lysed bacterial cells were found similar to those seen in farmed TBGS shrimp. In further tests, addition of DGF to cultures of VH1039 induced extreme but transitory toxicity of culture filtrates from 24 to 36 h. Treatment of DGF with a germicidal lamp (UV) for 30 min or with heat at 100degreeC for 15 min failed to stop shrimp mortality from mixed DGF/VH1039 injections. However, mortality was stopped if the heated DGF was treated with DNase. The results suggested that a bacteriophage may sometimes mediate the toxicity of *V. harveyi* in *Penaeus monodon* by the transfer of a toxin gene(s) or a gene(s) controlling toxin production

100. **Use of the polymerase chain reaction and denaturing gradient gel electrophoresis to study diversity in natural virus communities. Short, S. M., Suttle, C. A. (1999). *Hydrobiologia* 401:19-32.** Viruses are abundant members of marine and freshwater microbial communities, and are important players in aquatic ecology and geochemical cycles. Recent methodological developments have allowed the use of the polymerase chain reaction (PCR) to examine the diversity of natural communities of viruses without the need for culture. DNA polymerase genes are highly conserved and are, therefore, suitable targets for PCR analysis of microbes that do not encode rRNA. As natural virus communities are largely made up of dsDNA viruses, and as many dsDNA algal viruses encode their own DNA polymerase, PCR primers can be designed to amplify fragments of these genes. This approach has been used to examine the genetic diversity in natural communities of viruses that infect phytoplankton. Algal-virus-specific primers were used to amplify polymerase fragments from natural virus samples, demonstrating the presence of a diverse community of viruses closely related to those that are known to infect phytoplankton. We have modified this approach by using denaturing gradient gel electrophoresis (DGGE) to rapidly analyze PCR products. DGGE will permit rapid and efficient fingerprinting of natural marine viral communities, and allow spatial and temporal differences in viral community structure to be examined. This paper provides a brief overview of how PCR and DGGE can be used to examine diversity in natural viral communities drawing on viruses that infect phytoplankton as an example.

101. **Vibrio cholerae 0139 temperate phage: Characterization and role in modifying the expression of virulence chromosome genes. Smirnova, N. I., Yeroshenko, G. A., Schelkanova, Ye, Livanova, L. F., Konnov, N. P. (1999). *Molekulyarnaya Genetika Mikrobiologiya i Virusologiya* 3-9.** Restriction analysis of temperate cholera phage 139 isolated from *Vibrio cholerae* P16064, serogroup 0139, showed its DNA to be double-stranded linear with cohesive terminals. DNA-DNA hybridization on nylon membranes revealed that many *V. cholerae* strains of serogroup 0139 isolated in different regions contained a temperate cholera phage 139 in their genomes. Southern blot hybridization of chromosomal DNA PST-fragments with phage probe showed that the temperate phage 139 was identical to the temperate phage of serogroup II *V. eltor*. The phage integrated in tile chromosome near genes encoding motility (mot) and production of the capsule (cap) and purine (pur). Phage genome is apparently responsible for instability of cap, pur, and mot genes whose products are important for the development of an infectious process in cholera

102. **Genetic control of *Vibrio cholerae* pathogenicity: Temperate filamentous CTX bacteriophage coding for cholera toxin and the "pathogenicity island". Smirnova, N. I. (1999). *Molekulyarnaya Genetika Mikrobiologiya i Virusologiya* 3-11.** Reviews modern data on the genetic control of the key factors of *Vibrio cholerae* pathogenicity: cholera toxin and toxin-coregulated adhesion phili. Pays special attention to the temperate filamentous CTX bacteriophage, whose genome contains structural genes of cholera toxin, and the "pathogenicity island" carrying tcp genes responsible for the most important factor of the human small intestine colonization with *V. cholerae*. Discusses the mechanism of coordinated regulation of the activity of the main genes of V. cholerae pathogenicity genes

103. **Do viruses control the oceans? Suttle, C. A., Suttl (1999). *Natural History* 108:48-51.**

104. **Phage abortive infection of *Bacillus licheniformis* ATCC 9800; identification of the abiBL11 gene and localisation and sequencing of its promoter region. Tran, L. S. P., Szabo, L., Ponyi, T., Orosz, L., Sik, T., Holczinger, A. (1999). *Applied Microbiology and Biotechnology* 52:845-852.** The virulent bacteriophage BL11 infects almost all *Bacillus licheniformis* strains tested, including the industrial bacitracin-producing *B. licheniformis* 19. *B. licheniformis* ATCC 9800, however, was virtually insensitive to phage BL11 infection, and all of the few surviving progeny phages proved to be mutants. The phage-resistance mechanism was neither inhibition of adsorption, nor restriction or exclusion provided by a resident prophage, but was, instead, of another type. Phage BL11 adsorbed well on to ATCC 9800 cells, its DNA was injected, but replication of phage DNA was inhibited and the infected cells died. Thus, the mechanism of phage resistance was identified as abortive infection (AbiBL11). The so-called abiBL11 gene was identified on the chromosome of strain ATCC 9800 by Tn917PF1 transposon mutagenesis. Part of the abiBL11 gene from the phage-sensitive ATCC 9800::Tn917PFI was cloned. Gene-disruption analysis, based on Campbell-type integration, showed that a 0.3-kb EcoRI fragment contained the 5' end of abiBL11. The promoter region of abiBL11 was identified using promoter- and terminator-probe plasmids. The deduced sequence (206 amino acids) of the N-terminal part of abiBL11 showed no significant homology to known abortive-infection genes, but did show homology to a *Saccharomyces cerevisiae* gene coding for a serine/threonine protein kinase (RCK1)

105. **Blue-green algal viruses (cyanophages). Zhao, Y., Shi, Z., Huang, G., Wang, X. (1999). *Virologica Sinica* 14:100-105.**

106. **Practical use of adapted *Salmonella bacteriophage* for the treatment and prophylaxis of nosocomial salmonellosis.**

Akimkin, V. G., Bondarenko, V. M., Voroshilova, N. N., Darbeeva, O. S., Baiguzina, F. A. (1998). *Zhurnal Mikrobiologii Epidemiologii i Immunobiologii* 85-86.

107. **Use of processed solid residue of olive mill products to absorb *Escherichia coli* and bacteriophage T3 from drinking water. Al-Momani, F., Meqdam, M. M. M., Saadoun, I, Gharaibeh, S. H., Abu-El-Sha'r, W. Y. (1998). *Cytobios* 95:37-41.** The removal of bacteria and viruses from drinking water is of increasing interest particularly if the purification system is inexpensive and readily available. A new material obtained by locally processing the solid residues from olive mill products was investigated as a potential sorbent for removing micro-organisms from drinking water. Indicator micro-organisms, namely *Escherichia coli* and bacteriophage T3 were used in equilibrium batch mode experiments. Results indicated that the processed solid residue of olive mill products effectively removed 92.8% E. coli and bacteriophage T3 from the water. It is suggested that the olive mill products can be used successfully in treatment of drinking water containing microbial contaminants

108. **Molecular evolution of viruses - past and present, Part 2 - An introduction. Becker, Y. (1998). *Virus Genes* 16:7-11.** The evolution of viruses is reviewed within the perspective of the concepts on the evolution of the lipid membrane bound vesicular structures in the prebiotic soup through the ideas on evolution of cells during the RNA World and the transition into the DNA World. The ancient Archeae bacteria and their retrons that carry the bacterial reverse transcriptase gene and their unique protein splicing capability provide an indication of the evolutionary path for retroviruses and, independently, for RNA and DNA viruses of the prokaryotic Archeae bacteria and the eukaryotic yeast and fungi

109. **Comparison of elimination of bacteriophages MS2 and variant phiX-174 during sewage treatment by natural lagooning or activated sludges: A study on laboratory-scale pilot plants. Benyahya, M., Bohatier, J., Laveran, H., Senaud, J., Ettayebi, M. (1998). *Environmental Technology* 19:513-519.** Using appropriate laboratory pilot plants we studied phage elimination during sewage treatment by lagooning and activated sludges. Sewage fed into two types of pilot plant was seeded with a somatic coliphage (variant phiX-174) or an F-specific RNA phage (MS2). Samples were taken from inside the biological treatment tanks to follow phages disappearance. The kinetics of their elimination were compared with that of an inert tracer, rhodamine B. Other samples were taken at the outflow to evaluate the efficiencies of phage removal for the two treatment processes. The elimination of MS2 in the absence of any specific solid phase was also studied. Results show that rapid adsorption on solid particles was less marked for rhodamine than for the phages. The regression coefficients calculated for MS2 and variant phiX-174 were, respectively, 0.46 day-1 and 0.37 day^{-1} for lagooning, and 0.13 h-1 and 0.128 h-1 for activated sludges, whereas those of rhodamine were 0.069 day-1 and 0.024 h^{-1}. Thus elimination of the phages was faster than that of the tracer. This reflects the influence of factors acting exclusively on the viral particles. The phages do not therefore behave as inert molecules. The efficiencies of removal of the two types of phage were comparable for the two treatment processes. The extent of elimination was of the order of 2 log. The study of the elimination of MS2 in the absence of any specific solid phase showed that the floc of the activated sludges system favoured elimination more than the sediments in the lagooning system

110. **Effects of the abortive infection mechanism AbiK on the lactococcal phage p2. Boucher, I, Emond, E., Moineau, S. (1998). *Journal of Dairy Science* 81:4.**

111. **The bacteriophages. Champagne, C. P., Moineau, S. (1998). pp. 89-116 in Champagne, C. P. (ed.) *Production of Dairy Starter Cultures (in French)*.**

112. **The use of affinity adsorbents in expanded bed adsorption. Chase, H. A. (1998). *Journal of Molecular Recognition* 11:217-221.** The potential for the use of affinity ligands in expanded bed adsorption (EBA) procedures is reviewed. The use of affinity ligands in EBA may improve its use in direct recovery operations, as the enhanced selectivity of the adsorbent permits selective capture of the target from complex feedstocks and high degrees of purification. The properties of ligands suitable for use in EBA processes are identified and illustrated with examples. In addition to its use in the recovery of soluble products, such as proteins and nucleic acids, from particulate feedstocks, EBA can also be used to recover particulate entities, such as cells and packaged DNA (viruses and phages), from feedstocks. Affinity ligands coupled to appropriate chosen support materials will be required for such processes in order to achieve the necessary selectivity for the required particulate entity. The latter point is illustrated by the use of proteinaceous ligands immobilized to perfluorocarbon emulsions to achieve separations of microbial cells

113. **Technological and health benefits of dairy starter cultures. Daly, Charles, Fitzgerald, Gerald F., O'Connor, Lisa, Davis, Ruth (1998). *International Dairy Journal* 8:195-205.** Lactic acid bacteria are the focus of research efforts world-wide because of their central role in commercially important dairy fermentations. Significant advances have been made in elucidating the genetic, biochemical and physiological basis of many of the key technological traits of these bacteria. This review examines the recent progress that has been made in the areas of bacteriophage resistance, bacteriocins, proteolysis and carbohydrate metabolism, in the light of their industrial applications. In addition, the increasingly important role of lactic acid bacteria in the production of probiotic products and their potential as vaccine delivery vehicles are discussed

114. **Protecting the neighborhood: Extreme measures. Gottesman, S. (1998). *Proceedings of the National Academy of Sciences of the United States of America* 95:2731-2732.** In the unending wars of organism vs. organism, the growth of bacteriophage and the defenses raised by bacteria were among the first recognized and continue to provide new variations and insights on ways to defend oneself. A paper in this issue of the *Proceedings* demonstrates that prokaryotes, like eukaryotes, have chosen proteolytic self-destruction as a route to protection from attack, albeit a protection for the community rather than for the cell under attack (1).

115. **Microbial indicator reductions in alternative treatment systems for swine wastewater. Hill, V. R., Sobsey, M. D. (1998). *Water Science and Technology* 38:119-122.** Bacterial, viral and parasitic pathogens in swine wastes are of public health concern because many are able to infect humans. Hence, treatment processes must be effective in removing or destroying these microbes before wastewater discharge. Primary treatment by anaerobic lagoon is the current best management practice (BMP) for swine wastewater in the USA but alternative processes were also investigated for their potential to improve treatment. Wastewater samples were collected approximately monthly from March-December 1997 at a North Carolina swine nursery. Geometric mean concentrations for bacterial indicators (faecal coliforms, *E. coli*, enterococci and *C. perfringens* spores) in lagoon effluent were $3.3X10^5$, $2.8X10^5$, $3.4X10^5$ and $2.2X10^4$ CFU/100mL respectively. For somatic and male-specific coliphages they were $1.4X10^5$ and $5.0X10^3$ PFU/100mL respectively. Bacterial indicator levels in swine lagoon effluents are much higher than allowed for municipal wastewater effluents discharged to land or water. The anaerobic lagoon achieved

reductions of 1.1-2.2 log10 for all indicators except *C. perfringens* spores (0.2 log10). Of the secondary treatment processes, constructed wetlands achieved the best indicator microbe reductions ranging from 1.1-2.5 log10. A media filter and an overland flow system achieved mean indicator reductions of only 0.2-1.2 and 0.2-0.8 log10, respectively. The results indicate that a primary-secondary treatment system, an anaerobic lagoon and constructed wetlands, can achieve reductions of 2.9-4.8 log10 for bacterial and viral indicators and 1.5 log10 for *C. perfringens* spores

116. **Lysis of bacteriophages, *Lactococcus* spp., flow cytometric analysis. Hutter, K. J., Guo, X, Schueller, G., Suessmuth, R. (1998). *Advances in Food Sciences* 20:7-12.** Dairy products are not fermented by the natural microorganisms of milk but by inoculated starting cultures of *Lactococcus* spp. 70 to 80% of fermentation problems are caused by the induction of bacteriophages. Flow cytometry was used as a practicable method to control the growth and proliferation of bacteria by means of online DNA analysis at different points of time. Most of the Lactococcus cells are dying at the moment of lysis of bacteriophages. Therefore, only the resistant cells are detectable by flow cytometric analysis

117. **The technique for the lyophilizing preservation of the plague phages. Kadetov, V. V., Kurdyakova, T. A., Terent'ev, A. N., Kachkina, G. V., Borodina, T. N., Sayamov, S. R. (1998). *Biotekhnologiya* 63-67.** Optimum conditions for lyophilizing preservation of plague agents have been discussed which permit for them to retain the native biological characteristics under the significant reducing of the duration of the drying time

118. **Selfishness and death: Raison d'etre of restriction, recombination and mitochondria. Kobayashi, I (1998). *Trends in Genetics* 14:368-374.** Type II restriction-modification gene complexes, such as the EcoRI system, are not easily lost from their host cell. The descendants of cells that lose a restriction-modification gene complex are unable to modify a sufficient number of recognition sites in their chromosomes to protect them from lethal attack by the remaining molecules of restriction enzyme. This capacity to act as a selfish genetic element is likely to have contributed to the spread and maintenance of restriction-modification systems. Homologous recombination machineries of cells and viruses appear to be well adapted to cope with these elements. By extrapolation, the capacity of mitochondria to kill their host eukaryotic cell might have stabilized their initial symbiosis.

119. **Inactivation of phage Qbeta by 254nm UV light and titanium dioxide photocatalyst. Lee, Seockheon, Nakamura, Miyako, Ohgaki, Shinichiro (1998). *Journal of Environmental Science and Health Part A Toxic-Hazardous Substances & Environmental Engineering* 33:1643-1655.** The disinfection efficacy of UV light irradiation at wavelength of 254 nm over a titanium dioxide (TiO2) suspension was compared to that of UV alone. Bacteriophage Qbeta was used as a model virus for the study. Qbeta in sterilized pure water and TiO2 suspension was irradiated by a 0.4 mW/cm2 intensity of 254nm UV light. The UV light over TiO2 was more effective than 254nm UV alone in inactivating Qbeta. 3.5-log10 Qbeta inactivation was achieved by UV irradiation over TiO2 suspension (103 mg/L) after 2 minutes of irradiation, while UV alone inactivated 2-log10. Using a MPN-PCR method, a ca. 1-log10-unit decrease in Qbeta RNA concentration was detected after 3 minutes of photocatalytic irradiation. Th. decrease was explained by damage to nucleic acid of phage Qbeta due to radical oxidation, which is generated by photocatalysis

120. **Comparative adsorption of Norwalk virus, poliovirus 1 and F+ RNA coliphage MS2 to soils suspended in treated wastewater. Meschke, J. S., Sobsey, M. D. (1998). *Water Science and Technology* 38:187-189.** Enteric viruses such as Norwalk virus (NV) are important agents of waterborne disease from faecally contaminated groundwater. Viruses are more resistant to inactivation than most enteric bacteria and they may not be removed efficiently during land application. Adsorption is one of the major factors in viral removal and persistence in soils. The adsorption of NV by soils suspended in wastewater has not been determined. Therefore, we determined the adsorption of NV to six soils (Cecil clay-loam, Corolla sand, Georgia Kaolinite (clay), Wyoming Bentonite (clay), Ponzer organic muck and Flushing Meadows sand-loam) suspended in treated wastewater and compared it to that of poliovirus 1 (PV1) (strongly adsorbed) and MS2 (weakly adsorbed). NV is shown to be less sorptive than PV1 and more sorptive than MS2. Furthermore, relative virus adsorption among soils was similar for all three enteric viruses with viruses most adsorbed by clays and least adsorbed by sand and organic soils

121. **Advance in bacterial typing methods (a review). Milch, Hedda (1998). *Acta Microbiologica et Immunologica Hungarica* 45:401-408.** We give a short review about the two main groups of bacterial typing methods for epidemiological purposes: the phenotypic and genotypic methods. The advantage of the phenotypic methods is their feasibility for the less equipped laboratories, their disadvantages are the variability of the phenotypic properties, and their high labor requirement. The advantages of the genotypic typing methods are the higher discriminatory power and applicability of the same method for different species of bacteria. The disadvantage of these methods is that they are expensive and labour consuming. Beside the short description, we show the results of different authors obtained by the use of the molecular methods in the epidemiological practice and we call the attention to the insufficiency concerning the stability

122. **Starter cultures for Mozzarella cheese. Parente, E., Moschetti, G., Coppola, S. (1998). *Annali di Microbiologia ed Enzimologia* 48:89-109.** The composition of mixed and defined strain starter cultures for the production of Mozzarella cheese is described. The relationship between culture activities and cheese quality, phage related problems, propagation of starter cultures and approaches for culture characterization arc reviewed in detail

123. **Molecular evolution of a pathogenicity island from enterohemorrhagic *Escherichia coli* O157:H7. Perna, Nicole T., Mayhew, George F., Posfai, Gyorgy, Elliott, Simon, Donnenberg, Michael S., Kaper, James B., Blattner, Frederick R. (1998). *Infection and Immunity* 66:3810-3817.** We report the complete 43,359-bp sequence of the locus of enterocyte effacement (LEE) from EDL933, an enterohemorrhagic *Escherichia coli* O157:H7 serovar originally isolated from contaminated hamburger implicated in an outbreak of hemorrhagic colitis. The locus was isolated from the EDL933 chromosome with a homologous-recombination-driven targeting vector. Recent completion of the LEE sequence from enteropathogenic *E. coli* (EPEC) E2348/69 afforded the opportunity for a comparative analysis of the entire pathogenicity island. We have identified a total of 54 open reading frames in the EDL933 LEE. Of these, 13 fall within a putative P4 family prophage designated 933L. The prophage is not present in E2348/69 but is found in a closely related EPEC O55:H7 serovar and other O157:H7 isolates. The remaining 41 genes are shared by the two complete LEEs, and we describe the nature and extent of variation among the two strains for each gene. The rate of divergence is heterogeneous along the locus. Most genes show greater than 95% identity between the two strains, but other genes vary more than expected for clonal divergence among E. coli strains. Several of these highly divergent genes encode proteins that are known to be involved in interactions with the host cell. This pattern suggests recombinational divergence coupled with natural selection and has implications for our understanding of the interaction of both pathogens with their host, for the emergence of O157:H7, and for the evolutionary history of pathogens in general

124. **Biochemical and phylogenetic characterization of the dUTPase from the archaeal virus SIRV. Prangishvili, D., Klenk, H. P., Jakobs, G., Schmiechen, A., Hanselmann, C., Holz, I, Zillig, W. (1998). *Journal of Biological Chemistry* 273:6024-6029.** The derived amino acid sequence from a 474-base pair open reading frame in the genome of the *Sulfolobus islandicus* rod-shaped virus SIRV shows striking similarity to bacterial dCTP deaminases and to dUTPases from eukaryotes, bacteria, Poxviridae, and Retroviridae. The putative gene was expressed in *Escherichia coli*, and dUTPase activity of the recombinant enzyme was demonstrated by hydrolysis of dUTP to dUMP. Deamination of dCTP by the enzyme was not detected. Phylogenetic analysis based on amino acid sequences of the characterized enzyme and its homologues showed that the dUTPase-encoding dut genes and the dCTP deaminase-encoding dcd genes constitute a paralogous gene family. This report is the first identification and functional characterization of an archaeal dUTPase and the first phylogeny derived for the dcd-dut gene family

125. **Survival and transfer of faecal indicator organisms of wastewater effluents in receiving lake waters. Rajala, R. L., Heinonen-Tanski, H. (1998). *Water Science and Technology* 38:191-194.** Water of Lake Kallavesi, which receives wastewater effluents, is used for abstraction of drinking water, for swimming and fishing. It is also used directly for washing and drinking water, both for humans and cattle, especially in summer time. These are the reasons for the present study to follow survival and transfer of faecal indicators downstream from the wastewater treatment plant. Samples were collected in winter and summer from the bottom of the lake at deep sites. At some of the sites the vertical distribution of microbes in summer was also studied. Indicators determined were faecal coliforms, enterococci, sulphite-reducing clostridia and coliphages. The farthest point was 35km for bottom samples. All the indicators could be found in sampling sites near to the discharge point with relatively high numbers. At distant sample sites, coliphages or enterococci were the most abundant. In the winter, coliphages were found up to 18km from the discharge point. In summer, indicators survived well. The results suggest that the direct use of lake water could be considered a health risk

126. **Yeast positive-stranded virus-like RNA replicons: 20 S and 23 S RNA terminal nucleotide sequences and 3' end secondary structures resemble those of RNA coliphages. Rodriguez-Cousino, Nieves, Solorzano, Alicia, Fujimura, Tsutomu, Esteban, Rosa (1998). *Journal of Biological Chemistry* 273:20363-20371.** *Saccharomyces cerevisiae* strains carry single-stranded RNAs called 20 S RNA and 23 S RNA. These RNAs and their double-stranded counterparts, W and T dsRNAs, have been cloned and sequenced. A few nucleotides at both ends, however, remained unknown. These RNAs do not encode coat proteins but their own RNA-dependent RNA polymerases that share a high degree of conservation to each other. The polymerases are also similar to the replicases of RNA coliphages, such as Qbeta. Here we have determined the nucleotide sequences of W and T dsRNAs at both ends using reverse transcriptase polymerase chain reaction-generated cDNA clones. We confirmed the terminal sequences by primer-extension and RNase protection experiments. Furthermore, these analyses demonstrated that W and T dsRNAs and their single-stranded RNA counterparts (i) are linear molecules, (ii) have identical nucleotide sequences at their ends, and (iii) have no poly(A) tails at their 3' ends. Both 20 S and 23 S IRNAs have GGGGC at the 5' ends and the complementary 5-nucleotides sequence, GCCCC-OH, at their 3' ends. S1 and V1 secondary structure-mapping of the 3' ends of 20 S and 23 S RNAs shows the presence of a stem-loop structure that partially overlaps with the conserved 3' end sequence. Nucleotide sequences and stem-loop structures similar to those described here have been found at the 3' ends of RNA coliphages. These data, together with the similarity of the RNA-dependent RNA polymerases encoded among these RNAs and RNA coliphages, suggest that 20 S and 23 S RNAs are plus-strand single-stranded virus-like RNA replicons in yeast

127. **Isolation of three different bacteriophage from mesophilic *Aeromonas* sp. that use different types of monopolar flagella as their primary receptor. Rubires, X, Merino, Susana, Aguilar, Alicia, Nogueras, Maria Merce, Tomas, Juan M. (1998). *FEMS Microbiology Letters* 161:53-57.** Bacteriophage PM4, PM5 and PM6 were isolated on different mesophilic *Aeromonas* strains. These bacteriophage use the flagellum as their primary bacterial receptor since purified flagella from these strains are able to inactivate these bacteriophages, independently, and the phage-resistant mutants are aflagellate and nonmotile. Furthermore, we showed that these bacteriophage may be useful to initiate the serotyping of mesophilic *Aeromonas* for the H-antigen (flagellum)

128. **Bacteriophage PRD1 and silica colloid transport and recovery in an iron oxide-coated sand aquifer. Ryan, Joseph N., Elimelech, Menachem, Ard, Rebecca A., Harvey, Ronald W., Johnson, Philip R. (1998). *Environmental Science & Technology* 33:63-73.** Bacteriophage PRD1 and silica colloids were co-injected into sewage-contaminated and uncontaminated zones of an iron oxide-coated sand aquifer on Cape Cod, MA, and their transport was monitored over distances up to 6 m in three arrays. After deposition, the attached PRD1 and silica colloids were mobilized by three different chemical perturbations (elevated pH, anionic surfactant and reductant). PRD1 and silica colloids experienced less attenuation in the contaminated zone where adsorbed organic matter and phosphate may be hindering attachment of PRD1 and silica colloids to the iron oxide coatings. The PRD1 collision efficiencies agree well with collision efficiencies predicted by assuming favorable PRD1 deposition on iron oxide coatings for which the surface area coverage was measured by microprobe analysis of sediment thin sections. zeta potentials of the PRD1, silica colloids, and aquifer grains corroborated the transport results, indicating that electrostatic forces dominated the attachment of PRD1 and silica colloids. Elevated pH was the chemical perturbation most effective at mobilizing the attached PRD1 and silica colloids. Elevated surfactant concentration mobilized the attached PRD1 and silica colloids more effectively in the contaminated zone than in the uncontaminated zone

129. **A comparative study on the frequency of prophages among natural isolates of *Salmonella* and *Escherichia coli* with emphasis on generalized transducers. Schicklmaier, P., Moser, E., Wieland, T., Rabsch, W., Schmieger, H. (1998). *Antonie van Leeuwenhoek* 73:49-54.** Several collections of natural isolates of the genus *Salmonella* and of the species *Escherichia coli* were studied for the release of viable temperate phages. The results indicated that functional prophage genomes may be a common constituent of all bacterial genomes of the investigated strains. About 99% of the *Salmonella* phages are capable of generalized transduction of chromosomal host markers and plasmids. The ratio of transducing *E. coli* phages is significantly lower

130. **A new bacteriophage typing scheme for *Proteus mirabilis* and *Proteus vulgaris* strains: 3. Analysis of lytic properties. Sekaninova, G., Rychlik, I, Kolarova, M., Pillich, J., Semenka, J., Zajicova, V (1998). *Folia Microbiologica* 43:136-140.** The lytic properties of 21 bacteriophages constituting a new typing set for *Proteus* were examined in 507 *Proteus mirabilis* and 29 *P. vulgaris* strains isolated from patients and healthy subjects. Comparison of their morphological, serological, genetic and lytic properties showed that, in the Myoviridae and Podoviridae families, some phages were so closely related that the presence of all of them in the set was redundant. Analysis of the lytic properties revealed that some of the bacteriophages were not active enough to facilitate the differentiation of Proteus strains. The size of the final typing set was reduced from 21 to 12 phages but it was suggested that, in order to improve the differentiation capacity of the set, new phages should be included

131. **Bacterioplankton dynamics in Lake Constance (Bodensee): Substrate utilization, growth control, and long-term trends. Simon, M., Bunte, C., Schulz, M., Weiss, M., Wuensch, C. (1998). *Ergebnisse der Limnologie* 195-221.** We studied the dynamics of bacterioplankton growth and the factors controlling it in Lake Constance between 1982 and 1997, but mainly during the last 8 years. In the course of this time, the lake experienced a significant oligotrophication due to an efficient decrease in the phosphorus load. The large changes in nutrient load and concomitant qualitative and quantitative changes in the phytoplankton community made it a particularly interesting time to study bacterial growth dynamics. Both bacterial production (BP) and bacterial numbers (BN) showed persistent annual patterns throughout the period. In most years, highest rates of BP and BN occurred towards the end of the phytoplankton spring bloom. During the clear-water phase, BP and BN varied depending on the grazing pressure by daphnids and decreased towards its end. During summer, BP and BN increased again and to varying extents until the autumnal decline. In 1995 and 1997, highest rates occurred in summer (August, September). In particular, BN remained lower in summer than during the previous part of the season. During the spring bloom, BP was closely correlated either to the biomass of ciliates or of daphnids, but only weakly to chlorophyll, indicating that grazing and thus release of dissolved organic matter by these two herbivores was the most important factor in bottom-up control of bacterial growth at this time. Dissolved free and combined amino acids as well as dissolved free and combined carbohydrates constituted the pool of labile dissolved organic matter to a great extent and were always the major bacterial substrates utilized. At maxima of BP, amino acids were preferred whereas carbohydrates were utilized to a greater extent at high and declining bacterial numbers. The bacterial growth efficiency changed seasonally, but in general ranged between 20 and 40%. During most of the growing season, bacterioplankton growth was co-limited by phosphorus and organic carbon whereas during winter only organic carbon was limiting. Temperature has relatively little direct impact on bacterioplankton growth in the epilimnion because the bacterial assemblages adapted fairly well to the changing ambient temperatures. In the deeper water, temperature directly controlled BP during most of the year. The major loss factors of bacterioplankton comprised phage-induced mortality and grazing by heterotrophic nanoflagellates (HNF), ciliates, and daphnids. On average, phages accounted for 1-24% of total mortality whereas grazing by HNF for 52-68%, by ciliates for 14-19%, and by daphnids for 9-12%. During the clear-water phase, however, grazing by daphnids dominated by more than 50%. During oligotrophication, the annual ratio of BP/primary production (PP) integrated from 0 to 20 m varied between 0.09 and 0.29, but without a clear-cut trend. In 1995 and 1996, bacterial growth rates were enhanced and the biomasses of daphnids and autotrophic picoplankton reduced as compared to the previous years. This suggests that grazing control of BP by HNF became more important than before in this late stage of oligotrophication

132. **RT-PCR amplification detects inactivated viruses in water and wastewater. Sobsey, M. D., Battigelli, D. A., Shin, G. A., Newland, S. (1998). *Water Science and Technology* 38:91-94.** Nucleic acid (NA) amplification techniques are useful to detect viruses in water and other environmental samples because they are highly sensitive, specific and can detect fastidious enteric viruses that do not grow well or not at all in cell cultures. However, RT-PCR was found to detect inactivated viruses. In terms of risks to public health this constitutes a false positive result, as inactivated viruses are no longer infectious. When poliovirus type 1 and coliphage MS2 were studied for (a) persistence in water and sewage and (b) inactivation in water by free chlorine, chlorine dioxide and UV radiation, RT-PCR assays underestimated virus inactivation. The use of multiple RT-PCR amplification sites, larger RT-PCR genomic targets and immunocapture RT-PCR sometimes reduced, but did not eliminate, the discrepancy between loss of infectivity and loss of RT-PCR titre. Virus presence based on RT-PCR detection must be interpreted with caution when predicting human health risks

133. **Construction of bacteriophage resistant strains of *Streptococcus thermophilus* by pGh9::ISS1 insertional mutagenesis. Sturino, J. M., Steele, J. L. (1998). *Journal of Dairy Science* 81:7.**

134. **DNA analysis of temperate bacteriophage Aavariant phi23 isolated from *Actinobacillus actinomycetemcomitans*. Willi, K., Meyer, J. (1998). *Molecular & General Genetics* 258:323-325.** The DNA of the temperate bacteriophage Aavariant phi23 isolated from the oral bacterium *Actinobacillus actinomycetemcomitans* was examined structurally both in the phage head and in the prophage. The DNA in phage particles comprises 44 kb linear molecules with a terminal redundancy of 1.6 kb, which represent circular permutations. Thus, DNA is packaged into phage heads by the headful mechanism. The Aavariant phi23 prophage is integrated into the host chromosome

135. **The effect of storage and ozonation on the physical, chemical, and biological characteristics of swine manure slurries. Wu, J. J., Park, S. H., Hengemuehle, S. M., Yokoyama, M. T., Person, H. L., Masten, S. J. (1998). *Ozone Science & Engineering* 20:35-50.** The reduction of odor emanating from wasted swine manure is a very challenging environmental engineering problem. In an earlier work (Watkins et al., 1997), we showed the effect of ozone in reducing the odor and concentration of phenolic compounds in swine manure obtained from the pits under the slotted floors where the swine were housed. In this paper, we have expanded significantly upon the work of Watkins et al. by determining the effect of storage on the physical, chemical and biological characteristics of the swine manure slurry and whether the efficacy of ozonation is dependent upon storage time

136. **Properties of mycobacteriophage MTPH11. Zhilenkov, E. L., Shemyakin, I. G., Stepanshina, V. N., Korobova, O. V., Oborotov, M. V., Dorozhkova, I. R. (1998). *Mikrobiologiya* 67:660-665.** Some characteristics of the poorly studied phage MTPH11, which is used for identification of mycobacteria, are presented. The phage has an isometric head and a long noncontractile tail (B1 morphotype). The attachment apparatus of this phage includes a basal plate composed of two joint disks and a single tail fiber. The constant of phage adsorption on *Mycobacterium smegmatis* ATCC607 cells is 6.6 X 10-9 ml/min. The latent infection period in the MTPH11-host strain 607 system is 65 min; phage progeny ranges from 30 to 40 virions per one cell. The constant of phage inactivation with a homologous antiserum is 50 min-1. The buoyant density of intact MTPH11 virion in CsCl amounts to 1.520 g/cm3. The phage is susceptible to chloroform, retains lytic activity within a pH range of 5 to 9, and is resistant to inactivating agents. The G+C content of the phage DNA is 63 mol %

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Acknowledgements

Thanks to Hans Ackermann for his dedication to phage naming and patience with my HTMLing.
