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The Microbial Taxonomist

A Newsletter Published by Bergey's Manual Trust

Fred A. Rainey Elected to Chair of BMT

Fred A. Rainey is a native of Belfast, Northern Ireland. He obtained a BSc(Hons) in Microbiology and Microbial Technology in 1988 from University of Warwick. Fred's doctoral studies were carried out at the Thermophile Research Laboratory at the University of Waikato, Hamilton, New Zealand. In 1991 Fred joined the group of Erko Stackebrandt at the University of Queensland, Brisbane, Australia. In 1993, when Erko Stackebrandt became the Director and CEO of the German Collection of Microorganisms and Cell Cultures (DSMZ), Fred joined the DSMZ and set up the molecular identification laboratory and services.

It was at the beginning of 1997 that Fred moved to the United States and accepted his first academic appointment at Louisiana State University in the Department of Biological Sciences. At LSU Fred had a successful academic career both in teaching, research and administration. From 2004 to 2008 he served as the Associate Dean of the College of Basic Sciences. In the Fall semester of 2011 Fred was appointed the Director of the Department of Biological Sciences at the University of Alaska Anchorage.

Fred Rainey has been associated with Bergey's Manual Trust since 1997, first as an associate and since 2000 as a trustee (and secretary). He has contributed many chapters to Volumes 1–5 of the 2nd edition of *Bergey's Manual of Systematic Bacteriology* and was an Associate Editor of Volume 3, which covered the *Firmicutes*. Since his PhD studies Fred has been involved in bacterial systematics and has authored or coauthored over 200 papers in the field as well as some 85 book chapters. Fred's service to microbiology has included membership of the editorial boards of *Applied and Environmental Microbiology*, *Microbiology*, *International Journal of Systematic and Evolutionary Microbiology*, and *Extremophiles*. Fred sees his main role as Chair of Bergey's Manual Trust as facilitating the transition from the printed book to an up-to-date electronic product that will be accessible and useful to all microbiologists and others needing accurate and current information.

Join BISMiS or renew your membership today! See forms at end of this newsletter or join online at: www.bergeys.org/bismis.html

VOLUME 5 NEWS

Volume 5 of *Bergey's Manual of Systematic Bacteriology*, which focuses on the *Actinobacteria*, is in the final stages of production.

This volume is the largest of the three that I have managed, and will be more than 2000 pages in length, with 431 figures and 320 tables. Its size is such that it will need to be bound in two separate parts.

The first round of proofs was sent out to the authors in six batches beginning in August; I compiled their corrections with ours, and scanned and sent the corrected proofs to our typesetters, SPi. Revised proofs will arrive early December, and each correction will be checked against the first round. Once the pagination is finalized, the indexes will be prepared, and proofs will be checked again before final approval.

Volume 5 will be published in early 2012.

Aidan Parte, Managing Editor

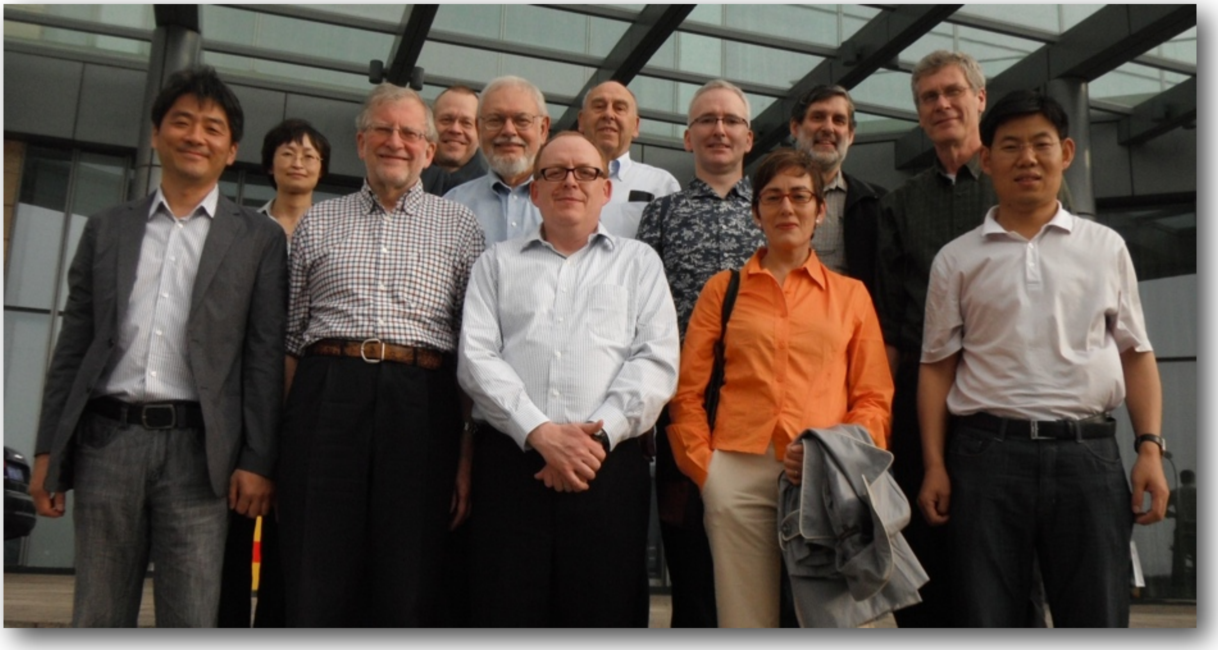
HIGHLIGHTS FROM ANNUAL MEETING IN BEIJING

This year the annual meeting of Bergey's Manual Trust was held in Beijing, China, on 17–18 May. In attendance were all six trustees (Jongsik Chun, Paul De Vos, Mike Goodfellow, Peter Kämpfer, Fred Rainey and Barny Whitman), emeritus trustees Karl Schleifer and Jim Staley, and our Managing Editor, Aidan Parte. Towards the onset of the meeting they were joined by Martha Trujillo following her election as a trustee. Two guests, Ying Huang and Wen-jun Li from the Institutes of Microbiology in Beijing and Kunming, respectively, participated in the open sessions of the meeting. In addition to standard business, notably reports from the Secretary, Treasurer, and Managing Editor, the primary issue addressed was the move toward an electronic publication of the next edition of *Bergey's Manual of Systematic Bacteriology*.

The final arrangements of the inaugural BISMiS conference were outlined by Goodfellow who was full of praise for the work done by Lixin Zhang, Liz Ashforth, and other members of the Local Organising Committee to ensure that the meeting was a success. Staley outlined the activities undertaken by BISMiS over the last year and presented plans for promoting the society at the forthcoming conference. He also indicated that Paul Lawson (University of Oklahoma) had agreed to serve as the Associate Editor of *The Bulletin of BISMiS*, the first issue of which had been edited by Jim Staley. This issue will become freely available on the BISMiS website once the second issue comes out. Some speakers who presented during the inaugural conference will contribute to the December issue of *The Bulletin*, whereas others will appear in a special issue of *Antonie van Leeuwenhoek*.

The trustees agreed that Bergey Medals for life-long contributions to prokaryotic systematics be awarded to Zhiheng Liu, Jisheng Ruan, James Tiedje, and Michael Goodfellow, whose term of office as a trustee had expired. It was also agreed that Goodfellow become an Emeritus Trustee. The trustees also agreed that Fred Rainey become Chairman of the Trust and that Martha E. Trujillo replace him as Secretary – see their biographies elsewhere in this issue. Rainey thanked the trustees for electing him as Chairman and thanked Goodfellow for all that he had done for BMT as a trustee, the Chair of the Trust and as an Editor of Volume 5.

The next meeting of BMT will be held in Anchorage, Alaska.



Attendees of the Trust meeting in Beijing, from left: Jongsik Chun, Ying Huang, Mike Goodfellow, Peter Kämpfer, Jim Staley, Fred Rainey, Karl Schleifer, Aidan Parte, Martha Trujillo, Paul De Vos, Barny Whitman and Wen-jun Li.

MARTHA E. TRUJILLO ELECTED AS TRUSTEE AND SECRETARY OF BMT

Martha Trujillo is Professor of Microbiology at the University of Salamanca in Spain. She is best known for her contributions to bacterial systematics and has published extensively in these fields. Martha is an associate editor of *Antonie van Leeuwenhoek* and the *International Journal of Systematic and Evolutionary Microbiology* and serves on several of the Taxonomic Subcommittees of the International Committee of the Systematics of Prokaryotes. In addition she is an associate editor of *Bergey's Manual of Systematic Bacteriology*, volume 5, to which she has made substantial contributions.

Martha's current research interests are focussed on the taxonomy and ecology of endophytic actinobacteria, bacterial communities which inhabit deteriorating stone monuments and on the search and interest in furthering the systematics of clinically significant actinomycetes, notably in those which cause actinomycetoma.

Martha was born in León, Mexico, and was educated in California before returning to Mexico where she gained a BSc in Pharmacy from the Autonomous Metropolitan University at UAM-Xochimilco, near Mexico City. She was awarded a PhD in actinobacterial systematics under the supervision of Mike Goodfellow at Newcastle University, Newcastle upon Tyne. Thereafter, she carried out postdoctoral work in the Department of Microbiology at Novartis Pharma in Basel, working closely with Jean-Jacques Sanglier. In 1998 she was appointed as a postdoctoral researcher at the University of Salamanca where she has also worked as a senior researcher, research assistant, and associate professor before assuming her present position. Martha is married and has two sons.

PETER H.A. SNEATH (1923–2011)

Peter Sneath was a transformative figure in the field of systematics. Peter had realized in the 1950's that when strains of bacteria are classified by a reasonably large number of detectable characters (50 or more) you have the basis for a numerical and statistical approach for the recognition of species and strains. It was, he recognized in essence, an approach to genotype before gene and protein sequences were available. With his colleague Robert Sokal he brought the concept to life and into practice in an enormously important book they coauthored in 1963 entitled *Principles of Numerical Taxonomy*. This book introduced taxonomists to a quantitative and statistical treatment of taxa based on phenetic analyses. Their taxonomic approach applies to species of plants and animals as well as microorganisms. This landmark book ushered in a new era of using computers for taxonomy.

Peter was always remarkably well informed, perceptive and prepared to think "out of the box". He promoted international and inter-disciplinary discussions of major issues of taxonomic assignment as, for example, reclassifying the blue-green algae as cyanobacteria along with his equally distinguished colleague Roger Stanier. He was an important cog in the planning, editing and publication of Bergey's manuals. Peter was a Trustee of Bergey's Manual Trust for 16 years and Chair for 4 years. He enthusiastically supported the reclassification of bacteria for the 2nd edition of *Bergey's Manual of Systematic Bacteriology* based on 16S rRNA gene sequence analyses as pioneered by Carl Woese. Peter was a Fellow of the Royal Society (London) and received honorary memberships in other microbiological societies. He was a man and scientist worth remembering. Peter's autobiography was published in 2010 in the first issue of *The Bulletin of BISMiS* (Volume 1: 77–83).

For his friends and close colleagues, Peter and his lovely wife, Joan, were great companions at many formal and informal meetings and all appreciated every chance to be together with them.

Robert G.E. Murray

JISHENG RUAN RECEIVES BERGEY MEDAL

Jisheng Ruan graduated from Beijing Agricultural University in 1953. His initial research interests were directed towards understanding the biology of bacterial plant pathogens. However, his scientific interests, and subsequently his career, were transformed in 1957 when he seized the opportunity to do a PhD at the Institute of Microbiology in Moscow under the supervision of Professor Krassilnikov, who at the time was a world leader in the biology of the actinomycetes. In Moscow he was rigorously trained in the theory and practice of prokaryotic systematics and introduced to his beloved friends, the streptomycetes. His research project was designed to unravel the biology of a group of actinomycetes using cultural, morphological, biochemical, and physiological criteria which held sway at the time.

The experience gained with Krassilnikov stood him in good stead as on his return to China in 1961 he was appointed to a position in the group of Professor Xunchu Yan at the newly established Institute of Microbiology of the Chinese Academy of Sciences in Beijing. Here, he was able to pursue his interests in the taxonomy of streptomycetes and was the first Chinese microbiologist to use electron microscopy for taxonomic purposes. He was also one of the first to realize that actinomycetes other than streptomycetes were a rich source of novel antibiotics. His taxonomic studies on the so called rare actinomycetes were not solely based on morphology but also on the application of chemotaxonomic procedures which were being developed at the time by Hubert and Mary Lechevalier in the Waksman Institute at Rutgers State University, New Brunswick, USA.

Another lucky break followed in 1981 when Jisheng was invited by Hubert Lechevalier to take up a two-year postdoctoral fellowship at the Waksman Institute to work on the chemotaxonomy of actinomycetes. His research work with the Lechevaliers' placed him firmly on the world stage and brought him into contact with leading figures in actinomycetes systematics, some of whom became collaborators and good friends. Notable amongst the latter were Professor Marian Mordarski (Institute of Immunology and Experimental Therapy, Wrocław, Poland), Dr Dwight Baker (Yale University), and Professor Mike Goodfellow (Newcastle University, Newcastle upon Tyne, UK).

Jisheng's work at the Waksman Institute was not only pivotal to his own career but also led to the introduction of modern taxonomic methods in China, for on his return to Beijing he set up a laboratory to promote the application and development of chemotaxnomic and molecular biological methods to clarify the systematics of actinomycetes. Much of his work was focussed on improving the systematics of frankiae, nocardioform actinomycetes and sporangia-forming taxa. Together with his colleagues he has published over 120 research papers and six books and trained innumerable graduate students.

Formal retirement from the Institute of Microbiology in 1994 gave Jisheng more scope to pursue his research, first in Singapore and then in Beijing. During this period he and his co-workers discovered four new genera (*Actinopolymorpha*, *Nonomuraea*, *Thermobifida* and *Thermobispora*) and revived the genus *Kitasatospora*. He also served as a long-term visiting professor at the Chinese Academy of Tropical Sciences in Haikou where he introduced graduate students to the intricacies of actinobacterial systematics and contributed to the research group of Kui Hong. In 2006, he was appointed as a consultant professor at his old institute in Beijing, a post which he still holds.

Now well into his eighth decade he is still making significant contributions to actinomycete systematics and has recently written another book – *Rapid Identification and Systematics of Actinobacteria* – together with Professor Ying Huang of the Institute of Microbiology in Beijing. Jisheng is a remarkable man whose verve and commitment to actinomycete systematics puts many younger colleagues to shame.

Mike Goodfellow

ZHIHENG LIU RECEIVES BERGEY MEDAL

Zhiheng Liu graduated from Beijing Agricultural University in 1964. He had chosen microbiology as his main subject and was fortunate to have been taught by two famous Chinese microbiologists, Professors Dafu Yu and Jilin Wu, who had been educated at Cornell University and Moscow State University, respectively. His life-long interest in the taxonomy of the actinomycetes was kindled during his final-year research project – "Isolation of Actinomycetes showing Activity against Gram-negative Bacteria" – which was carried out in the Institute of Microbiology in Beijing under the supervision of Jisheng Ruan. Following graduation he got caught up in the Great Cultural Revolution and spent 10 years as a farm laborer and worker in Xinjiang Province, Northwest China, where food was scarce, the summers fiercely hot, and the winters bitterly cold.

An opportunity opened up for Liu in 1978 following the re-introduction of the postgraduate education system in China. He successfully completed a highly competitive examination for an MSc place in the Graduate School of the Chinese Academy of Sciences. Here he was able to develop his interests in actinomycete systematics working under the tutelage of Academician Xunchu Yan. He was awarded an MSc in 1981 and in the same year was appointed to a position in the Institute of Microbiology in Beijing where he was to remain until his retirement in 2004. He became an Associate Professor in 1987 and a Full Professor in 1996.

It is difficult to do justice to all that Liu has achieved during his career at the Institute of Microbiology as his contributions have been many and varied. However, he was able to realize his dual interests in the taxonomy and exploitation of actinomycetes, as witnessed by the publication of over 150 research papers and appointment as a consultant to many biotech companies. His work on chemical and molecular systematics was promoted through several grant-funded collaborative projects, including those with Professor Michael Goodfellow (University of Newcastle, UK), Professor Marian Mordarski and Dr Andrzej Gamian (Institute of Immunology and Experimental Therapy, Wrocław, Poland), Dr Miroslav Petricek (Institute of Microbiology, Prague) and Professor Jean Swings (University of Ghent, Belgium). In addition, he has been and still is actively involved in the microbial aspects of the Chinese Space Programme.

Liu's contributions to research and teaching have been widely acclaimed in China. He received the Chinese Academy of Sciences Award (1988), the Technology Progress Prize of the Chinese Commission of Science (1997), the Huawei Teaching Award of the Chinese Academy of Sciences (1999) and Technology Progress Prizes from Hebei (1981) and Yunnan (2004) Provinces. In 1996, he was recognized to be an excellent teacher of postgraduate students by the Chinese Academy of Sciences. He has also served on several editorial boards and together with colleagues has published ten books in Chinese, including *Modern Actinomycete Biology and Biotechnology* (2004) and *Systematics of Actinomycetes* (2007).

Although retired, Liu still remains active. He is the Standing Director of the Chinese Society of Space Research, member of the National Expert Council of Space Sciences, Chairman of the Space and Origin of Life Committee, and is a Guest Professor at several institutes and universities. He continues to advise postgraduate students and played a significant role in ensuring the success of the Inaugural Meeting of Bergey's International Society for Microbial Systematics.

Mike Goodfellow

JAMES TIEDJE RECEIVES BERGEY MEDAL

The Trust voted to award the Bergey Medal to James Tiedje of Michigan State University. Professor Tiedje has made numerous important contributions to the field of microbial systematics. Among his research accomplishments, he and his student Kostas Konstantinidis pioneered the effort to use genomic sequences to better understand what comprises a prokaryotic species and higher taxa in a series of landmark papers. In addition, research in his laboratory has led to a better understanding of microbial biogeography. Among his other accomplishments, he enabled the move of the Ribosomal Database Project from the University of Illinois to Michigan State University, where it still remains. Furthermore, he led the effort to relocate Bergey's Manual Trust from Iowa State University to Michigan State University, where he supported its activities for several years until its relocation to the University of Georgia in 2006.

MICHAEL GOODFELLOW: THE MICROBIAL TAXONOMIST

To be invited to pen a few words on Michael Goodfellow is, at the same time, a great pleasure and a difficulty: how best to do justice to the varied achievements of someone who is so well-known to readers of *The Microbial Taxonomist* while attempting to reveal something new about the man? Many if not most people would be content to have made serious contributions in one field, but Mike's have been distinguished not only as a researcher but also as a committed educationalist and internationalist.

His research interests center on microbial systematics where his knowledge of the actinobacteria in particular is pre-eminent. As an early advocate of both numerical and polyphasic taxonomy, his outstanding overall contributions to bacterial taxonomy were recognized as a recipient of The Bergey Award in 1995. His notable achievements include the promotion of chemosystematics with Dave Minnikin where the introduction of procedures to detect polar lipid, menaquinone and mycolic acid patterns led to the reclassification of mycolic acid-containing bacteria, the validity of which has been underpinned and built upon subsequently by the introduction of molecular systematics. Similarly his work with the International Working Group on Mycobacterial Taxonomy led to a reappraisal of mycobacterial systematics and to the recognition of new causal agents of tuberculosis that in turn led to improved chemotherapy.

Mike's work for Bergey's Manual Trust (he completed his term as Board Chairman this year) and commitment to the preparation the 2nd edition of *Bergey's Manual of Systematic Bacteriology* has been heroic and the award recently of the Bergey Medal was richly deserved. It is no surprise that he was senior editor of Volume 5 of the *Manual*, which was devoted to the *Actinobacteria*. His professional support of microbiology has been manifold and includes service on the editorial boards of several journals, the Councils of learned societies, and numerous national and international advisory and evaluation panels. Moreover, his expertise has been sought by a number of pharmaceutical and biotechnology companies. Many of us know of Mike

REQUEST FOR NOMINATIONS FOR THE BERGEY AWARD

Nominations are sought for the 2013 Bergey Award.

The Award was initiated in 1979 to honor an individual for outstanding contributions to microbial taxonomy. The Award, donated by the Board of Trustees of Bergey's Manual Trust, consists of a certificate, a $2000 prize and expenses for travel to receive the Award at the society meeting. Previous winners of the Bergey Award are listed at the Bergey's website. Nominations in the form of a letter of nomination and a CV of the nominee should be forwarded to bergeys@uga.edu by 1 May 2012.

Goodfellow's commitment to higher education that, among other things, has resulted in a constant stream of British and overseas students graduating from his lab throughout his career. Few, I suspect, know of the equal passion he has for upholding and improving the quality and diversity of education at the secondary level: for nearly 40 years he has served as chairman of the governing body of one of the high schools in his adopted city of Newcastle for which he was honored recently by the award of Member of the British Empire (MBE) . His outlook and dedication, however, are decidedly international, be it in the context of providing training in his lab for foreign students, giving support for science initiatives in other countries – not least in the developing world – and organizing workshops with the aim of introducing new taxonomic concepts and practices. One example typifies his philosophy and action: in the Sudan his work is helping to highlight new causal agents of actinomycetoma with the intention of promoting more effective drug therapies to combat this awful and often neglected disease.

Like me, many people throughout the world will have worked with Mike Goodfellow and benefited from his intellect, and characteristic generosity and good humor. Mike and I have known each other for more than 50 years for many of which we have been research colleagues, fellow microbe hunters in varied and sometimes hazardous environments, and discussants of the world's politics, interactions that forge friendships that are special and cherished.

Alan Bull

INAUGURAL MEETING OF BISMIS IN BEIJING 19–23 MAY 2011

The inaugural meeting of Bergey's International Society for Microbial Systematics (BISMiS) occurred in Beijing, China, on 19–23 May 2011. The meeting, which was held at the Beijing Friendship Hotel, was sponsored by Bergey's Manual Trust and the Chinese Academy of Sciences. The program committee chaired by Lixin Zhang with Co-Chairs, Guoping Zhao, Li Huang and Zixin Deng worked closely with Michael Goodfellow, the Trustees and others to organize the program. More than 350 scientists and students attended the meeting, which had sessions on all aspects of microbial systematics. Nobel Laureate Barry Sharpless delivered the keynote speech entitled "Click Chemistry Evolving – Destinations Unknown" on 19 May, and Antonio Ventosa delivered his Bergey Award address entitled "Halophilic Microorganisms and Hypersaline Environments" on May 20.

Fred Rainey, as Secretary of BISMiS, supervised the online nomination and election of new officers for BISMiS including the President-Elect and Secretary. The nominees were Brian Austin and Milton da Costa for President-Elect and Martha Trujillo and Xiao-Hua Zhang for Secretary. At the close of the first BISMiS members' meeting, which was held on 22May, Fred Rainey announced the results of the election. The newly elected officers are Brian Austin and Martha Trujillo, who assumed their offices immediately following the BISMiS meeting. William Whitman will remain Treasurer and Fred Rainey is the new President.

The July issue of *The Bulletin of BISMiS*, Vol. 2, part 1, contains more detailed information about the meeting. Some of the speakers will publish articles in *Antonie van Leuwenhoek* and others will publish in *The Bulletin of BISMiS*.

The meeting was considered to be a great success by those who attended.

James Staley

GEORGY A. ZAVARZIN (1933–2011)

Georgy A. Zavarzin, a distinguished Russian microbiologist, passed away on 6 September 2011. This is a great loss not only for Russian microbiology, but for microbiology worldwide. G.A. Zavarzin was the author of many pioneering works in environmental microbiology and together with his coworkers, of many descriptions of new phylogenetic and metabolic groups of prokaryotes.

G.A. Zavarzin was born on 28 January 1933, into a family with deep scientific roots. His grandfather, academician Boris Isachenko was the director of Institute of Microbiology, Moscow, from 1937 to 1948, and the founder of microbial biogeochemistry in Russia. Nina Zavarzina, the daughter of Isachenko and mother of Georgy Zavarzin, was also a microbiologist and worked at the same Institute. However, it was Georgy Zavarzin's grandfather who influenced many of his choices. After the death of Isachenko in 1948, his grandson Georgy Zavarzin decided to become a microbiologist. He entered Moscow University and later started his PhD course in the Institute of Microbiology, USSR Academy of Sciences, under the supervision of academician A.A. Imshenetsky. Just before that (in 1952) Imshenetsky had succeeded in publishing a book in Russian of S.N. Winogradsky's works, a task considered almost impossible in the Soviet Union. Winogradsky, who discovered chemosynthesis and is considered to be a founder of environmental microbiology, emigrated from Russia during the revolution and because of that was *persona non-grata* in the Soviet Union. Following Winogradsky's research, Imshenetsky recommended Zavarzin to study the life cycle of *Nitrosococcus*, and this thesis work significantly influenced the life-long scientific preferences of Georgy. In the post-Soviet era not only was the name of Winogradsky given to the Institute of Microbiology in Moscow, but an extremely interesting biography of Winogradsky written by G.A. Zavarzin was published after a 20-year delay.

Georgy Zavarzin's scientific career advanced quickly and at 27 years old he was already the head of the Laboratory of Lithotrophic Microorganisms at the Institute of Microbiology. In the 1960s, when microbiology was mostly metabolism-oriented, Georgy started the investigations of metabolism of aerobic sulfur- and hydrogen-oxidizing bacteria. However, his first significant contribution to microbial diversity investigations was made at the end of the 1960s/beginning of the 1970s, as a new group of lithotrophic microorganisms, aerobic carbon monoxide oxidizers was described in collaboration with E. Sandjieva and A. Nozhevnikova. In spite of the Iron Curtain, his inability to travel abroad and publish in international journals, the interests of Georgy Zavarain continued to develope, mostly in parallel with the world trends, and sometimes, even ahead of them. The study of functional microbial diversity and ecology became the main goals of Zavarzin's team.

In the early 1970s, Georgy Zavarzin and his group started studying obligate anaerobes, firstly methanogens and their role in microbial communities and natural environments. Tatyana Zhilina, a younger coworker of Georgy Zavarzin, became his wife, and this union, in addition to a long and happy family life, resulted in the long-term and highly successful scientific research collaboration. Having become an extremely skillful microbiologist, Tatyana helped her husband to describe many new microorganisms representing novel taxa and/or metabolic groups.

Georgy Zavarzin was the first in Russia and one of the first in the world to become interested in microbial diversity of extreme environments. In the late 1970s he started microbiological investigations of the microbial communities in Uzon Caldera, Kamchatka. Together with Lyudmila Gerasimenko he studied the exchange of gases in thermophilic cyanbacterial mats, applying the results to the interpretation of the role of cyanobacteria in the transformation of the atmosphere of ancient Earth. His PhD student Viktor Kryukov isolated from Uzon hot spring the first representative of the order *Aquificales*, "*Calderobacterium hydrogenophilum*", later reclassified as a representative of the genus *Hydrogenobacter* with loss of priority. With Elizaveta Bonch-Osmolovskaya, Zavarzin isolated thermophilic and hyperthermophilic sulfur reducers, with Vitaly Svetlichny he discovered a new form of thermophilic process that later turned out to be widespread in the thermophilic world, anaerobic hydrogenogenic CO oxidation. Later, the investigations of metabolic diversity of thermophiles moved to a newly founded laboratory of Bonch-Osmolovskaya. Another "branch" of Zavarzin's "tree" was the laboratory of Svetlana Dedysh, studying diversity and ecology of microorganisms in peat bogs with extra low mineralization of water. Many novel environmentally relevant taxa were described by this group, including the planctomycete *Zavarzinella formoza*, isolated from a Siberian peat bog. Georgy Zavarzin was the first to isolate, in coauthoship with Lina Vasil'eva and her student Marina Omelchenko, a psychrophilic methanotroph *Methanococcus psychrophilus,* performing methane oxidation in tundra bogs.

From investigations in the early 1980s of hypersaline lagoons of Sivash Lake in Crimea, Tatyana Zhilina and Georgy Zavarzin described new halophilic methanogens, *Methanococcus halophilus* and *Metanohalobium evestigatum.* They also isolated the first halophilic homoacetogen *Acetohalobium arabaticum* and, later (in 1995) together with Fred Rainey and Erko Stackebrandt, described the new order *Halanaerobiales.* Especially significant and exciting results were obtained by Georgy and Tatyana when they studied the anaerobic microorganisms of soda lakes in the late 1980s; first Lake Magadi in Kenya, followed by the soda lakes of Tuva in Russia. From these habitats they succeeded in isolating and characterizing microorganisms representing all steps of the anaerobic carbon cycle in alkaline environments. Organotrophic alkaliphilic spirochaetes and anaerobic saccharolytic organisms of the novel genera *Halonatronum* and *Anoxynatronum* were isolated from Magadi and Siberia. Alkaliphilic homoacetogens turned out to be taxonomically diverse and were represented by the genera *Natroniella, Tindallia,* and *Natronoincola.* The PhD work of Elena Pikuta, supervised by Tatyana Zhilina, resulted in the isolation of the first alkaliphilic hydrogenotrophic sulfate reducers of the genera *Desulfonatronovibrio* and *Desulfonatronum.* The first anaerobic iron-reducing bacterium *Geoalkalibacter ferrihydriticus* was isolated by the younger daughter of George and Tatyana, Darya Zavarzina, in coauthorship with her parents. Extremely interesting are the recent studies of Tatyana Zhilina and Georgy Zavarzin describing the first alkaliphilic syntrophic acetate-oxidizing association. It consists of the novel organism *"Contubernalis alkaliaceticum",* a representative of the *Firmicutes,* growing in a co-culture with an alkalophilic hydrogenotrophic sulfate reducer (*Desulfonatronovibro or Desulfonatronum*) and is able to efficiently oxidize acetate. Another novel bacterium, *Alkaliflexus imshenetskii* gen. nov., sp. nov. belongs to the *Bacteroidetes* and is capable of anaerobic degradation of cellulosic substrates. The tandem of Tatyana Zhilina and Georgy Zavarzin represented a unique art form of microbiological work, which is so rare in our high-tech times. They developed novel complicated media, new tricks for the isolation of "difficult" microorganisms as well as being experts in light and electron microscopy, obtaining beautiful images of their overwhelming microorganisms.

At the same time, Georgy Zavarzin, though deeply attached to microbial world, always possessed a broader view of the impact of metabolic groups of microorganisms on global geochemical processes. His broader interests were connected with the microbial influence on the Earth's atmosphere and evolution of microbial communities on the Earth. He was the member of many international boards and committees, the author of a very popular course of lectures in Moscow University, devoted to environmental microbiology. Georgy never approved of studies that seemed routine to him, but always supported the research that he considered to be really novel. He was very generous, sharing his ideas not only inside his closest surroundings, but far beyond it. Together with his former students and coworkers, many people in Russia consider themselves his successors. His influence on Russian microbiology in the 20th century was extremely deep, and we will miss that a lot. Georgy Zavarzin's vivid interest in current research, encouraging remarks and fresh ideas will be missed forever. We share the grief of his family, will always remember our teacher, and will try to pass on to our students his high standards and his passion for the novel and the unstudied.

Elizaveta Bonch-Osmolovskaya

SPECIAL SYMPOSIUM ON SYSTEMATICS AT FEMS 2011

At the 2010 meeting of Bergey's Manual Trust in Seville it was decided to organize and to support a Special Symposium on Systematics at the FEMS meeting which took place on 27 June 2011 in Geneva, Switzerland. It was decided to focus the symposium on new developments in molecular biology, especially genomics, showing both the advantages and the problems with the use of the continuously growing genomic datasets, in taxonomy. For this reason the following title for the symposium was chosen, "The Impact of the Gene Sequence Data on Taxonomy – More Confusion or Finally a Solution?"

The event took place on the morning of Monday 27 June in Hall A and was chaired by Peter Kämpfer and Paul De Vos, both of whom presented their views on the current challenges in taxonomy.

THE FUTURE OF "POLYPHASIC APPROACH" IN PROKARYOTIC SYSTEMATICS – PETER KÄMPFER

The speaker stressed his attention on the observation that the enormous amounts of genome and gene sequence data will have a major impact on all disciplines of microbiology including taxonomy. However, the strong trend to replace the traditional "polyphasic approach" based on a consensus of genotypic and phenotypic methods by a merely sequence-based approach should be regarded with caution, because the understanding of the information behind the sequences has lagged far behind its accumulation. Unfortunately, the development and improvement of sophisticated phenotypic methods did not keep pace with the development of molecular methods.

For the two "showcase" genera *Acinetobacter* and *Streptomyces* the advantages and pitfalls of multilocus sequence typing (MLST) or multilocus sequence analysis (MLSA) was discussed in the light of the suitability of "housekeeping" genes for classification and identification at the species level. Here it was stressed that the information content for phylogenetic analyses, which is often not clear, the recognition of paralogous genes and conflicting tree topologies (problems with concatenation) and furthermore the impact of processes such as lateral gene transfer, gene duplication, recombination, rearrangements of genes in the genome, which is in many cases not clear and may be very different in different lineages, may have a strong impact on the outcome of any classification. It was concluded that these problems persist in the case of whole-genome comparisons.

It was finally concluded that prokaryotic taxonomy should be stable and predictable and in this regard, a most comprehensive phenotypic and genotypic characterization (in the framework of a polyphasic approach) is still necessary in characterization and classification (which is a prerequisite of identification). Only the interplay between genetic and phenotypic datasets provides a sound basis for the foundation of a more stable, in depth taxonomy of the prokaryotes. The more reliable the characterization and classification, i.e. the more comprehensive a "description", the greater chance one will have of being able to pick identification methods which are both accurate and have a long-term future!

BACTERIAL IDENTIFICATION: HOW FAR DO YOU WANT TO GO? – PAUL DE VOS

The speaker stated that one of the most important aspects of prokaryotic taxonomy concerns the identification of unknowns. The question was raised whether the fast-emerging sequence data can be integrated in the existing frame of bacterial systematics. As Bergey's taxonomic outline of prokaryotic systematics is based on 16S rRNA gene sequences, it already provides a partly positive answer. The difference between identification and typing was also tackled. The former being the appointing of an unknown up to the species and subspecies level or any higher level, while the latter focus on strain and clone differentiation. The high value of multilocus sequence analysis for bacterial systematics and in particular identification was also shown in two case studies with the prerequisites that a great variety of strains is sampled per taxon and that the core genes meet the following criteria (i) single locus status, (ii) independency of functionality from environmental behavior, (iii) sufficient length (approx. 1000 bp), and (iv) a meaningful translated gene product can be obtained from the sequence.

In addition, two more speakers showing some interesting aspects on novel developments in the "omic" sciences presented their views:

TOWARDS A DATA-BASED TAXONOMY – RAMON ROSSELLÓ-MÓRA

The speaker summarized the approaches in taxonomy that are centered on interactive databases. He presented the The All-Species Living Tree Project (LTP) (www.arb-silva.de/projects/living-tree), a curated 16S and 23S database containing only sequences corresponding to type strains with validly published names. The LTP database is a freely accessible service to the community of microbiologists and is meant to simplify the process of identifying new isolates and reconstructing phylogenies for taxonomic purposes. DNA sequences in public databases need to be approached with caution because apart from inconsistencies in the sequence itself, the link between the name given in the metadata (of the sequence database) and the sequence itself can, for various reasons, not be trusted. Sequences in the LTP are curated on these factors. He further presented the program JSpecies (www.imedea.uib.es/jspecies), a taxonomic interface that allows pair-wise genome comparisons to calculate Average Nucleotide Identity (ANI) and tetranucleotide regression. In the framework of JSpecies, Professor Rosselló-Móra also presented robust results showing that the DNA–DNA hybridization value cutoff of 70% could be equivalent to ANI of 96%. He also showed that to calculate this value between genomes, random partial sequencing of coverage of about 20% of each genome to be compared is sufficient. In addition, the power of MALDI-TOF methodology for classification and identification purposes was shown. Whole-cell profiles could be compared among strains, and the clusters observed reproduced the corresponding 16S rRNA lineages and the genomic circumscription based on DNA–DNA hybridization. Finally, the use of high-resolution mass spectrometry (Ion-Cyclotron Resonance Fourier Transform Mass Spectrometry, ICR-FT/MS) was presented as a possible new approach to profiling metabolic patterns of microorganisms by means of low-molecular-weight metabolites. However, this approach needs still further experimentation to understand its value.

MICROBIAL GENOMICS: IMPACT OF COMPARATIVE ANALYSES AND PAN-GENOME STUDIES – HERVÉ TETTELIN & DAVID RILEY

The speaker, Hervé Tettelin, used whole-genome sequencing (WGS) data to demonstrate that the number of genes that are in common between strains of a given species, the core genome, gradually decreased to about 75% of the genome size of any single strain when sequentially adding genomes in different combinations. The identification of distributed genes, shared by two or more but not all strains, and the discovery of new genes by including more WGS in the comparative analysis was likewise shown. This methodological approach allowed reconstructing the nature of the so-called species pan-genome being the sum of the core, distributed and strain-specific genomes. It appeared that different situations occur for different taxa (species). When the discovery of new genes declines relatively rapidly when more and more genomes of representatives of the same species are included in the analysis, a closed species-pan genome is the result where a finite number of genomes yield the entire gene repertoire accessible to the species. When the opposite trend is observed in the comparative analysis, the species pan-genome is open and the number of genomes required to characterize the gene repertoire is unknown but large. This may taxonomically lead to the interpretation that the species delineation is more or less restricted reflecting a more limited or wider "open" lifestyle of the organism. This depends on the presence or the absence of genes characteristic of the species' lifestyle that are often carried on mobile elements such as plasmids, phages and transposable elements.

CONCLUDING REMARKS

The symposium was well attended for the whole morning (620 attendees), demonstrating the strong interest of the microbiological community in taxonomic questions. It was concluded that genomic data will have a tremendous importance in taxonomy in the near future. However, it was also clear that the understanding of the information behind these data is essential in order to integrate these into a more sophisticated and overall accepted taxonomic system.

Bergey's International Society for Microbial Systematics (BISMiS)
Full Membership Application Form

The Society invites applications for full membership from any person who is interested in the subject of microbial systematics and holds a bachelor's degree in microbiology or a related subject.

The annual dues are US$ 50.00. Members are entitled to receive the online *Bergey's International Society for Microbial Systematics Bulletin* which is published twice a year, and the online Bergey's Manual Trust Newsletter. Full members will also receive a reduced registration fee for attendance of meetings.

Memberships will be renewed on 1 January of each year. Unless indicated otherwise, applications received before 1 November will be credited to the current year. Applications received after 1 November will become effective the following year. Return the form with payment to: **BISMiS, Bergey's Manual Trust, 527 Biological Sciences Building, The University of Georgia, Athens, GA 30602-2605, USA**.

Alternatively, please join BISMiS online using our secure credit card facility at www.bergeys.org/bismis.html.

First name: ________ Initial(s): ____ Last name: ________

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Highest degree: ______ Year received: ____ Subject: ________

Degree-granting institution: ________

Current position: ________

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Membership dues			Amount paid*
Full member	US$	50.00	______
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The Society invites applications for student membership from any person who is interested in the subject of microbial systematics and is enrolled as an undergraduate or graduate student in microbiology or a related subject.

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Alternatively, please join BISMiS online using our secure credit card facility at www.bergeys.org/bismis.html.

First name: ________ Initial(s): ____ Last name: ________

Title: ________ Email address: ________

Mailing address

Street: ________

City: ________ ________

State and Zip/Post Code: ________

Country: ________

Phone no. incl. Country/Area Code: ________

Degree in progress (BS, BA, MS or PhD, etc): ______ Subject: ________

Degree-granting institution: ________

Head of Department*: ________

**Head must write a brief supporting letter verifying that the student is in their department, and it must accompany the application. For online applications, please send letter to the address above or by email to bergeys@uga.edu.*

Applicant's signature: ________

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Student member	US$	30.00	________

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