Programme & Book of Abstracts

international conference

BISMiS

BISMiS

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

8 - 11 April 2018

Misty Hills Hotel & Conference Centre

Muldersdrift,
Johannesburg, South Africa

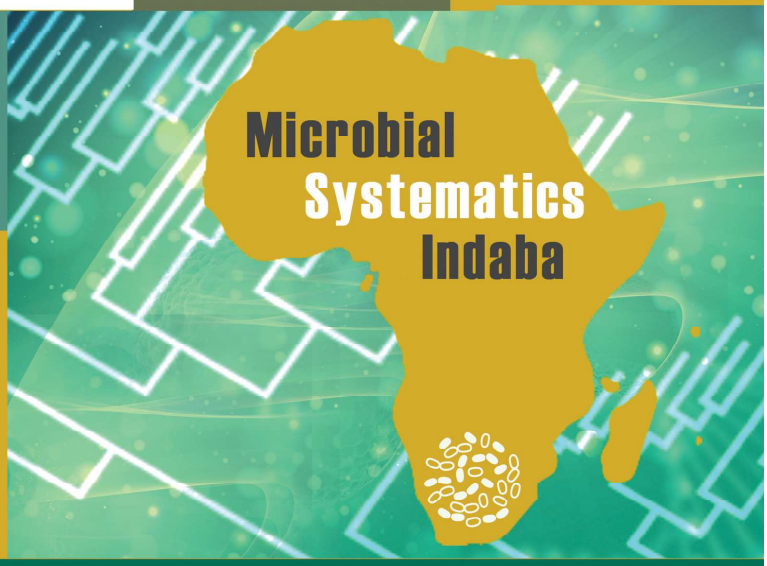

TABLE OF CONTENTS

MARTHA TRUJILO

Dear Friends and Colleagues,

Bergey'sInternational Society for Microbial Systematics was founded in 2009 to support and promote research in Microbial Systematics. One of the Society's main activities is the organization of its biannual meeting to facilitate communication and promote collaboration among taxonomists. The first BISMiS meeting was celebrated in 2011 in Beijing, followed by Edinburgh in 2014 and Pune in 2016.

In 2018 we will celebrate the fourth meeting in Muldersdrift (Johannesburg) joined by delegates from more than 13 countries. On this occasion the chosen Theme is "Microbial SystematicsIndaba". I have learned that the word INDABA means: "a group where in traditional African culture (Zulu or Xhosa), people get together to sort out the problems that affect them all, where everyone has a voice and where there is an attempt to find a common mind or a common story that everyone is able to tell when they go away from it".

Let's make BISMiS 2018 our Indaba and take this opportunity to discuss the current status of taxonomy and how whole genome sequencing and culture-free methods has impacted the discipline. One of the first consequences of this is the necessity to implement new approaches to the Classification and Identification of the vast Microbial World.

I would like to express my sincere appreciation to Professor Fanus Venter for agreeing to organize BISMiS 2018 and to all those who have helped him bring this exciting programme together.

I wish all attendants a great stay and a successful meeting.

Welcome to Muldersdrift!

Martha E. Trujillo
BISMiS President

STEPHANUS VENTER

Dear Delegate,

It is a privilege for me on behalf of the University of Pretoria to welcome you to BISMiS 2018. After three very successful meetings, BISMiS has become known as the foremost meeting for all microbiologists sharing a passion for bacterial systematics. We believe that BISMiS 2018 will again provide excellent opportunities to exchange scientific ideas, catch up with old friends and meet new colleagues.

This conference will have a true South African identity, as it will be based on the idea of an "indaba". An indaba, in the traditional African culture of Zulu and Xhosa speaking people, is a gathering where people get together to sort out the problems that affect them all. At these gatherings, everyone has a voice and an attempt is always made to find common ground and to decide collectively how to go forward. As part of the Indaba theme, we have invited researchers from different parts of the world to present lectures and facilitate discussions. We hope that BISMiS 2018 will truly be a "Microbial Systematics Indaba".

Finally I need to thank all our sponsors. Without your support, we would not be able to present this conference. I special word of thanks should go to the Bergey's Manual Trust for their generous support, including the Travel Awards for students and young investigators. I would like to encourage our delegates to support these companies, publishers and organisations as they are the true friends of our society.

Hope that you will enjoy every minute of your visit to South Africa!

Stephanus Venter
Department of Biochemistry, Genetics and Microbiology
University of Pretoria

RAMON ROSSELLO-MORA

Ramon Rossello-Mora is a scientific researcher at the Mediterranean Institute for Advanced Studies in Mallorca (Spain), a combined institute of the Spanish Council (CSIC) and the University of the Balearic Islands. He leads the Marine Microbiology Group (MMG) at the IMEDEA. This group mainly focuses on the diversity and systematics of environmental samples such as extreme saline habitats, anaerobic marine sediments and jellyfish microbiomes.

He is the author of over 140 publications in international journals and has an H factor of 42. His PhD thesis, obtained from the University of the Balearic Islands in 1992, dealt with the taxonomy and naphthalene degradation capabilities of Pseudomonas stutzteri. Afterwards he was a postdoctoral fellow at several institutes including the Technical University of Berlin (1992), Technical University of Munich (1993 - 1995), IMEDEA (1995 - 1997) and the Max Planck Institute for Marine Microbiology in Bremen (1997 - 1999). He was a Professor at the University of the Balearic Islands during period 2000 - 2001. He accepted a post as Researcher at the Spanish Council CSIC in 2001, where he is currently the leader of the laboratory of Marine Microbiology of the IMEDEA.

Ramon is executive editor of the journal Systematic and Applied Microbiology and was a member of the Judicial Commission of the ICSP for a period of 9 years (2005 - 2014). He was again re-elected to the commission in 2017. He is also member of the European Academy of Microbiology since 2016 and received the Bergey's Award for his contributions towards bacterial taxonomy in 2017.

A need for taxonomists to take actions before it's too late

Taxonomists are traditionally conservative in view of their own field's development. However, it is indisputable that in the advent of the current century, the progresses in molecular biology and high throughput methodologies are changing our "modus operandi" in our daily research activities. All –omics are opening the door to a modern, database-based, interactive and universal way of classifying microorganisms. Actually microbial taxonomy has always developed in parallel with the technological improvements in molecular biology by implementing technologies that may be useful for classification. Bacterial and archaeal taxonomy has been a pioneer in its approachwhere other taxonomies have followed by also implementing these methods.

However, in my opinion, bacterial and archaeal taxonomy suffers from several basic problems that need to be addressed suchas: the very high occurrence of single strain species descriptions (SSSD) that are based on very sparse genetic and metabolic traits, which often are of limited value; or the yet unclear role of whole genome sequences in classification. We may not want to recognize it, but the backbone of the classification system is mostly based on 16S rRNA gene phylogenetic reconstructions, and the species circumscriptions are based on genome to genome comparisons. Accurate and relatively cheap whole genome sequencing is now allowing the retrieval of valuable taxonomic information that surpasses the information presented in many of the current taxonomic papers. Even the phenotypic inference from the genomes can provide diagnostic traits that would be of higher value than many of the currently given metabolic tests. Relevant inferred phenotype could be tested once discovered.

But the most important problem is the impossibility to validly publish names for uncultured microorganisms. The need of depositing living material in public repositories as a requirement for accepting protologues under the bacteriological code is hampering the description of the vast microbial majority. There have been requests to accept DNA sequences as an alternative to type material, which would open the door to produce stable classification for the uncultured. The current bioinformatics tools allow for the retrieval of single (pan)genomes of all co-occurring populations of the same species. This, combined with the analysis of the gene content, phenotype inference and genealogies allows the classification of the uncultured at the same or even higher standards than for the cultured. Metagenomics is now a flowering field, with the exponential increase of information and discovery of microbial novelty. In this regard, molecular ecologists are in urgent need of a standardizedclassification before chaos occurs. However, the lack of activity of the responsible taxonomists in deciding how the field should move forwards is hampering a unified taxonomy.

Perhaps the solution is not to modernize by allowing cultured and uncultured bacteria to be classified using the same standards and nomenclatural code, but in creating an alternative nomenclature for the uncultured and to proceed orthogonally (i.e. no interaction, no feed-back), as has happened until now.

JONGSIK CHUN

Dr. Jongsik Chun serves as Member of Scientific Advisory Board at CosmosID, Inc. Dr. Chun recognized expert in the fields of microbial systematics, bioinformatics and genomics. Dr. Chun holds B.Sc. in Microbiology from Seoul National University and Ph.D. in Department of Microbiology, Computer Assisted Classification and Identification of Actinomycetes from University of Newcastle upon Tyne, U.K.

Database-driven taxonomic framework for Bacteria and Archaea

Prokaryotic taxonomy has been benefited from new technologies in the field of molecular biology, notably DNA sequencing, PCR and nucleic acid hybridization. Next-generation sequencing (NGS) provides affordable means of sequencing whole bacterial genomes and has great potential to enable the objective, robust and automated scheme for classification and identification of Bacteria and Archaea. Unlike phenotypic characteristics, consistent genome sequence data can be obtained regardless of the physiological state of cells. The use of genome data can readily facilitate automation of identification, as well as detect new species, in routine microbiological laboratories. For such a process, a high-quality, timely updated database is essential. Here, I will introduce the unified database of nomenclature, 16S rRNA genes, genome sequences and microbiome, previously introduced as EzBioCloud (formerly called EzTaxon). In this presentation, I will present (1) the strategy for quality-control of genome sequence data, (2) genome-based classification scheme, (3) the utility of Pacific Biosciences full-length 16S sequencing, and (4) application to metagenomics.

The presentation file will be posted at https://www.ezbiocloud.net/presentation/bismis2018 (at the time of the conference).

BRIAN HEDLUND

Brian P. Hedlund earned his Ph.D. from the University of Washington, Seattle, in 2000, and received his postdoctoral training with Karl Stetter at the University of Regensburg, Germany. He returned to the U.S.A. in 2003 as an Assistant Professor in the School of Life Sciences at the University of Nevada Las Vegas (UNLV) and has since been promoted to Professor.

Brian and his collaborators have made significant contributions to our understanding of the structure and function of microbial communities in geothermal springs, the function of the nitrogen biogeochemical cycle at high temperature, and the discovery of deep microbial lineages in geothermal springs through microbial cultivation, metagenomics, and single-cell genomics. Current efforts focus on linking phenome to genome in major, uncultivated microbial lineages in geothermal springs.

Brian is a member of Bergey's Manual Trust and editor for Bergey's Manual of Systematics of Archaea and Bacteria and Antonie van Leewenhoek. Dr. Hedlund regularly serves on grant panel review boards both domestically and internationally and has taught more than 2,500 students at UNLV.

Cultivation, physiology, genomic, and exometabolomic study of previously uncultivated *Chloroflexi* class TK10 (TK17), a global inhabitant of geothermal springs and other environments

Two novel thermophilic, aerobic, and heterotrophic rod-shaped bacteria, designated strain G233^T and YIM 72310^T, were isolated from sediments of Great Boiling Spring, Nevada, and Hamazui Spring in Rehai National Park, China. Based on phylogenetic analysis of both 16S rRNA genesand conserved, single-copy marker proteins, the two strains are the first cultivated representatives of the candidate class 'TK10' (SILVA taxonomy) or 'TK17' (Greengenes taxonomy), within the phylum *Chloroflexi*. Both strains are motile by means of flagella,which is the first documented example of flagellar motility in the *Chloroflexi*. Although both strains grew to high cell density on R2A medium, very few compounds, principally mono- and oligosaccharides, and sugar alcohols, were used as sole carbon and energy sources in defined media. However, both genomic predictions and exometabolomics profiles indicate a much broader heterotrophic repertoire for these organisms, including strong heterotrophic activity on a variety of phenolic compounds and heterocycles,as well as lipids and lipid derivatives. We suggest *Planoflexus* may specialize in digesting complex extracellular material in photosynthetic mats at the fringes of geothermal systems, from which they were isolated. On the basis of their unique phylogenetic placement and physiological characteristics, we propose these organisms as the first cultivated representatives of a novel class within the *Chloroflexi*, and suggest the names *Planoflexus thermophilus* sp. nov. and *Planoflexus flavus* sp. nov. for G233^T and YIM 72310^T, representatively. This study lays a foundation for understanding the physiology and ecological role of the TK10/17 class, which is globally distributed in both marine and terrestrial environments.

BP Hedlund1, E Zhou1,2, SC Thomas1, N Habib2, L-X Chen2, CO Seymour1, SK Murugapiran1, JA Dodsworth3, CR Mefferd1, L Liu2, W-D Xian2, X-Y Zhi4, K Louie5, BP Bowen5, TR Northen5, T. Woyke5, W-J Li2

WILLIAM WHITMAN

William "Barny" Whitman received his PhD in 1978 from The University of Texas at Austin with Bob Tabita studying the enzyme RuBisCO from Rhodospirillum rubrum. He continued his research on autotrophic prokaryotes during his postdoctoral studies with Ralph Wolfe at the University of Illinois at Urbana. He joined the Department of Microbiology at the University of Georgia in 1982 where his laboratory studies free-living prokaryotes of environmental importance.

His research attempts to understand the physiological, molecular biological and biochemical basis for the ecology and systematics of prokaryotes. This integrated approach has been applied to the methane-producing archaeon Methanococcus, the marine roseobacteria, and soil bacteria. Since 2006, he has served as Director of the Editorial Office for Bergeys Manual Trust and has worked on the 2nd edition of Bergey's Manual of Systematic Bacteriology, volumes 3-5, and the new online journal Bergey's Manual on Systematics of Archaea and Bacteria.

One goal of this work is to reconcile the taxonomy with the phylogeny and understand the biological basis for the prokaryotic groups.

Phylogenomic analyses of a clade within the roseobacter group suggest taxonomic reassignments of species of the genera *Aestuariivita*, *Citreicella*, *Loktanella*, *Nautella*, *Pelagibaca*, *Ruegeria*, *Thalassobius*, *Thiobacimonas*, and *Tropicibacter* and the proposal of the six novel genera *Cognatishimia*, *Cognatiyoonia*, *Flavimaricola*, *Limimaricola*, *Pseudaestuariivita*, and *Yoonia*.

Roseobacters are a diverse and globally abundant group of *Alphaproteobacteria* within the *Rhodobacteraceae* family. Recent studies and the cophenetic correlations suggest that the 16S rRNA genes are poor phylogenetic markers within this group. In contrast, the cophenetic correlation coefficients of the average amino acid identity (AAI) and RpoC protein sequences are high and likely more predictive of relationships. Amaximum likelihood phylogenetic tree calculated from 53 core genes demonstrated that some of the current genera were either polyphyletic or paraphyletic. The boundaries of bacterial genera were redefined based upon the AAI, the percent of conserved proteins (POCP), and phenotypic characteristics and resulted in the following taxonomic proposals. *Loktanella vestfoldensis, Loktanella litorea, Loktanella maricola, Loktanella maritima, Loktanella rosea, Loktanella sediminilitoris, Loktanella tamlensis*, and *Roseobactersp. CCS2* should be moved into the novel genus *Yoonia* with *Yoonia vestfoldensis* as the type species. *Loktanella hongkongensis, Loktanella cinnabarina, Loktanella pyoseonensis*, and *Loktanella soesokkakensis* should bemoved to the novel genus *Limomaricola* with *Limimaricola hongkongensis* as the type species. *Loktanella koreensis* and *Loktanella sediminum* should be moved into the novel genus *Cognatiyoonia* with the former as the type species. *Loktanella marina* should be move to the novel genus *Flavimaricola*. *Aestuariivita atlantica* should be moved to the novel genus *Pseudaestuariivita. Thalassobius maritima* should be moved to the novel genus *Cognatishimia*. Similarly, *Ruegeria mobilis, Ruegeria scottomollicae, Ruegeria sp. TM1040* and *Tropicibacter multivorans* should be moved to the genus *Epibacterium*. *Tropicibacter litoreus* should be moved into the genus *Ruegeria*. *Thalassobius abyssi* and *Thalassobius aestuarii* should be moved into the genus *Shimia*. *Citreicella marina, Citreicella thiooxidans, Pelagibaca bermudensis,* and *Thiobacimonas profunda* should be reclassified in the genus *Salipiger*. *Nautella italica* should be moved into the genus *Phaeobacter*. Because these proposals reclassify the type and only species of *Nautella*, *Pelagibaca*, and *Thiobacimonas*, these genera have no standing in this taxonomy. (We also thank Prof. Aharon Oren for his nomenclatural advice).

WEN-JUN LI

Dr.Wen-Jun Li is an internationally recognized scientist in the field of microbial systematics, who has isolated, identified and validly published many new prokaryotic taxa in the past 18 years, including 1 new classis (Thermoflexia), 7 new suborders/orders (Actinopolysporineae, Kineosporiineae, Jiangellineae, Thermoflexales, Kallotenuales, Egibacterales, Egicoccales), 13 new families (Egicoccaceae, Egibaceraceae, Kallotenuaceae, Thermoflexaceae, Actinopolysporaceae, Kineosporiaceae, Beutenbergiaceae, Cryptosporangiaceae, Jiangellaceae, Ruaniaceae, Yaniaellaceae, Sinobacteraceae, Aquichromatiaceae), over 55 new genera and 420 new species, from diverse terrestrial extremophilic environments, such as hot springs, salt lakes, saline mines, as well as traditional Chinese medicinal plant endophyte, karst caves and marine ecosystems.

He received his Ph.D in microbiology from Institute of Applied Ecology, Chinese Academy of Sciences in 2002. He was appointed as head of Actinobacterial research group and Vice Director of Yunnan Institute of Microbiology, Yunnan University, China since January of 2009, and Vice Dean of School of Life Sciences, Yunnan University, China since January of 2012, and now worked as Distinguished Professor in School of Life Sciences, Sun Yat-Sen University, Guangzhou, China. He has written three monographs and more than 620 publications and holds more than 20 authorized patents.

He has been appointed as the editorial board members of 7 peer-reviewed journals and was invited to be as reviewers for over 20 international journals. He was awarded as WFCC (The World Federation for Culture Collections) Skerman Award for Microbial Taxonomy in 2007, and some other ministry or provincial level Awards in 2005, 2007, 2009, 2010, 2013 and 2017, respectively, for his outstanding research achievements on microbial systematics. He has serviced as membership of the suborder Micrococcales International Committee on Systematics of Prokaryotes (ICSP) since 2008 and Charter member of Bergey's International Society for Microbial Systematics (BISMiS) from 2011, and recently, he was selected as Executive Board (EB) of International Committee on Systematics of Prokaryotes (ICSP) in Spain meeting at Valencia.

Update in the phylogeny and hierarchy of the members of the phylum *Actinobacteria*

It has been almost a decade since the last update on the hierarchy structure of members of the phylum *Actinobacteria*, which formed the backbone of the Bergey's Manual for *Actinobacteria* has been published. Since then, several new genera have been published, while some have been reclassified or promoted to a higher taxonomic level. While 16S rRNA gene sequences remain the basis for primary identification of bacteria, advancement in sequencing technology has provided easy access to detailed genomic information. This technological development has provided invaluable evidence for proper resolution in bacterial systema-tics. Furthermore, genome information can be retrieved and is available for many uncultured strains, which require proper recognition as they form an invaluable part of their distinct ecosystems. Certain actinobacterial genera with distinct physiological roles have been effectively published but have not been validly recognized. The genome information of all the strains of the phylum *Actinobacteria* with validly published names is also not yet available. It is therefore time to provide an update to the hierarchy of the higher orders of the members of the phylum *Actinobacteria* byconstructing a robust phylogenetic network. The 16S rRNA gene information of all the actinobacterial strains with validly published names, effectively published strains (to be validly recognized) and uncultured species whose genomes are available (to provide a proper phylogenetic position among the existing actinobacterial strains) will be used. An update of the phylogeny and reclassification of certain groups of actinobacteria will be presented.

SVETLANA DEDYSH

Svetlana N. Dedysh received her PhD in 1990 from The Moscow State University and joined the Laboratory of Soil Microbiology and Biokinetics at the Winogradsky Institute of Microbiology, where she started her research on methane oxidizing bacteria in northern wetlands. This research was carried out in a close collaboration with the Center for Microbial Ecology at The Michigan State University, USA, and the Max-Planck-Institute for Terrestrial Microbiology, Germany.

In 2005, Svetlana N. Dedysh defended her Doctoral dissertation on acidophilic methanotrophic bacteria. Since 2008, she is the head of the Laboratory of Wetland Microbiology at the Winogradsky Institute of Microbiology. Her main field of research is the microbiology of northern wetlands. Areas of research expertise are: 1) biology and ecology of methane-oxidizing bacteria; 2) microbial diversity in Sphagnum-dominated wetlands; 3) cultivation of bacteria from poorly studied phyla (Acidobacteria, Planctomycetes), 4) bacteria responsible for biopolymer degradation in northern wetlands.

She is the author of 4 novel bacterial families, 22 genera and 36 species descriptions. She has been a trustee of Bergey's Manual Trust and a member of Judicial Commission of the International Committee on Systematics of Prokaryotes since 2014.

Creating the taxonomic structure for the phylum *Acidobacteria*

The *Acidobacteria* is one of the globally distributed and highly diverse phyla of the domain *Bacteria*. These microorganisms inhabit a wide variety of terrestrial and aquatic habitats, and are particularly abundant in acidic soils, peatlands, and mineral iron-rich environments. The *Acidobacteria* raised considerable scientific interest at the turn of the century, when application of molecular techniques revealed the cosmopolitan distribution and high abundance of these microorganisms in various environments. The corresponding phylumhas been created in 1997 in order to accommodate the large number of 16S rRNA gene sequences, which have been retrieved from various soils by means of cultivation-independent molecular techniques. At that time, this phylum encountered only three species and four major subgroups (or "subdivisions") based on16S rRNA gene sequences. By 2007, the number of recognized subdivisions within the *Acidobacteria* increased to 26; each of them is assumed to be equivalent to a class level. The practice of using the category "subdivision" for describing the taxonomic position of a particular acidobacterium is clearly predominant in the scientific literature. Creating the taxonomic structure for this phylum is hampered by the fact thatacidobacteria remain a difficult object for microbiologists. At present, the taxonomically characterized diversity within this phylum is limited by 28 genera and 50 species, which represent only 7 out of 26 currently recognized subdivisions (SDs 1, 3, 4, 6, 8, 10 and 23). However, the corresponding family/order/class ranks have been defined only for some of thesebacteria. For example, the corresponding class ranks have been formally proposed only for SDs 1, 4, 8 and 10; the latter is not yet validly published. A number of orders and families remain to becircumscribed to accommodate the described representatives of SDs 3, 4, 6 and 23.This presentation will discuss and evaluate the criteria, which could be used for delineating high-level taxa within the *Acidobacteria*.

WILHELM DE BEER

Wilhelm de Beer is associate professor in the Department of Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), at the University of Pretoria. He received his M.Sc. degree in Microbiology at the University of the Free State, and his Ph.D. in Microbiology at the University of Pretoria.

He lectures mycology and his research is primarily about fungi associated with arthropods such as bark beetles, ambrosia beetles, and mites. More recently he also became involved in projects relating to the fungal associates of termites. The bulk of his more than 100 publications focuses on the ophiostomatoid fungi (Ophiostomatales and Microascales), with research topics ranging from taxonomy, phylogeny, population genetics, mating behavior, diagnostics, symbiotic relationships, invasion biology, to their causal roles as agents of sapstain and decay in timber, and of disease in trees and humans.

He currently serves as president of the African Mycological Association (AMA), and on the International Commission for the Taxonomy of Fungi (ICTF) and the Nomenclature Committee for Fungi (NCF).

The evolution of fungal taxonomy: from cryptic Latin diagnoses to genome-facilitated systematics

The Ascomycete order *Ophiostomatales* accommodates more than 320 species of mostly arthropod-associated species. These include some serious tree and human pathogens. The taxonomic history of this order largely reflects events that shaped Ascomycete systematics over the past two centuries. The first species of the order was described in 1823 in an 11-word Latin paragraph without illustration. This style persisted during the 19th century in most fungal species descriptions, but by the turn of the century, descriptions often became pages long as part of discussions on the biology of the fungus. During the 21st century detailed morphological studies led to species concepts being refined based on microscopy, ultrastructure, biochemical and physiological traits. However, monographs on genera were often hampered by their focus on either sexual or asexual state morphology, with such generic concepts often contradicting each other. In 1992 rDNA sequences for the first time showed that an asexual species could be placed among sexual species. Soon protein coding DNA sequences were used together with rDNA sequences to distinguish between cryptic species, reflecting phylogenetic relatedness, rather than phenotypic traits. The ability to link sexual and asexual states provided the impetus for the One Fungus One Name movement that in 2011 culminated in the abolishment of the dual nomenclature system, which allowed for one fungal species to have two or more names. During the past decade an improved understanding of population genetics, hybridization and horizontal gene transfer, aided by the availability of whole genome sequences, have been changing the way taxonomists define species and genera. One important challenge that remains unresolved, is the incorporation of environmental nucleic acid sequences (ENAS) into taxonomic studies. In a controversial case study, *Hawksworthiomyces* sequentia, known only from ITS sequences, has been described recently in the *Ophiostomatales*. However, the International Code for Nomenclature of Algae, Fungi and Plants, at present does not provide for the valid description of taxa for which specimens are not available. This issue will be debated at the International Mycological Congress in July 2018. As the integration of ENAS into taxonomic studies will greatly enhance our understanding of unculturable fungi in the environment, it is essential that the mycological community come up with a workable model that allows the naming of such species.

IAIN SUTCLIFFE

Iain SutCliffe took his degree and PhD at the University of Newcastle upon Tyne (1985), the latter supervised by Norman Shaw, an pioneer in using bacterial lipids for chemotaxonomy. Subsequent post-doctoral research in Newcastle included a Wellcome Trust Fellowship in Taxonomy, studying actinomycete lipoglycans as chemotaxonomic markers. After a Senior Lecturership at the University of Sunderland (1996-2004), he moved to Northumbria University, becoming Chair of Microbiology in 2007.

His research investigates the nature, biosynthesis and roles of membrane-anchored macromolecules within the cell envelopes of bacteria. Defining the nature and distribution of these macromolecules is of importance for understanding of microbial systematics, evolution and bacterium-environment interactions.

Contributions to systematics
Iain has published or contributed to more than 20 original papers relevant to systematics, primarily on microbial chemotaxonomy and novel species descriptions, and have published a further 8 commentaries or reviews contributing to the development of the discipline.

With Mike Goodfellow and Jongsik Chun, he edited New Approaches to Prokaryotic Systematics (2015). Volume 41, Methods in Microbiology (Elsevier). He has also organised and contributed several symposia on microbial systematics. In 2016 he was elected President-Elect of the Bergey's International Society for Microbial Systematics and in 2017 he was elected Chair of the Executive Board of the International Committee on Systematics of Prokaryotes.

Iain has been Editor-in-Chief, Antonie van Leeuwenhoek (2003-2007; 2009-present): during his tenure, the journal has developed as a major publisher of papers in microbial systematics, including significant numbers of prokaryotic species descriptions and special issues drawn from the 1st and 3rd meetings of Bergey's International Society for Microbial Systematics (Beijing and Pune). Most recently, with Martha Trujillo and Ramon Rosselló-Móra, they launched (jointly with Systematic & Applied Microbiology) the Digital Protologue Database as a significant new initiative in microbial systematics.

PROGRAMME COMMITTEE

Martha Trujillo
Iain Sutcliffe
Barny Whitman
Fred Rainey
Brain Hedlund
Stephanus Venter

CONFERENCE ORGANIZERS

Conference organizers
Stephanus Venter (University of Pretoria)
Carla de Jager (Carlamani Conferences and Events)
Amelia van Staden (Carlamani Conferences and Events)

Sunday 8 April 2018	
11h00	Depart on Tour to Sterkfontein Caves and Maropeng Visitor Centre
17h00	Return From Tour
18h00	Welcome function
Monday 9 April 2018	
07h30	Registration open
08h30	Opening **Martha Trujillo**
08h40	P1 Keynote: A need for taxonomists to take actions before it's too late **Ramon Rosselló-Móra**
09h30	Tea Break
10h00	Session 1 - Chairperson **Martha Trujillo**
10h00	P2 Keynote: Update in the phylogeny and hierarchy of the members of the phylum *Actinobacteria* **Wen-Jun Li**
10h30	1.1 Revisiting genotypic and phenotypic properties as an aid to circumscribe species of the genus **Salinispora Luis Maldonado**
10h50	1.2 The use of whole genome sequencing to confirm the recognition of *M. noduli* and *M. saelicesensis* **Raul Riesco**
11h10	1.3 Genome-scale data call for a taxonomic rearrangement of *Geodermatophilaceae* **Maria del Carmen Montero-Calasanz**
11h30	1.4 Diversity and distribution of sphingomonads **Yili Huang**
11h50	1.5 Genome-informed *Bradyrhizobium* taxonomy: where to from here? **Juanita Avontuur**
12h10	1.6 Divergence and gene flow in *Xanthomonas* plant pathogens **Marion Fischer-Le Saux**
12h30	Lunch
13h30	Session 2 - Chairperson **Barny Whitman**
13h30	P3 Keynote: Creating the taxonomic structure for the phylum *Acidobacteria* **Svetlana Dedysh**
14h00	2.1 A core-genome sequence based taxonomy of the family *Leptotrichiaceae* calculated using EDGAR 2.0 **Peter Kämpfer**

Monday 9 April 2018	
14h20	2.2 A global catalogue of microbial genomes - type strain sequencing project of WDCM **Juncai Ma**
14h40	2.3 Genome sequence-based criteria for species demarcation: Insights from the genus *Rickettsia* **Pierre-Edouard Fournier**
15h00	2.4 What exactly are bacterial subspecies? **Stephanus Venter**
15h20	Tea
15h50	Discussion: Where to with species descriptions (Leader **Martha Trujillo**)
17h00	Poster session with short introductions Group 1. Chairperson **Stephanus Venter**
18h30	Dinner
Tuesday 10 April 2018	
8h30	Session 3 - Chairperson **Brian Hedlund**
8h30	P4 Keynote: Phylogenomic analyses of a clade within the roseobacter group suggest taxonomic reassignments of species of the genera *Aestuariivita, Citreicella, Loktanella, Nautella, Pelagibaca, Ruegeria, Thalassobius, Thiobacimonas, and Tropicibacter* and the proposal of the six novel genera *Cognatishimia, Cognatiyoonia, Flavimaricola, Limimaricola, Pseudaestuariivita, and Yoonia* **Barny Whitman**
9h00	3.1 Actinobacterial biodiversity: a potential driver for the South African Bio-economy **Marilize Le Roes-Hill**
9h20	3.2 Identification and recovery of "missing microbes" from the gut microbiota of human populations living non-industrial lifestyles **Paul Lawson**
9h40	3.3 Capturing the hidden bacterial diversity at the Lonar Crater, India formed ~52000 years ago **Kamlesh Jangid**
10h00	3.4 Phylogenetic characterisation of Streptomyces species causing fissure scab of potatoes in South Africa **Michele Cloete**
10h30	Tea
11h00	Session 4 - Chairperson **Kamlesh Jangid**
11h00	P5 Keynote: Cultivation, physiology, genomic, and exometabolomic study of previously uncultivated Chloroflexi class TK10 (TK17), a global inhabitant of geothermal springs and other environments **Brian Hedlund**
11h30	4.1 Genomic diversity of human gut-associated Treponema inferred from shotgun metagenomic datasets **Krithivasan Sankaranarayanan**

Tuesday 10 April 2018	
11h50	4.2 Application of whole genome sequencing to exploring intra-generic heterogeneity **Vartul Sangal**
12h10	4.3 Relating tRNA gene diversity with the evolution of *Planctomycetes-Verrucomicrobia-Chlamydia* (PVC) and PVC-like bacteria **Bhagwan Rekadwad**
12h30	4.4 Phylogenomic analyses: The whole is greater than the sum of its parts **Marike Palmer**
12h50	Lunch
14h00	BISMiS AGM
15h00	Tea
15h30	Poster session with short introductions Group 2. Chairperson **Stephanus Venter**
16h30	Bergey Award lecture P6 Keynote: Database-driven taxonomic framework for Bacteria and Archaea **Jongsik Chun**
18h30	Conference dinner
Wednesday 11 April 2018	
8h30	Session 5 - Chairperson **Iain Sutcliffe**
8h30	P7 Keynote: The evolution of fungal taxonomy: from cryptic Latin diagnoses to genome-facilitated systematics **Wilhelm de Beer**
9h00	5.1 Bacterial species are sui generis evolutionary units **Marike Palmer**
9h20	5.2 Multiple uses of genome sequences in characterizing novel bacteria **Jeffrey Newman**
9h40	5.3 Importance of microbial culture collections (mBRC's) **Paul de Vos**
10h00	Tea
10h30	Discussion: Bacterial systematics: What lies ahead? (Leader: **Iain Sutcliffe**)
11h30	Closing **Iain Sutcliffe**
12h00	Lunch
13h00	Depart on Lion Park tour / Lion Park, Lesedi, Pilanesberg Tour

Bergey's Manual Trust

ORAL PRESENTATIONS INDEX

Oral Presentations

1.1 **Revisiting genotypic and phenotypic properties as an aid to circumscribe species of the genus *Salinispora***

LA Maldonado[1], L Contreras-Castro[2], JA Acevedo-Becerra[2], ME Esteva-García[2], JC Cancino-Díaz[2], CJ Hernández-Guerrero[3], S Martínez-Díaz[3], ET Quintana[2]

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The genus *Salinispora* Maldonado *et al*. 2005 was originally described to accommodate two actinobacterial species, namely *S. arenicola* and *S. tropica* recovered from marine sediments. A third species, *S. pacifica*, was described later (2013) and the genus solely encompasses marine obligate actinobacterial species of biotechnological importance. Description of novel salinisporae is difficult mainly due to the high level of similarity found between the three species at the 16S rRNA gene level, thus, alternative genes are needed to properly circumscribe and facilitate the description of putative novel candidates. Although there are phenotypic properties which helps to differentiate between the three species, genotypic data has contributed heavily to the circumscription of salinisporae. It is important to properly separate between the three species due to their secondary metabolism: *S. arenicola* produces ansamycins, *S. pacifica* cyanosporoside A and *S. tropica* salinisporamide A, to name a few. In this work, a collection of 50 salinisporae were recovered from the Sea of Cortez and their taxonomic position within the validly described species of the genus compared by using a collection of geno- and phenotypic properties. All of the isolates were found to be related to *S. arenicola* but some formed a distinct subclade after *atp*D, *gyr*B, *rpo*B, *sec*Y, and 16S gene analyses. A comparison of the sequences of the *rif*K gene also confirmed the separation of some of our isolates to *S. arenicola* hence suggesting (at least) a fourth species within the genus though genome sequencing plus ANI comparisons may also contribute to resolve the intrinsic relationship within the isolates and to *S. arenicola*. Regarding secondary metabolite production, the isolates show *in vitro* antibiotic activity against clinical isolates of *Staphylococcus aureus* and *Vibrio parahaemolyticus* thus enhancing the bioprospecting importance of our putative novel species.

1.2 **The use of whole genome sequencing to confirm the recognition of *M. noduli* and *M. saelicesensis***

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Micromonospora noduli, isolated from a nitrogen fixing nodule of *Pisum sativum* was formally described in 2016. The genomic delimitation of this species was based on 16S rRNA gene phylogeny, five partial core gene multilocus sequence analysis (MLSA) and DNA-DNA hybridization (DDH). The latter test showed that *M. saelicesensis*, also isolated from a nodule tissue, but in this case of the legume *Lupins angustifoius*, was the closest species, sharing a DDH value of 62.8% (63.4%). As part of a comparative genomics study of the species *Micromonospora saelicesensis*, ten strains that had a 16S rRNA gene identity above 99.5% with the type strain, were selected and their genomes sequenced. As previous analyses based on 16S rRNA gene phylogeny and MLSA also suggested that some of these strains were closely related to the species *M. noduli*, the genome of the type strain, GUI43^T, was also sequenced for comparison. Average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) analyses, with values just above the recommended threshold for the delimitation of species (96.64% and 71.20% respectively), highlighted the close relationship between *M. saelicensesis* and *M. noduli* type strains, questioning the species description of the latter one 2016. Phylogenomic analyses using whole-genome sequences of the 10 strains, separated them in two very closely related groups, one including the type strain of *M. saelisecensis* (ANI values ≥97.8% and dDDH ≥91.3%) and the other recovering *M. noduli* (ANI values ≥99.0% and dDDH≥92.3%), having between the two groups values just above the threshold for species delimitation (ANI values between 96.2% and 96.6% and dDDH between 71.1% and 71.8%). While these indices are slightly above the threshold, orthology analysis of protein coding genes showed significant differences between the two groups, and some of these were confirmed in wet-lab experiments. Thus, the data derived from the genomic analysis confirm that the species *M. saelicesensis* and *M. noduli* are very close but should be recognized as separated species, further supporting the separation of the two groups.

1.3 Genome-scale data call for a taxonomic rearrangement of *Geodermatophilaceae*

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Geodermatophilaceae (order *Geodermatophilales*, class *Actinobacteria*) form a comparatively isolated family within the phylum *Actinobacteria* and harbour many strains adapted to extreme ecological niches and tolerant against reactive oxygen species. Clarifying the evolutionary history of *Geodermatophilaceae* was so far mainly hampered by the insufficient resolution of the main phylogenetic marker in use, the 16S rRNA gene. In conjunction with the taxonomic characterisation of a motile and aerobic strain, designated YIM M13156^T and phylogenetically located within the family, we here carried out a phylogenetic analysis of the genome sequences now available for the type strains of *Geodermatophilaceae* and re-analysed the previously assembled phenotypic data. The results indicated that the largest genus, *Geodermatophilus*, is not monophyletic, hence the arrangement of the genera of *Geodermatophilaceae* must be reconsidered. Taxonomic markers such as polar lipids and fatty-acid profiles, cellular features and temperature ranges are indeed heterogeneous within *Geodermatophilus*. In contrast to previous studies, we also address which of these features can be interpreted as apomorphies of which taxon, according to the principles of phylogenetic systematics. We thus propose a novel genus, *Klenkia*, with the type species *Klenkia marina* sp. nov. and harbouring four species formerly assigned to *Geodermatophilus, G. brasiliensis, G. soli, G. taihuensis* and *G. terrae*. Emended descriptions of all species of *Geodermatophilaceae* are provided for which type-strain genome sequences are publicly available. Our study again demonstrates that the principles of phylogenetic systematics can and should guide the interpretation of both genomic and phenotypic data.

1.4 **Diversity and distribution of sphingomonads**

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It is believed that sphingomonads are ubiquitously distributed in environments. However the detailed information about their community structure and their co-relationship with environmental parameters remain unclear. In this study, novel sphingomonads-specific primers based on the 16S rRNA gene were designed to investigate the distribution of sphingomonads in 10 different niches. Both *in-silico* test and in-practice test on pure cultures and environmental samples showed that Sph384f/Sph701r was an efficient primer set. Illumina MiSeq sequencing revealed that community structures of sphingomonads were significantly different among the 10 samples, although 12 sphingomonad-genera were present in all samples. Based on RDA analysis and the Monte Carlo permutation test, sphingomonads community structure was significantly correlated with limnetic and marine habitat types. Among these niches, genus *Sphingomicrobium* showed strong positive correlation with marine habitats, whereas genera *Sphingobium*, *Novosphingobium*, *Sphingopyxis*, and *Sphingorhabdus* showed strong positive correlation with limnetic habitats. Our study provided direct evidence that sphingomonads were ubiquitously distributed in environments, and revealed for the first time that their community structure were correlated with habitats. Impressively, 12 out of 97 OTUs (unclassified *Sphingomonadaceae*) showed a similarity lower than 95% to known species, suggesting there were certain amounts of novel species or genera of *Sphingomonadaceae* in nature remained to be recognized. Using selective culture media we tried to isolate novel species from sphingomonads, and successfully obtained and identified 6 new species, for example *Sphingobacterium paludis*.

1.5 **Genome-informed *Bradyrhizobium* taxonomy: where to from here?**

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Bradyrhizobium is thought to be the largest and most diverse rhizobial genus, but this is not reflected in the number of formally described species. Although it was one of the first rhizobial genera to have been recognized, its taxonomy is complicated, and as a consequence, the description of new species is lagging behind other genera. Various contemporary studies are showing that genome sequence information may simplify species delineation and taxonomic decisions. Therefore, the growing availability of whole genome sequences for *Bradyrhizobium* will likely speed up the rate at which new species are delineated, characterized and formally described. In this study, we reviewed the current genomic resources for *Bradyrhizobium* available in the public domain. We then extracted the set of genes shared among all genomes (*Bradyrhizobium* and outgroups), and inferred a maximum likelihood phylogeny. A total of 152 *Bradyrhizobium* genomes are currently publicly available (for known species or isolates identified only to genus-level). Of the 33 formally described species, 26 have genome sequences available. The genomes of 19 strains of related species were included to represent outgroup taxa. Although some of the genomes have been assembled into one or a few scaffolds, most of the genomes are only available in draft form consisting of numerous fragments. As a result, only 383 genes with complete sequences could be identified within our taxon set of 171 isolates. Phylogenetic analysis separated the taxa into multiple clades, three of which corresponded to the so-called *B. japonicum*, *B. elkanii* and photosynthetic supergroups. This is the first robust *Bradyrhizobium* species phylogeny based on genome sequence information. This tree was used to evaluate the evolutionary relationships of the supergroups, to make decisions regarding discrepancies in species names and to identify isolates that should be moved to another genus. Furthermore, this study provides the basis for using genome sequence information as a resource to investigate biological traits important to the delineation of the supergroups.

1.6 **Divergence and gene flow in *Xanthomonas* plant pathogens**

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Plant health management of bacterial diseases relies on the capability to reliably detect and identify plant pathogenic bacteria. Systematics provides classification schemes, unambiguous names and identification tools to scientists and other stakeholders. However delineating stable taxonomic units, predictive of ecological, phenotypic, and phylogenetic properties, might be challenging in plant pathogenic species complexes. Xanthomonads are plant pathogenic bacteria responsible for economically important damages in many crops worldwide. As a whole, the genus *Xanthomonas* gather strains that are responsible for diseases on numerous plant species. However, each strain displays a narrow host range that is referred to in the pathovar concept. We address the question of the genetic structure, the species boundary and the nature of the evolutionary forces that shaped the diversity within two species, namely *Xanthomonas axonopodis sensu lato* whose taxonomy has been debated and *Xanthomonas arboricola* which encompasses both pathogenic and commensal strains. Thanks to CIRM-CFBP resources, large collections of strains were assembled. Population genetics based on the sequence analysis of seven housekeeping genes and population genomics using whole genome datasets were used to infer the evolutionary histories and gene flows. We also examined the gains and losses of virulence-associated genes along divergence. For *X. axonopodis*, the suggested evolutionary scenario involves a first step of generalist diversification that spanned over the last 25 000 years. A second step of ecology-driven specialization occurred during the past two centuries. Secondary contacts between host specialized strains probably occurred as a result of agricultural development and intensification, allowing genetic exchanges of virulence-associated genes. The barriers to gene flow identified did not always reflect the species delineation recently proposed based on average nucleotide identity (ANI). Using the known diversity of *X. arboricola*, we showed that it exhibits an epidemic population structure, within which epidemic clones emerged from a recombinant background population following virulence factor acquisition. Commensal strains have kept or lost the ancestral repertoire of virulence-associated genes. Some divergent strains might represent several new species based on ANI. Phytopathologists need both species and pathovar classification to manage pathogen emergence. Altogether, these studies highlight the major role of gene flow in plant pathogen diversification.

2.1 **A core-genome sequence based taxonomy of the family *Leptotrichiaceae* calculated using EDGAR 2.0**

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The family *Leptotrichiaceae* comprises the genera *Caviibacter*, *Leptotrichia, Oceanivirga, Sebaldella, Sneathia*, and *Streptobacillus*. All six genera form separate branches in the 16S rRNA gene sequence based phylogenetic trees and can therefore be clearly separated based on the 16S rRNA gene sequence phylogeny. The genera *Streptobacillus* and *Leptotrichia* are both monophyletic as indicated by the formation of distinct clusters in the phylogenetic tree including all type strains of the species assigned to the respective genera. Members are facultatively to obligate anaerobic organisms that stain as Gram-negative rods. All species described so far are non-motile and fermentative. Some species are fastidious and require serum or blood for growth and several of them have been isolated from human clinical specimens and are pathogenic to humans. Normally they occur in the human oral cavity and in the hindgut of termites. Most of the type strains of members of the family are already genome sequenced. For only two *Leptotrichia* type strains, genomes are not available so far. A core genome based phylogenetic tree of the genera assigned to the family *Leptotrichiaceae* based on amino acid sequences of a core gene set of 237 shared genes will be presented with the emphasis of core genome prediction and phylogenetic tree construction using the Neighbor joining method using EDGAR 2.0. The EDGAR 2.0 platform for comparative genomics will be discussed in more detail.

2.2 **A global catalogue of microbial genome: type strain sequencing project of WDCM**

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The WFCC-MIRCEN World Data Center for Microorganisms (WDCM, http://www.wdcm.org/) has long been committed to facilitating the application of cutting-edge information technology to improve the interchange of microbial data, promote the access and use of data and information, and coordinate international co-operation between culture collections, scientists and other user communities. To help numerous culture collections that cannot make their data available online, WDCM launched the Global Catalogue of Microorganisms (GCM) (http://gcm.wdcm.org/) project in 2012. Up to now, GCM (http://gcm.wdcm.org/) has become one of the largest data portals for public microbial collections and several international culture collection networks, providing data retrieval, analysis, and visualization system for microbial resources. Futhermore, GCM gradually developed into a knowledge base linking taxonomy, phenotype, omics data as well as relevant scientific papers and patents with its catalogue information, which currently consists of 402,778 strains and other holdings (plasmids and antibodys) deposited in 117 collections from 46 countries and regions. Recently, the WDCM announced the launching of the Global Microbial Type Strain Genome and Microbiome Sequencing Project during the 7th WDCM Symposium, indicating that the GCM project has begun a new stage (GCM 2.0). Focused on exploring the genomic information of microorganisms, this project plans to sequence all uncovered prokaryotic type strains together with select eukaryotic type strains, construct a database for genomics data sharing, and also provide an online data mining environment. Working groups responsible for selecting bacteria and fungal strains, drafting SOPs, managing intellectual property rights and legal issues and construction of the database have already embarked on the pioneer stage of GCM 2.0. The project will establish a cooperation network for type strain sequencing and functional mining, and complete genome sequencing of over 10000 species of microbial type strains in five years.

2.3 **Genome sequence-based criteria for species demarcation: insights from the genus *Rickettsia***

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With more than 100,000 bacterial genome sequences available in public databases, genomics has entered the routine workflow of many microbiology fields, including taxonomy. Rickettsiae are arthropod-associated bacteria, many of which are recognized human pathogens. Rickettsial taxonomy has long been impaired by the limited number of phenotypic criteria measurable for these strictly intracellular bacteria. In 2003, we proposed a MLST tool based on sequences from four genes, and these cutoff values have widely been used in the past decade. In the present study, we evaluated whether genome-based criteria could replace MLST for the taxonomic delineation of *Rickettsia* species. We studied 79 genomes from 34 species, including 27 species with standing in nomenclature and 7 as yet unofficial species. We compared the digital DNA-DNA hybridization (dDDH), OrthoANI and Average Genome Identity of Orthologous gene Sequences (AGIOS) parameters to classify rickettsial isolates at the genus, group, and species levels. To be classified as a member of the *Rickettsia* genus, a bacterial isolate should exhibit dDDH, OrthoANI, and AGIOS degrees of similarity with any of the 27 *Rickettsia* species of >16.8, >80.5 and >77.9%, respectively. A member of the typhus group must lack the *ompA* gene and have dDDH, OrthoANI and AGIOS values with *R. typhi* or *R. prowazekii* >42.5, >92.2, and >92.2%, respectively. A member of the transitional group must meet the following criteria: dDDH, OrthoANI and AGIOS values >44.0, >91.8 and >76.8%, respectively, with any member of this group. A member of the spotted fever group must exhibit the following criteria: dDDH, OrthoANI and AGIOS values with any member of this group >59.3, >95.1 and >94.6%, respectively. To be classified as a new *Rickettsia* species, an isolate should not exhibit more than one of the following nucleotide similarities with its closest phylogenetic neighbor species: >92.3, >99.2, and >98.6% for the dDDH, OrthoANI and AGIOS parameters, respectively. Using the latter criteria, "*R. monacensis"*, Rickettsia endosymbionts of *Ixodes scapularis* and *I. pacificus* and *R. gravesii* were classified as distinct new species. In contrast "*R. argasii*" and "*R. philipii*" belonged to the *R. heilongjiangensis* and *R. rickettsii* species, respectively.

2.4 **What exactly are bacterial subspecies?**

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Bacterial populations are constantly exposed to varying evolutionary forces, which could ultimately result in the formation of cohesive genetically isolated groups. Although these newly evolved groups are often phylogenetically and phenotypically well-defined, they still share a high level of similarity with their sister groups and is impossible to recognise as separate species when using the conventional quantitative DNA-DNA hybridisation or ANI cut-off values. A review of the literature indicated that most taxonomists classify such groups as sub-species. We predict that the use of an approach based on evolution (e.g. genealogical concordance) would have supported the hypothesis that such groups represent distinct species. This raises the question of how bacterial subspecies should be defined and if the use of this taxonomic category is still relevant. Several taxonomists have indicated that the sub-species category could also be used to communicate specific interspecies adaptive responses, but we believe that these variations are better captured with alternative terms to define the variable characteristic in question, such as pathovar, biovar or phylotype.

3.1 **Actinobacterial biodiversity: a potential driver for the South African Bio-economy**

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From an evolutionary perspective, emphasis has always been placed on the individual, regardless of their position in the Tree of Life. This way of thinking has changed over time as more information became available about the relationships between microbial populations and their animal and/or plant hosts and their environment, shifting the focus to the concept of holobionts as evolutionary units. Recently, it has been proposed that the 'real' driving force in evolution, is the processes that the individuals/populations are involved in and not necessarily the organisms themselves, a concept described as 'the singer, not the song'. In this sense, genomics as part of bacterial systematics has provided us with deeper insight into the potential functional role of the microbes under study and their involvement in driving specific environmental processes. Bearing all of this in mind, the genome sequences of 21 actinobacterial strains isolated from plant-rich environments were sequenced (Illumina MiSeq) and analysed for the presence of genes encoding for oxidative enzymes and the lipoprotein, expansin, proteins that are known to be involved in lignocellulose degradation. The genomes were annotated using RAST and evaluated for the presence of genes encoding for multi-copper oxidases (MCO), dye-decolourising (DyP-type) peroxidases, tyrosinases, lytic polysaccharide monooxygenases (LPMO), and expansins. Even though 16 actinobacterial genomes contained genes annotated as expansin homologues, only two genes were identified to encode for proteins with the amino acid signature unique to the carbohydrate-binding module family 63 (CMB-F63; expansins); all 21 genomes contained LPMO genes, with the majority showing phylogenetic relationship to chitin-binding LPMOs rather than cellulose-binding LPMOs; five different MCO superfamilies are represented, including the 'rare' two-domain MCOs; eight DyP-type peroxidases were detected; and nine contain the *melC1*/*melC2* genes required for the production of extracellular tyrosinases. Since South Africa wishes to become a global competitor in the field of enzyme production, this approach along with the potential for the application of these enzymes in the production of bulk or fine chemicals, necessitates a renewed drive in linking researchers involved in bacterial systematics with those involved in biodiscovery and the active development of the SA bio-economy.

3.2 **Identification and recovery of "missing microbes" from the gut microbiota of human populations living non-industrial lifestyles**

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The distal gut microbiota perform a wide range of functions that contribute to healthy human physiology, including nutrient processing, energy acquisition, vitamin synthesis, and immune system development. Disruptions in these microbial assemblages have been associated with a variety of metabolic and inflammatory disorders including Obesity, Type II Diabetes, Crohn's disease, Ulcerative colitis etc. Advances in high throughput sequencing has allowed for rapid characterization of the taxonomic diversity of the gut microbiome, and coupled with other approaches including meta-transcriptomics, meta-proteomics, and metabolomics, allows for systems level characterization of these ecologies. However, the vast majority of human microbiome studies are focused on populations living in urban/industrialized societies, often within a clinical context. Even large-scale endeavors like the Human Microbiome Project and the MetaHIT consortium, that seek to characterize the diversity of the human microbiome have ascertainment biases. Meta-analyses of taxonomic inventories across several studies collectively including over 3300 individuals from 14 populations, including 7 non-industrial populations demonstrate that the human gut microbiome has undergone significant changes in response to industrialization. This primarily manifests as an overall decrease in microbial richness, and the loss (extirpation) of specific microbial taxa from the gut of industrialized peoples. A well-known example of such a loss is *Treponema,* a genus commonly found in the gut of termites, cattle, and pigs. They also form a core component of the great ape gut microbiome, with high prevalence in orangutans, gorillas, chimpanzees, and bonobos. Among humans, their distribution is primarily associated with communities following traditional subsistence lifestyles including hunter-gatherers and rural agriculturalists, and by a distinct absence in urban, industrialized populations. Other taxa showing a similar trend are members of the genus *Prevotella,* and *Catenibacterium,* that have a much-reduced occurrence in industrialized people, while members of the genus *Succinivibrio*, *YS-2* (candidate phylum), and *Bacteroidales S24-7* (candidate family) are essentially absent in these populations. In this presentation, we will discuss the impact of this loss on gut microbial function, and high throughput cultivation efforts to isolate and characterize these "missing microbes" that may have led to the rise in gut related diseases that appear to be on the increase.

3.3 **Capturing the hidden bacterial diversity at the Lonar Crater, India formed ~52000 years ago**

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Impact craters are unique sites that mimic other primary succession habitats, such as high intensity fires and volcanism. The intense heat and pressures reached at the point of contact create sterile conditions at the immediate area of the impact. Given the importance of such sites in developing successional theories, we studied the soil microbial communities at the Lonar Crater, the only basalt crater in India that was formed through an oblique impact ~52000 years ago. It harbours a saline (1%) and alkaline (pH 9.8) lake which has been extensively studied. Although the soils at the crater represent valid Martian analogues, they have remained underexplored. We used Illumina sequencing of the bacterial 16S rRNA gene to assess their distribution along the crater elevation on two opposing slopes. Our usable data exhibited 77-87% Good's Coverage with 35943 to 61946 OTUs. Although Acidobacteria, Actinobacteria, Chloroflexi and Planctomycetes were the most abundant bacterial phyla, we detected decent abundance of rare phyla, such as Elusimicrobia, Ignavibacteriae, Latescibacteria, Microgenomates and Omnitrophica. While the South top communities were most diverse, the North top communities were least diverse with communities harboured at the Bottom of the crater exhibiting mid-diversity levels. PCO analysis showed a patterned distribution of the communities that was elevation dependant with communities at the bottom of the crater on opposing slopes clustering together whereas communities at the top were distinctly apart even from the opposing slopes. The bottom soils were significantly enriched with Acidobacteria and Latescibacteria but showed significantly fewer Aerophobetes and Chrloflexi. The availability of soil nutrients, C, N and P, played a major role in determining their distribution. Similarly, Ca and Mg seemed to influence the distribution of communities at low elevation. For instance, C/N and C/P ratio were positively correlated with the distribution of Acidobacteria and Latescibacteria, respectively. As few as 1974 members formed the core OTUs at Lonar soils. Our results suggest that the crater soils are rich in rare microbial taxa and require an extensive effort to capture the enormous diversity which remains hidden in this unique ecosystem.

3.4 **Phylogenetic characterisation of *Streptomyces* species causing fissure scab of potatoes in South Africa**

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Streptomyces species are the causal agents of potato scab, a disease characterised by blemishes on potato tubers that result in unmarketable tubers. A new distinct scab symptom, termed 'fissure scab', was reported in 2010 from isolated potato production regions in South Africa. Fissure scab of potatoes consists of 3 mm to 12 mm deep longitudinal fissures containing scab-like lesions. *Streptomyces* species were isolated from these lesions and Koch's postulates confirmed that these strains were responsible for the symptoms that were observed. The aim of this study was to identify the *Streptomyces* species involved with fissure scab in South Africa. In order to identify the species, multi locus sequence analyses (MLSA) was conducted on 48 isolates by sequencing a part of the 16S rRNA gene region, as well as partial gene regions of five housekeeping genes (*atpD*, *gyrB*, *recA*, *rpoB* and *trpB*). Phylogenetic trees were constructed for each gene region separately, where after the five housekeeping genes were concatenated and a single tree was constructed. The isolates responsible for the fissure scab symptoms grouped into three main clades, with clade 1 (12 isolates) grouping with *S. werraensis*. Clade 2 (14 isolates) grouped close to, but distinct from, *S. pseudogriseolus* and *S. gancidicus* and clade 3 (22 isolates) grouped close to, but distinct from, *S. flaveolus*. Clades 2 and 3 are considered novel species that are in the process of being described. Fissure scab in South Africa is therefore not caused by a single *Streptomyces* species, but a combination of different *Streptomyces* species. Further investigations into the distribution of these *Streptomyces* species in South Africa is in progress.

4.1 **Genomic diversity of human gut-associated *Treponema* inferred from shotgun metagenomic datasets**

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Shifts in human subsistence lifestyles, specifically the adoption of industrial agricultural practices has resulted in changes to the composition and diversity of the human gut microbiota. In addition to a decrease in overall microbial richness, these changes also include reduced prevalence and even complete absence of certain microbial taxa among industrialized populations. It is essential to understand the contribution of these "missing microbes" to overall gut function and to evaluate the impact of their loss on human health. Ideally, this would require isolation of these microbes in pure culture followed by functional characterization. However, challenges in obtaining viable samples (often collected from remote geographical locations), coupled with lack of information on nutrient requirements and growth conditions for several of these taxa, severely impact isolation based approaches. In contrast, advances in high-throughput sequencing and bioinformatics algorithms (genome assembly, binning, and annotation), now allow for reconstruction of partial and near-complete genomes from complex metagenomic datasets. In this study, we generated taxonomic inventories from published shotgun metagenomic datasets for over 3300 individuals (14 populations) and screened for the presence of *Treponema*. This analysis revealed the presence of multiple *Treponema* phylotypes among non-industrial populations. Shotgun metagenome datasets from individuals sharing specific phylotypes were merged and assembled using Ray-meta, followed by contig binning using MetaBAT. *Treponema* specific bins were identified using protein blast against the non-redundant protein sequence database from NCBI. A core set of marker proteins conserved across Spirochaetes was recovered for each reconstructed *Treponema* genome and used to visualize the biogeographic distribution of these strains across human populations.

4.2 **Application of whole genome sequencing to exploring intra-generic heterogeneity**

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Prokaryotic systematics provides the foundation for microbial research of ecological, industrial and medical importance. A species is typically defined as a group of closely related strains with a certain degree of phenotypic consistency, ≥70% pairwise DNA-DNA hybridization (DDH) values and >98.7% identity between 16S rRNA sequences. Determining these properties is time and labour-intensive and some techniques suffer from a lack of reproducibility and/or low resolution. Increasing evidence supports the incorporation of whole genome sequencing into prokaryotic systematics. We have applied whole genome sequencing to multiple taxa of actinobacteria and our analyses have revealed a high extent of heterogeneity within each taxon, suggesting that traditional systematic approaches lack sufficient resolution to reliably delineate them. For example, phylogenomic analyses of the genus *Amycolatopsis* revealed it to be quite heterogeneous, with some strains more closely related to members of the genus *Saccharomonospora* than the other *Amycolatopsis* strains. These findings are further supported by taxogenomic analyses including average nucleotide identity (ANI) and fragmented BLAST similarity (FBS) scores between each pair of strains in our dataset. Multiple strains of *Amycolatopsis orientalis* belong to distinct species that cluster with other species in different phylogenetic clades, this was found to be consistent with the digital DNA-DNA hybridisation (dDDH) values between these strains. Prokaryotic genera can be loosely defined based on <6% divergence of the 16S rRNA gene. We have previously identified prokaryotic generic boundaries separating different groups of species (FBS ≤ 6.9 and ANIb ≤ 74.8) based on a taxogenomic analyses of the genus *Rhodococcus*. The current genus *Amycolatopsis* also encompasses multiple species-groups that potentially equate to different genera when these cut-off values are applied. Our analyses also indicate similar problems within the genus *Modestobacter*, where some strains have been wrongly assigned to *Modestobacter marinus*. These analyses reveal a widespread problem of strain misidentification and misclassification using classical approaches and demonstrate that whole genome sequencing can resolve complex intra- and inter-generic structures and should be incorporated into prokaryotic systematics.

4.3 **Relating tRNA gene diversity with the evolution of Planctomycetes-Verrucomicrobia-Chlamydia (PVC) and PVC-like bacteria.**

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Prokaryotes are extremely diverse and contain feature-replete genomes allowing multiple physiological responses. An essential characteristic of most genomes is that they contain different tRNA genes. Since RNAs co-evolved with the proteins, their stored genetic information is more practical to assess evolutionary relatedness between taxa, especially in case the phylum contains very few representative species. We propose the use of tRNA gene diversity as a measure of evolutionary relationships among members of the phylum Planctomycetes, Verrucomicrobia and Chlamydia, collectively called PVC. Our analysis of seven available genomes (P=2, V=1, C=4) revealed that the number of tRNA genes per genome ranged from 35 to 40 in *Planctomyces* and *Chlamydia,* respectively. For Verrucomicrobia, the longest scaffold was available that contained four tRNA genes. While most tRNAs clustered with corresponding homologs in *E. coli* genome (NC000913), nearly 45% of tRNAs clustered with tRNAs coding different amino acids. Compared to *E. coli* tRNAs, *Planctomyces* were most similar followed by *Akkermansia, Isosphaera* and lastly *Chlamydia.* Within a phylum, clustering of tRNAs coding for different amino acids ranged from 8 to 10%. Further analysis of these tRNAs revealed striking sequence similarity with those from Cyanobacteria, Proteobacteria, Viridiplantae, Ascomycota and Basidiomycota (Eukaryota). Further analysis showed certain tRNAs that were identical with those from Viridiplantae suggesting possibilities of horizontal gene transfer or otherwise a different origin for PVC bacteria. While further quantitative analyses are required to test these possibilities, our work is a step forward into looking at tRNAs as a measure of evolutionary relatedness and possibly as a new tool for identification of bacteria.

4.4 **Phylogenomic analyses: The whole is greater than the sum of its parts**

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With the increased availability of genome sequences for bacteria, it has become routine practice to construct genome-based phylogenies. These phylogenies have formed the basis for various taxonomic decisions, especially for resolving problematic taxa. Despite the popularity of concatenating shared genes to obtain well-supported phylogenies, various issues regarding this combined evidence approach have been raised. These include the introduction of phylogenetic error into datasets, as well as incongruence due to organism level evolutionary processes. For this purpose, we evaluated the impact of phylogenetic conflict caused by organism level evolutionary processes on the established species hypothesis for *Pantoea*. This was achieved by exploring the presence and distribution of conflict at the gene partition and nucleotide levels, by identifying putative inter-lineage recombination events that might have contributed to such conflict. Furthermore, we determined whether sufficient signal was present to overshadow the phylogenetic conflict within smaller, randomly constructed datasets. Although no individual gene genealogies was fully congruent to the species hypothesis of *Pantoea*, the signal associated with specific nodes was distributed across the genome. Evidence of recombination across all lineages within the genus *Pantoea*, provides support for organism level evolutionary processes as a potential source of phylogenetic conflict. The randomly distributed signal was also sufficient to surpass the randomly distributed conflict within the dataset, to the extent that robust, well supported phylogenies, recovering the backbone of the *Pantoea* species hypothesis, was obtained with only 100 genes. This provides the ideal situation for phylogenetic inference, as the topology for the species hypothesis is not driven by single genes.

5.1 **Bacterial species are *sui generis* evolutionary units**

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Many of the gene flow barriers associated with genetic isolation during eukaryotic species divergence, are lacking in bacteria. In these organisms, the processes associated with horizontal gene transfer (HGT) may provide both the "homogenizing force" needed for genetic cohesion and the genetic variation essential to the speciation process. This is because HGT events can broadly be grouped into genetic conversions (where endogenous copies of genes or genetic material are replaced with exogenous homologs) and genetic introductions (where novel genetic material is transferred into a new host genetic background). Gene conversions therefore causes genetic homogenization of individuals within a niche. By contrast, HGT-based genetic introductions drive divergence of populations upon fixation of genetic variants. In this case divergence is driven by altering ecological characteristics of a population and allowing exploitation of additional niches. The effect of HGT in different bacterial species may vary tremendously, and can range from very low levels to rampant HGT, producing chimeric groups of isolates. These varying levels of HGT together with other evolutionary processes, like selection, can result in different groups of cohesive individuals or species that are not comparable. As a result, the conventional, cut-off based approaches for species delineation and definition is not sufficient. Rather, a pluralistic approach to bacterial species recognition is required to accommodate the varying evolutionary forces that result in the different evolutionary fates for bacterial species. We suggest that evolutionary history should form the basis of taxonomic decisions to obtain a more natural taxonomic hierarchy for bacteria, while previously established approaches can serve as methods for investigating cohesion within species. By doing so, we recognize that all bacterial species are unique and each of their own kind (*sui generis*) and can thus not be considered as equivalent groups.

5.2 **Multiple uses of genome sequences in characterizing novel bacteria.**

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Whole genome sequencing of novel bacterial species is becoming more common, and many type strains have already been sequenced through efforts such as the Genomic Encyclopedia of Bacteria and Archaea (GEBA). Whole genome sequences will likely be required for the publication of novel species in the near future. While many new species descriptions currently use the sequences to calculate G+C mol%, and digital DNA-DNA hybridization (dDDH) and average nucleotide identity (ANI) relative to other organisms, the genome also contains an information-rich evolutionary history of the organism that should be explored and correlated to the organism's phenotypes when possible. Average Amino Acid Identity (AAI) is an easily calculated metric that is better for comparing more distantly related organisms and can suggest whether they should be placed into a different genus (<70%) or family (<50%) from another organism. Protein coding gene complements can be compared to identify genes that are unique or shared among closely-related strains or species. Such gene sets can then be explored to predict unique or shared phenotypes for subsequent testing, or to explain already observed characteristics of the organisms. Ideally, the presence of specific genes could be correlated with commonly measured phenotypes such as response on Biolog plates or API test strips, antibiotic resistance profiles, and the production of specific molecules such as pigments, polar lipids, and polyamines. For cases in which genome similarity values are near a threshold to determine whether the organisms are in the same or different taxa, analysis of the genomes can suggest traits that define or distinguish specific taxa.

5.3 **Importance of microbial culture collections (mBRC's)**

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Ever since pure cultures of microorganisms were generated, preservation and exchange of microbial strains became a major concern. As a consequence, many culture collections where established at local, regional and national levels. Worldwide they are members of WFCC (World Federation of Culture Collections) and at the continental level of ECCO – (Europe); ANMR (Asia); USCCN (United States) and FELACC (Latin America). The WDCM (World Data Center for Microorganisms) catalogue offers info on their holdings.There are no strict rules - except for the description of new taxa – to stimulate or impose deposition of material of which scientifically important and costly research is published. Publishers act opportunistically by not demanding deposition of the material because there is no general policy and scientific correctness seems to be less important than commercial arguments. Microbial studies have evolved towards the generation of an overwhelming amount of genetic data (sequences) that are used in diversity studies. Hence, the biological material is not available and reference organisms are lacking for the numerous new phyla that have been discovered. A number of pro's and con's about the usefulness of culture collections can be debated. Among the pro's, the need for i) taxonomic references; ii) certified references for standardized testing and as key strains for epidemic outbreaks (human, animal and plant related) are mentioned. Further, the availability of cultures supports verification of published data and allows cumulative research. A number of con's are e.g.: i) the important financial burden for isolating, preserving and distributing of material; ii) the difficulty for BRC's to select for important 'key' cultures for preservation. A meaningful role of mBRC's in the future can only be met if i) adaptive funding models support collaborative actions; ii) redundancies of holdings are limited; iii) coordinated cultivation initiatives to extent the pure or enriched cultures are stimulated; iv) publishers and funding agencies impose the long term availability of the biological material studied; v) miniaturized preservation protocols are developed and vi) integrated data search becomes possible.

POSTER PRESENTATIONS

B1 **Trusting phylogeny or chemotaxonomy? A case study for *Turicella otitidis* including *Corynebacterium otitidis* comb. nov.**

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The actinobacterial genus *Turicella* was described to harbour clinical isolates, with *Turicella otitidis* the only species of this genus described to date. Due to its chemotaxonomic distinctiveness, *T. otitidis* was identified as a genus separate from *Corynebacterium*. However, according to phylogenetic trees based on ubiquitous single-copy genes in the genome, *Corynebacterium* is a paraphyletic group including *T. otitidis*. Also, trees concatenating menaquinone biosynthesis genes support the conclusion that *T. otitidis* is clustered in a unified group with *Corynebacterium* species. These results suggest that chemotaxonomy is not sufficient standard for classification compared to phylogenetic analysis. Based on this information, *T. otitidis* can be reclassified as a species belonging to *Corynebacterium* genus, i.e. as *Corynebacterium otitidis* comb. nov.

B2 **An EzBioCloud based k-mer database for an accurate metagenomic taxonomy classification**

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Knowing the composition of a metagenomic sample has been a challenge for the last decade. Being able to detect the taxa in a given sample could give a lot of insight into its environment. Having a good reference database is an important element of such ability to detect taxa accurately, and in the last few years, more genomes have been annotated in public databases. Unfortunately, some species are better represented than others, and not all the genomes went through the same quality control process, which results in some of them being of low quality or being positioned in the wrong taxa. Also, the computational requirements for such a process increases according to the number of genomes in the database and the number of reads in a given sample. Several methods and databases have been developed together to help microbiologists in their metagenomic taxonomic analyses. Most of them have focused on speed efficiency due to the high number of short reads included on each metagenomic shotgun dataset. In this study, we focus on the impact that a high-quality and normalized database can have on a well-known heuristic for sequence classification, the exact match k-mer algorithm. This method, together with the EzBioCloud database, which contains genomes that are validated with several quality control processes, allows us to have a fast, efficient and more accurate taxonomy classification system. We will compare our database with the standard NCBI refseq database, and we will show how our selection and normalization of genomes from EzBioCloud results in a more accurate taxonomy profiling. We will also show that creating a database with an equal number of genomes per species creates an unbiased and more accurate classification system, especially for those species that are underrepresented in the NCBI database.

B4 **KI-S: a tool for very fast taxonomic comparison of genomic sequences**

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In bacterial systematics, the use of average nucleotide identities (ANI) is now widely used to group bacterial genomes in phylogenetic groups or cliques. However, the computational time of this distance parameter which uses the BLAST algorithm, could be long and could be a limiting factor to study large datasets. As an example, 56000 bacterial genomes were available in the integrated microbial genomes (IMG) database the 1st September 2017. Here, we propose to use the percentage of shared *k*-mers between two genomes to estimate their phylogenetic relatedness. Using a dataset of 944 publicly available genomes of the *Pseudomonas* genus, we compared the distances based on *k*-mers with ANI values as well as the computational time of these two methods. Because, the trees generated from huge distance matrices are often hard to read, we have developed tools that provide original visual representations of these matrices. The "Ki-S" tool that we propose, allows to generate the matrices of ANIb and *k*-mers distances in a *Galaxy* environment and provides original visual representations to improve the visualization and analysis of large similarity matrices.

B5 **Developing a molecular consensus between multiple phylogenies: A case study of the genus *Aeromonas***

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Taxonomy of the genus *Aeromonas* has been controversial since its original description nearly 125 years ago. There is lack of congruence between 16S rRNA gene sequence similarity and DNA-DNA hybridization (DDH) values within *Aeromonas*. The taxonomic incongruence is further exacerbated due to the dual distinction of species either as genomospecies based on DDH or as phenospecies based on conventional biochemical characteristics. Single gene sequencing has only helped marginally and Multi Locus Sequence Typing (MLST) has therefore been proposed. However, there are at least four sets of MLST genes which have shown potential with other taxa that are currently in use for the genus *Aeromonas*. Because of the lack of statistical and evolutionary evidence, results from these schemas have been incongruent, and there are several taxa within *Aeromonas* with pending inconsistencies. For instance, the potential of a multigene approach to delineate species identity of *Aeromonas* strains isolated from diverse sources and different geographical regions was assessed. Individual gene phylogenies based on the 16S rRNA (1.5 kb), 23S rRNA (2.75 kb), *gyrB* (1.15 kb) and *rpoD* (840 bp) genes were constructed and their robustness was assessed using multiple statistical parameters, such as the cophenetic correlation coefficient, distortion coefficient, the Kishino-Hasegawa test, the Shimodairo-Hasegawa test, estimated likelihood weight and percentage sequence similarity (*S*). Although protein-coding genes were more accurate in differentiating closely related strains, none of the molecular chronometers agreed unanimously with each other. In order to resolve such inconsistencies, we propose to use whole-genome sequences (WGS) to rationally arrive at a core-genome MLST for the genus *Aeromonas.* This will be followed by narrowing down this core gene set in an evidence-based manner to arrive at the least number of genes that have the same discriminating power as that of whole genome taxonomy. We will then statistically validate these developed MLST schema on environmental isolates of *Aeromonas.* Based on the use of WGS to resolve the confusion in other incongruent taxa, we propose that the status of genomospecies in *Aeromonas* will also be resolved with the calculation of *in-silico* DDH values on these whole-genomes.

B8 **Culture dependent and culture independent studies on Socorro island (Revillagigedo archipelago) suggests an intrinsic diversity of actinobacterial species**

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The Revillagigedo archipelago, a recently named Mexican National Park, encompasses three islands. The biggest of those, the Socorro Island, is a well known resource of natural diversity and endemism. For instance, it contains -at least- thirty-nine plants that are unique to the ecosystem. On the contrary, no microbial studies have been conducted, thus its intrinsic microbial diversity is unknown, notably actinobacteria (Gram positive bacteria with a high content of GC). In this study, five soil samples were collected from different locations on the island (between December 2016 and January 2017) and employed for culture-dependant experiments oriented to the isolation of actinobacteria by using Glucose Yeast Malt extract agar (GYM) supplemented with antibiotics, namely nystatin [50 µg/mL] and rifampicin [15 µg/mL]. After a 4 weeks incubation period, thirty colonies chosen by morphological features resembling actinobacteria were taken randomly and purified and subcultured for further studies, including a specific PCR for Actinobacteria and 16S rRNA gene sequencing. Phylogenetic trees were constructed with the obtained sequences and were assigned to at least three different genera, with the genus *Streptomyces* not only being the most predominant but also representing several putative novel species. A pool of DNA extracted from the five samples was sent for a metagenomic analyses and it also suggests a high degree of microbial diversity. To our knowledge, this could be considered as the first systematic study regarding the actinobacterial diversity on the Revillagigedo archipelago. Due to the unique property of the actinobacteria as a prolific group for secondary metabolite production, the Revillagigedo Island certainly contains bacteria worth studying for bioprospective areas.

B9 **A novel soil bacterium *Hymenobacter humicola* sp. nov. 3isolated in Antarctica**

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A set of seven psychrotrophic bacterial strains was isolated from different soil samples collected at deglaciated northern part of James Ross Island (Antarctica) in the years 2013 and 2014. All isolates were rod-shaped, Gram-negative, non-motile, catalase positive and oxidase negative, and produced moderately slimy red-pink pigmented colonies on R2A agar. A polyphasic taxonomic approach based on 16S rRNA gene sequencing, extensive biotyping using conventional tests and commercial identification kits, fatty acid profile, MALDI-TOF MS, automated ribotyping and chemotaxonomy were applied to the isolates in order to clarify their taxonomic position. Phylogenetic analysis based on 16S rRNA gene showed that all isolates belonged into the genus *Hymenobacter* with the closest relative being *Hymenobacter aerophilus* DSM 13606^T, exhibiting 98.53% 16S rRNA pairwise similarity. The major components in cellular fatty acid composition were Summed Feature 3 ($C_{16:1}$ *ω7c*/ $C_{16:1}$ *ω6c*), C $_{16:1}$ *ω5c*, Summed Feature 4 ($C_{17:1}$ anteiso B/iso I), $C_{15:0}$ anteiso and $C_{15:0}$ iso. The menaquinone systems of the type strain CCM 8763^T contained MK-7 as the major respiratory quinone. The predominant polar lipids were phosphatidylethanolamine and unknown phospholipid. A moderate to minor amounts of three unknown polar lipids, four unknown aminophospholipids, one unknown glycolipid and one unknown phospholipid were present. Based on obtained results, we propose a novel species for which the name *Hymenobacter humicola* sp. nov. is suggested, with the type strain CCM 8763^T.

B10 **Genomic encyclopedia of bacterial and archaeal type strains: the genomes and pangenomes of soil and plant-associated prokaryotes and newly described type strains**

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The Genomic Encyclopedia of *Bacteria* and *Archaea* (GEBA) project was launched by the JGI in 2007 as a pilot project to sequence about 250 bacterial and archaeal genomes of elevated phylogenetic diversity. Here, this approach was extended to type strains of prokaryotes associated with soil or plants and their close relatives as well as type strains from newly described species. Individual investigators were invited to submit DNA from any of these type strains to JGI for sequencing and annotation. Since the project began in the Fall of 2013, individual investigators proposed 1312 type strains for genome sequencing, and 746 of these strains were approved. The major reason the projects were not approved was that sequencing was in progress elsewhere. Sequences for 571 genomes have been completed or are in progress. Projects approved were largely for type strains from soils, plant associated and saline soils and were contributed by investigators from 14 nations, chiefly India, Spain, United Kingdom, South Africa, and China. In addition, 285 type strains were provided by the China General Microbiological Culture Collection Center (CGMCC), which possesses a large collection of type strains isolated in China. Additional type strains have also been provided by the Colección Española de Cultivos Tipo (CECT). Therefore, this project has significantly increased the number of genome sequences for type strains, especially among plant and soil associated species. In the Fall of 2016, an additional phase of the project (GEBA IV) was initiated to sequence pangenomes of plant and soil associated species. So far, 13 investigators have expressed the intention to contribute DNA from 275 stains for the determination of 29 new pangenomes. So far, 67 sequences are completed or in progress.

B11 **Diverse alpha- and beta-rhizobia nodulate *Vachellia karroo* in South Africa**

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Vachellia karroo (previously *Acacia karroo*) is an iconic southern African legume tree species. It occurs across a wide range of habitats and is a well-known invader of the Grassland biome in South Africa. Very little is known regarding the identity and diversity of the symbiotic nitrogen fixing rhizobia associated with this plant species, and therefore we aimed to determine the range of rhizobia with which *V. karroo* interacts across its distribution range in South Africa. For this purpose, 88 bacterial isolates were obtained from trapping experiments with *V. karroo* rhizosphere soil collected in seven biomes and six provinces in South Africa. PCR amplification and sequencing of the housekeeping loci, 16S rRNA and *recA*, were performed to determine the identity and diversity of rhizobial symbionts. Our results showed that 66 of the examined bacteria represent diverse alpha-rhizobia from respectively *Ensifer*, *Mesorhizobium*, *Rhizobium* and *Bradyrhizobium* in the class Alpha-Proteobacteria. The remaining 19 isolates were beta-rhizobia belonging to the genus *Paraburkholderia*. The largest collection of isolates (32) belonged to the genus *Ensifer* and was encountered in six biomes, with most isolates (13) occurring in the Grassland biome. In this biome, *V. karroo* also associated with the highest number of different genera (*Ensifer*, *Mesorhizobium*, *Rhizobium* and *Paraburkholderia*). The second largest group consisted of 26 isolates of *Mesorhizobium* occurring across 5 biomes with most isolates (14) found in the Savanna biome. Several lineages in these two genera did not contain any validly named species and potentially represent novel species. The third largest group

consisted of the 19 *Paraburkholderia* isolates, found in three biomes with the majority associated with the Fynbos biome. Our study is therefore the first to show an association between *Paraburkholderia* and a species in the mimosoid clade in South Africa. We are also the first to report the presence of these rhizobia in South African biomes other than the Fynbos. Overall, our findings highlight the ability of *V. karroo* to interact with diverse (and possibly novel) rhizobial symbionts across a large geographic range, which might contribute significantly to the invasiveness and adaptability of this legume in certain environments.

B12 **The genetic characterization of *Streptomyces* isolates causing fissure scab on potatoes in the Limpopo Province**

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Fissure scab is a newly discovered potato disease, associated with previously unreported *Streptomyces* species in South Africa. The symptoms of fissure scab include deep longitudinal cracks or fissures of up to 12 mm in depth that reduce the cosmetic value and marketability of the potato tubers. Little is known about the causal agent of fissure scab. *Streptomyces* spp. were isolated from 29 potato tubers obtained from three farms in the Limpopo Province. The aim of the study was to genetically characterize the *Streptomyces* spp. causing fissure scab on potatoes in Limpopo. The characterization of the isolates was done by DNA sequencing with primers specific for the 16S rRNA gene. The presence of two of the pathogenicity genes commonly found in the pathogenicity island (PAI) of pathogenic *Streptomyces* species were determined using primers specific for these genes. A phylogenetic tree was constructed for the 16S rRNA gene region and it was observed that the *Streptomyces* isolates causing fissure scab were grouped into three clades, where one clade was grouped with *S. werraensis*. About 48% of the isolates were found to have the necrosis-inducing gene on the PAI, but the thaxtomin gene was absent. Further characterisation of *Streptomyces* isolates associated with fissure scab in South Africa is underway by means of Multi Locus Sequence Analyses of five housekeeping genes. This will be done to determine the diversity of *Streptomyces* spp. associated with fissure scab, as well as the genetic diversity within each species.

B13 **Morphological characterisation of *Streptomyces* species associated with fissure scab of potatoes in South Africa**

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Streptomyces species are the causal agents of several scab diseases on potato tubers. A new type of scab symptom, caused by *Streptomyces* species, was reported from South Africa in 2010. The isolates obtained from the symptoms were characterised by DNA sequencing and were grouped into three clades. Isolates from clade 1 grouped with *S. werraensis* while clades 2 and 3 grouped away from all known *Streptomyces* species and are considered as 2 novel species. The aim of this study was to determine the morphological characteristics of these strains by means of scanning electron microscopy (SEM) and growth on different culture media. SEM revealed that clades 1 and 3 had mycelia in open loops, while clade 2 had simple spirals. The spores of all three clades were spiny, with some spores in clade 1 being warty. Isolates belonging to clade 3 produced diffusible pigments in culture media, which made it possible to distinguish these cultures from clades 1 and 2. Although the culture morphology of clades 1 and 2 were similar, the distinct spirals of clade 2 and the profusion of single spores from clade 1 made it possible to distinguish between these clades. DNA sequencing is needed to accurately identify *Streptomyces* species, however, cultural characteristics are still useful for initial grouping of isolates in order to choose representative strains to sequence. The different culture media that are available is a quick and easy way to ascertain which carbon sources the bacteria can utilise. This information is valuable when investigating the ecology of the *Streptomyces* species in order to understand their role and function in the soil.

B14 *Micromonospora* species isolated from high altitude Atacama Desert soils

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Small numbers of *Micromonospora* strains were isolated from two locations on Cerro Chajnantor below the site of the Atacama Large Millimeter Array (ALMA) observatory east of San Pedro de Atacama, Chile. The ALMA 4 strains (isolates 4G51, 4G53, 4G55 and 4G57) were collected at 4,000 metres and the ALMA 5 strain (isolate 5R2A7) from 5,046 metres by plating out soil suspensions onto Gauze's No 1 and R2A agar, respectively. The ALMA 4 strains were unusual as they formed dry, filamentous colonies covered by white aerial hyphae while the ALMA 5 strain produced typical micromonosporal - like colonies. 16S rRNA gene sequence analyses showed that isolates 4G51, 4G53 and 4G57 formed a clade that was loosely associated with the type strain of *Micromonospora costi*; the remaining strains, isolates 4G55 and 5R2A7, were most closely related to *Micromonospora palomenae* and *Micromonosora coriariae*, respectively. In silico digital DNA/DNA relatedness values and extensive phenotypic data clearly showed that isolates 4G51 and 5R2A7 represent new species of *Micromonospora* thereby showing that Atacama Desert soils are a rich source of novel filamentous actinobacteria. The genomes of the novel isolates were found to contain putatively new biosynthetic gene clusters adding to the view that micromonosporae from extreme habitats should feature more prominently in bioprospecting campaigns.

B15 **Diversity of Actinobacteria in Indonesian arid habitats as a source of novel antimicrobial drug leads**

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The discovery of novel antimicrobial compounds that can be developed for pharmaceutical purposes has now changed towards the isolation and screening of rare and novel actinobacteria from unexplored and underexplored extreme environments. Based on the premise that exploring such kind of environments will give a higher probability of finding undiscovered novel actinobacteria taxa which can serve as sources of novel compound chemistry. Actinobacteria inhabiting arid habitats have been known to possess unique physiological and biochemical features as well as to produce niche specific-secondary metabolites which enable their survival under harsh environmental pressures such as low moisture, high temperature and high UV radiation. In this study, a culture-dependent method was used to selectively isolate, dereplicate and genotypically characterise the actinobacterial diversity using 16S rRNA gene marker in two Indonesian arid habitat soils, namely Parangkusumo coastal sand dunes (PRKS01) and Mount Bromo sea of sand (BRMO01). A total of 87 actinobacterial isolates were isolated from those samples with 67 and 20 isolates from PRKS01 and BRMO01, respectively. The dereplication process using a colour-grouping technique presumptively classified these isolates into 36 colour groups with 21 single membered-colour groups and 15 multi-membered colour groups. The phylogenetic analysis based on 16S rRNA gene sequencing showed 58% of the isolates belong to the genus *Streptomyces* and the remainder to genera such as *Dermococcus, Arthrobacter, Pseudonocardia, Kocuria, Verrucosispora, Microbacterium, Gordonia, Janibacter* and *Amycolatopsis*. Moreover, three isolates (PRKS01-14a, PRKS01-29 and PRKS01-65) are indicated to be potentially novel species with ≤99.3% similarity index against the described type strains in EzTaxon. These isolates share high similarity of their 16S rRNA sequences with *Arthrobacter pascens* DSM 20545T (98.35%), *Streptomyces yogyakartensis* NBRC 100779T (99.36%), and *Streptomyces nogalater* JCM 4799T (99.22%), respectively. An antiSMASH analysis of the PRKS01-65 genome indicates this strain as a potential antimicrobial producer. Fifty-three out of 92 biosynthetic gene clusters (BGCs) encode for various types of antimicrobials, including Type I polyketide synthases (T1pks), Type II

polyketide synthases (T2pks), Type III polyketide synthases (T3pks), Non-ribosomal peptide synthesis (NRPS), Bacteriocin, and others. Interestingly, ~60% of the compounds predicted still remain unidentified.

B17 **Optimization of motoho, a fermented sorghum beverage from Southern Africa**

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The demand for traditional products in the urban population has been met by upgrading household fermentation techniques to an industrial scale. Motoho is a traditionally fermented Southern African sorghum porridge or beverage. The use of a defined starter culture can decrease the variability which is inherent in traditionally fermented foods as well as enhance the quality of these foods. This study aimed to use lactic acid bacterial strains, *Lb. fermentum* and *Lb. plantarum* either singly or in combination as starter cultures to decrease the variability of motoho. The enzyme activity of phytase and tannase during the fermentation process was determined using enzyme assays. The tannase activity observed during the fermentation of motoho was between 0.49 to 0.79 U/ml, higher than that obtained from KBR9 *Bacillus cereus* which produced tannase of 0.22U/ml. The phytase activity was between 0.11 to 0.25 U/ml, which was lower than phytase values of 236.8±22.8 and 348.7±17.4U/ml which were obtained from lactic acid bacteria used in the fermentation of *ben-saalga*, pearl millet gruel. The low phytase values for motoho could be attributed to variables in process temperature and fermentation techniques.

B19 **Diversity and characterization of staphylococci associated with animals from Antarctica**

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Members of the genus *Staphylococcus* are a major group of bacteria inhabiting the skin, skin glands, and mucous membranes of humans, other mammals, and birds. Staphylococci are widespread in nature and occupy a variety of niches, however, there is very limited information available on isolates from Antarctica. Here we describe the diversity of staphylococci (n=40) isolated from penguin beak, feather and cloak swabs, fresh seagull, skua bird and penguin droppings and seal nose and anus swabs in the James Ross Island and Seymour Island, Antarctica. Sampling of these isolates was performed with cells growing on TSA agar in the Johann Gregor Mendel Czech Antarctic Station in period from 2013 to 2016. The preliminary identification to the genera level was performed by sequencing of partial 16S rRNA gene. Extensive phenotypic characterization was performed using the commercial kits API ID 32 Staph and STAPHYtest 24 and by conventional biochemical, physiological and growth tests relevant for the genus *Staphylococcus*. However, the phenotypic identification of many isolates provided only doubtful or unacceptable profiles. Therefore, the strains were identified by additional techniques, repetitive sequence-based PCR fingerprinting using the $(GTG)_5$ primer, sequencing of partial *rpoB* gene, and MALDI-TOF MS. All these methods have provided reliable identification into the species level and showed similarity to reference type strains investigated simultaneously. The results showed that the isolates represented specific ecovars. The species classification in the analyzed set of strains was as follows: *Staphylococcus delphini* (n=8), *Staphylococcus saprophyticus* (n=2), *Staphylococcus warneri* (n=2), *Staphylococcus epidermidis* (n=1), *Staphylococcus aureus* (n=4), *Staphylococcus haemolyticus* (n=6), *Staphylococcus schleiferi* (n=3), *Staphylococcus sciuri* (n=12), *Staphylococcus vitulinus* (n=1), and *Staphylococcus* sp. from *S. sciuri* complex (n=1). The antibiotic resistance pattern was tested by the disc diffusion method on Mueller-Hinton agar. The strains were predominantly susceptible to tested antibiotics except for penicillin G and ceftazidime. In summary, strains are characterized by significant phenotypic diversity and their biochemical profiles may differ from the key characteristics used in the identification schemes.

B20 **Study of microbial contamination in meat sold in butcheries and supermarkets around Mafikeng, North West Province**

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Raw meat samples (50 chicken, 50 pork and 50 beef) consisting of muscle, liver and kidney from chicken, pork and beef were tested and analyzed. The identification of the isolates were performed with conventional, as well as with and molecular methods based on 16S rRNA species specific gene amplification by PCR. This study indicates without a doubt the relatively high occurrence of pathogenic organisms in 30 of the samples (40%) with the presences of *Enterococcus mundtii*, *Bacillus* sp., *Bacillus cereus*, *Enterococcus* sp. and *Escherichia* sp.. The antimicrobial profile of eight isolates showed high resistance against atibiotics for *Macrococcus caseolyticus* (66.6%), followed by *Enterococcus* sp. (10%), *Enterococcus faecalis* (10%), *Enterococcus mundtii* (3.33%), *Escherichia* sp. (3.33%), *Bacillus* sp. (3.33%) and *Bacillus cereus* (3.33%). The majority of isolates were resistance to tetracyclines and some isolates showed resistance to multiple antibiotics. It was observed that more bacteria were isolated from samples collected at butcheries than at supermarkets. Due to the presence and potential hazard of pathogens in meat samples, the monitoring of these pathogens in different kinds of meat is vital to ensure public health.

B22 **Studies on the efficient degradation of phthalates by Gordonia sp. YC-RL2 and Mycobacterium sp. YC-RL4**

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Phthalic acid esters (PAEs) are widely used as plasticizers to improve the flexibility of plastic products. The PAEs have properties of carcinogenic and estrogenic, and are extremely difficult to be degraded under natural condition. The isolated strains Gordonia alkanivorans YC-RL2 and Mycobacterium sp.YC-RL4 were capable of degrading PAEs effectively, including degrade dimethyl phthalate (DMP), diethyl phthalate (DEP), dibutyl phthalate (DBP), dicyclohexyl phthalate (DCHP), and di-(2-ethylhexyl) phthalate (DEHP). The optimal temperature and pH for DEHP degrading was 30 °C and 8.0. Based on metabolites detected by HPLC-MS, the degradation pathway of DEHP was deduced where the strains transformed DEHP into benzoic acid (BA) via phthalic acid (PA) and mono (2-ethylhexyl) phthalate (MEHP). The alpha/beta hydrolase (DphM1) responsible for PAEs hydrolysis was identified from genomic library of YC-RL4. This enzyme had identity of 30%-40% with the known PAEs esterase, such as EstSP1, EstS1, EstG, M673 PAEs hydrolase, DphB and M11 PAEs hydrolase. DphM1 could hydrolyze all of 13 kinds of PAEs tested, especially ones with bulky side chain. The optimal catalytic condition of DphM1 towards PAEs was 30 °C and pH8.0. Kinetic analysis showed that DphM1 preferred to DMP, DEP and DCHP with high catalytic efficiency, and also could degrade recalcitrant substance DEHP, DOP and BBP, which was the vantage of DphM1 compared to counterparts reported. Based on the result of molecular docking, DphM1 and DMP could interact perfectly with binding energy of -69.125/mol. Some hydrophilic such as His148, Ser210, Asp209 and His336 might contribute to binding substrate or catalysis. A series of mutants will be constructed to evaluate the function of putative active residues.