United States Culture Collection Network 2015 meeting

Endangered and Orphaned Collections

At the US Department of Agriculture National Center for Genetic Resources Preservation, Fort Collins, Colorado.

Agenda

Monday, October 12

3:00	Check In
6:00	ad hoc dinner

Tuesday, October 13

8:00 am	Check in and coffee Poster hanging	NCGRP Conference Room
9:00 am	Welcome	S. Greene, NCGRP H. Blackburn, USDA
9:30 – 10:45	Presentations and discussion	K. McCluskey, FGSC History and context of the USCCN
		David Nobles, UTEX Succession and success at UTEX
		Todd Ward, USDA NRRL Preserving public and patent collections
		Stephanie Greene, NCGRP S#@t happens: ensuring survival through security backup
10:45- 11:00	break	
11:00- 11:40	Invited presentation	Chris Richards, USDA NCGRP Prioritizing preservation
11:40 – 12:00	Success story	Kyria Boundy-Mills, UC Davis Preserving yeasts of yesterday and today, for discoveries of tomorrow
12:00 – 1:30	Catered lunch at NCGRP	Poster viewing
1:30 – 3:00	presentations and discussion	Roland Roberts, NSF Living Collections at the NSF
		Cliff Duke, ESA Is there interest in a broader living collection RCN?
		Greg Dye, Duke The Duke Lemur Center
		Patrick Griffiths The Montgomery Botanic Center

3:15 – 4:45	NCGRP Tour	
6:00- 8:00	Dinner at Hilton Hotel	
7:00	Keynote Speech	Jan Leach, CSU Phytobiomes and Culture Collections: Challenges and Opportunities

Wednesday, Oct 14

8:00 am	Coffee and Posters	
9:00 – 10:45	presentations and opportunities	Richard Humber, USDA ARS Entomopathogenic fungi Carolyn D. Silflow, UMN, The Chlamydomonas Resource Center Kim Webb, USDA Collaboration for Plant Pathogen Strain Identification (CPPSI): A case study in developing a pathogen distribution system for industry needs". Lisa Gribble The US Dept of State wants us to think about Biosecurity John Wertz, Yale Long term stability for E. coli
10:45- 11:15	break	
11:15- 12:00	Invited presentation	Barbara W. Johnson, CDC The Arthropod-borne virus reference collection of the Centers for Disease Control and Prevention
12:00 – 1:30	Lunch	
1:30 – 3:00	Presentations from a larger community	James Scott, Toronto Preserving the UAMH collection Matt Ryan, CABI International developments – Continuation of MIRRI, the Nagoya Protocol and the UK BRC Initiative Micah Krichevsky Incorporating the USFCC Kyria Boundy-Mills The J. Roger Porter award Kevin McCluskey Wrap up and next steps
3:00	Adjournment	

USCCN Meeting at the USDA National Center for Genetic Resources Preservation

October 13-14, 2015

Invited Speakers

Jan Leach

Dr. Jan Leach is the Associate Dean for Research in the College of Agriculture and a University Distinguished Professor at Colorado State University. In her role as Associate Dean for Research, she provides strategic vision for research within the College, and works with faculty to build collaborative research teams. Her research group studies the molecular basis of durable plant disease resistance. Other projects in her laboratory are related to bioenergy (genetics of biomass production) and understanding the interactions of bacteria-insects-plants in plant health. Dr. Leach is the immediate past Chair of the American Phytopathological Society Public Policy Board where she has been a strong supporter of the value of culture collections. She was on the original APS ad hoc working group that led to this RCN and participated in the first USCCN meeting at the FGSC.

McNally, K. L., Childs, K. L., Bohnert, R., Davidson, R. M., Zhao, K., Ulat, V. J., ... & Leach, J. E. (2009). Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. *Proceedings of the National Academy of Sciences*, *106*(30), 12273-12278.

Gaines, T. A., Zhang, W., Wang, D., Bukun, B., Chisholm, S. T., Shaner, D. L., ... & Westra, P. (2010). Gene amplification confers glyphosate resistance in Amaranthus palmeri. *Proceedings of the National Academy of Sciences*, *107*(3), 1029-1034.

Salzberg, S. L., Sommer, D. D., Schatz, M. C., Phillippy, A. M., Rabinowicz, P. D., Tsuge, S., ... & Bogdanove, A. J. (2008). Genome sequence and rapid evolution of the rice pathogen Xanthomonas oryzae pv. oryzae PXO99A. *BMC genomics*, *9*(1), 204.

Chris Richards

Dr. Richards is a plant population geneticist with the USDA, ARS at the NCGRP in Fort Collins, CO, and an Affiliate Faculty in the Departments of Biology and Soil and Crop Sciences at Colorado State University. He obtained his MS Degree at Stanford University and his PhD at Duke University. His work at the USDA includes the analysis of population genetics of captive populations in regard to genebanking and relies on statistical methods that reveal population diversity and structure and also allow evaluation of genetic changes over time. Of special relevance to plant genetic resource conservation is the study of the impact of genetic bottlenecks and history of domestication.

Richards, C. M. (2000). Inbreeding depression and genetic rescue in a plant metapopulation. *The American Naturalist*, *155*(3), 383-394.

Volk, G. M., Richards, C. M., Reilley, A. A., Henk, A. D., Forsline, P. L., & Aldwinckle, H. S. (2005). Ex situ conservation of vegetatively propagated species: development of a seed-based core collection for Malus sieversii. *Journal of the American Society for Horticultural Science*, *130*(2), 203-210.

McCouch, S., Baute, G. J., Bradeen, J., Bramel, P., Bretting, P. K., Buckler, E., ... Richards, C. M.... & Zamir, D. (2013). Agriculture: feeding the future. *Nature*, *499*(7456), 23-24.

Barbara Johnson

Barbara J. B. Johnson, PhD , is a supervisory research microbiologist with the US Centers for Disease Control and Prevention, Division of Vector-Borne Diseases, in Fort Collins, Colorado. She conducts research to improve the laboratory diagnosis of Lyme disease and other tick-borne illnesses, prevent Lyme disease by vaccination, and understand the

pathogenesis of Borrelia burgdorferi infection. Dr. Johnson holds a doctoral degree in biochemistry from the University of Wisconsin, Madison.

Johnson, B. J., Pilgard, M. A., & Russell, T. M. (2014). Assessment of new culture method for detection of Borrelia species from serum of Lyme disease patients. Journal of clinical microbiology, 52(3), 721-724.

Swei, Andrea, Brandy J. Russell, Samia N. Naccache, Beniwende Kabre, Narayanan Veeraraghavan, Mark A. Pilgard, Barbara JB Johnson, and Charles Y. Chiu. "The genome sequence of Lone Star virus, a highly divergent bunyavirus found in the Amblyomma americanum tick." (2013): e62083.

Johnson, Barbara JB. "4 Laboratory Diagnostic Testing for Borrelia burgdorferi Infection1." Lyme disease: an evidence-based approach. Cambridge (MA): CAB International (2011): 73-88.

Information about participants and their collections

Anne Alvarez, University of Hawaii

"Pacific Bacterial Collection" at the University of Hawaii, College of Tropical Agriculture and Human Resources

There are 6, 171 strains on the acquisition list consisting of plant -associated bacteria, including epiphytes, soil saprophytes, and plant pathogens isolated from diseased agricultural crops, seed and propagative materials used in international trade. Strains were collected from 1973 to 2015 and maintained by Anne Alvarez, Plant Pathologist, Department of Plant and Environmental Protection Sciences, CTAHR.

The taxonomic emphasis of the collection is bacterial plant pathogens representing most common genera and species. The best represented genera are Xanthomonas, Pseudomonas, Erwinia, Pectobacterium, Dickeya, Ralstonia, and Clavibacter. These strains have been widely described in publications, but there is no public catalog. Strains have been exchanged with others and no fees are required. The collection was funded in part by numerous small grants from federal, state, private industry and international organizations (Rockefeller Foundation). No funds were specifically for collection development. All grant funds came from organizations that funded studies on epidemiology and control of bacterial diseases of various tropical and subtropical crops. Some of our cultures have been deposited into various national and international collections, such as ATTC and identities were validated on submission. This collection is presently endangered and the University has no succession plan.

Alvarez, Anne M. "Integrated approaches for detection of plant pathogenic bacteria and diagnosis of bacterial diseases." *Annu. Rev. Phytopathol.* 42 (2004): 339-366.

Sueno, W. S. K., Marrero, G., de Silva, A. S., Sether, D. M., & Alvarez, A. M. (2014). Diversity of Dickeya strains collected from pineapple plants and irrigation water in Hawaii. *Plant Disease*, *98*(6), 817-824.

Davis, J., Fricke, W. F., Hamann, M. T., Esquenazi, E., Dorrestein, P. C., & Hill, R. T. (2013). Characterization of the bacterial community of the chemically defended Hawaiian sacoglossan Elysia rufescens. *Applied and environmental microbiology*, *79*(22), 7073-7081.

A. Rick Bennett, University of Kentucky

Dr. Bennett joined the University of Kentucky, College of Agriculture, Food and Environment as Associate Dean for Research on June 1, 2015. He also serves as Director of the Kentucky Agricultural Experiment Station. Previously, Dr. Bennett spent over 17 years in various positions with the U.S. Department of Agriculture, Agricultural Research Service, including National Program Leader for Plant Health in which he provided leadership for visioning and strategic planning. He has been actively engaged in several national research initiatives including the formation of the U.S. Culture Collection Network. He has engaged prominent leaders in U.S. research communities from government, academia and industry to build interdisciplinary coalitions to address emerging challenges in agriculture. Dr. Bennett has been an advocate for agricultural research in public policy forums and is the immediate past President of the American Phytopathological Society.

Boundy-Mills, Kyria, Matthias Hess, A. Rick Bennett, Matthew Ryan, Seogchan Kang, David Nobles, Jonathan A. Eisen et al. "The United States Culture Collection Network (USCCN): Enhancing Microbial Genomics Research through Living Microbe Culture Collections." *AEM* 81, no. 17 (2015): 5671-5674.

Harvey Blackburn, USDA National Center for Genetic Resources Preservation

The mission of the Plant and Animal Genetic Resources Preservation Unit is to acquire, preserve, and evaluate genetic resources from plants, animals, microbes, aquatic organisms and insects; coordinate their availability, conservation, and utilization; and to provide optimum access to desirable genes and gene complexes. With stakeholders from diverse

communities including commercial cattle breeders and Navajo-Churro sheep producers, the animal germplasm unit preserves semen and embryos to assure valuable breeding stock is available for future breeding efforts.

Blackburn, H. D. "The national animal germplasm program: challenges and opportunities for poultry genetic resources." *Poultry science* 85, no. 2 (2006): 210-215.

Blackburn, H. D. "Development of national animal genetic resource programs." Reproduction, Fertility and Development 16, no. 2 (2003): 27-32.

Blackburn, H. D., S. R. Paiva, Stephan Wildeus, Will Getz, D. Waldron, R. Stobart, D. Bixby et al. "Genetic structure and diversity among sheep breeds in the United States: identification of the major gene pools." Journal of animal science 89, no. 8 (2011): 2336-2348.

Blackburn, H. D., Y. Plante, G. Rohrer, E. W. Welch, and S. R. Paiva. "Impact of genetic drift on access and benefit sharing under the Nagoya Protocol: The case of the Meishan pig." Journal of animal science 92, no. 4 (2014): 1405-1411.

Deepak Bokati, Noble Foundation

Our project focuses on isolating axenic shoot and root, fungal and bacterial endophytes of winter wheat and Bermuda grass of southern Oklahoma. Then the goal is to sequester beneficial microbes via high throughput screening for endophytes associated with heat tolerance, nitrogenase, phosphate solubilization and ACC deaminase traits.

My interest in this meeting is to extend my knowledge in maintaining fungal and bacterial culture stocks. Due to increasing amount of the cultures, we are planning to incorporate the barcoding system to better organize/manage the culture stocks.

The taxonomic emphasis is broad, any culturable fungal (PDA media) and bacterial (869 media) endophytes are included. The collection does not include materials collected from nature after 1993. While the collection does not have a public catalog, isolates are shared with no fee. The collection does not have a dedicated website, nor does it hold any external certifications. Support is entirely from The Samuel Roberts Noble Foundation, Ardmore OK. http://www.noble.org/

Herrera, José, Ravin Poudel, and Deepak Bokati. "Assessment of root-associated fungal communities colonizing two species of tropical grasses reveals incongruence to fungal communities of North American native grasses." Fungal Ecology 6.1 (2013): 65-69.

Herrera, J., Poudel, R., Nebel, K. A., & Collins, S. L. (2011). Precipitation increases the abundance of some groups of root-associated fungal endophytes in a semiarid grassland. Ecosphere, 2(4), art50.

Kyria Boundy-Mills, Phaff Yeast culture collection

Thousands of yeast strains were isolated by Herman Phaff from the 1940s through 1990s, and are preserved in the Phaff Yeast Culture Collection at the University of California Davis. They continue to be used at UC Davis and by researchers around the world, thanks in part to a recent award from the US National Science Foundation to validate species ID, and for remote cryopreservation. Valuable characterization data will be made available to users of the collection via a new database and website, using BioloMICS. Deposit of ribosomal sequences in GenBank will make the strains more useful and visible to researchers globally.

Phaff isolated yeasts from around the world for his foundational studies of yeast ecology and taxonomy. The yeasts continue to be utilized by researchers around the world in innovative ways. Recent uses include major multi-institutional projects such as the Thousand Fungal Genomes project and biofuels research at government agency research labs, as well as smaller projects on ecology, comparative genomics, taxonomy, yeast-insect associations, food fermentations, and food spoilage.

The yeasts are also used for research at UC Davis. Access to the fourth largest yeast collection in the world (containing 7,000 strains, over 800 species) allows research approaches that are possible in very few labs. The advantage of screening numerous strains to identify those with valuable combinations of characteristics has been demonstrated repeatedly. Recent

publications from our lab describe screening of large numbers of Phaff collection strains, up to 180 yeast strains, and have resulted in discovery of yeasts able to utilize specific carbon sources and tolerate inhibitors [1], or tolerate ionic liquids [2]. Of the 70 known oleaginous (high lipid) yeast species, 17 were discovered in the last 3 years at UC Davis, using Phaff collection yeasts [3]. A particularly exciting development is discovery of yeasts that can synthesize and secrete glycolipids, natural biosurfactants that have industrial value.

These exciting discoveries demonstrate the importance of preserving yeasts in pubic repositories, and the importance of supporting those repositories to ensure that innovative discoveries continue.

1. Sitepu, I., et al., Carbon source utilization and inhibitor tolerance of 45 oleaginous yeast species. Journal of Industrial Microbiology and Biotechnology., 2014. 41: p. 1061-1070.

2. Sitepu, I., et al., Yeast tolerance to the ionic liquid 1-ethyl-3-methylimidazolium acetate. FEMS Yeast Res, 2014. 14(8): p. 1286-1294.

3. Sitepu, I., et al., Oleaginous yeasts for biodiesel: Current and future trends in biology and production. Journal of Biotechnology Advances, 2014. 32(7): p. 1336-1360.

Daniel Brown, The Mollicutes Collection of Cultures and Antisera

The purpose of this collection is to conserve lyophilized cultures of organisms referable to the Class Mollicutes, redistribute these upon request on a non-profit basis, replenish selected strains as necessary, and serve as a repository for new specimens of mollicutes and specific antisera against them that may be contributed by independent investigators. The collection encompasses all axenically cultured organisms referable to the Class, except that U.S. Select Agent organisms are specifically excluded. The collection is presently located at the University of Florida and supported by the non-profit International Organization for Mycoplasmology. This assemblage of Mycoplasma spp. and related organisms originated at the U.S. National Institute of Allergy and Infectious Diseases under the direction of Joseph G. Tully around 1980. A second component, limited to isolates from plants and insects, originated at the U.S. Department of Agriculture under the direction of Robert F. Whitcomb. The ex-NIAID component includes about 6,000 specimens including at least the type strain of all species of Acholeplasma, Entomoplasma and Mesoplasma listed in Bergey's Manual; 116 of the current 121 species of Mycoplasma; Ureaplasma urealyticum and U. parvum but no other ureaplasmas; and 32 of the 37 species of Spiroplasma, plus many non-type strains of S. melliferum. The ex-USDA component consists of about another 6,000 vials of lyophilized culture material. Some of the spiroplasma specimens are labeled to genus, species and strain level, but the majority are not yet assigned to species or serogroup. A third component of the collection comprises about 18,000 vials of specific polyclonal rabbit or equine antisera against many of the strains, either unconjugated or directly conjugated with fluorescein isothiocyanate. The Global Catalogue of Microorganisms (http://gcm.wfcc.info/) includes a searchable inventory of the more than 200 species and 1500 strains in The Mollicutes Collection (World Federation of Culture Collections member acronym TMC; World Data Centre for Microorganisms collection number 858). A general website is available at IOM-Online.org. Specimens are available on a non-profit basis for $100 USD each ($50 USD each for IOM members) plus shipping. To request specimens or for further information contact Dr. Daniel R. Brown at drbrown@ufl.edu. The collection includes isolates collected from nature after 1993.

Calcutt MJ, Foecking MF. 2015. Comparative analysis of the Mycoplasma capricolum subsp. capricolum GM508D genome reveals subrogation of phase-variable contingency genes and a novel integrated genetic element. Pathog Dis. 2015 Aug;73(6):ftv041. doi: 10.1093/femspd/ftv041.

Calcutt MJ, Foecking MF, Fox LK. 2014. Complete genome sequence of the bovine mastitis pathogen Mycoplasma californicum strain ST-6T (ATCC 33461T). Genome Announc. 2(4):e00648-14. doi:10.1128/genomeA.00648-14.

Wise KS, Calcutt MJ, Foecking MF, et al. 2012. Complete genome sequences of Mycoplasma leachii strain PG50T and the pathogenic Mycoplasma mycoides subsp. mycoides small colony biotype strain Gladysdale. J Bacteriol. 194:4448-9. doi: 10.1128/JB.00761-12.

Brown DR, Farmerie WG, May M, et al. 2011. Genome sequences of Mycoplasma alligatoris A21JP2T and Mycoplasma crocodyli MP145T. J Bacteriol. 193:2892-3. doi: 10.1128/JB.00309-11.

Regassa LB, Stewart KM, Murphy AC, et al. 2004. Differentiation of group VIII Spiroplasma strains with sequences of the 16S-23S rDNA intergenic spacer region. Can J Microbiol. 50(12):1061-7.

Carolee T. Bull, Penn State University

My interest in living microbe collections goes back many years and includes activities with the American Phytopathological Society ad hoc working group on culture collections that led variously to this RCN.

My personal research collection was first called the Bull Salinas Collection (BS for short) and now will become the Bull Penn Collection (BP for short). This is a collection of phytobacterial plant pathogens from the United States with few from other countries. Type and pathotype strains of many species and pathovars of Pseudomonas and Xanthomonas are present in the collection but not available for distribution except as DNA. The vast majority of the collection was collected since 1993 and a public catalog is under development as a class project at PSU. Strains are shared for valid research projects and we don't charge a fee. We do limit the number of strains distributed unless we have a research collaboration with the group. Some strains have MTAs that prevent their distribution. The collection was developed from appropriated CRIS base funding from the USDA/ARS. Contributions from grants and support of the California Leafy Greens Research Board also supported isolation and taxonomy. Currently Penn State University is supporting the collection. A back up of the collection is currently stored at the NCGRP in Colorado with the UDSA and the original collection is at PSU.

Bull, Carolee T., and Steven T. Koike. "Practical Benefits of Knowing the Enemy: Modern Molecular Tools for Diagnosing the Etiology of Bacterial Diseases and Understanding the Taxonomy and Diversity of Plant Pathogenic Bacteria." Annual review of phytopathology Vol. 53: 157-180 (2015).

Sarris, P. F., Trantas, E. A., Baltrus, D. A., Bull, C. T., Wechter, W. P., Yan, S., ... & Goumas, D. E. (2013). Comparative genomics of multiple strains of Pseudomonas cannabina pv. alisalensis, a potential model pathogen of both monocots and dicots. PLoS One, 8(3), e59366.

Bull, C. T., Clarke, C. R., Cai, R., Vinatzer, B. A., Jardini, T. M., & Koike, S. T. (2011). Multilocus sequence typing of Pseudomonas syringae sensu lato confirms previously described genomospecies and permits rapid identification of P. syringae pv. coriandricola and P. syringae pv. apii causing bacterial leaf spot on parsley. Phytopathology, 101(7), 847-858.

Michael Coffey, World Phytophthora Genetic Resource Collection (WPC)

The origins of this important collection were in the research work of Professor Erwin and Professor Zentmyer at the University of California, Riverside Erwin collected mainly isolates from alfalfa and Zentmyer isolates of P. cinnamomi and P. palmivora from cacao. In 1962, the first accessions of the World Phytophthora Genetic Resource Collection (WPC) were placed in glass culture tubes and a great adventure began. The oldest deposition of the existing cultures is P0127, an isolate of Phytophthora medicaginis from Australia. In 1986 a major development was the provision of funds by the UC Genetic Resources Conservation Program (UC GRCP) for Imperiled Microbial Collections to allow the WPC to be stored under liquid nitrogen using cryogenic techniques. UC GRCP was terminated in June 2008. The WPC has grown in stature over the last 25 years increasing in size from 600 to over 15,000 accessions of Phytophthora (July 2008) of the more than 90 species or taxa which represent this most important plant pathogen. Many of the accessions have been intensively studied over the years and thus the WPC is not only unique in size but also in terms of its importance as a genetic World resource. In addition to living cultures, the WPC has a DNA bank. Standard charges are $295 per culture but for orders of 10 isolates or more they are US$250 per culture, and for orders of 20 or more US$150 per culture or DNA or frozen tissue. Samples from the from the DNA and tissue bank are $275 per 50uL sample of 10ng/uL PCR quality DNA; US$400 per 250mg fresh weight frozen tissue shipped with dry-ice. The University of California recently purchased freezers to replace obsolete cryopreservation systems, although these do not entirely relieve the need to purchase liquid nitrogen for the collection.

Robideau, G. P., De, C. O. C. K., ARTHUR, W., COFFEY, M. D., VOGLMAYR, H., BROUWER, H., ... & ANDRÉ LÉVESQUE, C. (2011). DNA barcoding of oomycetes with cytochrome c oxidase subunit I and internal transcribed spacer. Molecular ecology resources, 11(6), 1002-1011.

Martin, F. N., Blair, J. E., & Coffey, M. D. (2014). A combined mitochondrial and nuclear multilocus phylogeny of the genus Phytophthora. Fungal Genetics and Biology, 66, 19-32.

Chen, W., Djama, Z. R., Coffey, M. D., Martin, F. N., Bilodeau, G. J., Radmer, L., ... & Lévesque, C. A. (2013). Membrane-based oligonucleotide array developed from multiple markers for the detection of many Phytophthora species. Phytopathology, 103(1), 43-54.

Tyler Dreaden, University of Florida

The collection includes Cronartium quercuum f.sp. fusiforme. Accessions were derived from single uredinial pustule and verified using SSR markers. See http://www.mdpi.com/1999-4907/6/8/2739 for more information.

Current projects Fr1 fusiform rust gene cluster (linkage group 2) by screening a larger number (~400) of Fr1 segregating pine progeny. This includes a phenotyping step that requires inoculation of the segregating progeny with SC20-21 (Avr1/Avr1).

Future projects may include: Fine mapping of other Fr loci, monitoring virulence in the field, testing galls from outbreaks using isolates segregating for known avirulence loci, and Cqf re-sequencing experiments require controlled inoculations.

Nearly two decades of research on the host-pathogen interaction in fusiform rust of loblolly pine is detailed. Results clearly indicate that pathotype-specific genes in the host interacting with pathogen avirulence cause resistance as defined by the non-gall phenotype under favorable environmental conditions for disease development. In particular, nine fusiform rust resistance genes (Fr genes) are described here including the specific methods to determine each and their localization on the reference genetic map of loblolly pine. Understanding how these and other apparent Fr genes in loblolly pine and other rust-susceptible pines impact resistance screening, parental and progeny selection, and family and clonal deployment is an important area in forest genetics research and operational tree breeding. The documentation of these Fr genes is a key piece of information towards gaining that understanding and ultimately improving breeding and deployment strategies.

Amerson, H.V.; Nelson, C.D.; Kubisiak, T.L.; Kuhlman, E.G.; Garcia, S.A. Identification of Nine Pathotype-Specific Genes Conferring Resistance to Fusiform Rust in Loblolly Pine (Pinus taeda L.). Forests 2015, 6, 2739-2761.

Clifford Duke, Ecological Society of America

My interest in this meeting stems from leadership of the Ecological Society of America's Sustaining Biological Infrastructure (SBI) program (see www.esa.org/sbi). This program is based in part on our August 2012 workshop "Strategies for Developing and Innovating Living Stocks Collections." This NSF-sponsored workshop brought together managers of living stocks collections, policy professionals, and agency representatives to craft strategies for developing and innovating the nation's living stocks collections. A full workshop report is available here. The SBI, also sponsored by NSF, aims to provide project directors with the core business planning, marketing, and communication skills they need to ensure their resource can continue delivering services that are recognized and valued for their contributions to scientific research. The SBI training initiative focuses on the role of strategic business planning and analysis in driving successful research infrastructure projects, with the ultimate goal of building sustainable projects and project funding. For scientists directing infrastructure projects, achieving sustainability means implementing operationally-sound practices, developing a strong, achievable business plan, and continually maintaining relevance and value to the user community. Currently, we offer a 3-day course each June, with the next course scheduled for June 21-23, 2016. Email me (csduke@esa.org) or check the SBI website if you would like information on how to apply.

Duke Lemur Center

Greg Dye – operations and finance
Erin Ehmke – live colony and biobank research
Sarah Zehr – data management

The Duke Lemur Center (DLC) holds the distinction of being the largest living collection of endangered primates in the world, both in numbers of species and in number of individuals held. Currently, it houses nearly 250 individuals across 18 species of prosimian primates. Over its history, the DLC has housed, cared for, and made available for study over 4200 animals across 40 taxa including lemurs, lorises, galagos, and tarsiers. The endangered status of the species in the collection makes it extremely unlikely that a scientific resource of this magnitude and diversity could ever be re-created. Biological specimens are collected opportunistically (e.g., during routine physical exams and necropsies) and total more than 10,000 samples of various types (e.g., blood, serum, urine, hair, organ tissues, cadavers, etc.). The recent release of a publically available datasets based on nearly 50 years of life history data and medical records allow studies using our living colony and biobank to employ a holistic approach. Large sample sizes, longitudinal data and samples that in many cases span an animal's entire life, exact dates of events, and large numbers of individuals from closely related yet biologically diverse primate taxa make the DLC resource unique, The scientific endeavors at the DLC span a remarkable array of disciplines, including aging, behavior, cognition, epigenetics, genomics, phylogeography, physiology and virology.

Zehr, S. M., Roach, R. G., Haring, D., Taylor, J., Cameron, F. H., & Yoder, A. D. (2014). Life history profiles for 27 strepsirrhine primate taxa generated using captive data from the Duke Lemur Center. Scientific data, 1.

Rea, M. S., Figueiro, M. G., Jones, G. E., & Glander, K. E. (2014). Daily activity and light exposure levels for five species of lemurs at the duke lemur center. American journal of physical anthropology, 153(1), 68-77.

McKenney, E. A., Rodrigo, A., & Yoder, A. D. (2015). Patterns of Gut Bacterial Colonization in Three Primate Species. PLoS ONE, 10(5).

David Geiser, PSU Fusarium Resource Center

Research in my lab focuses on the molecular evolutionary genetics of fungi, mostly in the realm of molecular phylogenetics and systematics at the species level. We apply these tools mostly to identify and better understand the fungal culprits in plant and animal diseases and toxicoses. Unfortunately, identifying fungi using traditional micromorphological tools is very difficult, and tends to lead to species concepts that are too broad. We use the tools of multilocus molecular phylogenetics to recognize and identify species, which provides a much more objective and reliable framework for understanding the biology of these fungi.

As Director of the Fusarium Research Center at Penn State, I also curate the world's largest collection of cultures of Fusarium, one of the most important genera of toxigenic and pathogenic fungi. We are nearing 20,000 accessions and provide isolates to certified researchers, and also provide identification and other services. Most of the research in my lab naturally involves this important genus, but I am also involved in projects in a variety of other fungi.

Aoki, T., O'Donnell, K., and Geiser, D.M. 2014. Systematics of key phytopathogenic Fusarium species: current status and future challenges. J. Gen. Plant Path. 80: 189-201.

Short, D.P.G., O'Donnell, K., and Geiser, D.M. 2014. Clonality, recombination, and hybridization in the plumbing-inhabiting human pathogen Fusarium keratoplasticum inferred from multilocus sequence typing. BMC Evolutionary Biology 14:91.

Park, B., Martin, F., Geiser, D.M., Kim, H.S., Mansfield, M.A., Nikolaeva, E., Park, S.Y., Coffey, M.D., Russo, J., Kim, S.H., Balci, Y., Agad, G., Burgess, T., Grunwald, N.J., Cheong, K., Choi, J., Lee, Y.H., and Kang, S. 2013. Phytophthora Database 2.0: Update and Future Direction. Phytopathology 103: 1204-1208.

Ma, L., Geiser, D.M., Proctor, R.H., Rooney, A.P., O'Donnell, K., Trail, F., Gardiner, D.M., Manners, J.M., and Kazan, K. 2013. Fusarium Pathogenomics. Annu. Rev. Microbiol. 67: 399-416.

Jessie Glaeser, US Forest Service

The Center for Forest Mycology Research (CFMR) is home to the world's largest collection of wood-inhabiting fungi with 20,000 living cultures and 50,000 dried specimens. These collections constitute a library of the fungal kingdom that is used by researchers throughout the world. The taxonomic emphasis is primarily basidiomycete fungi associated with wood decay and include a large collection of imperfect fungi related to *Pseudogymnoascus destructans*, causal agent of white-nose syndrome of bats. The collection includes material collected in nature after 1993. Isolates are shared and there is no fee. The collection does not have external certification.

The CFMR collections have provided many valuable and historic contributions to: Basic research on biosystematics and evolution of fungi, Identification of forest and wildlife pathogens, invasive species, Basic research on the mechanisms of wood decay and development of new wood preservatives, Identification of important pharmaceuticals and biotechnological processes – biopulping, bioremediation, bioenergy, Development of sustainable management guidelines to minimize impacts on forest health from disease and bioenergy harvest. The database of cultures and dried specimens can be searched at: http://www.fpl.fs.fed.us/research/centers/mycology/culture-collection.shtml

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Patrick Griffiths, Montgomery Botanical Center

The Montgomery Botanical Center is one of the living collections that is participating to see how the microbial collection RCN is organized and functioning. The taxonomic emphasis of the collection includes Arecaceae, Cycadaceae and Zamiaceae. It includes materials collected from nature after 1993 and these are listed in our public database here: http://www.montgomerybotanical.org/Pages/Collection_Database.htm. The general website for the Montgomery Botanical Center is http://www.montgomerybotanical.org.

The collection is accredited by NAPCC and ArbNet. Registered as Scientific Institution for CITES (USFWS). https://www.publicgardens.org/content/napcc-collections-institution / http://www.arbnet.org/morton-register/accredited-arboreta/all / https://www.cites.org/eng/common/reg/si/US

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Elaine W. Gunter, ISBER/Specimen Solutions

Co-founded (and still a very active member of) ISBER, the International Society for Biological and Environmental Repositories in 2000, and served as its first president (www.isber.org). ISBER now has more than 1000 members & institutions world-wide and an official journal, Biopreservation & Biobanking. Contributed to ISBER's Best Practices in Specimen Banking I, II, &III. Continued to serve as ISBER Newsletter editor (see "publications" tab at ISBER website) for quarterly publication through 2013, and on subcommittees for marketing, publishing, nominations, biospecimen research and proficiency testing. Joined planning committee to create SEBIG (Southeast Biorepository Interest Group) and hold local events for Southeastern US, 2013.

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Grizzle W, Gunter E, Sexton K, Bell W. Quality Management of Biorepositories. Biopreservation and Biobanking. June 2015; 13(3):183-194

Stephanie Greene

Dr. Greene obtained her Ph.D. in Agronomy (Plant Breeding) at Kansas State University in 1992. She was curator of the USDA-ARS National Temperate Forage Legume Germplasm Unit Forage Legume resource from 1994 until she joined the NCGRP as a Plant Geneticist in 2014.

My priority goals are the strategic expansion and effective management of the National Plant Germplasm System's (NPGS) temperate forage legume collection of Medicago (alfalfa), perennial Trifolium (clover) and Lotus (trefoil), that consists of 16,000 accessions representing 380 species. Recent activities have focused on identifying and filling gaps in the taxonomic, ecogeographic, and genetic coverage of the collections, especially for crop wild relatives, relying heavily on geospatial analysis. Management efforts have focused on regeneration and seed monitoring using best management gene banking practices. Our goal is the rapid distribution of vigorous, true-to-type seeds to researchers and breeders. As resources permit, I have been characterizing the collection with genetic markers and evaluating priority agronomic traits. Current research activities are focused on tracking from cradle to grave, transgene flow from genetically-engineered alfalfa to identify and mitigate routes of seed and pollen transmission to support coexistence among diverse alfalfa producers.

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Richard Humber, USDA ARS

The USDA-ARS Collection of Entomopathogenic Fungal Cultures (ARSEF) began as a private research collection in an ARS laboratory in Orono, Maine, and in now operates in the USDA-ARS Robert W. Holley Center for Agriculture and Health on the Cornell University campus in Ithaca, NY. ARSEF was formally registered with the WDCM in 1982, and is one of only three such registered microbial germplasm collections operated by the Agricultural Research Service. The collection is the world's largest, most diverse, and most comprehensive repository for cultures of fungal pathogens affecting insects and other invertebrates. It currently comprises nearly 13000 isolates representing more than 700 taxa of fungi isolated from 1300 hosts or substrates from 2400 collections sites from 112 countries of the world. The vast majority of the holdings are of ascomycete fungi in Hypocreales, (Sordariomycetes) and phylum Entomophthoromycota. The collection includes materials collected from nature after 1993. The collection has a public catalog available via the homepage here: http://www.ars.usda.gov/Main/docs.htm?docid=12125. Isolates are shared with US scientists freely while foreign and commercial users pay shipping or small fees.

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Hibbett DS, Binder M, Bischoff JF, et al. 2007. A higher-level phylogenetic classification of the Fungi. Mycol. Res. 111: 509-547.

Huang B, Humber RA, Hodge KT. 2007. A new species of Conidiobolus from Great Smoky Mountains National Park. Mycotaxon 100: 227-233.

John F. Leslie, Director, Fungal Genetics Stock Center, Kansas State University

University Distinguished Professor in Plant Pathology, and Director of the FGSC since 2014, Dr. Leslie was on the FGSC external advisory board since the collection was housed at the University of Kansas Medical Center. As a strong proponent of living microbe collections, Dr. Leslie uses his world caliber Fusarium collection in a variety of projects.

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Saleh, A.A., H.U. Ahmed, T.C. Todd, S.E. travers, K.A. Zeller, J.F. Leslie and K.A. Garrett. 2010. Relatedness of Macrophomina phaseolina isolates from tallgrass prairie, maize, soybean and sorghum. Molecular Ecology 19:79-91.

Voss, H., Bowden, R.L., Leslie, J.F., Miedaner, T. 2010. Variation and transgression of aggressiveness among two Gibberella zeae crosses developed from highly aggressive parental isolates. Phytopathology 100:904-912.

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Kevin McCluskey, Fungal Genetics Stock Center, Kansas State University

The FGSC collection was established in 1960 and moved several times to accommodate the needs or retirement of the directors. The director has always been a tenured faculty member with limited day-to-day collection responsibilities. After the NSF changed its funding the FGSC looked to its community for support and the Kansas State University College of Agriculture provided a home for the FGSC in the Department of Plant Pathology. The FGSC will be expected to be self-supporting in the long-term. The collection was moved in one day and the entire resource, including historical documents, weighed 7 tons.

Over many years, the FGSC has maintained orphaned and endangered resources by using the "deposit, storage, distribution" approach where non-core resources are preserved but not accessioned. Most recently this has led to the availability of a collection of Allomyces (water mold) strains which were sent to the FGSC in 1995 and never used until new genome sequencing makes them valuable. They were also important in having been collected internationally prior to the implementation of the CBD. Other orphaned collections at the FGSC include the Perkins wild-type Neurospora collection, the DeSerres DOE mutation analysis set, several researchers private mutant strain collections, genome and genome sequencing libraries, SNP mapping primer sets, and gene deletion and tagged integrant strain sets for Cryptococcus, Candida, and Magnaporthe.

Baker, S. E., Schackwitz, W., Lipzen, A., Martin, J., Haridas, S., LaButti, K., ... & McCluskey, K. (2015). Draft genome sequence of Neurospora crassa strain FGSC 73. *Genome announcements*, *3*(2), e00074-15.

Smith, D., McCluskey, K., & Stackebrandt, E. (2014). Investment into the future of microbial resources: culture collection funding models and BRC business plans for biological resource centres. *SpringerPlus*, *3*(1), 1-12.

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Ulrich Melcher, Oklahoma State University

Dr. Melcher, Regents' Professor Emeritus in the Department of Biochemistry and Molecular Biology, has been interested in discovering and documenting the diversity of plant associated viruses and led an early century effort to uncover viruses in non-cultivated environments. He is an Affiliated Member of the National Institute for Microbial Forensics and Food and Agricultural Biosecurity, with interests in understanding pathogengenome evolution, detection, screening and diversity of plant associated microbes and their interactions with each other and the environment. Specific interests include Spiroplasma and their phages, Serratia marcescens, tobamoviruses and caulimoviruses. These interests led the Virology Committee of the American Phytopathological Society to recommend his participating of their behalf in the Steering Committee of the USCCN.

Dutta, M., Ali, A., and Melcher, U. (2015) Detection, discrimination and discovery of a new Tobacco streak virus strain. J. Virol.Method 221:15-21. doi:10.1016/j.jviromet.2015.03.025 Supplemental material (with omitted figures).

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Melcher, U., Verma, R., and Schneider, W. (2014) Metagenomic search strategies for interactions among plants and multiple microbes. Frontiers in Plant Science, 5:268 doi: 10.3389/fpls.2014.00268.

Stobbe, A. H., Schneider, W. L., Hoyt, P.R., and Melcher U. (2014) Screening metagenomic data for viruses using the e-probe diagnostic nucleic acid Assay (EDNA) Phytopathology. 104:1125-1129. doi.org/10.1094/PHYTO-11-13-0310-R

David Nobles, UTEX

The UTEX Culture Collection of Algae includes over 3,000 different strains of living algae, representing most major taxa. Cultures in the Collection are used for research, teaching, biotechnology development, and various other projects throughout

the world. UTEX supports this community of users through the provision of algal cultures along with a variety of other goods and services. This website contains a listing of the cultures maintained by UTEX, conditions for their maintenance, information regarding the purchase of cultures, and various other features of UTEX. Fees are charged for a variety of different products. In addition to cultures, the collection provides specialized equipment and training.

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Nobles D and Brown R. (2008) Transgenic expression of Gluconacetobacter xylinus strain ATCC 53582 cellulose synthase genes in the cyanobacterium Synechococcus leopoliensis strain UTCC 100. Cellulose 15: 691.

Sara Robinson, Oregon State University

My collection focuses on a very small category of fungi - those that create penetrating, permanent color inside stressed and dead wood. This group includes many white rot basidiomycete fungi capable of forming zone lines for various reasons, and some select ascomycete fungi that secrete pigment deeply into wood. The collection houses fungi within this category from all over the world, including our primary tropical collection point - the Amazon rainforest of Peru, but also including tropical forests in Australia, temperate forests in Chile, and forests across the USA and Canada. The primary interest for this is to provide a comprehensive collection of spalting fungi (fungi which are used to color wood for decorative purposes). Spalting is an ancient art form and is enjoying a resurgence in popularity in North America, South America, and Europe. There are many questions related to how different fungi form spalting and how they interact, and the research done on the collection fungi seeks to answer many of these questions while providing a central repository for spalting fungi. The collection includes isolates collected from nature after 1993 and has a public catalog (via http://www.northernspalting.com). A small fee is charged for sharing isolates. There is no external support for the collection.

Robinson, S.C., Weber, G., Hinsch, E., Vega Gutierrez, S., Pittis, L., Freitas, S. 2014. Utilizing extracted fungal pigments for wood spalting – a comparison of induced fungal pigmentation to fungal dyeing. Journal of Coatings, article ID 759073, doi: 10.1155/2014/759073

Weber, G., Chen, H-L., Hinsch, E., Freitas, S., Robinson, S.C. 2014. Pigments extracted from the wood-staining fungi Chlorociboria aeruginosa, Scytalidium cuboideum, and S. ganodermophthorum show potential for use as textile dyes. Coloration Technology 130(6):445-452

Robinson, S.C., Weber, G., Hinsch, E. 2014. Inducing zone lines and melanin formation for decorative purposes on North American western wood species, with an emphasis on conifers. International Wood Products Journal 5(4):196-199

Tudor, D., Margaritescu, S., Sánchez-Ramírez, S., Robinson, S.C., Cooper, P.A., Moncalvo, J.M. 2014. Morphological and molecular characterization of the two known North American Chlorociboria species and their anamorphs. Fungal Biology 118(8): 732-742

Natalia Risso Fonseca

USDA Forest Service – Rocky Mountain Research Station, Forest and Woodland Ecosystem Program,Forestry Sciences Laboratory, 1221 South Main, Moscow, ID 83843

The Moscow fungal archive collection houses over 15,000 living specimens of forest fungi including root-disease pathogens (Armillaria spp., Fusarium spp., Phellinus spp., Heterobasidion spp.), white-pine-blister-rust pathogen, fungal endophytes, fungal saprophytes, and wood decay fungi. The collection comprises current and historical collections included in published and unpublished studies of at least 50 current and former Forest Service scientists and forest health professionals that date

back at least 40 years. These fungi originated from 35 states and ca 27 countries, and most fungal isolates have the associated collection and environmental data (collector, date, location, host, etc.). This collection represents a multi-million dollar investment from the Forest Service to obtain these biological materials and it provides an invaluable resource for forestry research that is unavailable elsewhere, although the collection does not have a public catalog. The collection facility is certified by USDA APHIS-PPQ (Plant Protection and Quarantine) as a containment facility for tree-associated pathogens of national and international origin, which requires permits and strict guidelines for maintaining these collections. Potential uses of this fungal collection include 1) development of DNA-based methods for identification of forest fungi, 2) determining evolutionary/genetic relationships among fungi, 3) determining effects of climate change on the distribution of forest pathogens and associated fungi, 4) developing methods to predict potentially invasive pathogens before they arrive, 5) monitoring changes in forest fungi over time, 6) development of biological control methods, and 7) numerous other research topics.

Currently, no biological technician is devoted to maintaining these culture collections (the former collection curator was reassigned in 2007 due to repetitive motion injury). Thus, this fungal collection continues to degrade over time because personnel and funding are not available to maintain this irreplaceable biological resource. The collection shares cultures and does not charge fees.

Kim, M.-S.; Klopfenstein, N.B.; Hanna, J.W.; Cannon, P.; Medel, R.; López, A. 2010. First report of Armillaria root disease caused by Armillaria tabescens on Araucaria araucana in Veracruz, Mexico. Plant Disease 94(6): 784. http://www.fs.fed.us/rm/pubs_other/rmrs_2010_kim_m003.pdf

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Elías-Román, R.D.; Guzmán-Plazola, R.A.; Klopfenstein, N.B.; Alvarado-Rosales, D.; Calderón-Zavala, G.; García-Espinosa, R.; Mora-Aguilera, A.; Kim, M.-S. 2013. Incidence and phylogenetic analyses of Armillaria spp. associated with root disease in peach orchards in the State of Mexico, Mexico. Forest Pathology 43: 390-401. http://www.fs.fed.us/rm/pubs_other/rmrs_2013_elias_roman_r002.pdf

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Klopfenstein, N.B.; Hanna, J.W.; Cannon, P.G.; Medel-Ortiz, R.; Alvarado-Rosales, D.; Lorea-Hernández, F.; Elías-Román, R.D.; Kim, M.-S. 2014. First report of the Armillaria root-disease pathogen, Armillaria gallica, associated with several woody hosts in three states of Mexico. Plant Disease 98: 1280. http://apsjournals.apsnet.org/doi/abs/10.1094/PDIS-04-14-0349-PDN

Matthew Ryan, CABI

The CABI Genetic Resources Collection includes Filamentous fungi, yeast and bacteria. Given this broad distribution, our focus is primarily on organisms related to agriculture and the environment. The collection includes materials collected from nature after 1993 and has a public catalog at http://cabi.bio-aware.com/. Isolates are exchanged with other culture collections and a fee is charged for other users. CABI supports the collection (their website is www.cabi.org) and the collection has accreditation for their ID service (UKAS ISO 17025).

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Ryan, M., & Ritchie, B. J. (2012). Storage of Fungal Plant Pathogens. *Fungal Plant Pathogens*, 223.

Broughton, R., Buddie, A. G., Smith, D., & Ryan, M. J. (2012). The effect of cryopreservation on genomic stability in strains of the fungus Trichoderma. *CryoLetters*, *33*(4), 299-306.

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Carolyn Silflow
Matt Laudon
The Chlamydomonas Resource Center. Silflow, Carolyn D., Laudon, Matt C., and Lefebvre, Paul A. Dept. of Plant Biology, University of Minnesota, St. Paul, MN 55108

The unicellular green alga Chlamydomonas reinhardtii has been a powerful model system for biological research for well over 50 years. It has been used for basic research into processes such as photosynthesis and flagellar motility and more recently, for applied research in biofuels. Many tools are available to support this research including the sequenced genomes of the nucleus, chloroplast, and mitochondrion. The NSF supported Chlamydomonas Resource Center serves as a central repository to receive, catalog, preserve, and distribute high-quality and reliable wild-type and mutant cultures of Chlamydomonas as well as useful molecular genetic tools. The Center was initiated in 1978 at Duke University and moved in 2004 to the University of Minnesota. An on-line ordering system and database facilitates the distribution of the collection (http://chlamycollection.org). Some strains in the center date back to the 1950s, allowing intergenerational collaborations between former and current researchers. The nearly 4000 wild-type and mutant accessions currently in the collection will be supplemented with approximately 50,000 additional strains in the next five years as a result of an insertional mutagenesis project lead by Martin Jonikas at the Carnegie Institution. The Center supports research by high school and undergraduate students through the distribution of science fair and educational kits. We have approximately 20 field isolates of Chlamydomonas, some of which are interfertile with the standard laboratory strains. Collection of field isolates is not part of the mission of the Center. ? Yes. Distribution of Chlamydomonas strains and other materials such as plasmids is facilitated by an on-line ordering system. In 2014, more than 1500 strains and more than 200 plasmids were distributed worldwide as part of 565 orders. Fee structure is $20 per strain or plasmid for academic users and $200 for corporate users (plus shipping costs). We offer reduced pricing for undergraduate research and new faculty members at small colleges. Yearly pre-paid subscriptions are available at two levels: $400 for up to five orders comprising up to 50 cultures total and $800 for up to 15 orders comprising up to 150 cultures total.

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Anne Vidaver, University of Nebraska

I’m retired (professor emerita) with a culture collection of about 3,000 strains of bacteria accumulated over 45 years. The collection includes plant pathogens, unusual nitrogen fixing bacteria and endophytes, a few of which show promise in biological control of corn pathogens. No one is being hired to work with these bacteria. Thus far, they are under control of the Dept. Head. Many of the isolates represent first reports including the first dsRNA virus , phi 6, which is not in the Canadian bacteriophage collection, and also is being used by several investigators as a model system for membrane-enclosed, dsRNA viruses. The collection does not have a public catalog and includes material collected between 1966 and 2009.

Isolates are shared, although shipping and handling fees are billed to the recipient. Some cultures are also in type collections, such as ATCC. Material Transfer Agreements can complicate strain sharing.

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Smidt, M. L. and A.K. Vidaver. 1987. Variation among strains of Clavibacter michiganense subsp. nebraskense. Phytopathology 77: 388-392.

Flynn, P. and A.K. Vidaver .1995. Xanthomonas campestris pv. asclepiadis. pv. nov., causative agent of bacterial blight of milkweed (Asclepias spp.). Plant Dis. 79: 1176-1180.

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Todd Ward, USDA ARS

The ARS Culture Collection (NRRL) is one of the largest public collections of microorganisms in the world, containing approximately 93,000 strains of bacteria and fungi. This collection has a very broad taxonomic emphasis, encompassing a diverse array of bacteria and fungi that can be grown and maintained under fairly standard conditions in BSL2 laboratory facilities. The collection includes materials collected from nature before and after 1993 and has a public catalog (http://nrrl.ncaur.usda.gov). The collection is housed within the Mycotoxin Prevention and Applied Microbiology Research Unit at the National Center for Agricultural Utilization Research in Peoria, Illinois. The scientists and staff of the ARS Culture Collection conduct and facilitate microbiological research that advances agricultural production, food safety, public health, and economic development. These goals are pursued through in-house research that improves understanding and utilization of microbiological diversity and through efforts to enhance the value and accessibility of microbial accessions. The ARS Culture Collection is also an international patent strain depository recognized under the Budapest Treaty, and facilitates technological innovation by enabling scientists to simultaneously fulfill microbial culture deposition requirements in association with patent applications in the United States and any of the 139 countries that are contracting parties of the Budapest Treaty. Scientific expertise is provided by five Ph.D. microbiologists/geneticists, who have authored more than 700 scientific publications. However, the ARS Culture Collection project provides sufficient support for just one of these positions. Permanent technical support for collection operations is provided by two microbiology technicians and a computer assistant. Approximately 5-6,000 cultures are distributed without charge from the collection each year, which represents more than a $1 million annual in-kind contribution to microbiological research and biotechnological innovation. In addition, we distribute several hundred isolates from the ARS Patent Collection each year, and we charge a $20 fee for each isolate. Cost recovery fees for deposits and distributions from the ARS Patent Culture Collection are authorized and set forth under Title 7 of the Code of Federal Regulations. The fee structure for this collection has not changed in more than 20 years, and a request to raise these fees to achieve cost recovery has been submitted. This collection has included a patent collection since 1949 and has been an International Depository Authority under the Budapest Treaty since 1981.

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Kimberly Webb, USDA ARS

Sugarbeet is the source of more than half of the domestic sugar that is produced in the United States providing the U.S. with a viable domestic sweetener industry that produces an annual estimated $262.2 billion. Importantly, sugarbeet is the most valuable crop in crop rotations in many growing areas of the United States and plant diseases remain an important source of crop and sugar losses throughout these growing regions. Thus, it is essential to continue to understand and develop improved disease resistance in sugarbeet in order to minimize losses in economic potential.

The plant pathology program is responsible for characterizing the interaction of major sugar beet pathogens (i.e. Cercospora beticola, Rhizoctonia solani, and Fusarium oxysporum) with sugar beet in order to provide new information that will facilitate the development of improved sugar beet germplasm with greater disease resistance and assist in the development of innovative management principles. Using applied, biochemical, and molecular technologies we try to describe how sugarbeet pathogens cause disease, in the hope that novel pathways may be developed to better control those pathogens. A second focus of the project is to determine the genetic relationship and spatial scale of the pathogen populations that affect sugarbeet, in order to more fully understand the disease interactions and how they may differ throughout the many production regions.

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John Wertz, Yale University

The CGSC recently accepted the phage T4 culture collection from Evergreen State College because Dr. Kutter is retiring and it was being orphaned. Similarly, it is considering taking in the E. coli C collection following the recent death of Joe Bertani. So this is definitely a topic close to my heart.

This collection includes only non-pathogenic strains of Escherichia coli: predominantly K-12 derivatives, but a few B strains. It includes cultures of wild-type contributed from a number of laboratories and a few thousand derivatives carrying one or up to 29 mutations from among 3500 mutations in (or included in deletions spanning) more than 1300 different loci. Some combinations were constructed particularly for mapping purposes and are still used for teaching and for rapid localization,

some for manifestation of a particular phenotype, some strains for transferring a particular region or for complementation analysis. Some plasmids, e.g., the Clarke and Carbon collection, F-primes, a number of toolkit plasmids, and a few classic plasmids are included, but it is not a comprehensive collection of plasmids. The CGSC Database of E. coli genetic information includes genotypes and reference information for the strains in the CGSC collection, the names, synonyms, properties, and map position for genes, gene product information, and information on specific mutations and references to primary literature. The public version of the database includes this information and can be queried directly via this CGSC DB WebServer.

We have recently acquired most of the strains from the Keio Collection of systematic individual gene knockout (deletion/kan insertion) strains. These strains were developed by a collaboration of Nara Institute, Keio University, and Purdue Univ. Strains from this collection are currently available from the CGSC, as well as from the National Institute of Genetics in Japan. See Baba et al. 2006, Mol. Syst. Biol. 2: 2006 0008. The CGSC is not yet distributing whole sets of the Keio strains, however Open Biosystems has started distributing the full collection. In addition to continuous support from the National Science Foundation for over 30 years, it has been necessary since 1988 to make charges to users. In order to meet our costs and funding requirements, we are asking academics and non-profits to pay a portion of the costs associated with distributing strains. The fee is in the form of a $35 distribution fee for each order placed plus $8 per strain ordered. (So for example 2 strains would cost a total of $51). The fee for strains distributed on 96-well plates as large sets are $1.25 per strain. Currently only the YFP fusion library is available in 96-well plate format. Exceptions will be made for investigators making recent or large contributions to the Center and for persons without institutional resources for paying such a cost. These rates went into effect March 15th, 2014. We waive these charges for researchers and teachers who lack funds to pay them. The per-strain charge to for-profit companies, beginning January 2nd, 2013 is $120/strain.

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Sara Yentsch, National Center for Marine Algae and Microbiota

The NCMA originated from private culture collections established by Dr. Luigi Provasoli at Yale University and Dr. Robert (Bob) R. L. Guillard at Woods Hole Oceanographic Institution (Bob Guillard's 90th birthday was featured in: Andersen, R.A. 2011. Celebrating Bob Guillard's 90th. Phycological Newsletter 47(2): 10-12.). Initially, algal cultures of scientific interest or for aquaculture were generously provided by them to colleagues, thereby fostering research on marine phytoplankton, back then it was called the Culture Collection of Marine Phytoplankton (CCMP). In time, the task of maintaining and distributing cultures became too large.

Initially, the collection was housed at Woods Hole Oceanographic Institution, Massachusetts. In the autumn of 1981 Dr. Bob Guillard and Jeff Brown (who is still a curator at the NCMA) drove the Collection to Bigelow Laboratory for Ocean Sciences, Maine. In 1985, the facility was changed from a "Collection" to a "Center" to reflect the wider service-orientated mission of the facility. When the Center was established, it was named in honor of Dr. Luigi Provasoli and Dr. Bob Guillard as a tribute to their many and lasting contributions to the culture of marine phytoplankton. The NCMA earned its "National" title through an act of Congress (as the CCMP), so it was important to include the word in the new name to maintain its visibility as a national facility. "Center" (as stated above) reflects a wider, service-orientated mission (as opposed to calling it a collection). "Marine" differentiates it from the other major algal collection in the United States, the University of Texas Culture Collection of Algae, which focuses on freshwater algae. Including "Algae" in the title was an important move to position the NCMA more visibly in the private sector since researchers, particularly those in the algae biomass industry, use the term 'algae', rather than 'phytoplankton' for searches. Finally, "microbiota" is an inclusive generic name that encompasses bacteria, archaea, and viruses, and keeps the new name from becoming too long and cumbersome.

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This information was provided by participants or is excerpted from their collection website and other published public information. All of this information will be considered in preparation of a manuscript from this meeting. Participants will be able to access this document at the USCCN website and are invited to provide editorial input regarding their contributions.

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