2013 JGI User Meeting

TUESDAY EVENING POSTER SESSION

March 26, 2013 - Walnut Creek Marriott, Walnut Creek, CA

Posters alphabetical by first author. *Presenting author

	Authors	Title
1	George E. **ANASONTZIS*** (George.anasontzis@chalmers.se), Dang Tat Thanh, Nguyen Thanh Thuy, Dinh Thi My Hang, Vu Nguyen Thanh, and Lisbeth Olsson	Screening the tropical fungal biodiversity of Vietnam for biomass modifying enzymes, with secretome and transcriptome analyses
2	Adam **ARKIN*** (aparkin@lbl.gov), Robert Cottingham, Sergei Maslov, Rick Stevens, Dylan Chivian, Parmavir Dehal, Christopher Henry, Folker Meyer, Jennifer Salazar, Doreen Ware, David Weston, Brian Davison*, and Elizabeth M. Glass	KBase: An integrated knowledgebase for predictive biology and environmental research
3	Richard **BARAN*** (RBaran@lbl.gov), Benjamin P. Bowen, Nicholas Jose, Vamsi Moparthi, Cheryl A. Kerfeld, Ferran Garcia-Pichel, Muriel Gugger, and Trent R. Northen	Comparative metabolite profiling of cyanobacteria
4	R. **BERLEMONT*** (rberlemo@uci.edu), S.D. Allison, J.B.H. Martiny, E. Brodie, and A.C. Martiny	Metagenomics for plant litter deconstruction in natural and perturbed environments
5	Ranjita **BISWAS**, Nannan Jiang, Lee R. Lynd, and Adam Guss* (gussam@ornl.gov)	Metabolic engineering of *Clostridium thermocellum* for biofuel production from cellulosic substrates
6	Eric M. **BOTTOS,** Charles K. Lee* (cklee@waikato.ac.nz), Daniel Laughlin, and S. Craig Cary	Environmental drivers of microbial ecology in the dry valleys of Antarctica
7	Natalie **BREAKFIELD*** (nbreakfield@gmail.com), Sur Herrera Paredes, Derek Lundberg, Sarah Lebeis, Scott Clingenpeel, Tijana Glavina del Rio, Julien Tremblay, Susannah Tringe, and Jeff Dangl	The characterization of endophytic rhizobacteria isolates from *Arabidopsis thaliana*
8	Thomas **BRETTIN*** (brettints@ornl.gov), Robert Olson, Ross Overbeek, Terry Disz, Bruce Parello, Shiran Pasternak, James Gurtowski, Folker Meyer, Michael Galloway, Steve Moulton, Dan Olson, Shane Canon, Shreyas Cholia, Dantong Yu, Shinjae Yoo, Pavel Novichkov, Daniel Quest, Narayan Desai, Jared Wilkening, Miriam Land, Scott Deviod, Adam Arkin, Robert Cottingham, Sergei Maslov, and Rick Stevens	The KBase architecture and infrastructure design
9	Erick **CARDENAS POIRE*** (carden24@mail.ubc.ca), Kendra Mitchell, Melanie Scofield, Steven Hallam, and William H. Mohn	Forest harvesting alters the genetic potential for lignocellulose decomposition in soil communities
10	Alexander **CHURKIN,** Eviatar Nevo, Danny Barash* (dbarash@cs.bgu.ac.il)	The detection of riboswitches in stressful environments using genome-wide methods
11	Milica **CIRIC*** (Milica.Ciric@agresearch.co.nz), Dragana Gagic, Christina D. Moon, Graeme T. Attwood, Eric Altermann, Sinead C. Leahy, Chris J. Creevey, and Jasna Rakonjac	Metasecretome phage display — a new approach for harvesting surface and secreted proteins from microbial communities
12	Paramvir S. **DEHAL*** (psdehal@lbl.gov), Christopher S. Henry* (chenry@mcs.anl.gov), Aaron Best, Ben Bowen, Steven Brenner, Chris Bun, Steven Chan, John-Marc Chandonia, Neal Conrad, Matt DeJongh, Paul Frybarger, Keith Keller, Pavel S. Novichkov, Ross Overbeek, Fangfang Xia, Adam P. Arkin, Robert Cottingham, Sergei Maslov, and Rick Stevens	The DOE Systems Biology Knowledgebase: Microbial Science Domain
13	Andreas **DESINIOTIS,** Vassili N. Kouvelis, Karen Davenport, David Bruce, Chris Detter, Roxanne Tapia, Cliff Han, Miriam L. Land, Loren Hauser, Yun-Juan Chang, Chrongle Pan, Lynne A. Goodwin, Tanja Woyke, Nikos C. Kyrpides, Milton A. Typas, and Katherine M. Pappas* (kmpappas@biol.uoa.gr)	Genomic analysis of *Zymomonas mobilis* subsp. *mobilis* ATCC 29191: Comparative, structural and functional insights
14	Tania L. **GONZALEZ** and Ming C. Hammond* (mingch@berkeley.edu)	Application of parallel promoter stacking to the study of effector-triggered immunity in plants
15	Sean P. **GORDON*** (Sean.Gordon@ars.usda.gov), Henry Priest, David L. Des Marais, Wendy Schackwitz, Melania Figueroa, Joel Martin, Jennifer N. Bragg, Ludmila Tyler, Cheng-Ruei Lee, Doug Bryant, Wenqin Wang, Joachim Messing, Kerrie Barry, David Garvin, Hikmet Budak, Metin Tuna, Thomas Mitchell-Olds, William F. Pfender, Thomas Jeunger, Todd C. Mockler, and John P. Vogel	Genome diversity in *Brachypodium distachyon*: Deep sequencing of highly diverse natural accessions
16	Alex **GREENSPAN*** (greenspan@ucdavis.edu), Donghyun Kim, Aamir Khan, Rajeev Varshney, and Douglas Cook	Genome-level diversity of nitrogen-fixing symbionts of chickpea: Insights into the effect of domestication on symbiotic nitrogen fixation
17	Erik R. **HAWLEY***, Thomas D. Lorenson, and Matthias Hess (matthias.hess@tricity.wsu.edu)	Analysis of microbial communities associated with natural oils that seep into the Santa Barbara Channel: Linking community dynamics with biological hydrocarbon degradation
18	Guillermina **HERNANDEZ-RAQUET*** (hernandg@insa-toulouse.fr), Sandrine Païssé, Adèle Lazuka, Lucas Auer, Sophie Bozonnet, and Michael O'Donohue	Lignocellulose bioconversion by engineered mixed cultures
19	Valeria **JIMENEZ*** (vjimenez@mbari.org), Chia-Lin Wei, Chee-Hong Wong, Chew Yee Ngan, and Alexandra Z. Worden	Nitrogen metabolism in plants and green algae: a case study using *Micromonas*
20	M. Senthil **KUMAR,** Denis Bertrand, Song Gao, and Niranjan Nagarajan* (nagarajann@gis.a-star.edu.sg)	SIGMA: A Bayesian model based clustering approach for reconstructing individual genomes from shotgun sequencing of microbial communities

21	Sadhana **LAL*** (sadhana.lal@gmail.com), Umesh Ramachandran, Riffat Munir, Richard Sparling, and David B. Levin	*In silico* identification of core metabolic pathways in *C. termitidis* strain C1112 (DSM 5398) and comparative bioinformatics with other cellulolytic *Clostridium* species
22	Peter E. **LARSEN*** (plarsen@anl.gov), Shalaka Desai, Sarah Zerbs, Avinash Sreedasyam, Geetika Trivedi, Leland J. Cseke, and Frank R. Collart	Delineating molecular interaction mechanisms in an *in vitro* microbial-plant community
23	Sarah L. **LEBEIS*** (lebeis@live.unc.edu), Sur Herrera Paredes* (sur00mx@gmail.com), Derek S. Lundberg, Natalie W. Breakfield, Scott Yourstone, Jase Gehring, Stephanie Malfatti, Scott Clingenpeel, Tijana Glavina del Rio, Philip Hugenholtz, Susannah Green Tringe, and Jeffery L. Dangl	Modulation of root microbiome community assembly by the plant immune response
24	Jackson Z. **LEE*** (Jackson.z.lee@nasa.gov), Angela M. Detweiler, Mike D. Kubo, R. Craig Everroad, Tori M. Hoehler, Peter K. Weber, Jennifer Pett-Ridge, Leslie E. Prufert-Bebout, and Brad M. Bebout	Metagenomic and metatranscriptomic sequencing of a hypersaline mat diel
25	Hilary **LEUNG*** (hilaryl@mail.ubc.ca), Roland Wilhelm, Kendra Mitchell, and William Mohn	Characterization of hemicellulolytic soil microbial communities in disturbed forest stands using stable isotope probing
26	Hsiao-Pei **LU**, Yu-bin Wang, Chun-Yen Lin, Shiao-Wei Huang, Chih-Hao Hsieh, and Hon-Tsen Yu* (ayu@ntu.edu.tw)	Integrated metagenome and metatranscriptome reveal adaptive ability for sugar degradation, detection and uptake by the cecal microbiota in the leaf-eating flying squirrel (*Petaurista alborufus lena*)
27	Derek **LUNDBERG*** (derek.lundberg@gmail.com), Scott M. Yourstone* (scott.yourstone81@gmail.com), Devin Coleman-Derr, Susannah Green Tringe, Jeffrey L. Dangl, and Piotr A. Mieczkowski	Critical advances in amplicon sequencing efficiency
28	Folker **MEYER*** (folker@anl.gov), Dylan Chivian, Andreas Wilke, Naryan Desai, Jared Wilkening, Kevin Keegan, William Trimble, Keith Keller, Paramvir Dehal, Robert Cottingham, Sergei Maslov, Rick Stevens, and Adam Arkin	The DOE Systems Biology Knowledgebase: Microbial ommunities Science Domain
29	Angela D. **NORBECK*** (angela.norbeck@pnnl.gov), David Brown, Kevin Fox, David Cowley, and Samuel Purvine	Data integration and analysis processing at EMSL
30	Christian **OLSEN** (Christian@biomatters.com), Kashef Qaadri,, Matthew Shoa-Azar, Joan Wong, Trung Nguyen, George Rudenko, Tina Huynh, Aravind Somanchi, Jeff Moseley, Scott Franklin, and Shane Brubaker*	Haplotype assembly refinement and improvement
31	Hailan **PIAO*,** Stephanie Malfatti, Alexander Sczyrba, Julien Tremblay, Robin Ohm, Kanwar Singh, Fernanda Haffner, Stefan Bauer, David Culley, Kenneth Bruno, Kerrie Barry, Feng Chen, Scott Baker, Susannah Tringe, Igor Grigoriev, Roderick Mackie, and Matthias Hess (matthias.hess@tricity.wsu.edu)	Rumen systems microbiology: Towards a functional systems-level understanding of the microbial community and the biomass degradation process in the cow rumen
32	Ahmed **SAID,** Mohamed Ghazy* (mghazy@aucegypt.edu), Mohamed Maged, Amged Ouf, Ari Ferrira, Rania Siam, and Hamza El Dorry	A metagenomic approach for identification of novel enzymes from the Red Sea Atlantis II brine pool
33	Christopher W. **SCHADT*** (schadtcw@ornl.gov), Migun Shakya, Michael Robeson, Neil Gottel, Hector Castro, Zamin Yang, Marilyn Kerley, Gregory Bonito, Dale Pelletier, Susanna Tringe, Stephanie Malfatti, Kanwar Singh, Tijana Glavina del Rio, Sagar Utturkar, Tatiana Karpinets, Jesse Labbe, Wellington Muchero, Steven D. Brown, Francis Martin, Mircea Podar, Rytas Vilgalys, Mitchel J. Doktycz, and Gerald Tuskan	Roles of genotype-by-environment interactions in shaping the root-associated microbiome of *Populus*
34	Justin **SIEGEL*** (siegeljb@uw.edu)	Computational Design and Experimental Characterization of a Novel Carbon Fixation Pathway
35	Sebastian **SUDEK*** (ssudek@mbari.org), R. Craig Everroad, Alyssa Gehman, and Alexandra Z. Worden	Diversity of picophytoplankton along a physico-chemical gradient in the Northeastern Pacific
36	Ramon **TERRADO,** Adam Monier, and Connie Lovejoy* (connie.lovejoy@bio.ulaval.ca)	Nitrogen assimilation pathways in Arctic microalgae
37	Doris **TISCH,** Andre Schuster and Monika Schmoll* (monika.schmoll@ait.ac.at)	Carbon source and light dependent regulation of gene clusters in *Trichoderma reesei (Hypocrea jecorina)*
38	H. **VanSTEENHOUSE*** (hvansteenhouse@bionanogenomics.com), A. Hastie, E. Lam, H. Dai, M. Requa, M. Austin, F. Trintchouk, M. Saghbini, H. Cao	Structural variation detection and *de novo* assembly in complex genomes using extremely long single-molecule imaging
39	Doreen **WARE** (ware@cshl.edu), David Weston, Sergei Maslov, Shinjae Yoo, Dantong Yu, Michael Schatz, James Gurtowski, Matt Titmus, Jer-ming Chia, Sunita Kumari, Andrew Olson, Shiran Pasternak, Jim Thomason, Ken Youens-Clark, Mark Gerstein, Gang Fang, Daifeng Wang, Pam Ronald, TaeYun Oh, Chris Henry, Sam Seaver, Priya Ranjan*, Mustafa Syed, Miriam Land, and Adam Arkin	The DOE Systems Biology Knowledgebase: Plants Science Domain
40	Roland **WILHELM*** (rwilhelm@mail.ubc.ca)**,** David VanInsberghe, Steven Hallam, and William W. Mohn	Intra-genus diversity of *Bradyrhizobium spp.* isolated from bulk forest soil — an examination of free-living versus nodulating lifestyles
41	Hugh **YOUNG*** (hugh.young@ars.usda.gov), James Schnable, Michael Freeling, and John Vogel	Transformation of *Brachypodium distachyon* to analyze CNS enhancer activity and genome fractionation in maize
42	Yaoping **ZHANG**, David Keating, Irene Ong, Sean McIlwain* (smcilwain@glbrc.wisc.edu), Jeff Grass, Donna Bates, Alan Higbee, Josh Coon, Tricia Kiley, Yury Bukhman, Mingjie Jin, Ven Balan, Bruce Dale, Mary Lipton, Josh Aldrich, and Bob Landick	Lignocellulose-derived inhibitors from ammonia pre-treated biomass activate specific regulatory circuits and inhibit bacterial conversion of xylose to ethanol