
BIOGRAPHICAL SKETCH

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NAME Susannah Green Tringe	POSITION TITLE Senior Scientist		
eRA COMMONS USER NAME	ORCID 0000-0001-6479-8427		
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Harvard University, Cambridge, MA	A.B.	1994	Physics
Stanford University, Stanford, CA	Ph.D.	2000	Biophysics
University of New Mexico, Albuquerque, NM	Postdoctoral	2003	Molecular Genetics and Microbiology
DOE Joint Genome Institute, Walnut Creek, CA	Postdoctoral	2006	Genomics

A. Positions and Honors.

Positions and Employment

1994-2000 Graduate student, Radiation Oncology, Stanford University, Stanford, CA
2000-2003 Postdoctoral fellow (Ruby lab), Molecular Genetics and Microbiology, University of New Mexico Medical School, Albuquerque, NM
2003-2006 Postdoctoral fellow (Rubin lab), DOE Joint Genome Institute, Walnut Creek, CA
2006-2010 Research Scientist, DOE Joint Genome Institute, Walnut Creek, CA
2010-2011 Metagenome Program Deputy Lead, DOE Joint Genome Institute, Walnut Creek, CA
2010-2013 Career Research Scientist, DOE Joint Genome Institute, Walnut Creek, CA
2010-2011 Microbial Systems Group Lead, DOE Joint Genome Institute, Walnut Creek, CA
2011 Visiting Associate Professor, University of California, Berkeley, CA
2011-2015 Metagenome Program Lead, DOE Joint Genome Institute, Walnut Creek, CA
2013-2019 Staff Scientist, DOE Joint Genome Institute, Walnut Creek, CA
2015- Deputy Director, User Programs, DOE Joint Genome Institute, Walnut Creek, CA
2015- Adjunct Associate Professor, University of California, Merced, CA
2019- Senior Scientist, Lawrence Berkeley National Laboratory, Berkeley, CA
2020- Division Director, Environmental Genomics and Systems Biology Division, Lawrence Berkeley National Laboratory, Berkeley, CA (Interim May 2020-Jan 2021)

Other Experience and Professional Memberships

1992 Course assistant, Mathematics 21a: Multivariable Calculus, Harvard University, Cambridge, MA
1994 Teaching fellow, Applied Math 105b: Vector Calculus and Differential Equations, Harvard University, Cambridge, MA
1994- Member, American Association for the Advancement of Science
1996-1998 Teaching assistant, Cancer Biology 263: Apoptosis, Stanford University, Stanford, CA
2002-2004 Member, International Society for Computational Biology
2007- Member, American Society for Microbiology
2009- Member, Society for Industrial Microbiology
2010- Member, International Society for Microbial Ecology
2010- Review editor, Frontiers in Microbiology
2011-2013 Scientific Advisory Board, Hydrocarbon Metagenomics, Genome Alberta
2014- Scientific Advisory Committee, Plant-Microbial Interfaces SFA, Oak Ridge National Laboratory
2015-2016 Scientific Advisory Committee, Principles of Microbial Community Design FSFA, Pacific Northwest National Laboratory
2012- Editorial Board, Microbiome
2013- Editorial Board, Scientific Data
2015- Senior editor, mSphere

2017- Chair, Research Oversight Committee for Algal Blooms, Treatment, Risk Assessment, Prediction and Prevention (ATRAPP) project funded by Genome Canada / Genome Quebec

2017- Member, Research Oversight Committee for Managing Microbial Corrosion in Canada's Offshore and Onshore Oil Production Operations project funded by Genome Canada / Genome Alberta

2017- Member, Research Oversight Committee for GENICE: Microbial Genomics for Oil Spill Preparedness in Canada's Arctic Marine Environment project funded by Genome Canada / Genome Alberta

2017- Member of the External Advisory Board for the International Conference on Arabidopsis Research (ICAR) in 2020

2018-2019 Member, Scientific Advisory Board for the Environmental Molecular Sciences Laboratory (EMSL) at Pacific Northwest National Laboratory (PNNL)

2018- Member, Scientific Advisory Committee for ENIGMA: Ecosystems and Networks Integrated with Genes and Molecular Assemblies project funded by the US Department of Energy

2018- Member, Sigma Xi

2019- Senior editor, International Society for Microbial Ecology (ISME) Journal

2019- Associate editor, Science Advances

2020- Member, Scientific Advisory Committee for the DOE Systems Biology Knowledgebase (Kbase)

Honors

1993 Phi Beta Kappa

1994 *summa cum laude*, Harvard College, Physics

1996-1999 Lucille P. Markey Fellowship in Molecular Mechanisms of Disease

1999 AACR-Pharmacia & Upjohn Young Investigator award

2006 First author on publication named "New Hot Paper" by Essential Science Indicators

2011 DOE Early Career Research Program Award

2011 Named one of Popular Science's "Brilliant 10" for 2011

2013 Featured in "Women @ Energy" highlighting female scientists in the DOE

2014 Named to "Women @ the Lab" recognizing female scientists at LBNL

2016 Berkeley Lab Director's Award for Service

2018 AAAS Fellow

2019-2020 Clarivate Web of Science Highly Cited Researcher

2021 Department of Energy E. O. Lawrence award

B. Peer-reviewed publications (160 total published or in press; in chronological order. H-index 73)

1. Pargellis, A. N., **Green, S.**, and Yurke, B. Planar XY-model dynamics in a nematic liquid crystal system. *Physical Review E* 49: 4250-4257, 1994.
2. Fried, L. M., Koumenis, C., Peterson, S. R., **Green, S. L.**, Van Zijl, P., Allalunis-Turner, J., Chen, D. J., Fishel, R., Giaccia, A. J., Brown, J. M., and Kirchgessner, C. U. The DNA damage response in DNA-dependent protein kinase-deficient SCID mouse cells: Replication protein A hyperphosphorylation and p53 induction. *Proceedings of the National Academy of Sciences* 93: 13825-13830, 1996.
3. **Green, S. L.**, and Giaccia, A. J. Tumor Hypoxia and the Cell Cycle: Implications for Malignant Progression and Response to Therapy. *The Cancer Journal from Scientific American* 4: 218-223, 1998.
4. Denko, N. C., **Green, S. L.**, Edwards, D., and Giaccia, A. J. p53 checkpoint-defective cells are sensitive to x-rays, but not hypoxia. *Experimental Cell Research* 10: 82-91, 2000.
5. **Green, S. L.**, Freiberg, R. A., and Giaccia, A. J. p21Cip1 and p27Kip1 regulate cell cycle re-entry after hypoxic stress but are not necessary for hypoxia-induced arrest. *Molecular and Cellular Biology* 21: 1196-1206, 2001.
6. Hammond, E.M., **Green, S.L.**, and Giaccia, A.J. Comparison of hypoxia-induced replication arrest with hydroxyurea and aphidicolin-induced arrest. *Mutation Research* 532: 205-213, 2003.

7. **Tringe, S.G.**, Wagner, A. and Ruby, S.W. Enriching for direct regulatory targets in perturbed gene-expression profiles. *Genome Biology* 5: R29, 2004.
8. **Tringe, S.G.**, von Mering, C., Kobayashi, A., Salamov, A.A., Chen, K., Chang, H.W., Podar, M., Short, J.M., Mathur, E.J., Detter, J.C., Bork, P., Hugenholtz, P., and Rubin, E.M. Comparative Metagenomics of Microbial Communities. *Science* 308: 554-557, 2005.
9. **Tringe, S.G.** and Rubin, E.M. Metagenomics: DNA sequencing of environmental samples. *Nature Reviews Genetics* 6: 805-814, 2005
10. **Tringe, S.G.**, Willis, J., Liberatore, K. and Ruby, S.W. The WTM genes in budding yeast amplify expression of the stress-inducible gene RNR3. *Genetics* 174: 1215-1228, 2006.
11. von Mering, C., Hugenholtz, P., Raes, J., **Tringe, S. G.**, Doerks, T., Jensen, L. J., Ward, N., Bork, P. Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. *Science* 315: 1126-1130, 2007.
12. Warnecke, F., Luginbühl, P., Ivanova, N., Ghassemian, M., Richardson, T.H., Stege, J.T., Cayouette, M., McHardy, A.C., Djordjevic, G., Aboushadi, N., Sorek, R., **Tringe, S.G.**, Podar, M., Martin, H.G., Kunin, V., Dalevi, D., Madejska, J., Kirton, E., Platt, D., Szeto, E., Salamov, A., Barry, K., Mikhailova, N., Kyrpides, N.C., Matson, E.G., Ottesen, E.A., Zhang, X., Hernandez, M., Murillo, C., Acosta, L.G., Rigoutsos, I., Tamayo, G., Green, B.D., Chang, C., Rubin, E.M., Mathur, E.J., Robertson, D.E., Hugenholtz, P., Leadbetter, J.R. Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. *Nature* 450: 560-566, 2007.
13. **Tringe, S.G.**, Zhang, T., Liu, X., Yu, Y., Lee, W.H., Yap, J., Yao, F., Suan, S.T., Ing, S.K., Haynes, M., Rohwer, F., Wei, C.L., Tan, P., Bristow, J., Rubin, E.M. and Ruan, Y. The airborne metagenome in an urban environment. *PLoS One* 3: e1862, 2008. doi: 10.1371/journal.pone.0001862.
14. Kalyuzhnaya M.G., Lapidus A., Ivanova N., Copeland A.C., McHardy A.C., Szeto E., Salamov A., Grigoriev I.V., Suciú D., Levine S.R., Markowitz V.M., Rigoutsos I., **Tringe S.G.**, Bruce D.C., Richardson P.M., Lidstrom M.E., Chistoserdova L. High-resolution metagenomics targets specific functional types in complex microbial communities. *Nature Biotechnology* 26: 1029-1034, 2008. doi: 10.1038/nbt.1488.
15. **Tringe, S.G.**, Hugenholtz, P. A renaissance for the pioneering 16S rRNA gene. *Current Opinion in Microbiology* 11: 442-446, 2008. doi: 10.1016/j.mib.2008.09.011.
16. Walsh, D.A., Zaikova, E., Howes, C.G., Song, Y.C., **Tringe, S.G.**, Tortell, P.D., Hallam, S.J. Metagenome of a Versatile Chemolithoautotroph from Expanding Oceanic Dead Zones. *Science* 326:578-582, 2009. doi: 10.1126/science.1175309.
17. Duncan, K.E., Gieg, L.M., Parisi, V.A., Tanner, R.S., **Tringe, S.G.**, Bristow, J., Suflita, J.M. Biocorrosive Thermophilic Microbial Communities in Alaskan North Slope Oil Facilities. *Environmental Science & Technology* 43: 7977-7984, 2009. doi: 10.1021/es9013932.
18. Hemme, C.L., Deng, Y., Gentry, T.J., Fields, M.W., Wu, L., Barua, S., Barry, K., **Tringe, S.G.**, Watson, D.B., He, Z., Hazen, T.C., Tiedje, J.M., Rubin, E.M., Zhou, J. Metagenomic Insights into Evolution of a Heavy Metal-Contaminated Groundwater Microbial Community. *ISME Journal* 4: 660-672, 2010. doi: 10.1038/ismej.2009.154.
19. Ivanova, N., **Tringe, S.G.**, Liolios, K., Liu, W.T., Morrison, N., Hugenholtz, P., Kyrpides, N.C. A call for standardized classification of metagenome projects. *Environmental Microbiology* 12: 1803-1805, 2010. doi: 10.1111/j.1462-2920.2010.02270.x.

20. Pope, P.B., Denman, S.E., Jones, M., **Tringe, S.G.**, Barry, K., Malfatti, S.A., McHardy, A.C., Cheng, J.-F., Hugenholtz, P., McSweeney, C.S., Morrison, M. Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. *Proceedings of the National Academy of Sciences* 107: 14793-14798, 2010. doi: 10.1073/pnas.1005297107.
21. Cuvelier, M.L., Allen, A.E., Monier, A., McCrow, J.P., Messie, M., **Tringe, S.G.**, Woyke, T., Welsh, R.M., Ishoey, T., Lee, J.-H., Binder, B.J., Latasa, M., Guigand, C., Buck, K.R., DuPont, C.L., Hilton, J.A., Thiagarajan, M., Caler, E., Lasken, R., Chavez, F.P., Worden, A.Z. Targeted metagenomics and ecology of globally important uncultured eukaryotic phytoplankton. *Proceedings of the National Academy of Sciences* 107: 14679-14684, 2010. doi: 10.1073/pnas.1001665107.
22. Hollister, E.B., Forrest, A.K., Wilkinson, H.H., Ebbole, D.J., Malfatti, S.A., **Tringe, S.G.**, Holtzapple, M.T., Gentry, T.J. Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. *Applied Microbiology and Biotechnology* 88: 389-99, 2010. doi: 10.1007/s00253-010-2789-7.
23. He, S., Wurtzel, O., Singh, K., Froula, J.L., Yilmaz, S., **Tringe, S.G.**, Wang, Z., Chen, F., Lindquist, E.A., Sorek, R., Hugenholtz, P. Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. *Nature Methods* 7: 807-12, 2010. doi: 10.1038/nmeth.1507.
24. Suen, G., Scott, J.J., Aylward, F.O., Adams, S.M., **Tringe, S.G.**, Pinto-Tomás, A.A., Foster, C.E., Pauly, M., Weimer, P.J., Barry, K.W., Goodwin, L.A., Bouffard, P., Li, L., Osterberger, J., Harkins, T.T., Slater, S.C., Donahue, T.J., Currie, C.R. An insect herbivore microbiome with high plant biomass-degrading capacity. *PLoS Genetics* 6: e1001129, 2010. doi: 10.1371/journal.pgen.1001129.
25. Lykidis, A., Chen, C.-L., **Tringe, S.G.**, McHardy, A., Copeland, A., Kyrpides, N.C., Hugenholtz, P., Macarie, H., Olmos, A., Monroy, O. and Liu, W.-T. Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. *ISME Journal* 5: 122-30, 2011. doi: 10.1038/ismej.2010.125.
26. Hess, M., Sczyrba, A., Egan, R., Kim, T.-W., Chokhawala, H., Schroth, G., Luo, S., Clark, D.S., Chen, F., Zhang, T., Mackie, R.I., Pennacchio, L.A., **Tringe, S.G.**, Visel, A., Woyke, T., Wang, Z., Rubin, E.M. Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. *Science* 331: 463-467, 2011. doi: 10.1126/science.1200387.
27. Pope, P.B., Smith, W., Denman, S.E., **Tringe, S.G.**, Barry, K., Hugenholtz, P., McSweeney, C.S., McHardy, A.C., Morrison, M. Isolation of Succinivibrionaceae Implicated in Low Methane Emissions from Tammar Wallabies. *Science* 333: 646-648, 2011. doi: 10.1126/science.1205760.
28. Li, L.L., Taghavi, S., McCorkle, S.M., Zhang, Y.B., Blewitt, M.G., Brunecky, R., Adney, W.S., Himmel, M.E., Brumm P., Drinkwater C., Mead, D.A., **Tringe, S.G.**, van der Lelie, D. Bioprospecting metagenomics of decaying wood: mining for new glycosyl hydrolases. *Biotechnology for Biofuels* 4: 23, 2011. doi: 10.1186/1754-6834-4-23.
29. Gori, F., **Tringe, S.G.**, Kartal, B., Marchiori, E., Jetten, M. The metagenomic basis of anammox metabolism in Candidatus "Brocadia fulgida." *Biochemical Society Transactions* 39: 1799-1804, 2011. doi: 10.1042/BST20110707.
30. Godoy-Vitorino, F., Goldfarb, K.C., Karaoz, U., Leal, S., Garcia-Amado, M.A., Hugenholtz, P., **Tringe, S.G.**, Brodie, E.L., Dominguez-Bello, M.G. Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. *ISME Journal* 6: 531-41, 2012. doi: 10.1038/ismej.2011.131.
31. Berg Miller, M.E., Yeoman, C.J., Chia, N., **Tringe, S.G.**, Angly, F.E., Edwards, R.A., Flint, H.J., Lamed, R., Bayer, E.A., White, B.A. Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. *Environmental Microbiology* 14: 207-227, 2012. doi: 10.1111/j.1462-2920.2011.02593.x.

32. Harhangi, H.R., Le Roy, M., van Alen, T., Hu, B.L., Groen, J., Kartal, B., **Tringe, S.G.**, Quan, Z.X., Jetten, M.S., Op den Camp, H.J. Hydrazine synthase, a unique phylomarker to study the presence and biodiversity of anammox bacteria. *Applied and Environmental Microbiology* 78: 752-758, 2012. doi: 10.1128/AEM.07113-11.
33. Aylward, F.O., Burnum, K.E., Scott, J.J., Suen, G., **Tringe, S.G.**, Adams, S.M., Barry, K.W., Nicora, C.D., Piehowski, P.D., Purvine, S.O., Starrett, G.J., Goodwin, L.A., Smith, R.D., Lipton, M.S., Currie, C.R. Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. *ISME Journal* 6: 1688-1701, 2012. doi: 10.1038/ismej.2012.10.
34. Brisson, V.L., West, K.A., Lee, P.K.H., **Tringe, S.G.**, Brodie, E.L., Alvarez-Cohen, L. Metagenomic Analysis of a Stable Trichloroethene-Degrading Microbial Community. *ISME Journal* 6: 1702-1714, 2012. doi: 10.1038/ismej.2012.15.
35. Mason, O.U., Hazen, T.C., Borglin, S., Chain, P.S.G., Dubinsky, E.A., Fortney, J.L., Han, J., Holman, H.Y.N., Hultman, J., Lamendella, R., Mackelprang, R., Malfatti, S., Tom, L.M., **Tringe, S.G.**, Woyke, T., Zhou, J., Rubin, E.M., Jansson, J.K. Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. *ISME Journal* 6: 1715-1727, 2012. doi: 10.1038/ismej.2012.59.
36. Kozubal, M.A., Macur, R.E., Jay, Z.J., Beam, J.P., Malfatti, S.A., **Tringe, S.G.**, Kocar, B.D., Borch, T., Inskeep, W.P. Microbial iron cycling in acidic geothermal springs of Yellowstone National Park: Integrating molecular surveys, geochemical processes and isolation of novel Fe-active microorganisms. *Frontiers in Microbiology* 3: 109, 2012. doi: 10.3389/fmicb.2012.00109.
37. van de Vossenberg, J., Woebken, D., Maalcke, W.J., Wessels, H.J.C.T., Dutilh, B.E., Kartal, B., Janssen-Megens, E.M., Roeselers, G., Yan, J., Speth, D., Gloerich, J., Geerts, W., van der Biezen, E., Pluk, W., Francoijs, K.J., Russ, L., Lam, P., Malfatti, S.A., **Tringe, S.G.**, Haaijer, S.C.M., Op den Camp, H., Stunnenberg, H.G., Amann, R., Kuypers, M.M.M., Jetten, M.S.M. The metagenome of the marine anammox bacterium "*Candidatus Scalindua profunda*" illustrates the versatility of this globally important nitrogen cycle bacterium. *Environmental Microbiology* 15: 1275-89, 2013. doi: 10.1111/j.1462-2920.2012.02774.x.
38. van der Lelie, D., Taghavi, S., McCorkle, S.M., Li, L.-L., Malfatti, S.A., Monteleone, D., Donohoe, B.S., Ding, S.-Y., Adney, W.S., Himmel, M.E., **Tringe, S.G.** The metagenome of an anaerobic microbial community decomposing poplar wood chips. *PLoS One* 7: e36740, 2012. doi: 10.1371/journal.pone.0036740.
39. Baelum, J., Borglin, S., Chakraborty, R., Fortney, J.L., Lamendella, R., Mason, O.U., Auer, M., Zemla, M., Bill, M., Conrad, M.E., Malfatti, S.A., **Tringe, S.G.**, Holman, H.Y., Hazen, T.C., Jansson, J.K. Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. *Environmental Microbiology* 14: 2405-2416, 2012. doi: 10.1111/j.1462-2920.2012.02780.x.
40. Hollister, E.B., Forrest, A.K., Wilkinson, H.H., Ebbole, D.J., **Tringe, S.G.**, Malfatti, S.A., Holtzapple, M.T., Gentry, T.J. Mesophilic and Thermophilic Conditions Select for Unique but Highly Parallel Microbial Communities to Perform Carboxylate Platform Biomass Conversion. *PLoS ONE* 7: e39689, 2012. doi: 10.1371/journal.pone.0039689.
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42. Gilbert, J., Li, L.L., Taghavi, S., McCorkle, S.M., **Tringe, S.**, van der Lelie, D. Bioprospecting metagenomics for new glycoside hydrolases. *Methods in Molecular Biology* 908: 141-151, 2012. doi: 10.1007/978-1-61779-956-3_14.
43. Worden, A.Z., Janouskovec, J., McRose, D., Engman, A., Welsh, R.M., Malfatti, S., **Tringe, S.G.**, Keeling, P.J. Global distribution of a wild alga revealed by targeted metagenomics. *Current Biology* 22: R675-577, 2012. doi: 10.1016/j.cub.2012.07.054.

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45. Hunt, D.E., Lin, Y., Church, M.J., Karl, D.M., **Tringe, S.G.**, Izzo, L.K., Johnson, Z.I. The relationship between abundance and specific activity of bacterioplankton in open ocean surface waters. *Applied and Environmental Microbiology* 79: 177-84, 2013. doi: 10.1128/AEM.02155-12.
46. Burow, L.C., Woebken, D., Marshall, I. P.G., Lindquist, E.A., Bebout, B.M., Prufert-Bebout, L., Hoehler, T.M., **Tringe, S.G.**, Pett-Ridge, J., Weber, P.K., Spormann, A.M., Singer, S.W. Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. *ISME Journal* 7: 817-829, 2013. doi: 10.1038/ismej.2012.150.
47. Gori, F., **Tringe, S.G.**, Folino, G., van Hijum, S.A.F.T., Op den Camp, H.J.M, Jetten, M.S.M., Marchiori, E. Differences in sequencing technologies improve the retrieval of anammox bacterial genome from metagenomes. *BMC Genomics* 14:7, 2013. doi: 10.1186/1471-2164-14-7.
48. Sentchilo, V., Mayer, A.P., Guy, L., Miyazaki, R., **Tringe, S.G.**, Barry, K., Malfatti, S., Goessman, A., Robinson-Rechavi, M., van der Meer, J.R. Community-Wide Plasmid Gene Mobilization and Selection. *ISME Journal* 7: 1173-1186, 2013.
49. Beck, D.A., Kalyuzhnaya, M.G., Malfatti, S.A., **Tringe, S.G.**, Glavina del Rio, T., Ivanova, N., Lidstrom, M.E., Chistoserdova, L. A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the *Methylococcaceae* and the *Methylophilaceae*. *PeerJ* 1: e23, 2013. doi: 10.7717/peerj.23.
50. DeAngelis, K.M., D'Haeseleer, P.D., Chivian, D., Simmons, B., Arkin, A.P., Mavromatis, K., Malfatti, S., **Tringe, S.**, Hazen, T.C. Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. *Standards in Genomic Sciences* 7:382-398, 2013. doi: 10.4056/sigs.3377516.
51. Peiffer, J.A., Spor, A., Koren, O., Jin, Z., **Tringe, S.G.**, Dangl, J.L., Buckler, E.S., Ley, R.E. Diversity and heritability of the maize rhizosphere microbiome under field conditions. *Proceedings of the National Academy of Sciences* 110: 6548-6553, 2013. doi: 10.1073/pnas.1302837110.
52. He, S., Ivanova, N., Kirton, E., Allgaier, M., Bergin, C., Scheffrahn, R.H., Kyrpides, N.C., Warnecke, F., **Tringe, S.G.**, Hugenholtz, P. Comparative metagenomic and metatranscriptomic analysis of hindgut paunch microbiota in wood-feeding and dung-residing higher termite species (*Nasutitermes corniger* and *Amitermes wheeleri*). *PLOS One* 8: e61126, 2013. doi: 10.1371/journal.pone.0061126.
53. Dodsworth, J.A., Blainey, P.C., Murugapiran, S.K., Swingley, W.D., Ross, C.A., **Tringe, S.G.**, Chain, P.S.G., Raymond, J., Quake, S.R., Hedlund, B.P. Single-cell genomics and metagenomics suggest a fermentative, saccharolytic lifestyle for members of the OP9 lineage. *Nature Communications* 4: 1854, 2013. doi: 10.1038/ncomms2884.
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C. Research Support

Ongoing Research Support

"ECON: Enhancing Camelina Oilseed Production with Minimum Nitrogen Fertilization in Sustainable Cropping Systems," proposal to Department of Energy Systems Biology Research to Advance Sustainable Bioenergy Crops. PI for JGI subcontract, \$2,000,000 over 5 years, start date 9/15/2020.

"Community metabolism and greenhouse gas fluxes in industrial salt ponds pre- and post-restoration" proposal to the Environmental Molecular Sciences Laboratory supporting NMR and organic matter characterization of pond sediment, 10/1/2019-9/30/2021.

"Microbiology of Produced Water Recycling and Reuse" proposal to the Lawrence Berkeley National Laboratory (LBNL) Laboratory Directed Research and Development (LDRD) program. \$200,000 per year, renewable for one year, start date 10/1/2018.

"Systems Analysis of the Physiological and Molecular Mechanisms of Sorghum Nitrogen Use Efficiency, Water Use Efficiency and Interactions with the Soil Microbiome" proposal to Department of Energy Systems Biology Research to Advance Sustainable Bioenergy Crops. PI for JGI subcontract, \$1,007,000 over 5 years, start date 9/15/2015. In no-cost extension through FY21.

Past Research Support

"Molecular underpinnings of methane emissions from unrestored industrial salt ponds" proposal to the Environmental Molecular Sciences Laboratory supporting NMR analyses of pond sediment. 3/15/2019-5/1/2019.

"Next Generation Ecosystem Experiments in the Arctic (NGEE-Arctic)." Proposal to DOE Joint Genome Institute Community Sequencing Program 2013, co-PI Janet Jansson. 10/15/2012-10/15/2015.

"PGRP-GEPR-Defining Plant-Associated Metagenomes" proposal to National Science Foundation, co-PIs Jeff Dangl (University of North Carolina) and Ruth Ley (Cornell University). PI for JGI subcontract, \$1,387,591, 5/6/2010 – 3/31/2015.

"Microbial community impact on carbon sequestration in managed wetland 'carbon farming'" proposal to DOE Joint Genome Institute Community Sequencing Program 2011, co-PIs Susannah Tringe, Mark Waldrop, Lisamarie Windham-Myers and Tanja Woyke. 300 Gb sequence data on Illumina sequencing platform. 11/1/2010-10/31/2013.

“Meta-‘omics’ analysis of microbial carbon cycling responses to altered rainfall inputs in native prairie soils” proposal to DOE Office of Biological and Environmental Research, PI David Myrold. \$65,500 salary support. 6/1/2010-5/31/2013.

“INSPIRE Track 2: Defining the Organizational Principles of Microbial Communities Colonizing Plant Roots” proposal to National Science Foundation, Co-PIs Jeff Dangl (University of North Carolina), Vladimir Jovic, Elizabeth Shank, Pieter Dorrestein and Ruth Ley. PI for JGI subcontract, \$412,436 over 3 years, start date 9/1/2014.

“Microbial communities in biological carbon sequestration.” DOE Early Career Research Program Award. \$2,500,013 over 5 years. Start date 8/15/11. No cost extension to 8/14/17.