

BIOGRAPHICAL SKETCHNAME: **Igor Grigoriev**eRA COMMONS USER NAME: **IVGRIGORIEV**POSITION TITLE: **Adjunct Professor (UC Berkeley), Senior Scientist (Lawrence Berkeley National Laboratory), and Program Head (Joint Genome Institute)****EDUCATION/TRAINING**

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
Moscow Engineering Physics Institute, Russia	B.A./M.S.	02/1994	Biophysics
Research Institute for NII Genetika, Moscow, Russia	Ph.D.	12/1997	Molecular Biology
University of California Berkeley, Berkeley, CA	Postdoc	03/2001	Computational Structural Genomics

A. Personal Statement

My long-standing interests are in computational analyses and predictions for biomolecules from their sequences. During my Ph.D. and postdoctoral studies, I developed methods for protein structure prediction in genome-wide applications. I built gene-finding tools to search for protein kinases in the human genome during my work in biotech/pharma industry (US Patents #20050125852 and #20040009549). At the Joint Genome Institute, my lab developed and used pipelines for genome annotation and analysis. I established a successful program to sequence and annotate over 1500 fungal genomes (mycocosm.jgi.doe.gov) a growing number of algal genomes (phycocosm.jgi.doe.gov), transforming mycology and phycology into genomics-driven fields. I have also been an independent Principal Investigator with several NSF and DOE grants for comparative and functional genomics. I established collaborations with many research labs around the world and lead a group of ~15 employees (including 10 PhD level scientists) focused computational biology and genomics.

I use comparative genomics to identify common principles and mechanisms across different levels of biological diversity. Just in the last four years our collaborative efforts led to three important discoveries: a *new genetic code* (A.1), the *first fungal cellulosome* (A.2), and a *new epigenetic mark* in fungi (A.3) as well as genome-based prediction of fungal pathogens using machine learning (A.4).

- A.1 Riley R, Haridas S, Wolfe KH, Lopes MR, Hittinger CT, Göker M, Salamov AA, Wisecaver JH, Long TM, Calvey CH, Aerts AL, Barry KW, Choi C, Clum A, Coughlan AY, Deshpande S, Douglass AP, Hanson SJ, Klenk HP, LaButti KM, Lapidus A, Lindquist EA, Lipzen AM, Meier-Kolthoff JP, Ohm RA, Otilar RP, Pangilinan JL, Peng Y, Rokas A, Rosa CA, Scheuner C, Sibirny AA, Slot JC, Stielow JB, Sun H, Kurtzman CP, Blackwell M, **Grigoriev IV**, Jeffries TW. (2016) Comparative genomics of biotechnologically important yeasts. *Proc Natl Acad Sci U S A*. 113(35):9882-9887.
- A.2 Haitjema C, Gilmore S, Henske J, Solomon K, de Groot R, Kuo K, Mondo S, Salamov A, LaButti K, Zhao Z, Chiniquy J, Barry K, Brewer H, Purvine S, Wright A, Hainaut M, Boxma B, van Alen T, Hackstein J, Henrissat B, Baker S, **Grigoriev IV**, O'Malley M (2017) A parts list for fungal cellulosomes revealed by comparative genomics. *Nature Microbio*. 2:17087.
- A.3 Mondo SJ, Dannebaum RO, Kuo RC, Louie KB, Bewick AJ, LaButti K, Haridas S, Kuo A, Salamov A, Ahrendt SR, Lau R, Bowen BP, Lipzen A, Sullivan W, Andreopoulos BB, Clum A, Lindquist E, Daum C, Northen TR, Kunde-Ramamoorthy G, Schmitz RJ, Gryganskyi A, Culley D, Magnuson J, James TY, O'Malley MA, Stajich JE, Spatafora JW, Visel A, **Grigoriev IV**. (2017) Wide-spread adenine N6-methylation of active genes in fungi. *Nature Genet*. 49(6):964-968.
- A.4 Haridas S, Albert R, Binder M, Bloem J, LaButti K, Salamov A, Andreopoulos B, Baker SE, Barry K, Bills G, Bluhm BH, Cannon C, Castanera R, Culley DE, Daum C, Ezra D, González JB, Henrissat B, Kuo A, Liang C, Lipzen A, Lutzoni F, Magnuson J, Mondo SJ, Nolan M, Ohm RA, Pangilinan J, Park HJ, Ramírez L, Alfaro M, Sun H, Tritt A, Yoshinaga Y, Zwiers LH, Turgeon BG, Goodwin SB, Spatafora JW, Crous PW, **Grigoriev IV**. (2020) 101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. *Stud Mycol*. 96:141-153.

B. Positions and Honors

Positions and Employment

- 1996-98 **Junior Scientist**, Bioinformatics Dept., State Research Institute NII Genetika, Moscow, Russia,
1998-01 **Postdoctoral Fellow**, Department of Chemistry, University of California, Berkeley, CA
2001-03 **Bioinformatics Scientist**, Sugen Inc./Pharmacia Corp./Pfizer, South San Francisco, CA,
2003-09 **Group Leader**, Genome Annotation, Joint Genome Institute, Walnut Creek, CA
2010-17 **Staff Scientist**, Lawrence Berkeley Laboratory, Berkeley, CA
2009-- **Head**, Fungal and Algal Program, Joint Genome Institute, Walnut Creek/Berkeley, CA
2013-- **Adjunct Professor**, Department of Plant & Microbial Biology, University of California, Berkeley, CA
2017-- **Senior Staff Scientist**, Lawrence Berkeley Laboratory, Berkeley, CA

Honors and Awards

- 1992 Gold Medal, World Computer Olympiad (Artificial Intelligence), London UK
2012 Berkeley Lab Director's Award for Exceptional Achievements in Science
2014-- Highly Cited Researcher, top 1% (Thomson Reuters, 2014-16; Web of Science, 2017-2019)

Other Experience

- 2003-- Organizer of over 50 genomics workshops
2009-- Reviewer for *Science*, *Nature*, *Genome Research*, *Genome Biology*, *BMC* and *PLoS* journals
2009-- Grant Proposal Reviewer (GIS IBISA-France, 2009; NIH Study Section, 2013; KAUST, 2017)
2013 Guest Editor for *PLoS Genetics*
2014-- Editorial Board of *BMC Fungal Biology and Biotechnology*
2015-- Editorial Board of *AIMS Microbiology*
2015-2016 Guest Editor *Frontiers in Microbiology*
2017-2018 Co-editor, *Fungal Genomics, Methods in Molecular Biology* (Elsevier)

C. Contribution to Science

Over 250 publications including 10 book chapters and 2 patents cited over 46,050 times (H-index = 86) according to Google Scholar (https://scholar.google.com/citations?user=Z_xp9ngAAAAJ&hl=en).

1. Filling gaps in the Tree of Life with genome information is critical to explore the molecular basis of complexity, diversity and evolutionary history of eukaryotes. We sequenced and analyzed many first-of-its-kind genomes including the first genome of a tree (poplar) cited over 3,000 times, and ancient plants; the first amoeboid flagellate (1.a), choanoflagellate (1.b), crustacean (1.c), and diverse metazoa; the first haptophyte (1.d) and diverse algae; fungi including early diverging sequenced from single cells (1.e), and protists. Collectively, these provide a unique resource for comparative analysis of eukaryotic genomes.

- 1.a Fritz-Laylin LK, Prochnik SE, Ginger ML, Dacks JB, Carpenter ML, Field MC, Kuo A, Paredez A, Chapman J, Pham J, Shu S, Neupane R, Cipriano M, Mancuso J, Tu H, Salamov A, Lindquist E, Shapiro H, Lucas S, **Grigoriev IV**, Cande WZ, Fulton C, Rokhsar DS, Dawson SC. (2010) The genome of *Naegleria gruberi* illuminates early eukaryotic versatility. *Cell*. 140(5):631-642.
- 1.b King N, Westbrook MJ, Young SL, Kuo A, Abedin M, Chapman J, Fairclough S, Hellsten U, Isogai Y, Letunic I, Marr M, Pincus D, Putnam N, Rokas A, Wright KJ, Zuzow R, Dirks W, Good M, Goodstein D, Lemons D, Li W, Lyons JB, Morris A, Nichols S, Richter DJ, Salamov A, Sequencing JG, Bork P, Lim WA, Manning G, Miller WT, McGinnis W, Shapiro H, Tjian R, **Grigoriev IV**, Rokhsar D. (2008) The genome of the choanoflagellate. *Nature*. 451, 783-788.
- 1.c Colbourne JK, Pfrender ME, Gilbert D, Thomas WK, Tucker A, Oakley TH, Tokishita S, Aerts A, Arnold GJ, Basu MK, Bauer DJ, Cáceres CE, Carmel L, Casola C, Choi JH, Detter JC, Dong Q, Dusheyko S, Eads BD, Fröhlich T, Geiler-Samerotte KA, Gerlach D, Hatcher P, Jogdeo S, Krijgsveld J, Kriventseva EV, Kültz D, Laforsch C, Lindquist E, Lopez J, Manak JR, Muller J, Pangilinan J, Patwardhan RP, Pitluck S, Pritham EJ, Rechtsteiner A, Rho M, Rogozin IB, Sakarya O, Salamov A, Schaack S, Shapiro H, Shiga Y, Skalitzky C, Smith Z, Souvorov A, Sung W, Tang Z, Tsuchiya D, Tu H, Vos H, Wang M, Wolf YI, Yamagata H, Yamada T, Ye Y, Shaw JR, Andrews J, Crease TJ, Tang H, Lucas SM, Robertson HM, Bork P, Koonin EV, Zdobnov EM, **Grigoriev IV**, Lynch M, Boore JL. (2011) The ecoresponsive genome of *Daphnia pulex*. *Science*. 331(6017):555-561.
- 1.d Read B, Kegel J, Klute M, Kuo A, Lefebvre SC, Maumus F, Mayer C, Miller J, Monier A, Salamov A, Young J, Aguilar M, Claverie JM, Frickenhaus S, Gonzalez K, Herman EK, Lin YC, Napier J, Ogata H, Sarno AF, Shmutz J, Schroeder D, de Vargas C, Verret F, von Dassow P, Valentin K, Van de Peer Y,

Wheeler G; *Emiliania huxleyi* Annotation Consortium, Dacks JB, Delwiche CF, Dyhrman S, Glockner G, John U, Richards T, Worden AZ, Zhang X, **Grigoriev IV**. (2013) Pan-genome of the phytoplankton *Emiliania* underpins its global distribution. *Nature*, 499(7457):209-213.

- 1.e Ahrendt SR, Quandt CA, Ciobanu D, Clum A, Salamov A, Andreopoulos B, Cheng JF, Woyke T, Pelin A, Henrissat B, Reynolds NK, Benny GL, Smith ME, James TY, **Grigoriev IV**. (2018) Leveraging single-cell genomics to expand the fungal tree of life. *Nature Microbiol.* 3(12):1417-1428.

2. Principles of genome organization and evolution have been derived from comparative genomics of diverse eukaryotes. We observed dramatic expansions of transposons and gene families as well as whole-genome duplications (2.a). We proposed auxiliary and dispensable chromosomes in fungi and algae to be the keys to species evolution and pathogenicity (2.b, 2.c). We also reported transfers of genes and genome fragments between and within chromosomes (2.c), between cellular compartments (2.d), and between species and domains of life (A.2). In addition, algal genomes displayed introners, non-canonical splice sites, and overlapping genes (1.d, 2.b).

- 2.a Corrochano LM, Kuo A, Marcet-Houben M, Polaino S, Salamov A, Villalobos-Escobedo JM, Grimwood J, Álvarez MI, Avalos J, Bauer D, Benito EP, Benoit I, Burger G, Camino LP, Cánovas D, Cerdá-Olmedo E, Cheng JF, Domínguez A, Eliáš M, Eslava AP, Glaser F, Gutiérrez G, Heitman J, Henrissat B, Iturriaga EA, Lang BF, Lavín JL, Lee SC, Li W, Lindquist E, López-García S, Luque EM, Marcos AT, Martin J, McCluskey K, Medina HR, Miralles-Durán A, Miyazaki A, Muñoz-Torres E, Oguiza JA, Ohm RA, Olmedo M, Orejas M, Ortiz-Castellanos L, Pisabarro AG, Rodríguez-Romero J, Ruiz-Herrera J, Ruiz-Vázquez R, Sanz C, Schackwitz W, Shahriari M, Shelest E, Silva-Franco F, Soanes D, Syed K, Tagua VG, Talbot NJ, Thon MR, Tice H, de Vries RP, Wiebenga A, Yadav JS, Braun EL, Baker SE, Garre V, Schmutz J, Horwitz BA, Torres-Martínez S, Idnurm A, Herrera-Estrella A, Gabaldón T, **Grigoriev IV**. (2016) Expansion of signal transduction pathways in fungi by extensive genome duplication. *Curr Biol.* 26(12): 1577-1584.

- 2.b Worden AZ, Lee JH, Mock T, Rouze P, Simmons MP, Aerts A, Allen AE, Cuvelier ML, Derelle E, Everett MV, Foulon E, Grimwood J, Gundlach H, Henrissat B, Napoli C, McDonald SM, Parker MS, Rombauts S, Salamov A, Von Dassow P, Badger JH, Coutinho PM, Demir E, Dubchak I, Gentemann C, Eikrem W, Gready JE, John U, Lanier W, Lindquist EA, Luks S, Mayer KFX, Moreau H, Not F, Otilar R, Panaud O, Pangilinan J, Paulsen I, Piegu B, Poliakov A, Robbens S, Schmutz J, Toulza E, Wyss T, Zelensky A, Zhou K, Armbrust EV, Bhattacharya D, Goodenough UW, Van de Peer Y & **Grigoriev IV** (2009) Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes *Micromonas*. *Science*. 324:268-272.

- 2.c Ohm RA, Feau N, Henrissat B, Schoch CL, Horwitz BA, Barry KW, Condon BJ, Copeland AC, Dhillon B, Glaser F, Hesse CN, Kosti I, Labutti K, Lindquist EA, Lucas S, Salamov AA, Bradshaw RE, Ciuffetti L, Hamelin RC, Kema GH, Lawrence C, Scott JA, Spatafora JW, Turgeon BG, de Wit PJ, Zhong S, Goodwin SB, **Grigoriev IV**. (2012) Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen *Dothideomycetes* fungi. *PLoS Pathog.* 8(12):e1003037

- 2.d Curtis BA, Tanifuji G, Burki F, Gruber A, Irimia M, Maruyama S, Arias MC, Ball SG, Gile GH, Hiraoka Y, Hopkins JF, Kuo A, Rensing SA, Schmutz J, Symeonidi A, Elias M, Eveleigh RJ, Herman EK, Klute MJ, Nakayama T, Oborník M, Reyes-Prieto A, Armbrust EV, Aves SJ, Beiko RG, Coutinho P, Dacks JB, Durnford DG, Fast NM, Green BR, Grisdale CJ, Hempel F, Henrissat B, Höppner MP, Ishida KI, Kim E, Kořený L, Kroth PG, Liu Y, Malik SB, Maier UG, McRose D, Mock T, Neilson JA, Onodera NT, Poole AM, Pritham EJ, Richards TA, Rocap G, Roy SW, Sarai C, Schaack S, Shirato S, Slamovits CH, Spencer DF, Suzuki S, Worden AZ, Zauner S, Barry K, Bell C, Bharti AK, Crow JA, Grimwood J, Kramer R, Lindquist E, Lucas S, Salamov A, McFadden GI, Lane CE, Keeling PJ, Gray MW, **Grigoriev IV**, Archibald JM. (2012) Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. *Nature*. 492(7427): 59-65.

3. Fungal genomics for bioenergy is one of the focus areas of our research. For bioenergy production, fungi are efficient decomposers of plant biomass and sugar fermenters. Fungal symbionts and pathogens determine a sustainable growth of biofuel feedstocks. We led comparative genomics of large groups of plant biomass decomposers (3.a-3.c), yeast species specializing on different sugars from plant biomass (A.2), plant symbionts (3.d) and pathogens (A.4; 2.c). In addition to building comprehensive catalogs of genes, pathways, and hosts, these analyses demonstrated interesting cases of gene family evolution including conservation of biological mechanisms and convergent evolution (3.a; 3.d).

- 3.a Floudas D, Binder M, Riley R, Barry K, Blanchette RA, Henrissat B, Martínez AT, Otilar R, Spatafora JW, Yadav JS, Aerts A, Benoit I, Boyd A, Carlson A, Copeland A, Coutinho PM, de Vries RP, Ferreira P, Findley K, Foster B, Gaskell J, Glotzer D, Górecki P, Heitman J, Hesse C, Hori C, Igarashi K, Jurgens JA, Kallen N, Kersten P, Khajamohiddin A, Kohler A, Kues U, Kumar TKA, Kuo A, LaButti K, Larrondo LF, Lindquist E, Ling A, Lucas S, Lundell T, Martin R, McLaughlin DJ, Morgenstern I, Morin E, Murat C, Nolan M, Ohm RA, Patyshakuliyeva A, Rokas A, Ruiz-Dueñas FJ, Sabat G, Salamov A, Samejima M, Schmutz J, Slot JC, John FS, Stenlid J, Sun H, Sun S, Tsang A, Wiebenga A, Young D, Pisabarro A, Eastwood DC, Martin F, Cullen D, **Grigoriev IV**, Hibbett DS (2012) The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 1.d fungal genomes. **Science**. 336(6089):1715-1719.
- 3.b Riley R, Salamov AA, Brown DW, Nagy LG, Floudas D, Held BW, Lévasséur A, Lombard V, Morin E, Otilar R, Lindquist EA, Sun H, LaButti KM, Schmutz J, Jabbour D, Luo H, Baker SE, Pisabarro AG, Walton JD, Blanchette RA, Henrissat B, Martin F, Cullen D, Hibbett DS, **Grigoriev IV**. (2014) Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. **Proc Natl Acad Sci U S A**. 111(27):9923-9928.
- 3.c Solomon KV, Haitjema CH, Henske JK, Gilmore SP, Borges-Rivera D, Lipzen A, Brewer HM, Purvine SO, Wright AT, Theodorou MK, **Grigoriev IV**, Regev A, Thompson DA, O'Malley MA (2016) Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. **Science**. 351(6278):1192-1195.
- 3.d Kohler A, Kuo A, Nagy LG, Morin E, Barry KW, Buscot F, Canbäck B, Choi C, Cichocki N, Clum A, Colpaert J, Copeland A, Costa MD, Doré J, Floudas D, Gay G, Girlanda M, Henrissat B, Herrmann S, Hess J, Högberg N, Johansson T, Khouja HR, LaButti K, Lahrmann U, Lévasséur A, Lindquist EA, Lipzen A, Marmeisse R, Martino E, Murat C, Ngan CY, Nehls U, Plett JM, Pringle A, Ohm RA, Perotto S, Peter M, Riley R, Rineau F, Ruytinx J, Salamov A, Shah F, Sun H, Tarkka M, Tritt A, Veneault-Fourrey C, Zuccaro A; Mycorrhizal Genomics Initiative Consortium, Tunlid A, **Grigoriev IV**, Hibbett DS, Martin F. (2015) Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. **Nature Genet**. 47(4):410-415.

4. Multi-omics exploration of genome function and regulation. We discovered new transcription factors and regulatory cascades in model fungus *Neurospora crassa* with Fungal ENCODE project (4.a; 4.b). Combining comparative genomics with metabolomics of *Aspergillus* species we decoded synthesis of natural products (4.c). Differential expression of *Daphnia* genes (1.c) and of alleles in diatom *Fragilariopsis cylindrus* (4.d) illustrated genome responses to environmental perturbations. We also studied roles of 5mC or 6mA DNA methylations in gene regulation in early diverging fungi (A.3; 4.e).

- 4.a Hurley JM, Dasgupta A, Emerson JM, Zhou X, Ringelberg CS, Knabe N, Lipzen AM, Lindquist EA, Daum CG, Barry KW, **Grigoriev IV**, Smith KM, Galagan JE, Bell-Pedersen D, Freitag M, Cheng C, Loros JJ, Dunlap JC.(2014) Analysis of clock-regulated genes in *Neurospora* reveals widespread posttranscriptional control of metabolic potential. **Proc Natl Acad Sci U S A**. 111(48):16995-7002.
- 4.b Wu VW, Thieme N, Huberman LB, Dietschmann A, Kowbel DJ, Lee J, Calhoun S, Singan VR, Lipzen A, Xiong Y, Monti R, Blow MJ, O'Malley RC, **Grigoriev IV**, Benz JP, Glass NL. (2020) The regulatory and transcriptional landscape associated with carbon utilization in a filamentous fungus. **Proc Natl Acad Sci U S A**. 117(11):6003-6013.
- 4.c Kjærboelling I, Vesth TC, Frisvad JC, Nybo JL, Theobald S, Kuo A, Bowyer P, Matsuda Y, Mondo S, Lyhne EK, Kogle ME, Clum A, Lipzen A, Salamov A, Ngan CY, Daum C, Chiniquy J, Barry K, LaButti K, Haridas S, Simmons BA, Magnuson JK, Mortensen UH, Larsen TO, **Grigoriev IV**, Baker SE, Andersen MR. (2018) Linking secondary metabolites to gene clusters through genome sequencing of six diverse *Aspergillus* species. **Proc Natl Acad Sci U S A**. 115(4):E753-E761.
- 4.d Mock T, Otilar RP, Strauss J, McMullan M, Paajanen P, Schmutz J, Salamov A, Sanges R, Toseland A, Ward BJ, Allen AE, Dupont CL, Frickenhaus S, Maumus F, Veluchamy A, Wu T, Barry KW, Falciatore A, Ferrante MI, Fortunato AE, Glöckner G, Gruber A, Hipkin R, Janech MG, Kroth PG, Leese F, Lindquist EA, Lyon BR, Martin J, Mayer C, Parker M, Quesneville H, Raymond JA, Uhlig C, Valas RE, Valentin KU, Worden AZ, Armbrust EV, Clark MD, Bowler C, Green BR, Moulton V, van Oosterhout C, **Grigoriev IV**. (2017) Evolutionary genomics of the cold-adapted diatom *Fragilariopsis cylindrus*. **Nature**. 541(7638):536-540.
- 4.e Bewick AJ, Hofmeister BT, Powers RA, Mondo SJ, **Grigoriev IV**, James TY, Stajich JE, Schmitz RJ. (2019) Diversity of cytosine methylation across the fungal tree of life. **Nature Ecol Evol**. 3(3):479-490.

5. Genomic tools for bioengineering applications. Genomic blueprint provides parts list for biological engineering. After finding genes involved in xylose-fermenting yeast *Pichia stipitis* (5.a) we contributed to

engineering of xylose-fermenting *S.cerevisiae* strains (5.b) and expanded the catalog of genes and pathways involved in the fermentation of other sugars (A.1). We explored fungal thermophiles as potential hosts for industrial applications (5.c). Along with transposon mutagenesis in oleaginous *Rhodospiridium turrloides* (5.d) and interspecific yeast hybrid (5.e), these examples illustrate our experience in engineering eukaryotic genomes.

- 5.a Jeffries TW, **Grigoriev IV**, Grimwood J, Laplaza JM, Aerts A, Salamov A, Schmutz J, Lindquist E, Dehal P, Shapiro H, Jin YS, Passoth V, Richardson PM. (2007) Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast *Pichia stipitis*. **Nature Biotechnol.** 25(3):319-26.
- 5.b Wohlbach DJ, Kuo A, Sato TK, Potts KM, Salamov AA, Labutti KM, Sun H, Clum A, Pangilinan JL, Lindquist EA, Lucas S, Lapidus A, Jin M, Gunawan C, Balan V, Dale BE, Jeffries TW, Zinkel R, Barry KW, **Grigoriev IV**, Gasch AP. (2011) Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. **Proc Natl Acad Sci U S A.** 108(32):13212-13217.
- 5.c Berka RM, **Grigoriev IV**, Otilar R, Salamov A, Grimwood J, Reid I, Ishmael N, John T, Darmond C, Moisan MC, Henrissat B, Coutinho PM, Lombard V, Natvig DO, Lindquist E, Schmutz J, Lucas S, Harris P, Powlowski J, Bellemare A, Taylor D, Butler G, de Vries RP, Allijn IE, van den Brink J, Ushinsky S, Storms R, Powell AJ, Paulsen IT, Elbourne LD, Baker SE, Magnuson J, Laboissiere S, Clutterbuck AJ, Martinez D, Wogulis M, de Leon AL, Rey MW, Tsang A. (2011) Comparative genomic analysis of the thermophilic biomass-degrading fungi *Myceliophthora thermophila* and *Thielavia terrestris*. **Nature Biotechnol.** 29(10):922-927.
- 5.d Coradetti ST, Pinel D, Geiselman G, Ito M, Mondo S, Reilly MC, Cheng YF, Bauer S, **Grigoriev IV**, Gladden JM, Simmons BA, Brem R, Arkin AP, Skerker JM. (2018) Functional genomics of lipid metabolism in the oleaginous yeast *Rhodospiridium toruloides*. **Elife.** 7. pii: e32110.
- 5.e Weiss CV, Roop JI, Hackley RK, Chuong JN, **Grigoriev IV**, Arkin AP, Skerker JM, Brem RB. (2018) Genetic dissection of interspecific differences in yeast thermotolerance. **Nature Genet.** 50(11):1501-1504.

D. Research Support

Ongoing Research Support

#DE-AC02-05CH11231 (Mouncey, N., Director) 10/01/2019 – 09/30/2020 (ongoing)

Department of Energy Office of Science

The DOE Joint Genome Institute

Goals: JGI is a national user facility for large-scale, cost effective genome sequencing and DNA synthesis of genes that are of DOE mission importance and to make a significant contribution to genomic sciences.

#DEB 1456588 (Hibbett, D – Lead PI; Grigoriev, I – Co-PI) 04/01/2015 – 3/31/2021

National Science Foundation

Evolution of complex morphologies in the mushroom-forming fungi (Agaricomycetes): a comparative phylogenetic, phylogenomic, and developmental approach

Goals: Investigate genetic mechanisms of developmental and morphological evolution in Agaricomycetes to provide baseline information on the mechanisms of fungal development and gene regulation

#NL/DE-EE0032266/WBS1.3.2.110 (Grigoriev, I - PI) 10/01/2016 – 09/30/2022

Department of Energy Office of Energy Efficiency & Renewable Energy/BioEnergy Technology Office

Genetic blueprint of microalgae carbon productivity

Goals: Develop functional genomics pipeline to produce multi-omics data sets, metabolic model, and gene targets for improving industrial algal strains

#DE-SC0016365 (Bruns, T – Lead PI; Grigoriev, I - Co-PI) 07/01/2016 – 06/30/2020

Department of Energy Office of Science

Determination of the roles of pyrophilous microbes in the breakdown and sequestration of pyrolyzed forms of SOM

Goals: Dissect the effects of microbes on post-fire soil carbon dynamics by using experimental “pyrocosms”, highly controlled production of ¹³C-labeled pyrolyzed substrates, multi-omics, and stable isotope techniques

#DE-SC0020351 (Whitman, T- Lead PI, Grigoriev, I – Co-PI) 07/01/2019 – 06/30/2022

Department of Energy Office of Science

Title: *Dissection of carbon and nitrogen cycling in post-fire soil environments using a genome-informed experimental community*

Goals: Assess the interaction between N availability and PyOM mineralization by post-fire microbial communities and define the network of microbial interactions that facilitate PyOM breakdown over time

#DE-SC0019357 (Schilling J- Lead PI, Grigoriev, I – Co-PI)

10/01/2018 – 09/30/2021

Department of Energy Office of Science

Title: Gene regulatory networks enabling fungi to selectively extract sugars from lignocellulose

Goals: Brown rot-specific gene regulation patterns will be identified and characterized, enabling in vivo manipulations such as CRISPR/Cas9 and metabolomics to map metabolite expression feedback over time, producing an integrated regulatory model for brown rot fungi

Completed Research Support (during the past three years)

#DEB-1354625 - (James, T - PI)

03/01/2014 – 02/28/2018

National Science Foundation

Unveiling the diversity and ecological role of the obligate parasitic fungi in phylum Cryptomycota

Goals: Investigate the biological and genetic diversity of a recently discovered group of fungi known as Cryptomycota, abundant in the environment DNA, using microscopy and single cell genomics methods

#IOS 1456958 (Grigoriev, I - PI)

04/01/2015 – 3/31/2020

National Science Foundation

Collaborative Research: Functional and evolutionary bases of substrate- specificity in wood-decaying basidiomycetes

Goals: Study mechanisms of substrate specificity in wood-decaying Agaricomycetes using analyses of genes expressed during decay and physical/chemical characterization of the decay process