

# **Curriculum Vitae**

## **Gerald K. Sims**

*Department of Entomology Plant Pathology and Weed Science, New Mexico State University,  
Las Cruces, NM 88003, gksims@nmsu.edu*

### **Education/Training**

B.S., McNeese State University, 1978  
M.S., Louisiana State University, 1981, thesis title: *Associative dinitrogen fixation (acetylene reduction) on grasses of Louisiana*  
Ph.D., Purdue University, 1985, thesis title: *Degradation of pyridine derivatives by soil microorganisms*  
Mediator Training, Dept. Health and Human Services, Washington, DC, 1994  
Congressional Briefing Training, Government Affairs Institute, Georgetown University, 2004  
USDA-ARS Leader Training, Beltsville, MD, 2004  
Research Position Evaluation System Training, Beltsville, 2004  
Leadership Laboratory, Growth Dynamics, Albany, CA, 2005  
Advancing Leaders Program, New Mexico State University, 2013-2014  
Lead21, Leadership Course, 2014-2015

### **Current Position**

2012-present Professor and Department Head, Entomology Plant Pathology and Weed Science,  
New Mexico State University

### **Past Experience**

1985-1990 Assistant Professor, Department of Agronomy, Ohio State University  
1988, 1989 Visiting Scientist, Laboratory for Soil Microbiology, Pennsylvania State Univ.  
1990-1992 Project Leader, Dow Chemical, Midland, MI  
1990-1993 Adjunct faculty, Department of Agronomy, Ohio State University  
1992-2003 Microbiologist, USDA-ARS, Urbana, IL  
1992--2014 Joint Faculty Appointments, Dept. Crop Sciences, Dept. Natural Resources and Environ. Sci., UIUC  
2003-2012 Supvy. Microbiologist (Research Leader), USDA-ARS, Urbana, IL  
2007 (AUG-NOV) Acting National Program Leader, USDA-ARS, Beltsville, MD,  
2007 (SEP-NOV) Interim Director, Overseas Biological Control Laboratories (France, Australia, Argentina, China), USDA-ARS

### **Accomplishments-Service**

#### **NMSU Service**

Take a Microbe to Lunch: Nuances of Dining on Pesticides, ACES seminar, Aug 29, 2013

Environmental Microbiology: Gleaning Goodness from Garbage, PES seminar, Sept 6, 2013.  
2013 Regional ESA meeting welcome talk, Feb 25, 2013.  
2013 New Mexico Chile Conference welcome talk Feb 4, 2013.  
Display for Mayfield High School, Community Math and Science Night.  
Judge for the Southwest NM Regional Science and Engineering Fair  
Assisted development of entomology curriculum for Science Olympiad, Socorro, NM Tech.  
Assisted with Insect Expo at SW Regional ESA meeting.  
Developed Fright Night film festival series (2013-present).  
Search Committee, Environmental Soil Microbiology, Plant and Environmental Sciences, 2015.  
Search Committee, Soil Pedology, Plant and Environmental Sciences, 2016.  
Member Faculty Grievance Review Board, 2014-2016.

### **ARS Service**

#### **Location**

Safety (SHEM) Committee Member (1993; 2000-2002)  
Safety (SHEM) Committee Chair (1994-1996, 2001-2003)  
EEO committee (1994-1995)

#### **National**

Participant “Critical Issues for ARS Weed Science”, Beltsville, 6/5-7/1995  
Participant “Reducing Pesticide Risk” (NPS Workshop), 12/2-4/1997  
Served on Midwest Area Performance Review panel, NCAUR, Peoria, IL (10/21/1997)  
Representative for ARS to UIUC job fairs (1995, 1996; 1998-2008)  
Served as mediator (binding arbitration), ARS Coop Resolution program (two cases, 1997)  
Served in site review, NCSCRL, Morris, MN (5/21/1998)  
Member, Selection Committee, Microbiologist (2001)  
Chair, Selection Committee, Ecologist/Plant Physiologist/Agronomist (2003)  
Project Manager, demolition of an ARS farm building (2003)  
Chair, Selection Committee, Ecologist/Plant Physiologist/Agronomist (2004)  
Co-moderator, USDA National Program in Crop Protection and Quarantine Stakeholder Workshop, Miami (5/2008)  
Co-editor, USDA National Program in Crop Protection and Quarantine Action Plan (2008)

### **UIUC Service (awarded the UI College of ACES Service Recognition Award, 2007)**

#### **Department**

Agronomy Day Committee (1992-1995)  
Safety and Health Committee, Agronomy Dept. (1993-1995)  
Seminar Committee, Agronomy Dept. (1994-1996)  
Seminar Committee, NRES Dept. (1996-1997)

#### **University**

Howard Hughes (HHMI) UI Undergraduate Research Fellows Selection Committee (1999-2005)  
Graduate Policy Committee, Dept. NRES (2002-2004)  
Social Committee, Dept. NRES (2002-2004)

### **College**

UI ACES Open House Committee (2002-2004)  
Faculty Mentor Committees (service on three committees, 2001-present)  
Search Committee, Soil Microbiology Faculty Position, Dept. NRES (2004-2005)  
Space and Facilities Committee, Dept. Crop Sciences (2004-present)  
Awards and Recognition Committee, Dept. Crop Sciences (2004-present)  
Discussion panel member, Illinois Conference on Soil and Water Science: Our Science and Society, 16-Sept-2008, Mahomet, Illinois.

### **Professional Service**

#### **Regional**

CSRS-NCR-59 Technical Committee (Soil Organic Matter), 1985-1990 (Secretary, 1989-1990)

#### **National**

Membership Committee (National), American Society of Agronomy, 1986-1991  
Liaison, American Society of Agronomy/American Society for Microbiology, 1990-1993  
Environmental Quality Research Award Committee, American Society of Agronomy, 1992-1994  
ASA, SSSA session chair (Divisions S-3, S-4, A-5, S-11), 1990, 1992, 1995, 1998.  
Organizer, SSSA Symposium (S-2, S-3, S-11), "Nature and bioavailability of bound residues", 1992.  
Presiding Officer, C,N,P Transformations, Joint S-1/S-3 Symposium, Soil Science Society of American Annual Meeting, October 16, 1995.  
Coordinator, SSSA Symposium (S-9, S-11), "Characterization of clays and inorganic contaminants in soils", 1995.  
Soil Science Society of America Book Series Committee, 1992-1995  
Member, Book Feasibility Committee, Soil Science Society of America 1995-1996  
Chair, Book Feasibility Committee, Soil Science Society of America 1996-1997  
Organizer, SSSA Symposium (S-2, S-3, S-11), "Biodegradation of xenobiotics in soil: factors controlling kinetics", 1998.  
Panel member for pesticide fate, Water Quality and Management National Program Review, USDA-ARS, 3-6-Aug-1999.  
Expert Judge, The National Science Olympiad, 2005.  
Mentor, American Society for Microbiology Minority Mentorship Program, 2005-present.  
Minority mentors' representative, ASM 2006 General Meeting, Orlando FL, May 21-25, 2005.  
Environmental Quality Research Award Committee, American Soc. Agronomy, 2006-2008.  
Mentoring Committee, Society for Environmental Toxicology and Chemistry, 2007-present.  
Professional Awards Committee, Soc. for Environmental Toxicol. and Chemistry, 2007-present.  
Member, Charles Clark Award Committee, SSSA, 2015-present.  
Member, SSSA Research Award Committee, 2015-2016.  
Chair, SSSA Research Award Committee, 2015-present.

#### **International**

Agriculture and Food Editor, Encyclopedia of Earth, 2007-present.  
Editorial Board, International Journal of Agronomy, 2008-present.

Scientific Board for, Behnassi, M, Draggan, S, and Yaya, S (Eds.). 2011. Global food insecurity: Rethinking agricultural and rural development paradigm and policy, 1st Edition. Springer. 408 p. ISBN: 978-94-007-0889-1.

Scientific Board, Behnassi, M, Shahid, S.A., and D'Silva, J. (Eds.). 2011. Sustainable agricultural development: Recent approaches in resources management and environmentally-balanced production enhancement, 1st Edition. Springer. 278 p. ISBN: 978-94-007-0518-0.

Editorial Board, Journal of Bioremediation & Biodegradation.

Editorial Board for Oilseeds Crops: Agronomy, Science, and Technology, by Mohamed Fawzy Ramadan Hassanien, Guest Editors: Mohamed Fawzy Ramadan Hassanien, Sascha Rohn, Hesham Farouk Oraby, Bertrand Matthäus, and Abdalbasit Adam Mariod. Published by the International Journal of Agronomy.

*Other editing/reviewing.* J. Environ. Qual., Soil Sci. Soc. of Am. J., Soil Science, Soil Biol. and Biochem., J. Soil and Water Conservation, ASTM, Canadian J. Microbiol., Microbial Ecology, FEMS Microbial Ecology, Appl. Environ. Microbiol., J. Agric. Food Chem., Environ. Sci. and Technol., Marcel Dekker, John Wiley, Letters in Applied Microbiology. Proposals reviewed for International Science and Technology Center, National Science Foundation, BARD, USGS, USDA, NSF, Waste Materials Research Center, Illinois Groundwater Consortium, Auburn Univ., Univ. Delaware, and the Univ. Illinois.

### **Host for Visiting Scholars**

Ze'ev Ronan, Israel, 1989

Rambale Ankumah, Tuskegee University, 1996

Tammera Minnick, USA, 2008

Hao Zhang, China, 2008

Andres Gomez, Columbia, 2010

### **Consulting**

National Geographic Magazine; Reilly Tar and Chemical Co; ENSR (feasibility for natural attenuation of pyridine-contaminated aquifer, USEPA Superfund site No. IN000807107); Champaign City Council; Field Museum of Natural History; Mexico City Pollution Prevention and Control Office; International Ingredient Corp.; Chicago Dept. of Health; DuPont de Nemours, UK Central Science Laboratory (EBGM, York), Biotechnology Institute, Univ. Beijing (China), Georgia Academy of Science, Pict Sweet Foods, University of Vermont. New Mexico Secretary of Education (bark beetle research), University of Vermont (site review).

## **Accomplishments-Teaching**

### **Classroom instruction**

Ohio State University - Environmental Microbiology (Co-instructor, Microbiology Dept.), Soil Microbiology (Agronomy/Microbiology Depts.), Anaerobic Processes in Soils (Agronomy), Graduate Seminar (Agronomy Dept.), Graduate Colloquium (Agronomy Dept.), Undergraduate Colloquium (Agronomy Dept., 1991).

University of Illinois - Instructor for ACES Freshman Discovery (1996, 1998), Graduate Group Studies (1996, 1998); Graduate Seminar (F/S1995, F/S 1996), Special Problems, and Thesis Research. Guest lecturer for NRES 102 (Fundamentals of Env. Sci.), NRES 375 (Soil Microbiology), NRES 481 (Environmental Research Methods), CPSC 426 (Weed Mgt in Agronomic Crops), Senior Thesis in Microbiology (1996, 1997, 2000), Special Problems in Microbiology (2009), NRES 502 (Research Methods in NRES, 2011), HORT 505 (Research Methods in Horticulture, 2012).

New Mexico State University – Instructor for EPWS 100 (2015), EPWS 420/520 (2014, 2016); Guest lecturer EPWS 330.

## **Advising**

### *Undergraduate Advising:*

Undergraduate advisor, Dept. Agronomy, OSU (1986-1990). 1988-present, mentored 5 postdoctoral research fellows, major advisor for 9 Ph.D. and 12 M.S. candidates, service on >20 additional advisory committees. UI: Mentor for Jonathan Baldwin Turner program (1995,1996), Hank Beachell Future Leader Scholarship (ASA, 1999), McNair program for minority students (1994, 1996), Summer Research Opportunities Program for minority students (1995, 1996, 2003), Department of Microbiology Honors thesis program (1998, 1999, 2001), Howard Hughes Undergraduate Research Fellows program (1999), Special Undergraduate Research Experience program (1999, 2000, 2003, 2004), and the USDA 1890 National Scholar program (1998, 1999).

### *Graduate Advising:*

Advisees Earning Master of Science  
(Current Employment in Parentheses)

Dr. Staci R. Kehrmeyer (Kane). 1991. The effect of ammonium surfactant-clay complexes on bioavailability of naphthalene to *Pseudomonas putida*: bacterial growth and substrate degradation kinetics. Ohio State University (employer: Lawrence Livermore National Laboratory).

Dr. Edward J. O'Loughlin (co-advisor S. Traina), Adsorption and biodegradation of 2-methylpyridine in aqueous suspensions of specimen clay minerals. 1991. (employer: Argonne National Laboratory).

Nancy Greenan (co-advised with R.L. Mulvaney). A microscale method for colorimetric determination of urea in soil extracts. 1995 (employer: Private practice).

Eva Malkos (co-advised with L. Raskin). Bioremediation of naphthalene in soils of varying textures, nutrient concentrations, and hydrocarbon contents. 1996. (employer: Massachusetts Department of Environmental Protection).

Dr. Jason Tor. Trifluralin degradation under microbiologically induced nitrate and Fe(III) reducing conditions. 1996. (employer: Hampshire College).

Dr. Alison Cupples. The influence of environmental factors on cloransulam-methyl degradation 1999. (employer: Michigan State University).

- Frederique Bichat. Microbial utilization of heterocyclic nitrogen from atrazine. 1999. (employer: The French Environment and Energy Control Agency).
- Ryan Hultgren. Sorption and degradation of prosulfuron. 2000. (employer: Kennedy/Jenks Consultants).
- Dr. Indu Rupassara. Degradation of atrazine by plants and associated microorganisms. 2002. (employer: University of Illinois).
- Dr. Renee Mitchell, MD (Potera). Effects of acetolactate synthase inhibiting herbicides on soil microorganisms. 2003. (employer: The University of Texas Southwestern Medical Center).
- Brian Danzer. 2005. (employer: Rush University Medical Center).
- Scott Maxwell. Tetracycline and tylosin resistant bacteria isolated from swine effluent impacted environments. 2005. Deceased.
- Kerri Marsh (co-advised with R.L. Mulvaney). Availability of urea to autotrophic ammonia-oxidizing bacteria as related to the fate of <sup>14</sup>C- and <sup>15</sup>N-labeled urea added to soil. 2005. (employer: Private consulting).
- Elizabeth Shaffer. Atrazine biodegradation in a Cisne soil exposed to a major spill 2010. (employer: Malcolm Pirnie, Inc .)
- Andrea Skinner. Atrazine biodegradation in a Cisne soil exposed to a major spill. 2010. (employer: University of Illinois).
- Dr. Andres Gomez Zapata. (academic advisor at Universidad Nacional de Columbia G. Resterpo) Evaluacion de la actividad y la diversidad bacteriana can potencial bioremediator asociada a diferentes profundidades en el suelo del morro de Moravia mediante analisis de secuencias del Gen 16s rDNA. 2011. (employer: Craig Ventnor Institute).
- Tiffany A. Johnson (lead advisor Brad Lewis). Responses of blackmargined aphid densities to seasons changes in selected abiotic and biotic factors in pecan. 2016. (employer: New Mexico State University).

#### Advisees Earning PhD

- Dr. Ze'ev Ronen (lead advisor J.M.Bollag) Bioremediation of Subsurface Sediments and Groundwater Contaminated with Pyridine and Alkyl-pyridines. 1992. (employer: Ben Gurion.University).
- Dr. Mark Radosevich (co-advisor O. Tuovinen). 1994. (employer: University of Tennessee).
- Dr. Todd Mervosh Fate of the herbicide clomazone in soil, 1994. (employer: Connecticut Agricultural Experiment Station).
- Dr. Jennifer Crawford. Anaerobic dissipation of herbicides in microbiologically-induced soil redox regimes. 1996. (employer: Champaign Public Schools).
- Dr. Teresa Johnson. Microbial ecology: spatial aspects of pesticide degradation. 1999. (employer: Ohio State University).
- Dr. Sarah Taylor-Lovell (co-advisor Loyd Wax). Soybean response and weed control with flumioxazin, and sorption, degradation and weed control with isoxaflutole. 2000. (employer: University of Illinois).
- Dr. TaiFen Chu (co-advisor J. Stucki). Fate of atrazine and alachlor in redox-treated ferruginous smectite. 2001.
- Dr. Ramdas Kanissery. Bioavailability of metolachlor and glyphosate in aerobic and anaerobic soils. 2014. (employer: University of Florida).

*Other mentoring.* Host for exchange students from: Nancy, France (1996), Trenčín Slovakia (2005-2006), Gorinchem, The Netherlands (2006-2007). On-line mentor for American Society for Microbiology (2006-present), member of the Mentor Committee, Society for Environmental Toxicology and Chemistry (2007-present). Participated in the Minority Mentoring Program Mentor Round Table, May 21, 2006 at the 106<sup>th</sup> General Meeting of the American Society for Microbiology, May 21-25, 2006, Orlando, FL. NMSU Teaching Academy (>20 hours).

## **Accomplishments-Research**

### **Summary of Research Accomplishment Areas**

- Environmental behavior of N-heterocycles – This work influenced cleanup of a superfund site, resulted in useful isolates deposited with ATCC, and provided the environmental data used by numerous agencies globally, which appears on product labels, MSD sheets and toxicological profiles for certain chemicals.

- EPA registration studies for herbicides - Served on the registration committee for cloransulam-methyl and directed the compound's aerobic degradation study. Directed anaerobic studies for 2,4-D, ethalfluralin and benefin (contract lab), chaired registration committee for 100+ registration studies for diclosulam. Data used by USEPA in support of US registration of flumetsulam in 1994, cloransulam-methyl in 1997, diclosulam in 2000, and reregistration of ethalfluralin, benefin, and 2,4-D in 1995.

- Environmental process coupling as related to bioavailability – Numerous studies examined the coupling of sorption, degradation, and/or volatility for a number of compounds (solvents, PAHs, herbicides) in the soil environment. These studies established the mechanisms for resurgent activity of isoxaflutol, persistence carryover damage by prosulfuron, and factors that control degradation of atrazine in soil.

- Anaerobic transformations of herbicides – Several publications detail experiments with atrazine, dimethenamid, and trifluralin fate in flooded soils/sediments. Also, our lab provided the first proof for reductive debromination of a herbicide in pure culture, and the first report of any kind for reductive deiodination of a herbicide.

- Functional ecology of soil microorganisms – Non-symbiotic N<sub>2</sub>-fixing bacteria, assimilation of atrazine ring N (and lack of assimilation of ring C) by soil microbial communities, demonstrated direct utilization of urea by autotrophic NH<sub>4</sub>-oxidizing bacteria (C and energy), demonstrated the potential to use <sup>15</sup>N-DNA based stable isotope probing, first demonstration of linkage (using <sup>13</sup>C-DNA SIP) between bacterial phylogeny and function for degradation of a herbicide in soil.

### **Invited Presentations**

“Degradation of dinitroaniline herbicides under iron reducing conditions” American Society for Microbiology General Meeting, May 30- June 2, 2015, New Orleans, LA.

“Precision Zonal Management Systems for Resilient Cereal Yields and Ecosystem Services Under Variable Climates” (invitation to) N. Jordan. ASA, CSSA, and SSSA International Annual Meetings, Oct 21-24, 2012, Cincinnati, OH.

“Being Part of a Solution”. Department of Entomology, Plant Pathology, and Weed Science, New Mexico State university, Las Cruces, May 23, 2011.

- “Matrix Effects and Measuring Microbial Responses to Xenobiotics in Soil”. SSSA Annual Meeting, Long Beach, CA, Oct. 31 - Nov. 3, 2010.
- “Microbial Response to Introduced Substances in Terrestrial Environments – Coping With the Soil Matrix”. Challenges in Environmental Molecular Microbiology Workshop, Argonne National Laboratory, 2010.
- “Future Priorities for the Crop Protection and Quarantine Nation Program”, Office of National Programs, USDA-ARS, Beltsville, MD, January 8, 2009.
- “Biodegradation of organic compounds in soils”, Department of Land Resources and Environmental Sciences, Montana State University, Bozemen, MT, February 9, 2009.
- “Philosophy of Graduate Education”, Department of Land Resources and Environmental Sciences, Montana State University, Bozemen, MT, February 10, 2009.
- “Microbial Ecology of Herbicide Degradation – Potential and Limitations of Nucleic Acid Based Stable Isotope Probing” at 5th International Weed Science Congress, Vancouver, British Columbia, June 23–27, 2008.
- “Research Program Planning: Taking Advantage of Your Assets”, COLSA Open Forum Address, University of New Hampshire, Durham, April 23, 2008.
- Untitled presentation, Department of Crops, Soils, and Environmental Sciences, University of Arkansas, Fayetteville, June 11, 2008.
- “Ecology of atrazine natural attenuation in soil from a major spill” at Multiple stressors for the environment - present and future challenges and perspectives. SETAC Europe 17th Annual Meeting, Porto, Portugal, 20 - 24 May, 2007.
- “Bioavailability of xenobiotics in unsaturated soils – implications for nucleic acid based stable isotope probing” ASA-CSSA-SSSA International Annual Meetings, New Orleans, LA. Nov. 4-8, 2007.
- “Anaerobic degradation of Trifluralin” SETAC Europe 16th Annual Meeting, the Hague, The Netherlands, 7-11 May, 2006.
- “Examining the ecology of heterocyclic N utilization”, 11th International Symposium on Microbial Ecology, Vienna, Austria. August 20-25, 2006.
- “Investigating anaerobic microbial processes in agricultural soils using *Anaeromyxobacter dehalogenans* as a cosmopolitan model”, 11th International Symposium on Microbial Ecology, Vienna, Austria. August 20-25, 2006.
- “Interactions between microorganisms and weed seeds: implications for the microbial ecology of seed banks”, 10th International Symposium on Microbial Ecology (ISME) Microbial Planet: Sub-Surface to Space Cancun, Mexico, August 22-27, 2004.
- Maxwell, J., and G. K. Sims. 2003. Life Beneath Your Feet. ACES Open House, University of Illinois, March 11-12, 2003. A staffed, interactive presentation of microorganisms and their functions in soil and water.
- “Role of Uptake in Bioavailability of Herbicides to Microorganisms”, 10th IUPAC Intl. Congress on the Chemistry of Crop Protection, Basel, Switzerland, 4-9 August 2002.
- Larson, R. and G. Sims. 2002. Nitrate management for groundwater and drinking water protection. 12th Annual research planning conference, Illinois Groundwater Consortium, “Research on Agricultural Chemicals and Groundwater Resources”. Carbondale, IL April 22, 2002.
- Maxwell, J.S. L. Connor, K. Merrick, and G.K. Sims. 2002. Soil through the looking glass: Environmental microbiology. ACES Open House, March 8-9, 2002, University of Illinois at Urbana-Champaign.

- “The occurrence and diversity of antibiotic resistance genes in terrestrial ecosystems with and without impact from animal agriculture”, 9th International Symposium on Microbial Ecology, Amsterdam, The Netherlands. August 26-31, 2001.
- “Role of ionization in bacterial uptake and soil sorption of agrochemicals.” Groundwater quality 2001, 3rd Internat. Conf. on Groundwater Quality, Univ. of Sheffield, Sheffield, UK. 2001. (with R. Hultgren, A. Cupples, & R. Hudson).
- “Factors controlling degradation of pesticides in soil.” 9th Internat. Congress of Pesticide Chemistry. Royal Society of Chemistry and the International Union of Pure and Applied Chemistry. London, UK. 1998. (with A. Cupples & S. Hart).
- “Biodegradation as controlled by coupled processes.” Soil Sci. Soc. Amer. Nat. Meeting, Baltimore, MD. 1998. (with C. Bollin, S. Boyd, & L. Lee).
- “Factors controlling biodegradation of xenobiotics in soil.” Soil Sci. Soc. Amer. Nat. Meeting, Baltimore, MD. 1998.(with A. Cupples & D. Shelton).
- O’Loughlin, E. J., S. J. Traina, G. K. Sims. Effects of adsorption on the biodegradation of 2-methylpyridine. DuPont Agricultural Products, Wilmington, Delaware, 1997/ (with E. O’Loughlin and S.J. Traina).
- “A Day in the Life (What Faculty Really Do)” Address to the Ronald E. McNair Program, University of Illinois, 3/18/1997.
- Sims, G.K. Xenobiotic fate processes: Duking it out. University of Illinois at Urbana-Champaign. February 26, 1996.
- “Biodegradation of mixtures of xenobiotics.” Amer. Soc. Agron. Nat. Meeting, Seattle, WA. 1994. (with T. Johnson).
- “Aerobic biodegradation processes in soil.” Amer. Soc. Agron. Nat. Meeting, Seattle, WA. 1994. (with M. Cole)
- “Soil microbiology.” In Symp. on Soil Health: The basis of current and future production. Soil and Water Conservation Society. Decatur, IL. 1994.
- “Herbicide degradation.” Illinois Agricultural Pesticides Conf., Urbana, IL. 12/20/1994.
- “Impacts of surface crop residue on chemical processes and pesticide fate.” Amer. Soc. Agron. Nat. Meeting, Cincinnati, OH. 1993 (honorary).
- “Effects of Aging on Persistence of Pesticides” Department of Agronomy, Ohio State University, 5/13/1993.
- “Environmental Microbiology” Lecture for Microbiology 665. Ohio state University, 5/14/1993.
- “Environmental Fate of Herbicides” Ciba Plant Protection University Specialist Sessions. Urbana, IL, 12/14/1993.
- “Bioavailability of sorbed xenobiotics.” Dept. of Agronomy, Pennsylvania State Univ., University Park, PA. 10/2/1992 (honorary).
- “Extraction and characterization of bound residue of flumetsulam in aerobic soil systems.” Amer. Soc. Agron. Nat. Meeting, Minneapolis, MN. 1992. (with P. Havens, J. Smith, & R. Lehmann).
- “Nature and bioavailability of bound residues.” Amer. Soc. Agron. Nat. Meeting, Minneapolis, MN. 1992.
- Sims, G.K. Bioavailability of sorbed xenobiotics. The University of Southwestern Louisiana, 1991.
- Sims, G.K. Biodegradation of pyridine derivatives. Department of Microbiology, The Ohio State University, September 27, 1990.

- “Biodegradation of xenobiotic compounds in surface and subsurface environments.” Dept. of Soil Sci., Univ. of Arizona, Tucson. 1990.
- “Aerobic degradation of pyridines and derivatives.” Mini Symposium on Pyridines, Laboratory for Soil Microbiology, Pennsylvania State Univ., Toftrees Conference Center. 1989.
- “Bioremediation of pyridine derivative-contaminated environmental sites: aerobic degradation.” Reilly Industries, Indianapolis, IN. 1989.
- Sims, G.K. 1988. History of nitrate pollution from agriculture. Farmer-rancher sustainable agriculture workshop. Ohio State University, Columbus, OH, 18-Feb-1988 (Invited).
- Lal, R., J. Bigham, G. Sims, G. Hall, F. Miller, and T. Logan. 1988. Improving the prediction of upland erosion from agricultural lands in southeastern Ohio. 43rd Annual Meeting, Soil and Water Conservation Society, Columbus, OH, 31-Jul – 3-Aug-1988 (invited).
- Sims, G.K. 1989. Careers in Agronomy. Agriculture and Natural Resources Career Day, The Ohio State University, Columbus, Ohio, October 31, 1989 (Invited).
- Sims, G.K. 1989. Use of peer review in the classroom. Department of Agricultural Education, The Ohio State University, January 26, 1989.
- “Physiological responses of soil microorganisms exposed to agricultural chemicals.” In Symp. on Microbial Response to Chemical Contaminants in the Environment. Amer. Soc. for Microbiology Nat. Meeting, Miami, FL. 1988.
- Sims, G.K.** and S.J. Traina. 1988. Xenobiotics in Agriculture (Two Part Series). OASIS . Ag, The Ohio State University. April 9 and 16, 1988.
- Sims, G.** Level of Complexity of Water Quality Issues: Need for Basic Research. Water Quality Issues Update, Ohio State University Extension, March 3, 1988.

## Technology Transfer

- Bacterial strains deposited with the American Type Culture Collection ([www.atcc.org](http://www.atcc.org)):
- Arthrobacter crystallopoietes* (ATCC 49443)-Degrades pyridine.
- Micrococcus luteus* (ATCC 49442)-Isolated from soil. Degrades pyridine.
- Rhodococcus* sp (ATCC 49988)-Isolated from soil. Degrades many heterocyclic compounds
- Arthrobacter* sp. (ATCC 49987)-Isolated from superfund site (aquifer) degrades pyridines, homocyclic compounds
- Co-author 257 sequence submissions (uncultured isolates) to NCBI.
- Methods for NH<sub>4</sub>, NO<sub>2</sub> and NO<sub>3</sub> adopted by soil testing laboratories (Auburn University).
- Urea method adapted for commercial product Tribioscience Labs.
- Aerobic soil metabolism study used for registration of the herbicide, cloransulam-methyl.

## Funding

- Jordan, N., A. S. Davis, **G. K. Sims**, A. Yannarrell, K. Spokas, A. S. Grandy, S. Snapp, D. Mortensen, R. Smith and R. Koide. Precision zonal management systems for resilient cereal yields and ecosystem services under variable climates. NIFA Agriculture and Food Research Initiative Competitive Grants Program. January 2011-December 2015. \$5,000,000.
- Sims, G.K.**, J.C. Chee-Sanford, A.S. Davis, and M.M. Williams. Biologically and Ecologically Based Knowledge for Integrated Weed Management Systems. USDA-ARS No. 3611-22000-019-00D. 2010-2015. \$5,519,000.

- Sims, G.K.**, J.C. Chee-Sanford, A.S. Davis, and M.M. Williams. Factors Controlling Microbial Transformation of Herbicides, N Fertilizers, and Weed Seeds as Related to Biologically-Based Weed Management. USDA-ARS No. 3611-12220-007-00D. 2006-2011. \$1,496,690.
- Chee Sanford, J.C., **G.K. Sims**, M.M. Williams, and A.S. Davis. Biologically and Ecologically Based Knowledge for Integrated Weed Management Systems. USDA-ARS No. 3611-22000-018-00D. 2005-2010. \$4,022,245.
- Sims, G. K.** Anaerobic Microbial Degradation of Herbicides. USDA-ARS Competitive Postdoctoral Research Fellows Program, 2003-2005, \$80,000.
- Sims, G. K.** & R. A. Larson. Factors controlling persistence of antibiotics used in animal agriculture. Illinois Dept. of Natural Resources, Waste Management & Research Center, 2002-2004, \$83,722.
- Wander, M. M. & **G. K. Sims**. Evaluation of Bt toxin persistence in soils. Council on Food & Agricultural Research, 2001-2003 \$ \$117,000.
- Sprague, C.L., Young, B., Roskamp, G., Hager, A.G., Tranel, P.J., Riechers, D.L., Wax, L.M., Simmons, F.W., and **Sims, G. K.** University of Illinois Weeds Program Plan of Work for Soybean Research, Illinois Soybean Program Operating Board. 2001-2002 \$250,000.
- Sims, G.K.**, and L.M. Wax. Factors contributing to persistence of herbicides and strategies for reducing off-target impacts. USDA-ARS No. 3611-12220-006-00D. 2000-2005. \$1,476,285.
- Larson, R. A. & **G. K. Sims**. Nitrate management for groundwater and drinking water protection. Illinois Groundwater Consortium, 2000-2002 \$ 47,635.
- Sprague, C.L., Young, B., Roskamp, G., Hager, A.G., Tranel, P.J., Riechers, D.L., Wax, L.M., Simmons, F.W., and **Sims, G. K.** University of Illinois Weeds Program Plan of Work for Soybean Research, Illinois Soybean Program Operating Board. 2000-2001 \$250,000.
- Wax, L.M., E.W. Stoller, and **G.K. Sims**. Developing biological/ecological knowledge for enhancing weed management systems. 3611-22000-017-00D. 1999-2004. \$3,762,930.
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**Research Publications** (Hirsch index,  $h=31$  Google Scholar): (*authors in italics were students or post-doctoral fellows advised or co-advised by Sims*)

**In Review:**

Kanissery, R.G., A. Welsh, A. Gomez, L. Connor and **G.K. Sims**. (in review) Identification of metolachlor mineralizing bacteria in aerobic and anaerobic soils using DNA-stable isotope probing. Submitted to Biodegradation.

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### Teaching/Outreach Publications

*(authors in italics were students or post-doctoral fellows advised by Sims)*

21. **Sims, G.K.** 2014. "Soil degradation", in AccessScience@McGraw-Hill, <http://www.accessscience.com>, DOI 10.1036/1097-8542.757375.
20. National Program 304: Crop Protection & Quarantine Action Plan 2008-2013 (194 pages). Multiple authors, Co-edited with K. Hackett and K. Vick, August, 2008. [http://www.ars.usda.gov/research/programs/programs.htm?np\\_code=304&docid=17844](http://www.ars.usda.gov/research/programs/programs.htm?np_code=304&docid=17844).
19. USDA-ARS National Program 304 (Crop Protection and Quarantine) Accomplishment Report. 2008. Co-authored with M. Greenstone, E. Delfosse and K. Hackett. (289 pages). (<http://www.ars.usda.gov/SP2UserFiles/Program/304/NP304AccompRptFinal12-18.pdf>)
18. Avoiding harm from invasive species in FY 2007. A USDA Report to the Invasive Species Advisory Council and the National Invasive Species Council September, 2007.
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124. Sims, GK. 2015. Amino acids with high biosynthetic energy costs are conserved by soil communities. SSSA Annual Meeting, Minneapolis, MN. Nov. 15-18. Abstract 316-6 (poster #1303). Agron. Abstracts 102:104-2
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## Electronic Media

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**Sims, J.** 2013. What is an Entomologist? YouTube. URL:  
<https://www.youtube.com/watch?v=HwFVTQu84uE>

## Biological Resources (Technology Transfer)

Bacterial strains deposited with the American Type Culture Collection ([www.atcc.org](http://www.atcc.org)):  
*Arthrobacter crystallopoietes* (ATCC 49443)-Degrades pyridine.  
*Micrococcus luteus* (ATCC 49442)-Isolated from soil. Degrades pyridine.  
*Rhodococcus* sp (ATCC 49988)-Isolated from soil. Degrades many heterocyclic compounds  
*Arthrobacter* sp. (ATCC 49987)-Isolated from superfund site (aquifer) degrades pyridines, homocyclic compounds

### Genbank Accessions (gene sequences)

1. Uncultured bacterium clone H2 16S ribosomal RNA gene, partial sequence. 1,347 bp linear DNA. Accession number: JN039345.1 GI:338827807.
2. Uncultured *Pseudoxanthomonas* sp. clone G5 16S ribosomal RNA gene, partial sequence. 1,210 bp linear DNA . Accession number: JN039344.1 GI:338827806.
3. Uncultured *Brevundimonas* sp. clone G2 16S ribosomal RNA gene, partial sequence. 1,296 bp linear DNA. Accession number: JN039343.1 GI:338827805.
4. Uncultured *Alcaligenes* sp. clone F10 16S ribosomal RNA gene, partial sequence 1,371 bp linear DNA. JN039342.1 GI:338827804.
5. Uncultured *Alcaligenes* sp. clone E6 16S ribosomal RNA gene, partial sequence 1,380 bp linear DNA. JN039341.1 GI:338827803.
6. Uncultured *Micrococcus* sp. clone E1 16S ribosomal RNA gene, partial sequence 1,303 bp linear DNA. JN039340.1 GI:338827802.
7. Uncultured *Alcaligenes* sp. clone E5 16S ribosomal RNA gene, partial sequence 1,317 bp linear DNA. JN039339.1 GI:338827801.
8. Uncultured *Dietzia* sp. clone C12 16S ribosomal RNA gene, partial sequence 1,424 bp linear DNA. JN039338.1 GI:338827800.
9. Uncultured Pseudomonadaceae bacterium clone C3 16S ribosomal RNA gene, partial sequence 1,301 bp linear DNA. JN039337.1 GI:338827799.
10. Uncultured *Aquamicrobium* sp. clone D3 16S ribosomal RNA gene, partial sequence 1,248 bp linear DNA. JN039336.1 GI:338827798.
11. Uncultured *Arthrobacter* sp. clone B4 16S ribosomal RNA gene, partial sequence 1,332 bp linear DNA. JN039335.1 GI:338827797.
12. Uncultured *Ralstonia* sp. isolate TTGE gel band I3-20e 16S ribosomal RNA gene, partial sequence 514 bp linear DNA. HM583864.1 GI:301350800.
13. Uncultured *Acinetobacter* sp. isolate TTGE gel band I3-10b 16S ribosomal RNA gene, partial sequence 517 bp linear DNA . HM583863.1 GI:301350799.
14. Uncultured *Acinetobacter* sp. isolate TTGE gel band I3-10f 16S ribosomal RNA gene, partial sequence 494 bp linear DNA. HM583862.1 GI:301350798.
15. Uncultured *Flavobacterium* sp. isolate TTGE gel band I2-20a 16S ribosomal RNA gene, partial sequence 528 bp linear DNA . HM583861.1 GI:301350797.
16. Uncultured *Acinetobacter* sp. isolate TTGE gel band I2-10c 16S ribosomal RNA gene, partial sequence 526 bp linear DNA . HM583860.1 GI:301350796.
17. Bacterium P2-20-73 16S ribosomal RNA gene, partial sequence 1,401 bp linear DNA. HM583880.1 GI:301350816.
18. Bacterium P2-20-9 16S ribosomal RNA gene, partial sequence 1,388 bp linear DNA. HM583879.1 GI:301350815.
19. Bacterium P2-20-7 16S ribosomal RNA gene, partial sequence 1,390 bp linear DNA. HM583878.1 GI:301350814.
20. Bacterium P2-20-2 16S ribosomal RNA gene, partial sequence 1,389 bp linear DNA. HM583877.1 GI:301350813.
21. Bacterium P2-10-5 16S ribosomal RNA gene, partial sequence. 1,387 bp linear DNA. HM583876.1 GI:301350812.
22. Bacterium P2-10-1 16S ribosomal RNA gene, partial sequence. 1,388 bp linear DNA. HM583875.1 GI:301350811.
23. Bacterium P2-0-7 16S ribosomal RNA gene, partial sequence. 1,364 bp linear DNA. HM583874.1 GI:301350810.
24. Bacterium P2-0-1 16S ribosomal RNA gene, partial sequence. 1,431 bp linear DNA. HM583873.1 GI:301350809.

25. Bacterium P1-20-9 16S ribosomal RNA gene, partial sequence. 1,406 bp linear DNA. HM583872.1 GI:301350808
26. Bacterium P1-0-9 16S ribosomal RNA gene, partial sequence. 1,379 bp linear DNA. HM583871.1 GI:301350807
27. Bacterium P1-0-2 16S ribosomal RNA gene, partial sequence. 1,392 bp linear DNA. HM583870.1 GI:301350806
28. Bacterium I1-20-2 16S ribosomal RNA gene, partial sequence. 1,380 bp linear DNA . HM583869.1 GI:301350805
29. Bacterium I1-10-4 16S ribosomal RNA gene, partial sequence. 1,378 bp linear DNA . HM583868.1 GI:301350804
30. Bacterium I1-10-2 16S ribosomal RNA gene, partial sequence. 1,332 bp linear DNA HM583867.1 GI:301350803
31. Bacterium I1-0-5 16S ribosomal RNA gene, partial sequence. 1,352 bp linear DNA. HM583866.1 GI:301350802
32. Bacterium I1-0-1 16S ribosomal RNA gene, partial sequence. 1,349 bp linear DNA. HM583865.1 GI:301350801
33. Uncultured alpha proteobacterium clone S1-10-CL6 16S ribosomal RNA gene, partial sequence. 1,446 bp linear DNA . AY728074.1 GI:53759184
34. Uncultured beta proteobacterium clone S1-10-CL1 16S ribosomal RNA gene, partial sequence. 1,493 bp linear DNA. AY728073.1 GI:53759183.
35. Uncultured Bacteroidetes bacterium clone S1-9-CL10 16S ribosomal RNA gene, partial sequence. 1,485 bp linear DNA. AY728072.1 GI:53759182
36. Uncultured gamma proteobacterium clone S1-9-CL8 16S ribosomal RNA gene, partial sequence. 1,496 bp linear DNA . AY728071.1 GI:53759181
37. Uncultured alpha proteobacterium clone S1-9-CL5 16S ribosomal RNA gene, partial sequence. 1,443 bp linear DNA . AY728070.1 GI:53759180
38. Uncultured low G+C Gram-positive bacterium clone S1-6-CL19 16S ribosomal RNA gene, partial sequence. 1,238 bp linear DNA . AY728069.1 GI:53759179
39. Uncultured beta proteobacterium clone S1-6-CL16 16S ribosomal RNA gene, partial sequence. 1,491 bp linear DNA. AY728068.1 GI:53759178.
40. Uncultured low G+C Gram-positive bacterium clone S1-6-CL2 16S ribosomal RNA gene, partial sequence. 1,480 bp linear DNA. AY728067.1 GI:53759177
41. Uncultured Bacteroidetes bacterium clone S1-4-CL9 16S ribosomal RNA gene, partial sequence. 1,486 bp linear DNA. AY728066.1 GI:53759176.
42. Uncultured delta proteobacterium clone S1-4-CL8 16S ribosomal RNA gene, partial sequence. 1,511 bp linear DNA. AY728065.1 GI:53759175
43. Uncultured bacterium clone S4-8-CL10 16S ribosomal RNA gene, partial sequence, 1,444 bp linear DNA. EU769203.1 GI:192758226.
44. Uncultured bacterium clone S4-8-CL8 16S ribosomal RNA gene, partial sequence. 1,451 bp linear DNA. EU769202.1 GI:192758225
45. Uncultured bacterium clone S4-8-CL7 16S ribosomal RNA gene, partial sequence. 1,449 bp linear DNA. EU769201.1 GI:192758224.
46. Uncultured bacterium clone S4-8-CL2 16S ribosomal RNA gene, partial sequence. 1,446 bp linear DNA. EU769200.1 GI:192758223.
47. Uncultured bacterium clone S4-8-CL1 16S ribosomal RNA gene, partial sequence. 1,449 bp linear DNA . EU769199.1 GI:192758222.
48. Uncultured bacterium clone S4-6-CL9 16S ribosomal RNA gene, partial sequence. 1,501 bp linear DNA. EU769198.1 GI:192758221.
49. Uncultured bacterium clone S4-6-CL7 16S ribosomal RNA gene, partial sequence. 1,459 bp linear DNA. EU769197.1 GI:192758220

50. Uncultured bacterium clone S4-6-CL4 16S ribosomal RNA gene, partial sequence. 1,444 bp linear DNA. EU769196.1 GI:192758219.
51. Uncultured bacterium clone S4-4-CL10 16S ribosomal RNA gene, partial sequence. 1,447 bp linear DNA. EU769195.1 GI:192758218.
52. Uncultured bacterium clone S4-4-CL8 16S ribosomal RNA gene, partial sequence. 1,449 bp linear DNA. EU769194.1 GI:192758217.
53. Uncultured bacterium clone S4-4-CL5 16S ribosomal RNA gene, partial sequence. 1,446 bp linear DNA. EU769193.1 GI:192758216.
54. Uncultured bacterium clone S4-4-CL3 16S ribosomal RNA gene, partial sequence. 1,448 bp linear DNA. EU769192.1 GI:192758215.
55. Uncultured bacterium clone S4-4-CL1 16S ribosomal RNA gene, partial sequence. 1,449 bp linear DNA. EU769191.1 GI:192758214.
56. Uncultured bacterium clone S4-2-CL10RB 16S ribosomal RNA gene, partial sequence. 641 bp linear DNA. EU769190.1 GI:192758213.
57. Uncultured bacterium clone S4-2-CL10FA 16S ribosomal RNA gene, partial sequence. 634 bp linear DNA. EU769189.1 GI:192758212.
58. Uncultured bacterium clone S4-2-CL9 16S ribosomal RNA gene, partial sequence. 1,467 bp linear DNA. EU769188.1 GI:192758211.
59. Uncultured bacterium clone S4-2-CL5 16S ribosomal RNA gene, partial sequence. 1,448 bp linear DNA. EU769187.1 GI:192758210.
60. Uncultured bacterium clone S4-2-CL2 16S ribosomal RNA gene, partial sequence. 1,497 bp linear DNA. EU769186.1 GI:192758209.
61. Uncultured bacterium clone S4-2-CL1 16S ribosomal RNA gene, partial sequence. 1,499 bp linear DNA. EU769185.1 GI:192758208.
62. Uncultured bacterium clone S4-1-CL5 16S ribosomal RNA gene, partial sequence. 864 bp linear DNA. EU769184.1 GI:192758207.
63. Uncultured bacterium clone S3-10-CL8 16S ribosomal RNA gene, partial sequence. 526 bp linear DNA. EU769183.1 GI:192758206.
64. Uncultured bacterium clone S3-10-CL5 16S ribosomal RNA gene, partial sequence. 1,478 bp linear DNA. EU769182.1 GI:192758205.
65. Uncultured bacterium clone S3-10-CL3 16S ribosomal RNA gene, partial sequence. 576 bp linear DNA. EU769181.1 GI:192758204.
66. Uncultured bacterium clone S3-10-CL1 16S ribosomal RNA gene, partial sequence. 564 bp linear DNA. EU769180.1 GI:192758203.
67. Uncultured bacterium clone S3-5-CL4 16S ribosomal RNA gene, partial sequence. 634 bp linear DNA. EU769179.1 GI:192758202.
68. Uncultured bacterium clone S3-5-CL3RB 16S ribosomal RNA gene, partial sequence. 608 bp linear DNA. EU769178.1 GI:192758201.
69. Uncultured bacterium clone S3-5-CL3FA 16S ribosomal RNA gene, partial sequence. 640 bp linear DNA. EU769177.1 GI:192758200.
70. Uncultured bacterium clone S3-5-CL1 16S ribosomal RNA gene, partial sequence. 642 bp linear DNA. EU769176.1 GI:192758199.
71. Uncultured bacterium clone S3-4-CL5 16S ribosomal RNA gene, partial sequence. 1,198 bp linear DNA. EU769175.1 GI:192758198.
72. Uncultured bacterium clone S3-3-CL1 16S ribosomal RNA gene, partial sequence. 1,449 bp linear DNA. EU769174.1 GI:192758197.
73. Uncultured bacterium clone S2-8-CL9 16S ribosomal RNA gene, partial sequence. 759 bp linear DNA. EU769173.1 GI:192758196.
74. Uncultured bacterium clone S2-8-CL8 16S ribosomal RNA gene, partial sequence. 740 bp linear DNA. EU769172.1 GI:192758195.

75. Uncultured bacterium clone S2-8-CL7 16S ribosomal RNA gene, partial sequence.720 bp linear DNA.EU769171.1 GI:192758194.
76. Uncultured bacterium clone S2-8-CL4 16S ribosomal RNA gene, partial sequence.610 bp linear DNA.EU769170.1 GI:192758193.
77. Uncultured bacterium clone S2-8-CL2 16S ribosomal RNA gene, partial sequence.693 bp linear DNA.EU769169.1 GI:192758192.
78. Uncultured bacterium clone S2-5-CL44 16S ribosomal RNA gene, partial sequence.918 bp linear DNA.EU769168.1 GI:192758191.
79. Uncultured bacterium clone S2-2-CL10 16S ribosomal RNA gene, partial sequence. 620 bp linear. DNA . EU769167.1 GI:192758190.
80. Uncultured bacterium clone S2-2-CL9 16S ribosomal RNA gene, partial sequence.612 bp linear DNA.EU769166.1 GI:192758189.
81. Uncultured bacterium clone S2-2-CL7 16S ribosomal RNA gene, partial sequence.750 bp linear DNA.EU769165.1 GI:192758188.
82. Uncultured bacterium clone S2-2-CL1 16S ribosomal RNA gene, partial sequence.781 bp linear DNA.EU769164.1 GI:192758187.
83. Uncultured bacterium clone S1-10-CL9 16S ribosomal RNA gene, partial sequence.675 bp linear DNA.EU769163.1 GI:192758186.
84. Uncultured bacterium clone S4-2-CL6 16S ribosomal RNA gene, partial sequence. 1,490 bp linear DNA. EU769162.1 GI:192758185.
85. Uncultured bacterium clone S4-2-CL3 16S ribosomal RNA gene, partial sequence.1,448 bp linear DNA. EU769161.1 GI:192758184.
86. Uncultured bacterium clone S4-1-CL9 16S ribosomal RNA gene, partial sequence. 1,490 bp linear DNA. EU769160.1 GI:192758183.
87. Uncultured bacterium clone S4-1-CL8 16S ribosomal RNA gene, partial sequence. 1,312 bp linear DNA. EU769159.1 GI:192758182.
88. Uncultured bacterium clone S4-1-CL7 16S ribosomal RNA gene, partial sequence.922 bp linear DNA .EU769158.1 GI:192758181.
89. Uncultured bacterium clone S4-1-CL3 16S ribosomal RNA gene, partial sequence.1,490 bp linear DNA.EU769157.1 GI:192758180.
90. Uncultured bacterium clone S3-10-CL10 16S ribosomal RNA gene, partial sequence.1,493 bp linear DNA.EU769156.1 GI:192758179.
91. Uncultured bacterium clone S3-4-CL10 16S ribosomal RNA gene, partial sequence.1,493 bp linear DNA .EU769155.1 GI:192758178.
92. Uncultured bacterium clone S3-4-CL3 16S ribosomal RNA gene, partial sequence. 1,441 bp linear DNA. EU769154.1 GI:192758177.
93. Uncultured bacterium clone S3-3-CL7 16S ribosomal RNA gene, partial sequence. 1,446 bp linear DNA. EU769153.1 GI:192758176.
94. Uncultured bacterium clone S3-3-CL3 16S ribosomal RNA gene, partial sequence.1,450 bp linear DNA.EU769152.1 GI:192758175.
95. Uncultured bacterium clone S2-5-CL50 16S ribosomal RNA gene, partial sequence.1,456 bp linear DNA .EU769151.1 GI:192758174.
96. Uncultured bacterium clone S2-5-CL33 16S ribosomal RNA gene, partial sequence. 1,239 bp linear DNA .EU769150.1 GI:192758173.
97. Uncultured bacterium clone S2-5-CL29 16S ribosomal RNA gene, partial sequence.1,356 bp linear DNA .EU769149.1 GI:192758172.
98. Uncultured bacterium clone S2-5-CL23 16S ribosomal RNA gene, partial sequence.1,492 bp linear DNA.EU769148.1 GI:192758171.
99. Uncultured bacterium clone S2-5-CL15 16S ribosomal RNA gene, partial sequence.1,444 bp linear DNA.EU769147.1 GI:192758170.

100. Uncultured bacterium clone S2-5-CL11 16S ribosomal RNA gene, partial sequence.1,502 bp linear DNA.EU769146.1 GI:192758169.
101. Uncultured bacterium clone S2-5-CL7 16S ribosomal RNA gene, partial sequence.1,469 bp linear DNA .EU769145.1 GI:192758168.
102. Uncultured bacterium clone S2-5-CL1 16S ribosomal RNA gene, partial sequence.1,490 bp linear DNA .EU769144.1 GI:192758167.
103. Uncultured bacterium clone S2-2-CL4 16S ribosomal RNA gene, partial sequence.1,450 bp linear DNA .EU769143.1 GI:192758166.
104. Uncultured bacterium clone S2-5-CL39 16S ribosomal RNA gene, partial sequence.1,350 bp linear DNA .EU769142.1 GI:192758165.
105. Uncultured bacterium clone 15 16S ribosomal RNA gene, partial sequence.1,491 bp linear DNA. DQ398884.1 GI:89114018.
106. Uncultured bacterium clone 28 16S ribosomal RNA gene, partial sequence. 1,490 bp linear DNA. DQ398883.1 GI:89114017.
107. Uncultured bacterium clone 7 16S ribosomal RNA gene, partial sequence. 1,490 bp linear DNA. DQ398882.1 GI:89114016.
108. *Stenotrophomonas* sp. BBTR57 16S ribosomal RNA gene, partial sequence.1,506 bp linear DNA .DQ337605.1 GI:85002031.
109. *Serratia* sp. BBTR54 16S ribosomal RNA gene, partial sequence. 1,503 bp linear DNA .DQ337604.1 GI:85002030.
110. *Pseudomonas* sp. BBTR25 16S ribosomal RNA gene, partial sequence. 1,506 bp linear DNA. DQ337603.1 GI:85002029.
111. *Xanthomonas retroflexus* 16S ribosomal RNA gene, partial sequence. 1,506 bp linear DNA. DQ337602.1 GI:85002028.
112. *Serratia* sp. BBTR23 16S ribosomal RNA gene, partial sequence. 1,503 bp linear DNA. DQ337601.1 GI:85002027.
113. *Pseudomonas* sp. BBTR5 16S ribosomal RNA gene, partial sequence. 1,498 bp linear DNA . DQ337600.1 GI:85002026.
114. *Luteimonas* sp. CHNTR51 16S ribosomal RNA gene, partial sequence. 1,497 bp linear DNA. DQ337599.1 GI:85002025.
115. *Rhodanobacter* sp. CHNTR45 16S ribosomal RNA gene, partial sequence. 1,506 bp linear DNA. DQ337598.1 GI:85002024.
116. *Pseudoxanthomonas* sp. CHNTR38 16S ribosomal RNA gene, partial sequence. 1,506 bp linear .DNA . DQ337597.1 GI:85002023.
117. *Pseudomonas* sp. CHNTR36 16S ribosomal RNA gene, partial sequence. 1,498 bp linear DNA . DQ337596.1 GI:85002022.
118. *Luteimonas* sp. CHNTR31 16S ribosomal RNA gene, partial sequence. 1,506 bp linear DNA. DQ337595.1 GI:85002021.
119. *Bacillus* sp. CHNTR52 16S ribosomal RNA gene, partial sequence.1,517 bp linear DNA. DQ337594.1 GI:85002020.
120. *Denitrobacter* sp. BBTR53 16S ribosomal RNA gene, partial sequence. 1,504 bp linear DNA. DQ337593.1 GI:85002019.
121. *Herbaspirillum* sp. CHNTR44 16S ribosomal RNA gene, partial sequence. 1,494 bp linear DNA .DQ337592.1 GI:85002018.
122. *Oxalobacteraceae* bacterium CHNTR40 16S ribosomal RNA gene, partial sequence.1,490 bp linear DNA .DQ337591.1 GI:85002017.
123. *Denitrobacter* sp. CHNTR39 16S ribosomal RNA gene, partial sequence.1,504 bp linear DNA .DQ337590.1 GI:85002016.
124. *Chryseobacterium* sp. BBTR48 16S ribosomal RNA gene, partial sequence.1,478 bp linear DNA .DQ337589.1 GI:85002015.

125. *Chryseobacterium* sp. CHNTR56 16S ribosomal RNA gene, partial sequence.1,478 bp linear DNA .DQ337588.1 GI:85002014.
126. Soil bacterium CHNTR54 16S ribosomal RNA gene, partial sequence.1,491 bp linear DNA .DQ337587.1 GI:85002013.
127. *Paracoccus* sp. BBTR62 16S ribosomal RNA gene, partial sequence.1,424 bp linear DNA .DQ337586.1 GI:85002012.
128. *Kaistia* sp. BBTR58 16S ribosomal RNA gene, partial sequence. 1,450 bp linear DNA .DQ337585.1 GI:85002011.
129. *Bosea* sp. BBTR49 16S ribosomal RNA gene, partial sequence.958 bp linear DNA .DQ337584.1 GI:85002010.
130. *Ochrobactrum* sp. B2 BBTR46 16S ribosomal RNA gene, partial sequence.1,444 bp linear DNA .DQ337583.1 GI:85002009.
131. Alpha proteobacterium BBTR41 16S ribosomal RNA gene, partial sequence.1,446 bp linear DNA .DQ337582.1 GI:85002008.
132. *Rhizobium* sp. BBTR4 16S ribosomal RNA gene, partial sequence.1,442 bp linear DNA .DQ337581.1 GI:85002007.
133. *Rhizobium* sp. CHNTR68 16S ribosomal RNA gene, partial sequence.1,442 bp linear DNA .DQ337580.1 GI:85002006.
134. *Ochrobactrum* sp. CHNTR58 16S ribosomal RNA gene, partial sequence.1,445 bp linear DNA .DQ337579.1 GI:85002005.
135. *Rhizobium* sp. CHNTR53 16S ribosomal RNA gene, partial sequence.1,442 bp linear DNA .DQ337578.1 GI:85002004.
136. *Brevundimonas* sp. CHNTR43 16S ribosomal RNA gene, partial sequence. 1,422 bp linear DNA .DQ337577.1 GI:85002003.
137. *Pseudaminobacter* sp. CHNTR41 16S ribosomal RNA gene, partial sequence.1,445 bp linear DNA .DQ337576.1 GI:85002002.
138. *Sphingomonas* sp. CHNTR37 16S ribosomal RNA gene, partial sequence.1,448 bp linear DNA .DQ337575.1 GI:85002001.
139. *Ochrobactrum* sp. CHNTR30 16S ribosomal RNA gene, partial sequence. 1,444 bp linear DNA .DQ337574.1 GI:85002000.
140. *Ochrobactrum* sp. CHNTR29 16S ribosomal RNA gene, partial sequence.1,444 bp linear DNA .DQ337573.1 GI:85001999.
141. *Ochrobactrum* sp. CHNTR28 16S ribosomal RNA gene, partial sequence.1,444 bp linear DNA .DQ337572.1 GI:85001998.
142. *Rhizobium* sp. CHNTR26 16S ribosomal RNA gene, partial sequence.1,448 bp linear DNA .DQ337571.1 GI:85001997.
143. *Rhodococcus* sp. BBTR50 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337570.1 GI:85001996.
144. *Rhodococcus* sp. BBTR45 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337569.1 GI:85001995.
145. *Rhodococcus* sp. BBTR42 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337568.1 GI:85001994.
146. *Arthrobacter* sp. BBTR33 16S ribosomal RNA gene, partial sequence.1,487 bp linear DNA .DQ337567.1 GI:85001993.
147. *Rhodococcus* sp. BBTR18 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337566.1 GI:85001992.
148. *Leifsonia* sp. CHNTR47 16S ribosomal RNA gene, partial sequence.1,484 bp linear DNA .DQ337565.1 GI:85001991.
149. *Leifsonia* sp. CHNTR46 16S ribosomal RNA gene, partial sequence.1,484 bp linear DNA .DQ337564.1 GI:85001990.

150. *Rhodococcus* sp. CHNTR42 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337563.1 GI:85001989.
151. *Mycobacterium* sp. CHNTR34 16S ribosomal RNA gene, partial sequence.1,481 bp linear DNA .DQ337562.1 GI:85001988.
152. *Rhodococcus* sp. CHNTR32 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337561.1 GI:85001987.
153. *Variovorax* sp. BBCT26 16S ribosomal RNA gene, partial sequence.1,496 bp linear DNA .DQ337560.1 GI:85001986.
154. *Pseudomonas* sp. BBCT8 16S ribosomal RNA gene, partial sequence.1,485 bp linear DNA .DQ337559.1 GI:85001985.
155. *Bacteroidetes* bacterium CHNCT12 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA.DQ337558.1 GI:85001984.
156. *Chryseobacterium* sp. BBCT19 16S ribosomal RNA gene, partial sequence.1,480 bp linear DNA .DQ337557.1 GI:85001983.
157. *Chryseobacterium* sp. BBCT14 16S ribosomal RNA gene, partial sequence.1,478 bp linear DNA .DQ337556.1 GI:85001982.
158. *Chryseobacterium* sp. BBCT12 16S ribosomal RNA gene, partial sequence.1,479 bp linear DNA .DQ337555.1 GI:85001981.
159. *Labrys methylaminiphilus* 16S ribosomal RNA gene, partial sequence.1,448 bp linear DNA .DQ337554.1 GI:85001980.
160. *Sphingomonas* sp. BBCT69 16S ribosomal RNA gene, partial sequence.1,451 bp linear DNA .DQ337553.1 GI:85001979.
161. *Phyllobacterium* sp. BBCT68 16S ribosomal RNA gene, partial sequence.1,530 bp linear DNA .DQ337552.1 GI:85001978.
162. *Rhizobium* sp. BBCT66 16S ribosomal RNA gene, partial sequence.1,442 bp linear DNA .DQ337551.1 GI:85001977.
163. *Sinorhizobium* sp. BBCT64 16S ribosomal RNA gene, partial sequence.1,446 bp linear DNA .DQ337550.1 GI:85001976.
164. *Caulobacter* sp. BBCT22 16S ribosomal RNA gene, partial sequence.1,447 bp linear DNA .DQ337549.1 GI:85001975.
165. *Sphingomonas* sp. BBCT20 16S ribosomal RNA gene, partial sequence.1,448 bp linear DNA .DQ337548.1 GI:85001974.
166. *Caulobacter* sp. BBCT11 16S ribosomal RNA gene, partial sequence.1,447 bp linear DNA .DQ337547.1 GI:85001973.
167. *Rhodococcus* sp. BBCT 63 16S ribosomal RNA gene, partial sequence.1,476 bp linear DNA .DQ337546.1 GI:85001972.
168. *Microbacterium* sp. BBCT30 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337545.1 GI:85001971.
169. Swine effluent bacterium CHNDP4 16S ribosomal RNA gene, partial sequence.1,479 bp linear DNA .DQ337544.1 GI:85001970.
170. Swine effluent bacterium CHNDP11 16S ribosomal RNA gene, partial sequence.1,491 bp linear DNA .DQ337543.1 GI:85001969.
171. Swine effluent bacterium CHNDP10 16S ribosomal RNA gene, partial sequence.1,491 bp linear DNA .DQ337542.1 GI:85001968.
172. Swine effluent bacterium CHNDP1 16S ribosomal RNA gene, partial sequence.1,491 bp linear DNA .DQ337541.1 GI:85001967.
173. Swine effluent bacterium CHNDP38 16S ribosomal RNA gene, partial sequence.1,506 bp linear.DNA .DQ337540.1 GI:85001966.
174. *Psychrobacter* sp. CHNDP34 16S ribosomal RNA gene, partial sequence.1,500 bp linear DNA .DQ337539.1 GI:85001965.

175. *Staphylococcus* sp. CHNDP33 16S ribosomal RNA gene, partial sequence.1,515 bp linear DNA .DQ337538.1 GI:85001964.
176. *Brevibacterium* sp. CHNDP32 16S ribosomal RNA gene, partial sequence.1,487 bp linear DNA .DQ337537.1 GI:85001963.
177. Swine effluent bacterium CHNDP41 16S ribosomal RNA gene, partial sequence.1,504 bp linear DNA .DQ337536.1 GI:85001962.
178. *Schineria* sp. CHNDP40 16S ribosomal RNA gene, partial sequence.1,502 bp linear DNA .DQ337535.1 GI:85001961.
179. *Staphylococcus* sp. CHNDP23 16S ribosomal RNA gene, partial sequence.1,517 bp linear DNA .DQ337534.1 GI:85001960.
180. *Shigella* sp. BBDP81 16S ribosomal RNA gene, partial sequence.1,503 bp linear DNA .DQ337533.1 GI:85001959.
181. *Eubacterium* sp. BBDP67 16S ribosomal RNA gene, partial sequence.1,486 bp linear DNA .DQ337532.1 GI:85001958.
182. *Carnobacterium* sp. BBDP71 16S ribosomal RNA gene, partial sequence.1,523 bp linear DNA .DQ337531.1 GI:85001957.
183. *Bacteroides* sp. BBDP74 16S ribosomal RNA gene, partial sequence.1,490 bp linear DNA .DQ337530.1 GI:85001956.
184. *Bifidobacterium* sp. BBDP69 16S ribosomal RNA gene, partial sequence.1,492 bp linear DNA .DQ337529.1 GI:85001955.
185. *Lactobacillus* sp. BBDP73 16S ribosomal RNA gene, partial sequence.1,523 bp linear DNA .DQ337528.1 GI:85001954.
186. *Eubacterium* sp. BBDP70 16S ribosomal RNA gene, partial sequence.1,473 bp linear DNA .DQ337527.1 GI:85001953.
187. *Enterococcus* sp. BBDP57 16S ribosomal RNA gene, partial sequence.1,528 bp linear DNA .DQ337526.1 GI:85001952.
188. *Shigella* sp. BBDP80 16S ribosomal RNA gene, partial sequence.1,503 bp linear DNA .DQ337525.1 GI:85001951.
189. *Eubacterium* sp. BBDP17 16S ribosomal RNA gene, partial sequence.1,486 bp linear DNA .DQ337524.1 GI:85001950.
190. *Shigella* sp. BBDP15 16S ribosomal RNA gene, partial sequence.1,503 bp linear DNA .DQ337523.1 GI:85001949.
191. *Corynebacterium* sp. BBDP21 16S ribosomal RNA gene, partial sequence.1,480 bp linear DNA .DQ337522.1 GI:85001948.
192. *Carnobacterium* sp. BBDP54 16S ribosomal RNA gene, partial sequence.1,523 bp linear DNA .DQ337521.1 GI:85001947.
193. *Enterococcus* sp. BBDP31 16S ribosomal RNA gene, partial sequence.1,522 bp linear DNA .DQ337520.1 GI:85001946.
194. *Corynebacterium* sp. BBDP55 16S ribosomal RNA gene, partial sequence.1,481 bp linear DNA .DQ337519.1 GI:85001945.
195. Swine effluent bacterium BBDP62 16S ribosomal RNA gene, partial sequence.1,516 bp linear DNA .DQ337518.1 GI:85001944.
196. *Microbacterium* sp. BBDP58 16S ribosomal RNA gene, partial sequence.1,486 bp linear DNA .DQ337517.1 GI:85001943.
197. *Leucobacter* sp. BBDP56 16S ribosomal RNA gene, partial sequence.1,489 bp linear DNA .DQ337516.1 GI:85001942.
198. *Microbacterium* sp. BBDP82 16S ribosomal RNA gene, partial sequence.1,486 bp linear DNA .DQ337515.1 GI:85001941.
199. *Microbacterium* sp. BBDP66 16S ribosomal RNA gene, partial sequence.1,486 bp linear DNA .DQ337514.1 GI:85001940.

200. *Psychrobacter psychrophilus* 16S ribosomal RNA gene, partial sequence.1,503 bp linear DNA .DQ337513.1 GI:85001939.
201. *Dietzia* sp. BBDP51 16S ribosomal RNA gene, partial sequence.1,483 bp linear DNA .DQ337512.1 GI:85001938.
202. *Corynebacterium* sp. BBDP60 16S ribosomal RNA gene, partial sequence.1,481 bp linear DNA .DQ337511.1 GI:85001937.
203. *Microbacterium* sp. BBDP44 16S ribosomal RNA gene, partial sequence.1,488 bp linear DNA .DQ337510.1 GI:85001936.
204. *Corynebacterium* sp. BBDP43 16S ribosomal RNA gene, partial sequence.1,481 bp linear DNA .DQ337509.1 GI:85001935.
205. *Dietzia* sp. BBDP49 16S ribosomal RNA gene, partial sequence.1,480 bp linear DNA .DQ337508.1 GI:85001934.
206. *Dietzia* sp. BBDP47 16S ribosomal RNA gene, partial sequence.1,479 bp linear DNA .DQ337507.1 GI:85001933.
207. *Dietzia* sp. BBDP42 16S ribosomal RNA gene, partial sequence.1,479 bp linear DNA .DQ337506.1 GI:85001932.
208. *Escherichia* sp. BBDP27 16S ribosomal RNA gene, partial sequence.1,503 bp linear DNA .DQ337505.1 GI:85001931.
209. Swine effluent bacterium BBDP25 16S ribosomal RNA gene, partial sequence.1,514 bp linear DNA .DQ337504.1 GI:85001930.
210. *Escherichia* sp. BBDP20 16S ribosomal RNA gene, partial sequence,1,503 bp linear DNA ,DQ337503.1 GI:85001929,
211. Uncultured bacterium clone S1-4-CL5 16S ribosomal RNA gene, partial sequence,1,511 bp linear DNA ,AY725263.1 GI:52082683.
212. Uncultured bacterium clone S1-4-CL2 16S ribosomal RNA gene, partial sequence.1,490 bp linear DNA .AY725262.1 GI:52082682.
213. Uncultured bacterium clone S1-4-CL6 16S ribosomal RNA gene, partial sequence.1,473 bp linear DNA..AY725261.1 GI:52082681.
214. Uncultured bacterium clone S1-4-CL1 16S ribosomal RNA gene, partial sequence.1,498 bp linear DNA .AY725260.1 GI:52082680.
215. Uncultured bacterium clone S1-3-CL17 16S ribosomal RNA gene, partial sequence.1,504 bp linear DNA .AY725259.1 GI:52082679.
216. Uncultured bacterium clone S1-3-CL12 16S ribosomal RNA gene, partial sequence.1,506 bp linear DNA .AY725258.1 GI:52082678.
217. Uncultured bacterium clone S1-3-CL2 16S ribosomal RNA gene, partial sequence.1,485 bp linear DNA .AY725257.1 GI:52082677.
218. Uncultured bacterium clone S1-2-CL8 16S ribosomal RNA gene, partial sequence.1,487 bp linear DNA .AY725256.1 GI:52082676.
219. Uncultured bacterium clone S1-2-CL7 16S ribosomal RNA gene, partial sequence.1,500 bp linear DNA.AY725255.1 GI:52082675.
220. Uncultured bacterium clone S1-2-CL6 16S ribosomal RNA gene, partial sequence.1,445 bp linear DNA .AY725254.1 GI:52082674.
221. Uncultured bacterium clone S1-2-CL5 16S ribosomal RNA gene, partial sequence.1,490 bp linear DNA .AY725253.1 GI:52082673.
222. Uncultured bacterium clone S1-2-CL3 16S ribosomal RNA gene, partial sequence.1,487 bp linear DNA .AY725252.1 GI:52082672.
223. Uncultured bacterium clone S1-2-CL1 16S ribosomal RNA gene, partial sequence.1,503 bp linear DNA .AY725251.1 GI:52082671.
224. Uncultured bacterium clone S1-1-CL14 16S ribosomal RNA gene, partial sequence.1,338 bp linear DNA .AY725250.1 GI:52082670.

225. Uncultured bacterium clone S1-1-CL12 16S ribosomal RNA gene, partial sequence.1,397 bp linear DNA .AY725249.1 GI:52082669.
226. Uncultured bacterium clone S1-1-CL9 16S ribosomal RNA gene, partial sequence.1,463 bp linear DNA .AY725248.1 GI:52082668.
227. Uncultured bacterium clone S1-1-CL4 16S ribosomal RNA gene, partial sequence.1,444 bp linear DNA .AY725247.1 GI:52082667.
228. Uncultured bacterium clone S1-1-CL2 16S ribosomal RNA gene, partial sequence.1,491 bp linear DNA .AY725246.1 GI:52082666.
229. *Burkholderia* sp CHNCT10 16S ribosomal RNA gene, partial sequence.1,494 bp linear DNA .EF471225.1 GI:134304920.
230. *Brevundimonas* sp. BBDP1031 16S ribosomal RNA gene, partial sequence.1,416 bp linear DNA .EF471238.1 GI:134304933.
231. *Brevundimonas* sp. BBDP1037 16S ribosomal RNA gene, partial sequence.1,425 bp linear DNA .EF471237.1 GI:134304932.
232. *Brevundimonas* sp. BBDP1026 16S ribosomal RNA gene, partial sequence.1,416 bp linear DNA .EF471236.1 GI:134304931.
233. *Brevundimonas* sp. BBDP1024 16S ribosomal RNA gene, partial sequence.1,414 bp linear DNA .EF471235.1 GI:134304930.
234. *Bacillus* sp. BBDP1032 16S ribosomal RNA gene, partial sequence.1,488 bp linear DNA .EF471234.1 GI:134304929.
235. *Alcaligenes* sp. BBTR16 16S ribosomal RNA gene, partial sequence.1,507 bp linear DNA .EF471233.1 GI:134304928.
236. *Psychrobacter* sp. BBTR1010 16S ribosomal RNA gene, partial sequence.1,500 bp linear DNA .EF471232.1 GI:134304927.
237. *Psychrobacter* sp. BBTR1013 16S ribosomal RNA gene, partial sequence.1,491 bp linear DNA .EF471231.1 GI:134304926.
238. *Enterobacter* sp. BBTR105 16S ribosomal RNA gene, partial sequence.1,479 bp linear DNA .EF471230.1 GI:134304925.
239. *Pseudomonas* sp. CHNCT21 16S ribosomal RNA gene, partial sequence.1,498 bp linear DNA .EF471229.1 GI:134304924.
240. *Pseudomonas* sp. CHNCT24 16S ribosomal RNA gene, partial sequence.1,500 bp linear DNA .EF471228.1 GI:134304923.
241. *Denitrobacter* sp. CHNCT17 16S ribosomal RNA gene, partial sequence.1,502 bp linear DNA .EF471227.1 GI:134304922.
242. *Lysobacter* sp. BBCT65 16S ribosomal RNA gene, partial sequence.1,506 bp linear DNA .EF471226.1 GI:134304921.
243. *Dyella* sp. CHNCT14 16S ribosomal RNA gene, partial sequence.1,506 bp linear DNA .EF471224.1 GI:134304919.
244. *Dyella* sp. CHNCT13 16S ribosomal RNA gene, partial sequence.1,506 bp linear DNA .EF471223.1 GI:134304918.
245. *Dyella* sp. CHNCT5 16S ribosomal RNA gene, partial sequence.1,506 bp linear DNA .EF471222.1 GI:134304917.
246. *Variovorax* sp. CHNCT9 16S ribosomal RNA gene, partial sequence.1,496 bp linear DNA .EF471221.1 GI:134304916.
247. *Burkholderia* sp. CHNCT3 16S ribosomal RNA gene, partial sequence.1,494 bp linear DNA .EF471220.1 GI:134304915.
248. *Xanthomonas* sp. BBCT38 16S ribosomal RNA gene, partial sequence.1,506 bp linear DNA .EF471219.1 GI:134304914.
249. *Chryseobacterium* sp. BBCT31 16S ribosomal RNA gene, partial sequence.1,479 bp linear DNA .EF471218.1 GI:134304913.

250. *Chryseobacterium* sp. BBCT17 16S ribosomal RNA gene, partial sequence. 1,478 bp linear DNA .EF471217.1 GI:134304912.
251. *Lysobacter* sp. BBCT6 16S ribosomal RNA gene, partial sequence. 1,506 bp linear DNA .EF471216.1 GI:134304911.
252. Uncultured *Acinetobacter* sp. isolate TTGE gel band I2-10c 16S ribosomal RNA gene, partial sequence. 526 bp DNA linear ENV 24-MAY-2011. HM583860.1 GI:301350796
253. Uncultured *Flavobacterium* sp. isolate TTGE gel band I2-10c 16S ribosomal RNA gene, partial sequence. 526 bp DNA linear ENV 24-MAY-2011. HM583861.1 GI:301350797
254. Uncultured *Acinetobacter* sp. isolate TTGE gel band I3-10f 16S ribosomal RNA gene, partial sequence HM583862.1 GI:301350798
255. *Acinetobacter* sp. isolate TTGE gel band I3-10b 16S ribosomal RNA gene, partial sequence. 517 bp DNA linear ENV 24-MAY-2011. HM583863.1 GI:301350799
256. *Ralstonia* sp. isolate TTGE gel band I3-20e 16S ribosomal RNA gene, partial sequence. 514 bp DNA linear ENV 24-MAY-2011 HM583864.1 GI:301350800
257. Bacterium I1-0-1 16S ribosomal RNA gene, partial sequence. 1349 bp DNA linear BCT 24-MAY-2011 HM583865.1 GI:301350801
258. Bacterium I1-0-5 16S ribosomal RNA gene, partial sequence. 1352 bp DNA linear BCT 24-MAY-2011 HM583866.1 GI:301350802
259. Bacterium I1-10-2 16S ribosomal RNA gene, partial sequence. 1332 bp DNA linear BCT 24-MAY-2011 HM583867.1 GI:301350803