

GWYN A. BEATTIE

ROBERT EARLE BUCHANAN DISTINGUISHED PROFESSOR OF BACTERIOLOGY
Iowa State University, Department of Plant Pathology, Entomology & Microbiology
4005 ATRB, 2213 Pammel Drive, Ames, IA 50011-1101
(515)294-5571, gbeattie@iastate.edu

EDUCATION

1991 **PhD** in Molecular and Cellular Biology, University of Wisconsin-Madison
1985 **BA** in Chemistry, Carleton College, Northfield, MN

PROFESSIONAL EXPERIENCE

2010-present Professor, Iowa State University (ISU), Dept of Plant Pathology, Entomology & Microbiology
2020-2021 Interim Chair, Dept of Plant Pathology & Microbiology, ISU
2003-2010 Associate Professor, Dept of Plant Pathology, ISU
2003-2006 Chair, Interdepartmental Microbiology Graduate Program, ISU
2002-2003 Assistant Professor, Dept of Plant Pathology, ISU
1995-2002 Assistant Professor, Dept of Microbiology, ISU
1991-1995 Post-doctoral Associate with Steven Lindow, University of California-Berkeley

RESEARCH AREA

Phytobacteriology, with an emphasis on the genomics and ecology of phyllosphere bacteria and the virulence mechanisms of foliar and vascular bacterial pathogens; Ecophysiology, with an emphasis on bacterial responses to light and water stress; and Agricultural microbiomes, with a focus on root microbiomes associated with abiotic stress tolerance.

AWARDS AND HONORS (LAST 10 YEARS)

2020 American Phytopathological Society Fellow
2018 Regents Award for Faculty Excellence
2006-present - Robert Earle Buchanan Distinguished Professor of Bacteriology for Research and Nomenclature (Endowed Chair), Iowa State University

PROFESSIONAL SERVICE (LAST 10 YEARS)

Editorial Positions:

Senior Editor, *Molecular Plant-Microbe Interactions* (2010-2015)
Co-Editor of a *Molecular Plant-Microbe Interactions* Focus Issue (2014-2015)
Editorial Board, *Applied and Environmental Microbiology* (2003-2014)

Federal Grant & Program Review Panels:

Member, DOE-BER Focus Area Triennial Review Team (2016)
Member, DOE-BER Focus Area Triennial Review Team (2015)
Panel, NSF-IOS Symbiosis, Defense and Self-Recognition (2013)
Panel, NSF-BREAD (2012)

Advisory Panels & Councils:

Prokaryotic Super Program Advisory Board for the Joint Genome Institute (2019-present)
Agricultural Microbiomes Research Coordination Network Scientific Steering Committee (NSF-funded) (August 2017-present)

Pacific Northwest National Laboratory Scientific Advisory Committee for the Predicting Ecosystem Resilience through multiscale and integrative science (PREMIS) project (2016-2018)

California Dept of Food and Agriculture Pierce's Disease Research Scientific Advisory Panel (2015-2018)

Foundation for Food and Agricultural Research (FFAR) Plant Efficiency Advisory Council (2016)

Alliances

Member, Board of Directors, International Alliance for Phytobiomes Research (2016-present)

Member, Committee to establish a National Microbiome Data Collaborative (2017-2020)

Service to Professional Societies:

Chair, American Phytopathological Society Public Policy Board (2016-2020)

Member, American Phytopathological Society Public Policy Board (2014-2016)

Invited participant, APS Thought Leaders Meeting (2013)

Panel member, APS competition for "The Schroth Faces of the Future Symposium" (2012)

Federal Program Activities:

Invited speaker and participant, American Society for Microbiology (ASM) Microbiome Stakeholder Workshop, 2019, Washington, D.C.

Invited participant, NSF Microbiome Workshop: Deciphering the microbiome - Empowering theory, cross-system analyses, and innovative analytics to propel advances in microbiome science, 2019, Alexandria, VA.

Invited participant, APS Emerging Pathogens Initiative Workshop, 2019, Cleveland, OH.

Invited participant, Alternatives to Antibiotics, Research Gap Analysis Workshop, 2016, National Animal Disease Center, Ames, IA.

Invited participant, Office of Science Technology & Policy Microbiome Event, Announcement of Microbiome Initiative, 2016, White House, Washington, D.C.

Invited participant, American Academy of Microbiology Colloquium on "How microbes can help feed the world", 2012, Washington, D.C.

Service at Professional Conferences:

Scientific Committee, *Phytobiomes 2022*, Denver, CO

Scientific Committee, *11th International Symposium on Phyllosphere Microbiology*, 2022, Davis, CA

Co-organizer, *International Phytobiomes Conference*, 2018, Montpellier, France

Co-organizer, Agricultural Microbiomes Workshop: Building a global research community to stimulate collaboration, leverage data and research platforms, and optimize science, 2018, Boston, MA

Co-organizer, *Keystone Symposium on Phytobiomes: From microbes to plant ecosystems*, 2016, Santa Fe, NM

Session Co-organizer on "Applications of phytobiomes in plant disease management", APS meeting, 2016, Tampa, FL.

Co-organizer, *Phytobiomes Roadmap Writing Workshop*, 2015, The Samuel Roberts Noble Foundation, Ardmore, OK

Scientific Committee, *10th International Symposium on Phyllosphere Microbiology*, 2015, Ascona, Switzerland

Co-organizer, *Phytobiomes 2015: Designing a New Paradigm for Crop Improvement*, 2015, Washington, D.C.

Session Co-organizer on "Understanding Phytobiomes to Improve Agricultural Productivity", APS meeting, 2014, Minneapolis, MN

Session Organizer, 14th Meeting of the International Society of Microbial Ecology, 2012,
Copenhagen, Denmark

Service to Other Universities:

Member, Nominating committee for the Ethel K. Allen Memorial Chair in Phytobacteriology,
University of Wisconsin-Madison (2014, 2019)

Society Memberships:

American Society for Microbiology, National and North Central Branch
American Phytopathological Society, National and North Central Branch
International Society for Molecular Plant-Microbe Interactions
American Association for the Advancement of Science

PUBLICATIONS (LAST 10 YEARS)

Refereed Journal Articles

- Freitas, C., A. Parra, P. Souza; P. Aderkas, C. Borchers, **G.A. Beattie**, F. Silva, and R. Thornburg. 2022. Ornamental tobacco floral nectar is a rich source of antimicrobial peptides. Accepted by Plant Science 324:111427 doi.org/10.1016/j.plantsci.2022.111427
- Olawole, O.I., M.L. Gleason and **G.A. Beattie**. 2022. Expression and functional analysis of the type III secretion system effector repertoire of the xylem pathogen *Erwinia tracheiphila* on cucurbits. *Molecular Plant-Microbe Interactions* 35:768-778 doi.org/10.1094/MPMI-01-22-0002-R
- LaSarre, B., O.I. Olawole, A.A. Paulsen, L.J. Halverson, M.L. Gleason and **G.A. Beattie**. 2022. Complete genome sequences of four strains of *Erwinia tracheiphila*: A resource for studying a bacterial plant pathogen with a highly complex genome. *Molecular Plant-Microbe Interactions* 35:500-504. doi.org/10.1094/MPMI-01-22-0008-A
- Olawole, O.I., Q. Liu, C. Chen, M.L. Gleason and **G.A. Beattie**. 2021. The contributions to virulence of the effectors Eop1 and DspE differ between two clades of *Erwinia tracheiphila*. *Molecular Plant-Microbe Interactions* 34:1399-1408. [doi: 10.1094/MPMI-06-21-0149-R](https://doi.org/10.1094/MPMI-06-21-0149-R)
- Fu, B., Y. Zhai, M. Gleason and **G.A. Beattie**. 2021. Characterization of *Erwinia tracheiphila* bacteriophage FBB1 isolated from spotted cucumber beetles that vector *E. tracheiphila*. *Phytopathology* 111:2185-2194. [doi: 10.1094/PHYTO-03-21-0093-R](https://doi.org/10.1094/PHYTO-03-21-0093-R)
- Fu, B., O. Olawole and **G. A. Beattie**. 2021. Biological control and microbial ecology draft genome sequence data of *Glutamicibacter* sp. FBE-19, a bacterium antagonistic to the plant pathogen *Erwinia tracheiphila*. *Phytopathology* 111:765-768. [doi: 10.1094/PHYTO-09-20-0380-A](https://doi.org/10.1094/PHYTO-09-20-0380-A)
- Kang, I.-J., K. S. Kim, **G.A. Beattie**, H. Chung, S. Heu and I. Hwang. 2021. Characterization of *Xanthomonas citris* pv. *glycines* population genetics and virulence in a national survey of bacterial pustule disease in Korea. *Plant Pathology Journal* 37:652-661. [doi: 10.5423/PPJ.FT.11.2021.0164](https://doi.org/10.5423/PPJ.FT.11.2021.0164)
- Kang, I.-J., K.-S. Kim, **G.A. Beattie**, J.-W. Yang, K.-H. Sohn S. Heu and I. Hwang. 2021. Pan-genome analysis of effectors in Korean strains of the soybean pathogen *Xanthomonas citri* pv. *glycines*. *Microorganisms* 9:2065 [doi: 10.3390/microorganisms9102065](https://doi.org/10.3390/microorganisms9102065)
- Dundore-Arias, J.P., E.A. Eloie-Fadrosch, L.M. Schriml, **G.A. Beattie**, F.P. Brennan, P.E. Busby, R.B. Calderon, S.C. Castle, J.B. Emerson, S.E. Everhart, K. Eversole, K.E. Frost, J.R. Herr, A.I. Huerta, A. S. Iyer-Pascuzzi, A.K. Kalil, J.E. Leach, J. Leonard, J.E. Maul, B. Prithiviraj, M. Potrykus, N.R. Redekar, J.A. Rojas, K.A.T. Silverstein, D.J. Tomso, S.G. Tringe, B.A. Vinatzer, and L.L. Kinkel. 2020. Community-driven Metadata Standards for Agricultural Microbiome Research. *Phytobiomes Journal* 4:115-121. [doi: 10.1094/PBIOMES-09-19-0051-P](https://doi.org/10.1094/PBIOMES-09-19-0051-P)
- Bell, T., K.L. Hockett, R.I. Alcalá-Briseño, M. Barbercheck, **G.A. Beattie**, M.A. Bruns, J.E. Carlson, T. Chung, A. Collins, B. Emmett, P. Esker, K.A. Garrett, L. Glenna, B.K. Gugino, M.

- del Mar Jiménez-Gasco, L. Kinkel, J. Kovac, K.P. Kowalski, G. Kuldau, J.H.J. Leveau, M.J. Michalska-Smith, J. Myrick, K. Peter, M. Fernanda Vivanco Salazar, A. Shade, N. Stopnisek, X. Tan, A.T. Welty, K. Wickings and E. Yergeau. 2019. Manipulating wild and tamed phytobiomes: Challenges and opportunities. *Phytobiomes Journal* 3:3-21. doi: [10.1094/PBIOMES-01-19-0006-W](https://doi.org/10.1094/PBIOMES-01-19-0006-W).
- Leandro, L.F.A., S. Eggenberger, C. Chen, J. Williams, **G.A. Beattie** and M. Liebman. 2018. Cropping system diversification reduces severity and incidence of soybean sudden death syndrome caused by *Fusarium virguliforme*. *Plant Disease* 102:1748-1758. doi: [10.1094/PDIS-11-16-1660-RE](https://doi.org/10.1094/PDIS-11-16-1660-RE)
- Beattie, G.A.**, B.M. Hatfield, H. Dong and R.S. McGrane. 2018. Seeing the light: The roles of red- and blue-light sensing in plant microbes. *Annual Review of Phytopathology* 56:41-66. doi: [10.1146/annurev-phyto-080417-045931](https://doi.org/10.1146/annurev-phyto-080417-045931)
- Liu, Q., **G.A. Beattie**, E. Saalau Rojas and M.L. Gleason. 2018. Bacterial wilt symptoms are impacted by host age and involve net downward movement of *Erwinia tracheiphila* in muskmelon. *European Journal of Plant Pathology* 151:803-810. doi: [10.1007/s10658-018-1418-7](https://doi.org/10.1007/s10658-018-1418-7)
- McGrane, R. and **G.A. Beattie**. 2017. *Pseudomonas syringae* pv. *syringae* B728a regulates multiple stages of plant colonization via the bacteriophytochrome BphP1. *mBio* 8:301178-17. doi: [10.1128/mBio.01178-17](https://doi.org/10.1128/mBio.01178-17)
- Michelmore, R.W., G. Coaker, R. Bart, **G.A. Beattie**, A. Bent, T. Bruce, D. Cameron, J. Dangel, S. Dinesh-Kumar, R. Edwards, S. Eves-van den Akker, W. Gassmann, J. Greenberg, R. Harrison, P. He, L. Hanley-Bowdoin, J. Harvey, A. Huffaker, S. Hulbert, R. Innes, J.D. Jones, I. Kaloshian, S. Kamoun, F. Katagiri, J.E. Leach, W. Ma, J.M. McDowell, J. Medford, B. Meyers, R. Nelson, R.P. Oliver, Y. Qi, D. Saunders, M. Shaw, C. Smart, P. Subudhi, L. Torrance, B.M. Tyler, V. Valent and J. Walsh. 2017. Foundational and translational research opportunities to improve plant health. *Molecular Plant-Microbe Interactions* 30:515-516. doi: [10.1094/MPMI-01-17-0010-CR](https://doi.org/10.1094/MPMI-01-17-0010-CR)
- Shapiro, L.R., E.D. Scully, T.J. Straub, J. Park, A.G. Stephenson, **G. Beattie**, M. Gleason, R. Kolter, M. C. Coelho, C.M de Moraes, M.C. Mescher, and O. Zhaxybayeva. 2016. Horizontal gene acquisitions, mobile element proliferation, and genome decay in the host-restricted plant pathogen *Erwinia tracheiphila*. *Genome Biology and Evolution* 8:649-664 doi: [10.1093/gbe/evw016](https://doi.org/10.1093/gbe/evw016)
- Shapiro, L.R., E.D. Scully, D. Roberts, T.J. Straub, S.M. Geib, J. Park, A.G. Stephenson, E. Saalau Rojas, Q. Liu, **G. Beattie**, M. Gleason, C.M de Moraes, M.C. Mescher, S.G. Fleischer, R. Kolter, N. Pierce and O. Zhaxybayeva. 2015. Draft genome sequence of *Erwinia tracheiphila*, an economically important bacterial pathogen of cucurbits. *Genome Announcements-Prokaryotes* 3:e00482-15. doi: [10.1128/genomeA.00482-15](https://doi.org/10.1128/genomeA.00482-15)
- Saalau Rojas, E., J. C. Batzer, **G. A. Beattie**, S. J. Fleischer, L. R. Shapiro, M. A. Williams, R. Bessin, B. D. Bruton, T. J. Boucher, L. C. H. Jesse and M. L. Gleason. 2015. Bacterial wilt of cucurbits: Resurrecting a classic pathosystem. *Plant Disease* 99:564-574. doi: [10.1094/PDIS-10-14-1068-FE](https://doi.org/10.1094/PDIS-10-14-1068-FE)
- Yu, X., S. P. Lund, J. W. Greenwald, A. H. Records, R. A. Scott, D. Nettleton, S. E. Lindow, D. C. Gross and **G. A. Beattie**. 2014. Transcriptional analysis of the global regulatory networks active in *Pseudomonas syringae* during leaf colonization. *mBio* 5:e01683-14. doi: [10.1128/mBio01683-14](https://doi.org/10.1128/mBio01683-14)
- Freeman, B. C., C. Chen, X. Yu, L. Nielsen, K. Peterson and **G. A. Beattie**. 2013. Physiological and transcriptional responses to osmotic stress of two *Pseudomonas syringae* strains that differ

- in epiphytic fitness and osmotolerance. *Journal of Bacteriology* 195:4742-4752. doi: [10.1128/JB.00787-13](https://doi.org/10.1128/JB.00787-13)
- Chen, C., S. Li, D. R. McKeever and **G. A. Beattie**. 2013. The widespread plant-colonizing bacterial species *Pseudomonas syringae* detects and exploits an extracellular pool of choline in hosts. *The Plant Journal*. 75:891-901. doi: [10.1111/tpj.1226](https://doi.org/10.1111/tpj.1226) (This is a Faculty of 1000 Prime Recommended Read) (cover illustration)
- Wu, L, R. S. McGrane and **G. A. Beattie**. 2013. Light regulation of swarming motility in *Pseudomonas syringae* integrates signaling pathways mediated by a bacteriophytochrome and a LOV protein. *mBio* 3:e00334-13. doi: [10.1128/mBio.00334-13](https://doi.org/10.1128/mBio.00334-13) (cover illustration)
- Li, S., X. Yu, G. A. Beattie. 2013. Glycine betaine catabolism contributes to *Pseudomonas syringae* tolerance to hyperosmotic stress by relieving betaine-mediated suppression of compatible solute synthesis. *Journal of Bacteriology* 10:2415-2423. doi: [10.1128/JB.00094-13](https://doi.org/10.1128/JB.00094-13)
- Yu, X., S. P. Lund, R. A. Scott, J. W. Greenwald, A. H. Records, D. Nettleton, S. E. Lindow, D. C. Gross, and **G. A. Beattie**. 2013. Transcriptional responses of *Pseudomonas syringae* to growth in epiphytic versus apoplastic leaf sites. *Proc. Natl. Acad. Sci. U.S.A.*, 110:E425-E434. doi: [10.1073/pnas.1221892110](https://doi.org/10.1073/pnas.1221892110)

Book Chapters

- Etesami, H. and **G. A. Beattie**. 2017. Plant-microbe interactions in adaptation of agricultural crops to abiotic stress conditions, pp. 163-200. In: V. Kumar, M. Kumar, S. Sharma and R. Prasad (eds). *Probiotics and Plant Health*, Springer Nature Singapore Pte Ltd, Singapore. doi:[10.1007/978-981-10-3473-2_7](https://doi.org/10.1007/978-981-10-3473-2_7)
- Beattie, G. A.**, C. Chen, L. Nielsen and B. C. Freeman. 2016. Interstrain variation in the physiological and transcriptional responses of *Pseudomonas syringae* to osmotic stress, pp. 649-656. In: F. de Bruin (ed), *Stress and Environmental Regulation of Gene Expression and Adaptation in Bacteria*, Wiley-Blackwell Publishers.

Non-referred articles:

- Beattie, G.A.** 2018. Microbiomes: Metabolic coupling on roots. *Nature Microbiology* 3:396-397. doi: [10.1038/s41564-018-1039-1](https://doi.org/10.1038/s41564-018-1039-1)
- Etesami, H. and **G.A. Beattie**. 2018. Mining halophytes for plant growth-promoting halotolerant bacteria to enhance the salinity tolerance of non-halophytic crops. *Frontiers in Microbiology* 9:Article No. 148 doi: [10.3389/fmicb.2018.00148](https://doi.org/10.3389/fmicb.2018.00148)
- Beattie, G.A.** 2016. Plant Science: A war over water when bacteria invade leaves. *Nature* 539:506-507. doi: [10.1038/nature16319](https://doi.org/10.1038/nature16319)
- Beattie, G.A.** 2015. Microbiomes: Curating communities from plants. *Nature* 528:340-341. doi: [10.1038/539506a](https://doi.org/10.1038/539506a)
- Beattie, G.A.**, D. Desveaux and S. Kang. 2015. Focus on the good, the bad and the unknown: Genomics-enabled discovery of plant-associated microbial processes and diversity. *Mol. Plant-Microb. Interact.* 28:211 doi: [10.1094/MPMI-28-03-0211](https://doi.org/10.1094/MPMI-28-03-0211)

Extension and outreach publications:

- McCluskey, K., K. Boundy-Mills and **G.A. Beattie**. 2018. Complying with the Nagoya Protocol to the convention on biological diversity. *SIMB (Society for Industrial Microbiology) News* 68(1):8
- McCluskey, K. and **G.A. Beattie**. 2018. What you should know about obtaining and using organisms from other countries. *Phytopathology News* 52(2):22
- Beattie, G.A.** 2017. PPB Queries APS membership on advocacy targets. *Phytopathology News* 51(1):12
- Dundore-Arias, J.P. and **G.A. Beattie**. 2015. Phytobiomes in the classroom. *Phytopathology News* 49(4):47.