

Alexandra J Weisberg

CONTACT

Dept. of Botany and Plant Pathology
Oregon State University
4575 SW Research Way
Corvallis, Oregon, 97333, USA

Email: weisbeal@oregonstate.edu
Website: alexandra-weisberg.com
Twitter: [@weisbergaj](https://twitter.com/weisbergaj)

PROFESSIONAL EXPERIENCE

Postdoctoral Researcher, Oregon State University, Jeff Chang & Niklaus Grünwald labs
Research Associate, Postdoc 2019-Present
USDA NIFA Postdoctoral Fellow 2017-2019
Postdoctoral Scholar 2015-2017
Research Assistant, Virginia Tech, Boris Vinatzer lab 2014

EDUCATION

Virginia Polytechnic Institute and State University (Virginia Tech), Blacksburg, VA, USA
Ph.D., Genetics, Bioinformatics, and Computational Biology 2010–2014
John Jelesko lab
Dissertation: Investigations into the molecular evolution of plant terpene, alkaloid, and urushiol biosynthetic enzymes assoc. with Translational Plant Sciences program
B.S., Computer Science 2006–2009
Mathematics minor

FIRST AUTHOR PUBLICATIONS

34 publications (9 first author)

** indicates co-first authorship*

[Diversification of plasmids in a genus of pathogenic and nitrogen-fixing bacteria](#)

Weisberg A. J., Miller M., Ream W., Grünwald N. J., Chang J. H.
Philosophical Transactions of the Royal Society B 377.1842 (2021) p. 20200466.

[Genomic Approaches to Plant-Pathogen Epidemiology and Diagnostics](#)

Weisberg A. J., Grünwald N. J., Savory E. A., Putnam M. L., Chang J. H.
Annual Review of Phytopathology 59 (2021).

[Unexpected conservation and global transmission of agrobacterial virulence plasmids](#)

Weisberg A. J., Davis E. W., Tabima J., Belcher M. S., Miller M., Kuo C.-H., Loper J. E., Grünwald N. J., Putnam M. L., Chang J. H.
Science 368.6495 (2020).

[A novel species-level group of *Streptomyces* exhibits variation in phytopathogenicity despite conservation of virulence loci](#)

Weisberg A. J., Kramer C. G., Kotha R. R., Luthria D. L., Chang J. H., Clarke C. R.
Molecular Plant-Microbe Interactions (2020) *MPMI*–06.

Phytopathogenic *Rhodococcus* have diverse plasmids with few conserved virulence functions

Savory E. A. *, Weisberg A. J. *, Stevens D. M., Creason A. L., Fuller S. L., Pearce E. M., Chang J. H.
Frontiers in Microbiology 11 (2020) p. 1022.

Sequencing and *de novo* assembly of the *Toxicodendron radicans* (poison ivy) transcriptome

Weisberg A. J., Kim G., Westwood J. H., Jelesko J. G.
Genes 8.11 (2017) p. 317.

Evolutionary transitions between beneficial and phytopathogenic *Rhodococcus* challenge disease management

Savory E. A. *, Fuller S. L. *, Weisberg A. J. *, Thomas W. J., Gordon M. I., Stevens D. M., Creason A. L., Belcher M. S., Serdani M., Wiseman M. S., Grünwald N. J., Putnam M. L., Chang J. H.
eLife 6 (2017) e30925.

Gall-ID: tools for genotyping gall-causing phytopathogenic bacteria

Davis II E. W. *, Weisberg A. J. *, Tabima J. F., Grünwald N. J., Chang J. H.
PeerJ 4 (2016) e2222.

Similarity-based codes sequentially assigned to ebolavirus genomes are informative of species membership, associated outbreaks, and transmission chains

Weisberg A. J., Elmarakeby H. A., Heath L. S., Vinatzer B. A.
Open Forum Infectious Diseases 2 (2015) ofv024.

CO-AUTHOR
PUBLICATIONS

Application of whole genome sequencing to understand diversity and presence of genes associated with sanitizer tolerance in *Listeria monocytogenes* from produce handling sources

Bland R. N., Johnson J. D., Waite-Cusic J. G., Weisberg A. J., Riutta E. R., Chang J. H., Kovacevic J.
Foods 10.10 (2021) p. 2454.

Diversification of the Type VI Secretion System in *Agrobacteria*

Wu C.-F., Weisberg A. J., Davis E. W., Chou L., Khan S., Lai E.-M., Kuo C.-H., Chang J. H.
mBio 12.5 (2021) e01927–21.

Experimental evolution can enhance benefits of rhizobia to novel legume hosts

Quides K. W., Weisberg A. J., Trinh J., Salaheldine F., Cardenas P., Lee H.-H., Jariwala R., Chang J. H., Sachs J. L.
Proceedings of the Royal Society B 288.1951 (2021) p. 20210812.

Evolution of specialization in a plant-microbial mutualism is explained by the oscillation theory of speciation

Torres-Martínez L., Porter S. S., Wendlandt C., Purcell J., Ortiz-Barbosa G., Rothschild J., Lampe M., Warisha F., Le T., Weisberg A. J., Chang J. H., Sachs J. L.
Evolution 75.5 (2021) pp. 1070–1086.

Recurrent mutualism breakdown events in a legume rhizobia metapopulation

Gano-Cohen K. A., Wendlandt C. E., Al Moussawi K., Stokes P. J., Quides K. W., Weisberg A. J., Chang J. H., Sachs J. L.
Proceedings of the Royal Society B 287.1919 (2020) p. 20192549.

[A deoR-type transcription regulator is required for sugar-induced expression of Type III secretion-encoding genes in *Pseudomonas syringae* pv. tomato DC3000](#)

Turner S. E., Pang Y.-Y., O'Malley M. R., [Weisberg A. J.](#), Fraser V. N., Yan Q., Chang J. H., Anderson J. C.
Molecular Plant-Microbe Interactions 33.3 (2020) pp. 509–518.

[Antibacterial potential of secondary metabolites from Indonesian marine bacterial symbionts](#)

Nofiani R., [Weisberg A. J.](#), Tsunoda T., Panjaitan R. G. P., Brilliantoro R., Chang J. H., Philmus B., Mahmud T.
International Journal of Microbiology 2020 (2020).

[Phenotypic characterization and phylogenetic analysis of *Pseudomonas syringae* strains associated with canker disease on apricot in Iran within the context of the global genetic diversity of the *P. syringae* complex](#)

Vasebi Y., Khakvar R., Tian L., Moubarak P., Valentini F., [Weisberg A. J.](#), Vinatzer B. A.
European Journal of Plant Pathology 158 (2020) pp. 545–560.

[Biosynthesis of the nuclear factor of activated T cells inhibitor NFAT-133 in *Streptomyces pactum*](#)

Zhou W., Posri P., Abugrain M. E., [Weisberg A. J.](#), Chang J. H., Mahmud T.
ACS Chemical Biology (2020).

[The evolution, ecology, and mechanisms of infection by gram-positive, plant-associated bacteria](#)

Thapa S. P., Davis E. W., Lyu Q., [Weisberg A. J.](#), Stevens D. M., Clarke C. R., Coaker G., Chang J. H.
Annual Review of Phytopathology 57 (2019) pp. 341–365.

[Re-evaluation of a Tn 5:: gacA mutant of *Pseudomonas syringae* pv. tomato DC3000 uncovers roles for uvrC and anmK in promoting virulence](#)

O'Malley M. R., [Weisberg A. J.](#), Chang J. H., Anderson J. C.
PLOS One 14.10 (2019) e0223637.

[Genomic and metabolic differences between *Pseudomonas putida* populations inhabiting sugarcane rhizosphere or bulk soil](#)

Lopes L. D., [Weisberg A. J.](#), Davis E. W., Varize C. d. S., Pereira e Silva M. d. C., Chang J. H., Loper J. E., Andreote F. D.
PLOS One 14.10 (2019) e0223269.

[Tropical soils are a reservoir for fluorescent *Pseudomonas* spp. biodiversity](#)

Lopes L. D., Davis E. W., Pereira e Silva M. d. C., [Weisberg A. J.](#), Bresciani L., Chang J. H., Loper J. E., Andreote F. D.
Environmental Microbiology 20.1 (2018) pp. 62–74.

[Response to comments on "Evolutionary transitions between beneficial and phytopathogenic *Rhodococcus* challenge disease management"](#)

Chang J. H., Putnam M. L., Grünwald N. J., Savory E. A., Fuller S. L., [Weisberg A. J.](#)
eLife 7 (2018) e35852.

[Transient heterologous gene expression methods for poison ivy leaf and cotyledon tissues](#)

Dickinson C. C., [Weisberg A. J.](#), Jelesko J. G.
HortScience 53.2 (2018) pp. 242–246.

The population genetic test Tajima's D identifies genes encoding pathogen-associated molecular patterns and other virulence-related genes in *Ralstonia solanacearum*

Eckshtain-Levi N., Weisberg A. J., Vinatzer B. A.
Molecular Plant Pathology 19.9 (2018) pp. 2187–2192.

Genome variations between rhizosphere and bulk soil ecotypes of a *Pseudomonas koreensis* population

Lopes L. D., Pereira e Silva M. d. C., Weisberg A. J., Davis E. W., Yan Q., Varize C. d. S., Wu C.-F., Chang J. H., Loper J. E., Andreote F. D.
Environmental Microbiology 20.12 (2018) pp. 4401–4414.

Evolution of the US biological select agent *Rathayibacter toxicus*

Davis E. W., Tabima J. F., Weisberg A. J., Lopes L. D., Wiseman M. S., Wiseman M. S., Pupko T., Belcher M. S., Sechler A. J., Tancos M. A., Schroeder B. K., Murray T. D., Luster D. G., Schneider W. L., Rogers E. E., Andreote F. D., Grünwald N. J., Putnam M. L., Chang J. H.
mBio 9.4 (2018).

Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant-pathogen interactions in a tree

Muchero W., Sondreli K. L., Chen J.-G., Urbanowicz B. R., Zhang J., Singan V., Yang Y., Brueggeman R. S., Franco-Coronado J., Abraham N., Yang J.-Y., Moremen K. W., Weisberg A. J., Chang J. H., Lindquist E., Barry K., Ranjan P., Jawdy S., Schmutz J., Tuskan G. A., LeBoldus J. M.
Proceedings of the National Academy of Sciences 115.45 (2018) pp. 11573–11578.

A proposal for a genome similarity-based taxonomy for plant-pathogenic bacteria that is sufficiently precise to reflect phylogeny, host range, and outbreak affiliation applied to *Pseudomonas syringae* sensu lato as a proof of concept

Vinatzer B. A., Weisberg A. J., Monteil C. L., Elmarakeby H. A., Sheppard S. K., Heath L. S.
Phytopathology 107.1 (2017) pp. 18–28.

Morphological and transcriptomic evidence for ammonium induction of sexual reproduction in *Thalassiosira pseudonana* and other centric diatoms

Moore E. R., Bullington B. S., Weisberg A. J., Jiang Y., Chang J., Halsey K. H.
PLOS One 12.7 (2017) e0181098.

Isothermal amplification and lateral-flow assay for detecting crown-gall-causing *Agrobacterium* spp.

Fuller S. L., Savory E. A., Weisberg A. J., Buser J. Z., Gordon M. I., Putnam M. L., Chang J. H.
Phytopathology 107.9 (2017) pp. 1062–1068.

Microbe-ID: an open source toolbox for microbial genotyping and species identification

Tabima J. F., Everhart S. E., Larsen M. M., Weisberg A. J., Kamvar Z. N., Tancos M. A., Smart C. D., Chang J. H., Grünwald N. J.
PeerJ 4 (2016) e2279.

Genome-enabled phylogeographic investigation of the quarantine pathogen *Ralstonia solanacearum* race 3 biovar 2 and screening for sources of resistance against its core effectors

Clarke C. R., Studholme D. J., Hayes B., Runde B., Weisberg A., Cai R., Wroblewski T., Daunay M.-C., Wicker E., Castillo J. A., Vinatzer B. A.
Phytopathology 105.5 (2015) pp. 597–607.

Phylobiochemical characterization of class-Ib aspartate/prephenate aminotransferases reveals evolution of the plant arogenate phenylalanine pathway

Dornfeld C., Weisberg A. J., KC R., Dudareva N., Jelesko J. G., Maeda H. A.
Plant Cell 26.7 (2014) pp. 3101–3114.

MANUSCRIPTS
IN PREP OR
UNDER
REVISION

"Pangenome evolution reconciles robustness and instability of symbioses" Weisberg A.J., Rahman A., Backus D., Tyavanagimatt P., Chang J.H., Sachs J.L. under review at Nature Communications.

"Dynamic interactions between mega-sized symbiosis integrative and conjugative elements and bacterial chromosomes" Weisberg A.J., Sachs J.L., Chang J.H. follow-up to the above manuscript, prepared for submission to mBio.

"Genome resources for tumorigenic *Rhizobium* spp. isolated from blueberry plants with aerial crown gall" Weisberg A.J., Sanahuja G., Umble J., Miller M., Khalib N.A., Chang J.H., and Stockwell V.O. submitted to Phytopathology.

"*Streptomyces canutascabiei* sp. nov., which causes potato common scab and is distributed across the world" Clarke C., Nguyen H.P., Weisberg A.J., Chang J.H. submitted to IJSEM.

"Adaptation to a commercial quaternary ammonium compound sanitizer leads to cross-resistance to select antibiotics in *Listeria monocytogenes* isolated from fresh produce environments" Bland R., Waite-Cusic J., Weisberg A.J., Riutta E.R., Chang J.H., Kovacevic J. submitted to Frontiers in Microbiology.

"Dual Adhesive Unipolar Polysaccharides Synthesized by Overlapping Biosynthetic Pathways in *Agrobacterium tumefaciens*" Onyeziri M.C., Natarajan R., Hardy G.G., Xu J., Reynolds I.P., Kim J., Merritt P.M., Danhorn T., Hibbing M.E., Weisberg A.J., Chang J.H., Fuqua C. Preprint available at <https://www.biorxiv.org/content/10.1101/2021.04.22.440995v1>

"Modular evolution of secretion systems and virulence plasmids in a bacterial species complex" Chou L., Lin Y.C., Haryono M., Santos M.N.M., Cho S.T., Weisberg A.J., Wu C.F., Chang J.H., Lai E.M, Kuo C.H. Preprint available at <https://www.biorxiv.org/content/10.1101/2021.05.20.444927v2>

Plus two additional manuscripts in preparation.

FUNDING & FELLOWSHIPS	USDA NIFA Postdoctoral Fellowship	\$152,000	2016
	MPS program mini grant for dept. purchase of high memory server for assembly and transcriptomics. Kim G, Weisberg A, Fedkenheuer M, Fedkenheuer K, Fang Y	\$24,000	2013
	Molecular Plant Sciences program travel award for Workshop on Molecular Evolution at Woods Hole	\$2,000	2011
	Virginia Tech Scholars Award	\$2,000	2006
TEACHING	Instructor of record, BI 311 Genetics		Winter 2020
	<ul style="list-style-type: none"> • Required for undergraduates majoring in the life sciences 173 students 4 credit lecture and recitation 		
	Guest lecture, Plant Physiology , St. Mary's College of Maryland		Nov 2021
	<i>Invited as guest lecturer for a class discussion on genomic epidemiology in agriculture for BIOL 435: Plant Physiology at St. Mary's.</i>		
	Nanopore sequencing workshop , Oregon State University		Dec 2019
	<i>Led a workshop and discussion group on nanopore sequencing, including DNA extraction techniques, experiences with MinION sequencing, and ease of use.</i>		
	Microbial comparative genomics and Publication quality figures in R workshops , Virginia Tech		Nov 2019
<i>Invited to teach two workshops, one on microbial comparative genomics techniques and analyses, and another on making publication-quality figures in R. Graduate students in the Translational Plant Sciences program attended and performed analyses with example data.</i>			
Guest lecture, Microbial Forensics and Biosecurity , Virginia Tech		Nov 2019	
<i>Invited as guest lecturer on Agrobacterium and agricultural epidemiology methods and challenges for an undergraduate PPWS 4114 Microbial Forensics and Biosecurity class at Virginia Tech.</i>			
Microbiome Training Workshop , Oregon State University		May 2017	
<i>TA for a workshop on analyzing microbiome data.</i>			
OUTREACH	DNA Biology and Bioinformatics STEM Camp		Jul 2019
David Douglas High School/Nestucca High School, Oregon State University			
<i>Developed and led lab and bioinformatics sections as part of a 3 day summer STEM camp for underrepresented high school students from Portland, OR and Cloverdale, OR. Students learned to transcribe DNA to RNA and translate protein sequences, identify genes with BLAST, and examine 3D protein structure.</i>			

ASE Midsummer Conference Workshop Oregon State University Aug 2018
Taught as part of a hands-on workshop for high school STEM interns on the history of agriculture titled "AnthroBiology, Mutants, GMOs, and Big Data - The History of Food", examining the relationship of corn to teosinte and modern genetics of sweet corn.

DNA Biology and Bioinformatics STEM Camp Jul 2018
 David Douglas High School, Oregon State University
Developed and led lab and bioinformatics sections as part of a 3 day summer STEM camp for underrepresented high school students from Portland, OR. Students learned to transcribe DNA to RNA and translate protein sequences, identify genes with BLAST, and examine 3D protein structure.

DNA Biology and Bioinformatics STEM camps, Oregon State University 2015-2017
Developed and led lab sections and taught bioinformatics classes as part of 2-week summer STEM camps targeted at local and Portland,OR high school students.
 - *Students learned to extract DNA, run PCR, and perform either genome sequencing and assembly (2015,2016) or microbiome sequencing and analysis (2017).*
 - *Camps were developed to particularly encourage women and other underrepresented groups to consider pursuing a career in STEM fields.*

MENTORING

Undergraduates and Postbacc.

Riely White, Elizabeth Riutta, Emma Pearce, Kaavya Subramanian, Casey Huggins, Joey Edgerton, Dakota Backus, Heidi Lederhos, Michael Belcher, Ash Gill - *Oregon State University*

Oscar Tanner - *Virginia Tech*

High School students

Ella Rose, Parinita Tyavanagimatt

Visiting graduate students and postdocs

Kenjiro Quides, Lucas Dantas, Lorena Torres Martinez, Angela Porter

PROFESSIONAL SERVICE

Reviewer for the journals:

- Molecular Biology and Evolution (MBE)
- Molecular Plant-Microbe Interactions (MPMI)
- mSystems
- New Phytologist
- Phytopathology
- Science Advances

Postdoc member of departmental seminar committee	2021
Assisted with managing departmental computing infrastructure	2015-Present
Postdoc member of search committee for tenure track faculty position in the Department of Botany and Plant Pathology	2018
Plant Pathology, Physiology, and Weed Science GSO	2012-2014
Secretary/Treasurer, Virginia Tech	
Co-coordinator for Molecular Plant Science Discussion Group, Virginia Tech	2012-2014
Molecular Plant Sciences GSO Bioinformatics Committee member, Virginia Tech	2012-2014
Co-organized Workshop on whole genome/RNA-seq, Virginia Tech	Apr 2013
Co-organized PPWS Research Symposium, Virginia Tech	Oct 2012

MEMBERSHIPS	IS-MPMI - International Society for Molecular Plant-Microbe Interactions	
INVITED TALKS	Mid-Atlantic Plant Molecular Biology Society 2021 Towson, VA <i>MAPMBS 2021 meeting invited talk "Modularity underpins the evolution of nitrogen fixing symbiosis"</i>	Aug 2021
	Phytobiomes Alliance webinar <i>"Genomic approaches to the epidemiology and diagnostics of phytopathogens: tracking the global spread of agrobacteria"</i> Viewed by 75 attendees, >100 views online. https://www.youtube.com/watch?v=7d6oKrtXBsU	Jul 2020
	Departmental Seminar Virginia Tech, Blacksburg, VA <i>Genetics, Bioinformatics, and Computational Biology department seminar "Evolution and epidemiology of the natural genetic engineer Agrobacterium"</i>	Nov 2019
	Departmental Seminar University of Arizona, Tucson, AZ <i>School of Plant Sciences Departmental Seminar "Evolution of the Natural Genetic Engineer: Agrobacterium"</i>	Sep 2018
CONFERENCES & PRESENTATIONS	Departmental Seminar Oregon State University, Corvallis, OR <i>Botany and Plant Pathology Departmental Seminar "Modularity Underpins the Evolution of Nitrogen Fixing Symbiosis"</i>	Jan 2021
	Bioinformatics Users Group (BUG) Oregon State University, Corvallis, OR <i>"Getting started with Nanopore sequencing in the lab: i.e. you can do it, and it's not a random sequence generator anymore!"</i>	May 2020
	Departmental Seminar Oregon State University, Corvallis, OR <i>Botany and Plant Pathology Departmental Seminar "Mobilome flexibility confers robustness to good and bad symbionts of plants" tag team with Jeff Chang</i>	Apr 2020
	39th Crown Gall Conference University of Missouri, Columbia, MO <i>"Evolution and epidemiology of the natural genetic engineer Agrobacterium"</i>	Oct 2019
	CGRB Fall Conference Oregon State University, Corvallis, OR <i>lightning talk "Evolution and epidemiology of the natural genetic engineer Agrobacterium"</i>	Sep 2019
	2019 IS-MPMI XVIII Congress Glasgow, Scotland <i>poster "The genomic bases for cheating among wild populations of nodule-associated Bradyrhizobium"</i>	Jul 2019
	2019 IS-MPMI XVIII Congress Glasgow, Scotland <i>satellite conference invited talk/workshop "Genome Visualization Tools"</i>	Jul 2019

9th Yosemite Symbiosis Workshop Yosemite, CA <i>"The genomic bases for cheating among wild populations of nodule-associated Bradyrhizobium"</i>	May 2019
Plant & Animal Genome Conference XXVII San Diego, CA <i>"Evolution of the Natural Genetic Engineer: Agrobacterium"</i>	Jan 2019
NIFA Fellows Project Director's Meeting USDA NIFA, Washington, DC <i>poster "Characterizing Competitiveness And Persistence Of Agrobacteria In The Crown Gall Disease Niche"</i>	Aug 2018
Bioinformatics Users Group (BUG) Oregon State University, Corvallis, OR <i>"Characterizing the population genetic history of Rhodococcus and tracking disease outbreaks in the nursery industry"</i>	Nov 2017
38th Crown Gall Conference Oregon State University, Corvallis, OR <i>"Evolution of the Agrobacterium secondary and tertiary replicons"</i>	Oct 2017
Departmental Seminar Oregon State University, Corvallis, OR <i>Botany and Plant Pathology Departmental Seminar "Modeling the evolution of Agrobacterium Ti plasmids"</i>	Mar 2017
37th Crown Gall Conference Indiana University, Bloomington, IN <i>"The characterization of novel Ti plasmid types"</i>	Oct 2016
CGRB Fall Conference Oregon State University, Corvallis, OR <i>poster "Ti plasmids cluster genetically and cluster by Agrobacterium taxa and plant host type"</i>	Sep 2016
2016 IS-MPMI XVII Congress Portland, OR <i>poster "Ti plasmids cluster genetically and cluster by Agrobacterium taxa and plant host type"</i>	Jun 2016
36th Crown Gall Conference DowAgrosciences, Zionsville, IN <i>"Ti plasmids cluster according to opine type and are augmented by a large gene pool"</i>	Nov 2015
CGRB Fall Conference Oregon State University, Corvallis, OR <i>poster "Deep sequencing of crown gall-forming Agrobacterium genera reveals diversity in population structure and Ti plasmid sequence"</i>	Sep 2015
MPS Mini-Symposium Virginia Tech, Blacksburg, VA <i>"De novo assembly of the Toxicodendron radicans (poison ivy) transcriptome"</i>	Feb 2014

- Departmental seminar** Virginia Tech, Blacksburg, VA Nov 2013
*"De novo assembly of the *Toxicodendron radicans* (poison ivy) transcriptome"*
- Departmental seminar** Virginia Tech, Blacksburg, VA Apr 2013
"Examining the molecular evolution of neofunctionalization in plant secondary metabolism"
- MPS Mini-Symposium** Virginia Tech, Blacksburg, VA Mar 2012
poster "Identifying effectively-mutable protein space using measures of natural selection: a meta-analysis of two terpene synthase gene families"
- Banff Conference on Plant Metabolism** Banff, Alberta, Canada Jun 2010
poster "Molecular evolution of plant tyrosine and phenylalanine biosynthesis"
- MPS Mini-Symposium** Virginia Tech, Blacksburg, VA Jan 2010
poster "Molecular evolution of plant tyrosine and phenylalanine biosynthesis"

SOCIAL MEDIA
& PRESS

For *"Unexpected conservation and global transmission of agrobacterial virulence plasmids"* Science 368, 6495, eaba5256:
<https://www.sciencedaily.com/releases/2020/06/200604152111.htm>
https://www.eurekalert.org/pub_releases/2020-06/udoa-sdt052720.php
https://www.eurekalert.org/pub_releases/2020-06/osu-pdd052920.php
<https://www.agdaily.com/crops/researchers-develop-new-way-trace-global-spread-major-plant-disease/>
<https://phys.org/news/2020-06-global-major-disease.html>
https://www.seedquest.com/solutions.php?type=solutionid_article=117914
<https://www.technology.org/2020/06/05/successful-detailed-tracking-of-major-plant-diseases-global-spread/>
<https://www.nurserymag.com/article/scientitsts-successfully-track-detailed-spread-of-agrobacterium/>
<https://www.courthousenews.com/plant-detectives-develop-tool-to-track-spread-of-major-crop-disease/>
<https://www.producegrower.com/article/scientitsts-successfully-track-detailed-spread-of-agrobacterium/>
<https://www.farmprogress.com/crops/stopping-plant-disease>

For *"Evolutionary transitions between beneficial and phytopathogenic *Rhodococcus* challenge disease management"* eLife 6:e30925:
 Commentary in:
 Melnyk, RA and Haney, CH (2017) [Plasmid-powered evolutionary transitions](#). eLife 6:e33383.
 Tena, G (2018) [Dr. Rhodo and Mr. Coccus](#). Nature Plants. 4, 8(2018)

Podcast in Bacteriofiles:
<https://www.asm.org/index.php/podcasts/bacteriofiles/item/7305-plasmid-promotes-plant-pathogenesis-bacteriofiles-340>

Press releases in:

<http://www.nurserymag.com/article/bacterium-breakthrough/>

<https://content.govdelivery.com/accounts/USDANIFA/bulletins/1d37681>

<https://blog.plantwise.org/2017/12/15/rhodococcus-jekyll-and-hyde-bacteria-discovered-in-plant-nurseries/>

<http://extension.oregonstate.edu/news/release/2017/12/osu-plant-pathologists-discover-unusual-evolutionary-transition-common-bacteria>

<http://www.nurserymag.com/article/osu-discover-rhodococcus-bacteria-evolves/>

<https://www.sciencedaily.com/releases/2017/12/171212125356.htm>

<http://www.capitalpress.com/Nursery/20171219/researchers-developing-tools-to-track-harmful-bacteria>

<https://phys.org/news/2017-12-pathologists-unusual-evolutionary-transition-common.html>

<https://plantae.org/evolutionary-transitions-between-beneficial-and-phytopathogenic-rhodococcus/>

<http://www.westernfarmerstockman.com/technology/researchers-uncover-bacteria-change-tactic>

Interview about computing infrastructure and research at Oregon State featured in AMD keynote address at CES 2019

REFERENCES

Jeff H. Chang PhD

Postdoctoral co-advisor (lead).

Professor, Botany and Plant Pathology, Oregon State University

541.737.5278

Jeff.Chang@oregonstate.edu

4575 SW Research Way, Corvallis OR, 97333

Niklaus Grünwald PhD

Postdoctoral co-advisor (secondary).

Research Plant Pathologist, USDA ARS

541.738.4049

Nik.Grunwald@ars.usda.gov

3420 NW Orchard Avenue, Corvallis OR, 97331

John G. Jelesko PhD

PhD advisor.

Associate Professor, Plant Pathology, Physiology, and Weed Science, Virginia Tech

540.231.3728

jelesko@vt.edu

548 Latham Hall, Blacksburg VA 24061

Boris Vinatzer PhD

Mentor.

Professor, Plant Pathology, Physiology, and Weed Science, Virginia Tech

540.231.2126

vinatzer@vt.edu

551 Latham Hall, Blacksburg VA 24061