

Kelly Vining

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A. EDUCATION AND EMPLOYMENT INFORMATION

1. Education

PhD, University of New Hampshire, 2007.
Major: Genetics

MS, University of New Hampshire, 1999.
Major: Plant Biology

BA, University of Southern Maine, 1996.
Major: Biology

2. Employment history

(September 2015 - Present) Assistant Professor, Oregon State University.

(May 2014 - September 2015) Bioinformatic Analyst/Trainer, Oregon State University, Center for Genome Research and Biocomputing.

(January 2009 - April 2014) Faculty Research Associate, Oregon State University, Dept. of Forest Ecosystems and Society. *Additional title starting in 2011: Affiliate Faculty, Molecular and Cellular Biology Program.*

(June 2013 - November 2013) Research Support - Bioinformatics, US Department of Agriculture, Agricultural Research Service.

(July 2005 - December 2006) DNA Sequencing Facility Operator, Hubbard Center for Genome Studies.

(May 2002 - May 2007) Research/Teaching Assistant, University of New Hampshire.

B. TEACHING, ADVISING AND OTHER ASSIGNMENTS

Brief teaching philosophy

My goal is to provide students with a strong foundation of knowledge in areas that will serve them well in their careers. I emphasize practical examples from my own collaborative research projects in order to expose students to current, real-world examples and data sets. My courses involve biological data analysis and management, and introduction to the tools of bioinformatics. Since there is a diverse range of student

experience in these areas, I aim to strike a balance that serves everyone. I often ask students to work in teams in order to foster development of communication skills and a collaborative mindset. I strive to share my enthusiasm for plant genomics and breeding with students, as these disciplines are directly relevant to their career paths. Lastly, I am careful to listen to students, both one-on-one and via course evaluations, in order to continually improve my courses.

1. Instructional Summary

I am the lead instructor for one graduate-level on-site course that is offered in alternating fall terms. I revamped the course in 2018, reorganizing what had been a three-module course into a two-module offering with updated course material. I have participated in one team-taught graduate course, and have served as a faculty mentor for a course in the OSU Biological Data Sciences program that was initiated in 2017.

a. Credit Courses

Term	Course	Title	Credits	Enrollment
F 2018	MCB/PBG 621	Genetic Mapping and Association	1	11
F 2018	MCB/PBG 620	Introduction to Molecular Markers	1	13
F 2017	MCB 554	Genome Organization, Structure, and Maintenance	4	13
S 2017	BOT 599 ¹	Collaborative Problem Solving in Biological Data Sciences	3	10
F 2016	MCB/PBG 620	DNA Fingerprinting	1	10
F 2016	MCB/PBG 621	Genetic Mapping	1	9
F 2016	MCB/PBG 622	Mapping Quantitative Trait Loci	1	8

i. Guest Lectures

Term	Course	Title	Credits	Enrollment
W 2019	PBG431	Plant Genetics Recitation	1	15
F 2019	HORT 511	Research Perspectives in Horticulture	2	12
F 2018	HORT 511	Research Perspectives in Horticulture	2	11
F 2017	HORT 511	Research Perspectives in Horticulture	2	11
S 2016	MCB 599	Genotyping-By-Sequencing	NA	25
W 2016	MCB 599	RNA-seq Analysis	NA	20
F 2016	HORT 511	Research Perspectives in Horticulture	2	11
F 2015	HORT 511	Research Perspectives in Horticulture	2	11

b. Non-Credit Courses and Workshops

Term	Course	Title	Credits	Enrollment
S 2015	MCB 599 ²	Genotyping-By-Sequencing	NA	13

¹ Role: one of four faculty mentors in this course

² Role: sole instructor, two-week workshop

Summary table of teaching events since hire/last promotion

Topic	Total no. events	No. events outside region of responsibility	Total attendees
		International	
Field Day/Tour	4	1	130
School, Conference or Symposium	3	0	150
TOTAL	7	1	280

Field Day/Tour

- What Genomics Can Offer to Develop New Potato Varieties for the Industry, Hermiston Farm Fair, Hermiston, Oregon, December 2, 2015.
- Mint Industry Research Council Scientific Advisory Committee tour of OSU mint breeding program. Corvallis, Oregon, September 13, 2017.
- Application of Genomic Tools in Potato Breeding. HAREC Potato Field Day, Hermiston, Oregon, June 20, 2018.
- Aphid Resistance and Black Raspberry: Can DNA Show the Way? Presenter: Christina Mulch, M.S. Graduate Student. NWREC Caneberry Field Day, Aurora, Oregon. August 7, 2019.
- Disease resistance genes in potato: What are they, and how do they work? Hermiston Farm Fair, Hermiston, Oregon, December 4, 2019.

School, Conference or Symposium

- Bringing Genomics to Oregon Specialty Crops. Center for Genome Research and Biocomputing Fall Conference, Corvallis, Oregon, April 10, 2016.
- Identifying genes expressed during *Verticillium dahliae* infection of mint. Horticulture department seminar. February 29, 2016.
- Comparative RNA-seq for the investigation of tolerance to verticillium wilt in black raspberry, XIth International *Rubus* and *Ribes* Symposium, Asheville, North Carolina, June 21, 2015-June 24, 2015.

Workshops organized or co-organized

N/A

c. Curriculum Development

Credit

MCB 554, Genome Organization, Structure, and Maintenance. Developed new lectures, new class discussion exercises based on reading current and historical scientific research papers.

MCB/PBG 620/621, Molecular Markers, Genetic Mapping and Association. Revamped course material, and merged three separate modules into two, with an emphasis on current technologies and analysis methods.

Non-Credit
N/A

d. Graduate and Undergraduate Students and Postdoctoral Trainees

Graduate students advised

Mulch, Christina	M. S.	2020 (expected)	Horticulture (co-advised with Nahla Bassil)
Talbot, Samuel	M.S.	2022 (expected)	Horticulture
Omilani, Oluwafemi	Ph.D.	2023 (expected)	Horticulture (co-advised with Sagar Sathuvalli)
Skillin, Paul	M.S.	2023 (expected)	Horticulture

Graduate students Committee member

Cobertera, David	Ph.D.	2022 (expected)	Crop and Soil Sciences
Hu, Shengwei	Ph.D.	2021 (expected)	Crop and Soil Sciences
Veitch, Rebecca	Ph.D.	TBD	Comparative Health Sciences
Nahata, Surbhi	M.S.	2020	Environmental Science
Komaei, Golnaz	Ph.D.	2020	Horticulture
King, Ryan	M.S.	2019	Horticulture
Wada, Nami	M.S.	2019	Crop and Soil Sciences
Barrett, Damien	Ph.D.	2019	Microbiology
Chen, Hsuan	Ph.D.	2019	Horticulture
Vasquez, Javier	Ph.D.	2019	Crop and Soil Sciences
Finch, Kristin	Ph.D.	2019	Botany and Plant Pathology
Brandt, Kali	Ph.D.	2019	Crop and Soil Sciences
Merve Sekeri	M.S.	2019	Horticulture

Graduate students Graduate Council Representative

N/A

Undergraduate students advised

Ruby Clark	BA/BS	2021	Biochemistry/Molecular Biology, URSA Engage Program
Aishwarya Vellanki	BA/BS	2021	Computer Science, URSA Engage Program
Talbot, Samuel	BA/BS	2018	Crop & Soil Science (project mentor)
Vela, Saddle	BA/BS	2018	Botany and Plant Pathology (project mentor)

Summer 2017 grant recipient,

*Undergraduate Research, Innovation, Scholarship and Creativity (URISC).
Honorable mention for excellent lightning talk,
Summer Undergraduate Research Symposium, September 14, 2017.
Shoaff-Fellows, HenryBA/BS 2017 Biology (project mentor)*

Postdoctoral trainees

None

Visiting scientists hosted/trained

Qinghua “Mary” Ma, China, co-hosted December 2018- November 2019
Ruth Meiers, Wageningen University, The Netherlands, hosted June
2017-October 2017

e. Team or Collaborative efforts

Commitment to cross-disciplinary teaching across departments. Team-taught
MCB 554 Name collaborators, provide affiliate depts. Also BDS.

f. International Teaching

N/A

2. Student and Participant/Client Evaluation

a. Credit Courses

Summary of student evaluations of teaching (SET)²

Course	Term	Responses	Instructor rating			Course rating		
			Ind.	HOR T	CAS	Ind.	HORT	CAS
MCB/PBG 620	F 2018	6	5.9	5.6	5.3	5.9	5.6	5.3
MCB/PBG 621	F 2018	5	5.9	5.6	5.3	5.9	5.6	5.3
MCB 554	F 2017	8	5.3	5.8	5.3	5.0	5.6	5.1
MCB/PBG 620	F 2016	8	5.5	5.1	5.0	5.4	5.0	4.8
MCB/PBG 621	F 2016	7	5.3	5.3	5.3	5.0	5.1	5.0
MCB/PBG 622	F 2016	7	5.3	5.3	5.3	5.1	5.1	5.0

²Median ratings on a scale of 1-6: 1=poor, 6=excellent

b. Non-Credit Courses and Workshops

None

3. Peer Teaching Evaluations

Peer review for MCB554 conducted fall term 2017. Committee chair: Laurent Deluc.
Peer review for PBG/MCB620/621 conducted fall term 2018. Committee chair: John Lambrinos

4. Advising

N/A

5. Other Assignments

Research is the largest share of my appointment (60%). The over-arching focus of my research program is integration of plant breeding with the tools of modern genomics and bioinformatics. The projects focus on specialty crops that are important to Pacific Northwest agriculture. Building foundational genome resources for specialty crops and their wild relatives is a common theme among the projects, as is identifying genes and molecular markers linked to disease and pest resistance.

Collaborative Programs

I collaborate with Hermiston Agricultural Research Experiment Center (HAREC) potato breeder Vidyasagar Sathuvalli on projects to develop and utilize genome resources for potato by whole-genome sequencing of wild potato species. This project aims to identify genetic determinants of Columbia Root Knot Nematode (CRKN) resistance. I am the primary data analyst for these projects. I and also train Dr. Sathuvalli's students and postdocs in genomic analysis methods. This collaboration has led to my becoming involved in the international Potato Pan-Genome group.

I collaborate with researchers at the Corvallis USDA-ARS on a variety of projects with strawberry, black raspberry, blueberry, and mint. All projects involve genome sequencing, genetic linkage mapping, and molecular marker development. For all projects, I conduct data analyses and summarize results in peer-reviewed publications. We have published the first black raspberry genome sequence in 2016, which has been cited >50 times. Graduate student Christina Mulch, is co-advised with USDA-ARS geneticist Nahla Bassil. Christina's project is focused on identifying the genetic determinants of aphid resistance in black raspberry.

I collaborate with hazelnut breeder Shawn Mehlenbacher in the Department of Horticulture on genome resource development for hazelnut. I work directly on genome assembly and annotation, and serve as the bioinformatics trainer for Mehlenbacher lab personnel. We have produced the first chromosome-level assembly for hazelnut cultivar 'Jefferson', and are currently assembling and annotating hazelnut genomes for additional cultivars.

I collaborate with ornamental breeder Ryan Contreras on a project involving genetic linkage map development for lilac, and molecular marker identification for a reblooming trait that is important to the ornamental industry. I am involved in project planning, and also assist students with DNA analyses.

I continue to work with and advise Center for Genome Research and Biocomputing (CGRB) bioinformatics trainers on an ad-hoc basis.

Research Currently in Progress

Project: Mint varietal improvement through integrated genomics and breeding

Situation: The Pacific Northwest produces much of the U.S. crop of peppermint and spearmint, which are grown for their distilled oils. Verticillium wilt, caused by the fungus *Verticillium dahliae*, threatens the peppermint crop in particular. Since commercial peppermints are sterile polyploids, they are not directly amenable to traditional breeding approaches.

Approach: My mint research exploits fertile ancestral species of commercial mints. Using genomics tools, we have identified genes that appear to be involved in the disease resistance response in Verticillium wilt resistant mints. We have also shown for the first time that several genes in the essential oil biosynthesis pathway are represented by multiple copies in the genome. This finding hints at a complex regulatory mechanism, and has implications for breeding. My lab is now engaged in developing molecular markers for these traits that can be employed in marker-assisted selection. Grant funds for this project are obtained from Oregon Mint Commission and the national-level Mint Industry Research Council (ca. \$100,000).

Outcomes and Impact: My mint breeding program re-established mint breeding at OSU after a long absence. The sponsor commissions consist of mint growers, essential oil dealers, and consumer products sellers. A few of the companies have mint breeding operations, but these are entirely proprietary. Therefore, my breeding and genomics research work provides an important service to the industry as a whole. Groups from the commissions, as well as individual local mint growers, occasionally tour my lab and greenhouse. Stakeholders invariably say that they are impressed by and grateful for the research program. Information is disseminated to both sponsor commissions via their annual meetings, and to the Mint Industry Research Council Scientific Advisory Committee. Over time, I have seen a change in understanding of the genomics area of science among members. This has guided commission research priorities, and has led to continued funding.

Scholarship: My collaborators and I published the first-ever mint genome sequence for the species *Mentha longifolia* in 2017, a paper that has been cited 29 times to date. A manuscript reporting a chromosome-level update for this reference genome has recently been submitted for publication. A genetic diversity survey of USDA accessions of two other mint species, *M. aquatica* and *M. suaveolens*, was published in collaboration with USDA-ARS researchers in 2019. We were invited to submit a review article describing mint germplasm in the USDA National Clonal Germplasm repository; this manuscript is currently under review. I regularly present posters with recent findings at the annual Plant and Animal Genome meetings in San Diego.

Project: Assessing *Verticillium dahliae* diversity in Pacific Northwest mint growing regions

Situation: This project is an offshoot of the mint varietal improvement project. *Verticillium dahliae* is a soil-borne fungus that can persist in the soil for decades. Since mint is a

perennial crop, it is particularly vulnerable to fungal attack, which causes yield reduction and shortens the productive period of fields. Ultimately, growers take infested fields out of mint production. As we work to breed for mint resistance to *Verticillium* wilt disease, it is important to know about the genetic diversity of the fungus itself, so that we can predict how quickly the fungus might overcome mint genetic resistance.

Approach: I and collaborators collected mints from *Verticillium*-infested mint fields throughout Oregon, Washington, and Idaho. We sequenced the genomes of the collected samples, as well as archival samples from Midwestern states. We compared DNA sequences of the isolates to determine overall population structure and genetic diversity. Grant funds for this project were obtained from Oregon Mint Commission and the Mint Industry Research Council.

Outcomes and Impact: We determined that overall genetic diversity in *Verticillium dahliae* in the Pacific Northwest is low, but there are three genetically distinct groups. This was the first regional genetic survey done for this fungus. We also found one isolate that appeared to have resulted from fusion of two fungal strains. We shared this information directly with the growers who contributed samples to the project. This information helped to guide their management decisions. We also reported results to the sponsoring commissions at their annual meetings, and at the Mint Industry Research Council Scientific Advisory Committee meeting.

Scholarship: Results of this work were published in the journal *Phytopathology* in September 2019. This paper has already been cited.

Project: Building genomic resources for hazelnut

Situation: Oregon's Willamette Valley is home to 99% of hazelnut production in the United States (>\$120M/yr). The industry has recently undergone a rapid expansion: of the 80,000 planted acres, more than half are 1-5 years old. Additional plantings of 8,000 acres per year are expected. Trees can produce nuts for >50 years. Hazelnut orchards are perpetually under threat from the fungal disease Eastern Filbert Blight (EFB).

Approach: Genome-assisted breeding for EFB resistance is the approach taken by the OSU hazelnut breeding program. The Hybrid Hazelnut Research Consortium has access to a large collection of hazelnut germplasm, with many accessions exhibiting either qualitative or quantitative resistance to EFB. In my collaborative research program with hazelnut breeder Shawn Mehlenbacher, we are sequencing and annotating genomes of EFB-resistant trees, and using this information to map different sources of genetic resistance.

Outcomes and Impact: The OSU hazelnut breeding program is already using molecular markers for EFB resistance, and additional marker development is ongoing. We have produced the first chromosome-level assembly for EFB-resistant hazelnut cultivar 'Jefferson', which has narrowed the EFB resistance gene search to a small region of DNA containing fewer than 20 genes. The collaboration has led to direct funding to my lab from

the Oregon Hazelnut Commission (ca. \$100,000). Research progress is reported to the commission on an annual basis and presented at the Oregon Nut Growers Society's very well-attended (>500) annual meeting. The video of my winter 2020 meeting presentation is available on YouTube: <https://www.youtube.com/watch?v=hjPYwY4WbKY&t=11s>.

Scholarship: In 2019, I gave an invited talk in the 'Fruit and Nuts' workshop at the Plant and Animal Genome XXVII meeting. Later that year, our group presented a poster at the OSU Center for Genome Research and Biocomputing's fall conference. A manuscript describing the chromosome-level 'Jefferson' genome is in preparation.

Project: Development of potato cultivars with resistance to Columbia Root Knot Nematode

Situation: Columbia Root Knot Nematode (CRKN) is an important regional pest in Pacific Northwest potato production areas. Resistance to this pest has been found in wild potato species, and has been introgressed into breeding lines. However, some CRKN isolates have been identified that are able to overcome this resistance.

Approach: The genome of the wild potato species *Solanum bulbocastanum*, an importance source of CRKN resistance, has been sequenced and annotated. In addition, genomes of three isolates of the nematode pest have been sequenced. These resources are being used to study gene expression during pathogenesis, and to develop molecular markers for CRKN resistance.

Outcomes and Impact: Presentations have been made to potato growers and processors at annual Hermiston Farm Fair and Potato Field Days events (5,000 – 20,000 visitors).

Scholarship: I have presented posters and given talks at Potato Association of America and Plant and Animal Genome national meetings. Our group has published two peer-reviewed papers in 2019.

Project: Hemp genomic resource development.

Situation: University-based hemp research was enabled by the passage of the 2018 Farm Bill. Hemp is a relatively new crop for the state of Oregon. Most of the hemp being produced is for the non-drug CBD market. To be legally marketable, hemp plant extracts must have <0.3% of the drug molecule THC. Therefore, there is great interest in tracking genes related to CBD and THC production. The hemp research program in my lab started in 2019, and is funded by the hemp seed company OregonCBD.

Approach: Genomic resources are being developed hemp plants that are important to OregonCBD's breeding program. Whole-genome sequencing and gene annotation are jumping-off points for molecular marker development. Molecular markers are being developed to track genes encoding enzymes in the CBD/THC biosynthetic pathway. Planned work includes gene expression and epigenetics studies, as well as chromosome

manipulation to study whether increases in the number of sets of chromosomes in a hemp plant influences traits including essential oil quality.

C. SCHOLARSHIP AND CREATIVE ACTIVITY

Summary of peer-reviewed papers

Time frame	Refereed papers	Proceedings articles	Non-peer-reviewed materials
Since current appointment	20	2	2
Prior positions	10	7	0
TOTAL	30	9	2

1. Publications

a. Peer-reviewed

i. Refereed publications

Vining, K.J., Hummer, K.E., Bassil, N.V., Lange, B.M., Khoury, C., Carver, D. 2020. Crop wild relatives as germplasm resource for cultivar improvement in mint (*Mentha* L.). *Frontiers in Plant Science*. Invited review. (in press).

Role: wrote sections of manuscript, reviewed and revised manuscript.

Chen, H., Lattier, J.D., Vining, K., Contreras, R.N. 2020. Two SNP markers identified using GBS are associated with remontancy in a segregating F1 population of *Syringa meyeri* 'Palibin' x *S. pubescens* 'Penda' Bloomerang®. *J. Amer. Soc. Hort. Sci.* 145(1):104-109.

Role: advised on methods for data analysis, reviewed and revised manuscript

Vining K, Pandelova I, Hummer K, Bassil N, Contreras R, Neill K, Chen H, Parrish A, Lange M. 2019. Genetic diversity survey of *Mentha aquatica* L. and *Mentha suaveolens* Ehrh., mint crop ancestors. *Genetic Resources and Crop Evolution* 66:825-845.

Role: conceived experiment, collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Bali, S., Vining, K., Gleason, C., Majtahedi, H., Brown, C.R., Sathuvalli, V. (2019). Transcriptome profiling of resistance response to *Meloidogyne chitwoodi* introgressed from wild species *Solanum bulbocastanum* into cultivated potato. *BMC genomics* 20:907-925.

Role: analyzed data, reviewed and revised manuscript

Hernandez, F.J., Steffenson, B.J., Filichkin, T.P., Fisk, S.P., Helgersson, L.J., Meints, B., Vining, K.J., Marshall, D., del Blanco, I., Chen, X., Hayes, P. (2019).

Introgression of rpg4/Rpg5 into barley germplasm provides insights into the genetics of resistance to *Puccinia graminis* f. sp. tritici race TTKSK and resources for developing resistant cultivars. *Phytopathology*

<https://doi.org/10.1094/PHYTO-09-18-0350-R>

Role: advised on methods for data analysis, reviewed and revised manuscript

Dung, J.K.S., Knaus, B.J., Fellows, H.L.S., Grünwald, N.J., Vining, K.J. (2019). Genetic diversity of *Verticillium dahliae* isolates from mint detected with genotyping by sequencing. *Phytopathology*

<https://doi.org/10.1094/PHYTO-12-18-0475-R>.

Role: conceived experiment, collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Naithani, S.N., Gupta, P., Preece, J., Garg, P., Fraser, V., Padgitt-Cobb, L.K., Martin, M., Vining, K, Jaiswal., P. (2019). Involving community in genes and pathway curation. *Database*, Volume 2019, 1 January 2019, bay146.

Role: analyzed data, reviewed and revised manuscript.

Wallace, L., Arkwazee, H., Vining, K., Myers, J.R. (2018). Genetic diversity within snap beans and their relation to dry beans. *Genes* 9:587.

Role: analyzed data, reviewed and revised manuscript.

Bali, S., Patel, G., Novy, R., Vining, K., Thompson, A., Brown, C., Holm, D., Porter, G., Endelman, J., Sathuvalli, V. (2018). Evaluation of genetic diversity among Russet potato clones and varieties from breeding programs across the United States. *PLoS ONE* 13(8): e0201415.

Role: analyzed data, reviewed and revised manuscript.

Jibrán, R., Dzierzon, H., Bassil, N.V., Bushakra, J.M., Edger, P. P., Sullivan, S., Finn, C. E., Dossett, M., Vining, K. J., VanBuren, R., Mockler, T. C., Liachko, I., Kevin M. Davies, K.M., Foster, T.M., Chagné, D. (2018). Chromosome-scale scaffolding of the black raspberry (*Rubus occidentalis* L.) genome based on chromatin interaction data. *Horticulture Research* 5:8

<https://doi.org/10.1038/s41438-017-0013-y>

Role: analyzed data, reviewed and revised manuscript.

VanBuren, R., Wai, C. M., Colle, M., Wang, J., Sullivan, S., Bushakra, J. M., Liachko, I, Vining, K.J., Dossett, M., Finn, C.E., Jibrán, R., Chagne, D., Childs, K., Edger, P.P. Mockler, T.C., Bassil, N.V. (2018). A near complete, chromosome-scale assembly of the black raspberry (*Rubus occidentalis*) genome. *Gigascience*. 7.

Role: analyzed data, reviewed and revised manuscript.

Bushakra, J.M., Dossett, M., Carter, K.A., Vining, K.J., Lee, J.C., Bryant, D.W., VanBuren, R., Lee, J., Mockler, T.C., Finn, C.E., Bassil, N.V. (2018).

Characterization of aphid resistance loci in black raspberry (*Rubus occidentalis*

L.). *Molecular Breeding* 38:83.

Role: analyzed data, reviewed and revised manuscript.

Martin, R. C., Vining, K., Dombrowski, J. E. (2018) Genome-wide (ChIP-seq) identification of target genes regulated by BdbZIP10 during oxidative stress. *BMC Plant Biology* 18:58-70.

Role: analyzed data, wrote sections of manuscript, produced figures and tables, reviewed and revised manuscript.

Vining, K., Johnson, S. R., Ahkami, A., Lange, I., Parrish, A. N., Trapp, S. C., Croteau, R. B., Straub, S. C., Pandelova, I. G., Lange, B. M. (2017). Draft Genome Sequence of *Mentha longifolia* and Development of Resources for Mint Cultivar Improvement. *Molecular Plant* 10(2):323-339.

Role: Conceived study, collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Vining, K., Salinas, N., Tennessen, J. A., Zurn, J. D., Sargent, D. J., Hancock, J., Bassil, N. V. (2017). Genotyping-by-sequencing enables linkage mapping in three octoploid cultivated strawberry families. *PeerJ*, 5, e3731.

Role: analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

McCallum, S., Graham, J., Jorgensen, L., Rowland, L. J., Bassil, N. V., Hancock, J. F., Wheeler, E. J., Vining, K., Poland, J. A., Olmstead, J. W., Buck, E., Wiedow, C., Jackson, E., Brown, A., Hackett, C.A. (2016). Construction of a SNP and SSR linkage map in autotetraploid blueberry using genotyping by sequencing. *Molecular Breeding*, 36(4), 1–24.

Role: analyzed data, wrote sections of manuscript, reviewed and revised manuscript

VanBuren, R., Bryant, D., Bushakra, J. M., Vining, K., Edger, P. P., Rowley, E. R., Priest, H. D., Michael, T. P., Lyons, E., Filichkin, S. A., Dossett, M., Finn, C.E., Bassil, N.V., Mockler, T.C. (2016). The genome of black raspberry (*Rubus occidentalis*). *The Plant Journal*, 87(6), 535–547.

Role: analyzed data, wrote sections of manuscript, produced figures and tables, reviewed and revised manuscript

Bushakra, J. M., Bryant Jr., D., Dossett, M., Vining, K., VanBuren, R., Gilmore, B. S., Lee, J., Mockler, T. C., Finn, C. E., Bassil, N. V. (2015). A genetic linkage map of black raspberry (*Rubus occidentalis*). *Theoretical and Applied Genetics*, 128(8), 1631–1646.

Role: analyzed data, reviewed and revised manuscript

Vining, K., Davis, T. M., Jamieson, A. R., Mahoney, L. L. (2015). Germplasm resources for verticillium wilt resistance breeding and genetics in strawberry

(*Fragaria*). *Journal of Berry Research*, 5(4), 183–195.

Role: analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Vining, K., Romanel, E., Jones, R. C., Klocko, A. L., Alves-Ferreira, M., Hefer, C. A., Amarasinghe, V., Dharmawardhana, P., Naithani, S., Ranik, M., Wesley-Smith, J., Solomon, L., Jaiswal, P., Myburg, A. A., Strauss, S. H. (2015). The floral transcriptome of *Eucalyptus grandis*. *The New phytologist*, 206(4), 1406-22.

Role: analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Prior to current position

Myburg, A. A., Grattapaglia, D., Tuskan, G. A., Hellsten, U., Hayes, R. D., Grimwood, J., Jenkins, J., Lindquist, E., Tice, H., Bauer, D., Goodstein, D. M., Dubchak, I., Poliakov, A., Mizrachi, E., Kullam, A. R., Hussey, S. G., Pinard, D., van der Merwe, K., Singh, P., van Jaarsveld, I., Silva-Junior, O. B., Togawa, R. C., Pappas, M. R., Faria, D. A., Sansaloni, C. P., Petrolis, C. D., Yang, X., Ranjan, P., Tschaplinski, T. J., Ye, C. Y., Li, T., Sterck, L., Vanneste, K., Murat, F., Soler, M., Clemente, H. S., Saidi, N., Cassan-Wang, H., Dunand, C., Hefer, C. A., Bornberg-Bauer, E., Kersting, A. R., Vining, K., Amarasinghe, V., Ranik, M., Naithani, S., Elser, J. L., Boyd, A. E., Liston, A. I., Spatafora, J. W., Dharmawardhana, P., Raja, R., Sullivan, C., Romanel, E., Alves-Ferreira, M., Külheim, C., Foley, W., Carocha, V., Paiva, J., Kudrna, D., Brommonschenkel, S. H., Pasquali, G., Byrne, M., Rigault, P., Tibbits, J., Spokevicius, A., Jones, R. C., Steane, D. A., Vaillancourt, R. E., Potts, B. M., Joubert, F., Barry, K., Pappas, G. J., Strauss, S. H., Jaiswal, P., Grima-Pettenati, J., Salse, J., Van de Peer, Y., Rokhsar, D. S., Schmutz, J. (2014). *The genome of Eucalyptus grandis*. (7505th ed., vol. 510, pp. 356-62). Nature.

Role: analyzed data, wrote sections of manuscript, reviewed and revised manuscript

Bräutigam, K., Vining, K. J., Lafon-Placette, C., Fossdal, C. G., Mirouze, M., Marcos, J. G., Fluch, S., Fraga, M. F., Guevara, M., Abarca, D., Oystein, J., Maury, S., Strauss, S.H., Campbell, M. M., Rohde, A., Diaz-Sala, C., Cervera, M. (2013). Epigenetic regulation of adaptive responses of forest tree species to the environment. *Ecology and Evolution*, 3(2), 399–415.

Role: analyzed data, wrote sections of manuscript, reviewed and revised manuscript

Vining, K., Pomraning, K. R., Wilhelm, L. J., Ma, C., Pellegrini, M., Di, Y., Mockler, T. C., Freitag, M., Strauss, S. H. (2013). Methylome reorganization during in vitro dedifferentiation and regeneration of *Populus trichocarpa*. *BMC plant biology*, 13(1), 92.

Role: collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Vining, K., Pomraning, K. R., Wilhelm, L. J., Priest, H. D., Pellegrini, M., Mockler, T. C., Freitag, M., Strauss, S. H. (2012). Dynamic DNA cytosine methylation in the *Populus trichocarpa* genome: tissue-level variation and relationship to gene expression. *Bmc Genomics*, 13(1), 27.

Role: collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Slavov, G. T., DiFazio, S. P., Martin, J., Schackwitz, W., Muchero, W., Rodgers-Melnick, E., Lipphardt, M. F., Pennacchio, C. P., Hellsten, U., Pennacchio, L. A., others (2012). Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree *Populus trichocarpa* (3rd ed., vol. 196, pp. 713–725). *New Phytologist*.

Role: analyzed data, reviewed and revised manuscript

Vining, K., Contreras, R. N., Ranik, M., Strauss, S. H. (2012). Genetic Methods for Mitigating Invasiveness of Woody Ornamental Plants: Research Needs and Opportunities. *HortScience*, 47(9), 1210-1216.

Role: drafted manuscript, produced figures and tables, reviewed and revised manuscript

Strauss, S., Vining, K., Pomraning, K., Wilhelm, L., Dharmawardhana, P., Priest, H. (2010). *Exploring the developmental epigenome of Populus trichocarpa* (vol. 150, pp. 507). *Journal of Biotechnology*.

Role: wrote sections of manuscript, produced figures and tables, reviewed and revised manuscript

Vining, K., Davis, T. (2009). Isolation of a Ve homolog, mVe1, and its relationship to verticillium wilt resistance in *Mentha longifolia* (L.) Huds. *Molecular Genetics and Genomics*, 282(2), 173–184.

Role: collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Vining, K., Zhang, Q., Tucker, A., Smith, C. A., Davis, T. (2005). *Mentha longifolia* (L.) L.: a model species for mint genetic research. *HortScience*, 40(5), 1225–1229.

Role: collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

Vining, K., Loy, J. B. (1998). Born Naked: The Development of Hull-less Pumpkin Seeds. *HortScience*, 33(2), 208–208.

Role: collected raw data, analyzed data, drafted manuscript, produced figures and tables, reviewed and revised manuscript

ii. Juried exhibits

None

iii. Book chapters

None

iv. Extension publications

None

v. Proceedings articles

None

vi. Abstracts from conferences without published proceedings

None

b. Other Publications

i. Proceedings articles

Bushakra, J., Bassil, N., Weiland, J., Finn, C., Vining, K., Filichkin, S. A., Dossett, M., Bryant, D., Mocker, T. (2015). Comparative RNA-seq for the investigation of tolerance to *Verticillium* wilt in black raspberry. *XI International Rubus and Ribes Symposium 1133* (pp. 103–114).

Bushakra, J., Bryant, D., Dossett, M., Vining, K., Vanburen, R., Gilmore, B. S., Filichkin, S. A., Weiland, J., Peterson, M., Bradish, C., others (2015). Developing black raspberry genetic and genomic resources. [abstract]. International Rubus and Ribes Symposium.

Bryant, D., Bushakra, J., Dossett, M., Vining, K., Filichkin, S. A., Weiland, J., Lee, J., Finn, C., Bassil, N., Mockler, T. (2014). Building the genomic infrastructure in black raspberry. [abstract] *American Society of Horticulture Science Meeting*.

Vining, K., Pomraning, K. R., Wilhelm, L., Priest, H. D., Ma, C., Zhu, R., Etherington, E. R., Pellegrini, M., Mockler, T., Freitag, M., others (2011). Developmental variation in DNA methylation in poplar (*Populus trichocarpa*). *BMC Proceedings* (7th ed., vol. 5, pp. P177).

Mansfield, M., Vining, K., Townley, M., Davis, T. (2010). Using confocal microscopy to study the infection of *Mentha longifolia* by a GFP strain of the verticillium wilt pathogen. *Phytopathology* (6th ed., vol. 100, pp. S77–S77).

Vining, K., Davis, T. (2009). Screening for verticillium wilt resistance in diploid and octoploid strawberry germplasm. *Phytopathology* (6th ed., vol. 99, pp. S135–S135).

Mansfield, M., Vining, K., Townley, M., Davis, T. (2009). Tracking the timeline of the progression of verticillium wilt infection in tissue of susceptible and tolerant plants of *Mentha longifolia*. *Phytopathology* (6th ed., vol. 99, pp. S135–S135).

Vining, K., Zhang, Q., Smith, C., Davis, T. (2006). Identification of resistance gene analogs and verticillium resistance-like sequences in *Mentha longifolia* (6th ed., vol. 96, pp. S118–S119).

Vining, K., Loy, J. (1998). *Seed development and seed fill in hull-less seeded cultigens of pumpkin (Cucurbita pepo L.) Cucurbitaceae* vol. 98, pp. 64–69.

ii. Other authored content not peer reviewed

Bali, S., Graebner, R. C., Brown, C., Vining, K., Sathuvalli, V. (2017). Genetics and genomics of host resistance to Columbia root-knot nematode in potato (15th ed., vol. XVII, pp. 1-5). Potato Progress.

Boucher C., Vining K., Dung JK. (2016).

Prevalence of race 2 strains of *Verticillium dahliae* causing Verticillium wilt of mint in Oregon. Central Oregon Agricultural Research Center Annual Report. pp. 40-43.

2. Presentations to peers

Summary table of presentations to peers at professional meetings

Year	Regional	National	International	TOTAL	Invited
2015-current	15	14	1	30	2 national
2010-2014	9	13	9	31	
TOTAL	24	27	10	61	2 national/0 international

a. List of national presentations and those invited

Vining, K., Mint Industry Research Council Annual Meeting, "Mint Varietal Improvement: Building Genomic Resources," Scottsdale, AZ. (January 2020).

Vining, K. University of New Hampshire, Biological Sciences Seminar Series. "Specialty Crop Genomics: A Pacific Northwest Perspective" (Invited talk). Durham, NH. (September 2019).

Vining, K., Snelling, J., Mehlenbacher, S. Plant and Animal Genome (PAG XXVII) San Diego, CA. "Hazelnut Genome Resource Development" (Invited talk). (January 2019)

Vining, K., Mint Industry Research Council Annual Meeting, "Integrated Mint Breeding and Genomics – 2018 Progress," San Antonio, TX. (January 2019).

Vining, K., Mint Industry Research Council Scientific Advisory Committee Meeting, "Mint Varietal Improvement – 2018 Progress," Washington, DC. (September 2018).

Vining, K., Pandelova, I., Sathuvalli, V. American Society for Horticultural Sciences Annual Conference. A Chromosome-Level Reference Genome of Wild Diploid Potato Species *Solanum bulbocastanum*. Washington, DC. (July 2018).

Pandelova, I.G., Vela, S., Pariish, A.N., Lange, I., Lange, B.M., Vining, K. Plant and Animal Genome (PAG XXVI). A segregating population of *Mentha longifolia* enables molecular marker development for mint oil type, male fertility and Verticillium wilt resistance. San Diego, CA. (January 2018).

Vining, K., Mint Industry Research Council Scientific Advisory Committee Meeting, "Integrated Mint Breeding and Genomics – 2017 Progress," New Orleans, LA. (January 2018).

Vining, K., Mint Industry Research Council Scientific Advisory Committee Meeting, "Mint Varietal Improvement through Integrated Genomics and Breeding," Portland, OR. (September 2017).

Pandelova, I.G., Bali, S., Sathuvalli, V.R., Vining, K. American Society of Plant Biologists. "The wealth of wild relatives: a link connecting genomics and plant breeding," Honolulu, HI. (June 2017).

Vining, K., Mint Industry Research Council Annual Meeting, "Progress in Integrated Genomics and Mint Breeding," Coronado, CA. (January 2017).

Pandelova, I.G., Vining, K. Plant and Animal Genome (PAG XXV). Transcriptome Comparisons Identify Candidate Verticillium Wilt Resistance Genes in Mint (*Mentha* spp.). San Diego, CA. (January 2017).

Bali, S., Vining, K., Brown, C., Sathuvalli, V.R. Sol Genomics. "Development of high-throughput markers linked to Columbia Root Knot Nematode resistance in potato," Davis, CA. (September 2016).

Vining, K., Mint Industry Research Council Annual Meeting, "Mint Varietal Improvement," Las Vegas, NV. (January 2016).

Vining, K., Mint Industry Research Council Annual Meeting, "Development of mint genome resources at Oregon State University," Las Vegas, NV. (January 2015).

Vining, K., Mint Industry Research Council Scientific Advisory Committee Meeting, "Mint genome research at Oregon State University," Boston, MA. (September 2014).

Bryant, D. - Presenter, Bushakra, J. M. - Presenter, Dossett, M., Vining, K., Filichkin, S. A., Weiland, J. E., Lee, J., Finn, C. E., Bassil, N. W., Mockler, T., American Society for Horticultural Science (ASHS), "Building the genomic infrastructure in black raspberry," Orlando, FL. (July 2014).

Bushakra, J. M. - Presenter, Bryant, D., Bradish, C. M., Dossett, M., Vining, K., Weiland, J. E., Filichkin, S. A., Perkins-Veazie, P., Scheerens, J. C., e. a., American Society for Horticultural Science (ASHS), "Developing the genomic and genetic infrastructure for black raspberry," Orlando, FL. (July 2014).

Vining, K., Klocko, A., Romanel, E., Alves-Ferreira, M., Jones, R., Dharmawardhana, D. P., Naithani, S., Solomon, L., Amarasinghe, V., e. a., International Union of Forestry Research Organizations (IUFRO) Tree Biotechnology Conference, "Floral Transcriptome of *Eucalyptus grandis*," Asheville, NC. (May 2013).

Klocko, A., Vining, K., Amarasinghe, V., Alves-Ferreira, M., Dharmawardhana, D. P., Naithani, S., Sullivan, C., Jones, R., Jaiswal, P., Ranik, M., Plant and Animal Genome XXI, "Floral Transcriptome of *Eucalyptus grandis*," San Diego, CA. (January 2013).

Vining, K., Plant and Animal Genome XXI, "Methylome Changes During in Vitro Regeneration Of *Populus trichocarpa*," San Diego, CA. (January 2013).

Vining, K., Plant and Animal Genome XXI, "Methylome-Transcriptome Interplay During Acquisition and Release From Seasonal Dormancy In *Populus trichocarpa*," San Diego, CA. (January 2013).

Vining, K., Pomraning, K. R., Wilhelm, L. J., Pellegrini, M., Di, Y., Mockler, T., Freitag, M., Strauss, S. H., American Society of Plant Biologists, "DNA methylation dynamics during in vitro propagation of *Populus trichocarpa*," Austin, TX. (July 2012).

Lu, H., Vining, K., Ma, C., Dow, M., Thomson, J., Strauss, S., National Institute of Food and Agriculture Biotechnology Risk Assessment Grants Program Annual Project Director's Meeting, "Genetic Containment of Transgenic Trees Using Zinc-finger Nucleases," Riverdale, MD. (April 2012).

Vining, K., Pomraning, K. R., Wilhelm, L., Priest, H. D., Dolan, P., Ma, C., Zhu, R., Etherington, E. R., Mockler, T., Freitag, M., Strauss, S., American Society of Plant Biologists, "Genomic analysis of cytosine methylation in *Populus trichocarpa* tissues from differing developmental stages," Montreal, Quebec, Canada. (August 2010).

Vining, K., Plant and Animal Genome XVIII, "Epigenomic analysis of *Populus trichocarpa* tissues from differing developmental stages," San Diego, CA. (January 2010).

Strauss, S., Vining, K., Pomraning, K. R., Wilhelm, L., Dharmawardhana, D. P., Priest, H. D., Ma, C., Zhu, R., Etherington, E. R., Mockler, T., Freitag, M., DOE

Biomass Feedstock Grantee Workshop, "Methods for characterizing the developmental epigenome of *Populus trichocarpa*," San Diego, CA. (January 2010).

Vining, K., Plant and Animal Genome XXI, "Methylome-Transcriptome Interplay During Acquisition and Release From Seasonal Dormancy In *Populus trichocarpa*," San Diego, CA. (January 2010).

i. Regional presentations

Vining, K. Oregon Nut Growers Society Winter Meeting. "The Role of Genomics in the Hazelnut Industry," Corvallis, Corvallis, OR. (January 2020).

Vining, K., Lange, M. Oregon Mint Commission Annual Meeting. "Mint Varietal Improvement," Gleneden Beach, OR. (January 2020).

Vining, K., Dung, J.D. Oregon Mint Commission Annual Meeting. "Quantitative PCR Assay for Detection of Verticillium Wilt," Gleneden Beach, OR. (January 2020).

Snelling, J., Vining, K., Mehlenbacher, S.A. Oregon State University Center for Genome Research and Biocomputing Spring Conference. "Genomic Resources Improve Resolution of the Eastern Filbert Blight Locus in 'Jefferson' Hazelnut," Corvallis, OR (April 2019).

Vining, K. Oregon State University Center for Genome Research and Biocomputing Rural Data Science Workshop. "OSU Mint Genomics: Applications of Major Data to a Minor Crop," Corvallis, OR (April 2019).

Vining, K., Lange, M. Oregon Mint Commission Annual Meeting. "Mint Varietal Improvement," Gleneden Beach, OR. (January 2019).

Vining, K., Dung, J.D. Oregon Mint Commission Annual Meeting. "Improvement of the Mint Reference Genome and Further Analysis of *Verticillium dahliae* Genetic Diversity," Gleneden Beach, OR. (January 2019).

Vining, K., Dung, J.D. Oregon Mint Commission Annual Meeting. "Improvement of the Mint Reference Genome and Further Analysis of *Verticillium dahliae* Genetic Diversity," Gleneden Beach, OR. (January 2018).

Mulch, C. - Presenter, Bushakra, J., Bassil, N., Songhee, L., Peterson, M., Finn, C., Vining, K. Aphid Resistance Screening of *Rubus occidentalis* Seedlings using a rapid DNA extraction protocol with high resolution melting markers. American Phytopathological Society, Pacific Division Meeting. (June 2018).

Talbot, S. – Presenter, Vining, K. Chromosome-level Annotation of Mint Oil Biosynthesis Genes. Celebrating Undergraduate Excellence Symposium, Oregon

State University. (May 2018).

Vela, S. – Presenter, Pandelova, I., Vining, K. Testing of Candidate Genes for Pollen Fertility in Wild Mint Species. Celebrating Undergraduate Excellence Symposium, Oregon State University. (May 2018).

Vining, K., Dung, J.D. Oregon Mint Commission Annual Meeting. "Improvement of the Mint Reference Genome and Further Analysis of *Verticillium dahliae* Genetic Diversity," Gleneden Beach, OR. (January 2018).

Vining, K. Oregon Mint Commission Annual Meeting. "Progress in Integrated Genomics and Mint Breeding," Gleneden Beach, OR. (January 2017).

Vining, K. Oregon Mint Commission Annual Meeting. "Building Genome Resources for Mint," Gleneden Beach, OR. (January 2016).

prior to current position

Vining, K. Oregon Mint Commission Annual Meeting. "Update on Mint Genome Research at Oregon State University," Gleneden Beach, OR. (January 2015).

Bryant, D. - Presenter, Bushakra, J. M., Vining, K., Dossett, M., Finn, C. E., Filichkin, S. A., Weiland, J. E., Bassil, N. W., Mockler, T., 7th International Rosaceae Genomics Conference (RGC7), "Development of genomic resources in black raspberry," Seattle, WA. (June 2014).

Bryant, D. - Presenter, Bushakra, J. M., Vining, K., Dossett, M., Finn, C. E., Filichkin, S. A., Weiland, J. E., Bassil, N. W., Mockler, T., 7th International Rosaceae Genomics Conference (RGC7), "Development of genomic resources in black raspberry," Seattle, WA. (June 2014).

Bushakra, J. M. - Presenter, Bryant, D., Vining, K., Dossett, M., Mockler, T., Finn, C. E., Bassil, N. V., 7th International Rosaceae Genomics Conference (RGC7), "Linkage mapping of black raspberry," Seattle, WA. (June 2014).

Bushakra, J. M. - Presenter, Bryant, D., Vining, K., Dossett, M., Mockler, T., Finn, C. E., Bassil, N. V., 7th International Rosaceae Genomics Conference (RGC7), "Linkage mapping of black raspberry," Seattle, WA. (June 2014).

Klocko, A., Vining, K., Amarasinghe, V., Romanel, M., Alves-Ferreira, Dharmawardhana, D. P., Naithani, S., Sullivan, C., Jones, R., Jaiswal, P., International Plant & Animal Genome XXI, "Floral transcriptome of *Eucalyptus grandis*." (January 2013).

Vining, K., Pomraning, K. R., Wilhelm, L., Priest, H. D., Ma, C., Zhu, R., Etherington, E. R., Pellegrini, M., Mockler, T., Freitag, M., Strauss, S., International

Union of Forestry Research Organizations (IUFRO) Tree Biotechnology Conference, "Developmental variation in DNA methylation in poplar (*Populus trichocarpa*)," Arraial d'Ajuda, Bahia, Brazil. (June 2011).

Strauss, S., Vining, K., Pomraning, K. R., Wilhelm, L., Dharmawardhana, D. P., Priest, H. D., Shevchenko, O., Ma, C., Zhu, R., Etherington, E. R., e. a., 14th International Biotechnology Symposium and Exhibition - Biotechnology for the Sustainability of Human Society, "Exploring the developmental epigenome of *Populus trichocarpa*," Palacongressi, Rimini, Italy. (September 2010).

Strauss, S., Vining, K., Pomraning, K. R., Wilhelm, L., Dharmawardhana, D. P., Priest, H. D., Shevchenko, O., Ma, C., Zhu, R., Etherington, E. R., e., International Poplar Symposium, "Exploring the developmental epigenome of *Populus trichocarpa*," Orvieto, Italy. (September 2010).

b. List of international presentations and those invited

Mulch, C.M. Vining, K.J., Dossett, M., Finn, C.E., Bassil, N.V. – Presenter, Development of a robust RNA extraction protocol for black raspberry. International Society of Horticultural Sciences, Zürich, Switzerland. (June 2019).

prior to current position

Bushakra, J. M., Bryant, D., Vining, K., Dossett, M., Mockler, T., Finn, C. E. - Presenter, Bassil, N. V., International Horticultural Congress (IHC), "Developing a genotype by sequencing protocol for linkage map construction in black raspberry (*Rubus occidentalis* L.)," Brisbane, Australia. (August 2014).

Bryant, D. - Presenter, Bushakra, J. M., Vining, K., Dossett, M., Finn, C. E., Filichkin, S. A., Weiland, J. E., Bassil, N. W., Mockler, T., 7th International Rosaceae Genomics Conference (RGC7), "Development of genomic resources in black raspberry," Seattle, WA. (June 2014).

Bryant, D. - Presenter, Bushakra, J. M., Vining, K., Dossett, M., Finn, C. E., Filichkin, S. A., Weiland, J. E., Bassil, N. W., Mockler, T., 7th International Rosaceae Genomics Conference (RGC7), "Development of genomic resources in black raspberry," Seattle, WA. (June 2014).

Bushakra, J. M. - Presenter, Bryant, D., Vining, K., Dossett, M., Mockler, T., Finn, C. E., Bassil, N. V., 7th International Rosaceae Genomics Conference (RGC7), "Linkage mapping of black raspberry," Seattle, WA. (June 2014).

Bushakra, J. M. - Presenter, Bryant, D., Vining, K., Dossett, M., Mockler, T., Finn, C. E., Bassil, N. V., 7th International Rosaceae Genomics Conference (RGC7), "Linkage mapping of black raspberry," Seattle, WA. (June 2014).

Klocko, A., Vining, K., Amarasinghe, V., Romanel, M., Alves-Ferreira, ?, Dharmawardhana, D. P., Naithani, S., Sullivan, C., Jones, R., Jaiswal, P., International Plant & Animal Genome XXI, "Floral transcriptome of *Eucalyptus grandis*." (January 2013).

Vining, K., Pomraning, K. R., Wilhelm, L., Priest, H. D., Ma, C., Zhu, R., Etherington, E. R., Pellegrini, M., Mockler, T., Freitag, M., Strauss, S., International Union of Forestry Research Organizations (IUFRO) Tree Biotechnology Conference, "Developmental variation in DNA methylation in poplar (*Populus trichocarpa*)," Arraial d'Ajuda, Bahia, Brazil. (June 2011).

Strauss, S., Vining, K., Pomraning, K. R., Wilhelm, L., Dharmawardhana, D. P., Priest, H. D., Shevchenko, O., Ma, C., Zhu, R., Etherington, E. R., e. a., 14th International Biotechnology Symposium and Exhibition - Biotechnology for the Sustainability of Human Society, "Exploring the developmental epigenome of *Populus trichocarpa*," Palacongressi, Rimini, Italy. (September 2010).

Strauss, S., Vining, K., Pomraning, K. R., Wilhelm, L., Dharmawardhana, D. P., Priest, H. D., Shevchenko, O., Ma, C., Zhu, R., Etherington, E. R., e., International Poplar Symposium, "Exploring the developmental epigenome of *Populus trichocarpa*," Orvieto, Italy. (September 2010).

3. Grant and contract support

Total grant support since last promotion

I have generated \$1,651,754 in total support for my program in my current position.

Year(s), Title	Sponsoring Organization	\$ To My Program	Total \$	PI and Collaborators
2020-2022: Site-Specific Recombinases As Tools For Plant Genome Editing: Efficacy And Risk	USDA, Biotechnology Risk Assessment Research Grants Program	\$4,953	\$500,000	Vining, Strauss (PI), (OSU)
2020-2021: Hazelnut genome resource development	Oregon Hazelnut Commission	\$47,043	\$47,043	Vining
2020-2021: Mint varietal improvement through integrated genomics and breeding	Mint Industry Research Council	\$57,264	\$117,264	Vining, Lange, (WSU) co-PIs
2020-2021: Partial funding for OSU plant growth chamber	Mint Industry Research Council	\$25,000	\$25,000	Vining

2020-2021: Partial funding for OSU plant growth chamber	Oregon Mint Commission	\$25,000	\$25,000	Vining
2019-2020: Mint varietal improvement through integrated genomics and breeding	Mint Industry Research Council	\$69,138	\$129,138	Vining, Lange, (WSU) <i>co-PIs</i>
Year(s), Title	Sponsoring Organization	\$ To My Program	Total \$	PI and Collaborators
2019-2020: Verticillium Control Through Natural Antifungal Terpenoids	Mint Industry Research Council	\$25,660	\$37,660	Vining, Dung (OSU), Lange, (WSU) <i>co-PIs</i>
2020-2021: Development of aphid resistance resources in black raspberry	Northwest Center for Small Fruits Research	\$30,246	\$30,246	Vining
2019-2020: Hemp genome resource development	Oregon CBD (Gift from private company)	\$1,000,000	\$1,000,000	Vining
2019-2020: Developing genomic resources for hazelnut (<i>Corylus avellana L.</i>)	Oregon Hazelnut Commission	\$100,000	\$100,000	Vining
2018-2019: Mint varietal improvement through integrated genomics and breeding	Mint Industry Research Council	\$72,000	\$142,000	Vining, Lange, (WSU) <i>co-PIs</i>
2018-2019: Improvement of Mint Reference Genome, and Further Analysis of <i>Verticillium dahliae</i> Genetic Diversity	Oregon Mint Commission	\$15,400	\$21,086	Vining, Dung (OSU) <i>co-PIs</i>
2018-2020: Development of genomic resources and enhancement of breeding efficiency for important potato pests	Tri-State Potato Consortium	\$10,000	\$99,000	Vining, Sathuvalli, (OSU), Pappu, Gleason, (WSU), <i>co-PIs</i>
2018-2019: Development of Aphid Resistance Resources in Black Raspberry	North American Raspberry and Blackberry Association	\$4,867.08	\$4,867.08	Vining
2018-2019: Varietal Improvement in Mint Using Chromosome	OSU Agricultural Research	\$5,500	\$12,500	Vining, Contreras, (OSU)

Doubling	Foundation			
2018-2020: CRISPR-Cas9 mutagenesis for genetic containment of forest trees	USDA, Biotechnology Risk Assessment Research Grants Program	\$4,483	\$500,000	Vining, Strauss (PI), (OSU)
Year(s), Title	Sponsoring Organization	\$ To My Program	Total \$	PI and Collaborators
2016-2017: Mint varietal improvement through integrated genomics and breeding	Mint Industry Research Council	\$73,000	\$137,000	Vining, Lange (WSU), <i>co-PIs</i>
2015-2017: Comparative genomics of mint pathogenic <i>Verticillium dahliae</i> isolates	Oregon Mint Commission	\$27,750	\$27,750	Vining
2015-2016: Continued mint varietal improvement through integrated genomics and breeding	Mint Industry Research Council	\$54,450	\$54,450	Vining
Total		\$1,367,450	\$2,098,653	
Prior to current position				
2014-2015: Gene expression during <i>Verticillium</i> infection of mint	Mint Industry Research Council	\$24,700	\$24,700	Vining
2014-2015: Gene expression during <i>Verticillium</i> infection of mint	Oregon Mint Commission	\$22,300	\$22,300	Vining
2013-2014: Development of genomic resources for mint at Oregon State University	Oregon Mint Commission	\$19,820	\$19,820	Vining
Total		\$1,651,754	\$3,010,004	

4. Patent awards, cultivar releases, and inventions.

N/A

5. Other information appropriate to the discipline.

Membership in Professional Societies

American Society of Plant Biologists. (2009 - Present).

American Phytopathological Society. (2006 - Present).

D. SERVICE

1. University Service

a. Service to the Department

(2015 - Present), Chairperson, Horticulture Safety Action Team (HSAT).

Impact: Respond to general safety concerns voiced by department members. Lead efforts to keep shared teaching labs and shared growth chamber room in compliance with Environmental Health and Safety standards.

(2017), Authored summary letter for colleague Laurent Deluc's Peer Review of Teaching.

b. Service to the College

(2015-present) Committee Member, Variety Release Committee

(2019) Committee Member, Search Committee, Botany and Plant Pathology Dept., Assistant Professor.

c. Service to the University

(2020-present) Committee Chair, Oregon State University Global Hemp Innovation Center, Plant Breeding and Genomics Committee

(2020) Committee Member, Oregon State University Center for Genome Research and Biocomputing Strategic Planning Committee
Committee produced summary recommendations document for University Research Office.

(2020) Committee Member, Oregon State University Research Computing Task Force

(2019), Committee Member, Revisioning Molecular and Cellular Biology Program Committee.

(April 10, 2018), Presentation to Achievement Rewards for College Scientists (ARCS) Foundation.

(2017-2018) Committee Member, Search Committee, Center for Genome Research and Biocomputing Program Manager.

(2014-2017) Committee Member, Oregon State University President's Commission on the Status of Women.

(2017) Grant Proposal Reviewer, Internal, Large Grant Development.

(2012) Search Committee Member, Oregon State University Dept. of Forest Ecosystems and Society.

(2010) Search Committee Member, Oregon State University Dept. of Forest Ecosystems and Society.

2. Service to the Profession

a. Peer reviews of journal articles

I have served as a peer reviewer of journal articles for more than 17 scientific journals.

b. Grant panels

USDA-Specialty Crops Research Initiative, Citrus Disease Research and Extension Program, October 23-26, 2018.

3. Service to the Public – Professionally-related

N/A

4. Service to the Public – Non-Professionally-related

N/A

5. If service is a significant percentage of FTE, describe outcomes or impacts.

N/A

E. AWARDS

1. National and International Awards

None

2. State and Regional Awards

None

3. University and Community Awards

None

F. Diversity, Equity and Inclusion

2019: Faculty mentor: Undergraduate Research, Scholarship and the Arts (URSA) Engage Program. This program provides first and second year students, and transfer

students in their first year at OSU, opportunities to pursue research or creative activity under the guidance of an OSU mentor.

2019: Search Advocate Training. Search Advocates are trained, external search committee members who promote equity, validity, and diversity on OSU searches.

2017: Faculty participant, Louis Stokes Alliance for Minority Participation, Bridge Program. This program at Oregon State University is dedicated to increasing the number of traditionally underrepresented students successfully completing science, technology, engineering and mathematics (STEM) baccalaureate degree programs, in addition to increasing the number of students interested in and qualified for undergraduate research and graduate level studies.