

(Gernot Presting)
College of Tropical Agriculture and Human Resources
 (MBBE)

FTE Distribution: 25% I; 50% R; 25% A

Education

<u>Degree</u>	<u>University</u>	<u>Major</u>
Bachelors	University of Delaware (Newark, Delaware, U.S.A.)	Entomology and Plant Pathology
PhD	University of Wisconsin (Madison, Wisconsin, U.S.A.)	Plant Pathology

Professional Appointments

<u>Title</u>	<u>Employer</u>	<u>Dates Employed</u>
Assoc. Department Chair	<u>University of Hawai'i at</u>	2023 – 2024
Professor	<u>Mānoa</u> (Honolulu, HI, U.S.A)	2014 – present
Graduate Chair, MBBE	Dept. of Molecular Bio-sciences	2013 – 2014
Associate Professor	& Bioengineering	2009 – 2014
Assistant Professor		2004 – 2009
Senior Scientist, Data Mining	<u>Torrey Mesa Research</u> <u>Institute</u> of Syngenta (San Diego, California, U.S.A.)	2000 – 2003
Research Assistant Professor	<u>Clemson University</u> <u>Genomics Institute</u> (Clemson, South Carolina)	1998 – 2000
Postdoctoral Researcher	<u>IPK Gatersleben</u> , Germany	1996 – 1998
Postdoctoral Fellow	<u>Biotechnology Institute</u> , <u>Cornell University</u> (Ithaca, NY)	1992 – 1996
Research Geneticist	<u>U.S. Dept. of Agriculture</u> , (Prosser, WA)	1991 – 1992

Courses Taught

Course Number and Title (credits)

MBBE483 - Introduction to Bioinformatics Topics for Biologists (3cr.)

MBBE610 - Graduate Student Seminar (1cr.)

MBBE683 - Advanced Topics in Bioinformatics (4cr.)

Publications (reverse chronological order)

Book Chapters

5. Xie Z, **Presting G.** 2016. Chromatin immunoprecipitation to study the plant epigenome, In: *Plant Cytogenetics: Methods and Protocols*, eds Kianian FS & Kianian APM (Springer New York, New York, NY), pp 189-196.

4. **Presting G.** 2013. Maize centromeres, In: *Plant Centromere Biology*, Jiang J, Birchler J A, eds. John Wiley & Sons, pp. 25-38.
3. Lange BM, **Presting G.** 2004. Genomic survey of metabolic pathways in rice, In: *Recent Advances in Phytochemistry*, Romeo, John T., ed., Elsevier Science, Amsterdam, pp. 111-137.
2. Wing RA, Yu Y, **Presting G**, Frisch D, Wood T, Woo S-S, Budiman MA, Mao L, Kim HR, Rambo T, Fang E, Blackmon B, Goicoechea JL, Higingbottom S, Sasinowski M, Tomkins J, Dean RA, Soderlund C, McCombie WR, Martenson R, de al Bastide M, Wilson R, Johnson D. 2002. Sequence-tagged connector / DNA fingerprint framework for rice genome sequencing. In: *Rice Genetics IV*. pp. 215 to 225. The International Rice Research Institute. Science Publishers Inc. New Delhi, India.
1. **Presting G**, Budiman MA, Wood T, Yu Y, Kim HR, Goicoechea JL, Fang E, Blackman B, Jiang J, Woo SS, Dean RA, Frisch D, Wing RA. 2001. A framework for sequencing the rice genome. In: *Rice Biotechnology: Improving yield, stress tolerance and grain quality*, Jamie A. Goode and Derek Chadwick, eds., John Wiley & Sons, New York, pp. 236:13-27.

Refereed Journal Publications

58. Liu J, Seetharam AS, Chougule K, Ou S, Swentowsky KW, Gent JI, Llaca V, Woodhouse MR, Manchanda N, **Presting GG**, Kudrna DA, Alabady M, Hirsch CN, Fengler KA, Ware D, Michael TP, Hufford MB, Dawe RK. 2020. [Gapless assembly of maize chromosomes using long-read technologies](#). *Genome Biol.* 21(1):121. doi: 10.1186/s13059-020-02029-9.

57. **Presting G.** 2018. Centromeric retrotransposons and centromere function. *Current Opinion in Genetics & Development* 49:79-84.



56. Jiao Y, Peluso P, Shi J, Liang T, Stitzer MC, Wang B, Campbell M, Stein JC, Wei X, Chin C-S, Guill K, Regulski M, Kumari S, Olson A, Gent J, **Schneider KL**, **Wolfgruber TK**, May M, Springer N, Antoniou E, McCombie R, **Presting G**, McMullen M, Ross-Ibarra J, Dawe RK, Hastie A, Rank DR, Ware D. 2017. [Improved maize reference genome with single-molecule technologies](#). *Nature* 546:524-527. DOI:10.1038/nature22971.

55. **Wolfgruber TK**, **Nakashima MM**, **Schneider KL**, **Sharma A**, **Xie Z**, Albert PS, Xu R, Bilinski P, Dawe RK, Ross-Ibarra J, Birchler JA, **Presting G.** 2016. [High quality maize centromere 10 sequence reveals evidence of frequent recombination events](#). *Front. Plant Sci.* 7:308. DOI: 10.3389/fpls.2016.00308.



54. **Schneider KL, Xie Z, Wolfgruber TK, Presting G.** 2016. [Inbreeding drives maize centromere evolution.](#) *Proc Natl Acad Sci USA*. 113(8):E987-E996. DOI: 10.1073/pnas.1522008113
53. Sherwood AR, Carlile AL, Neumann JM, Kocielek JP, Johansen J, Lowe RL, Conklin KY, **Presting G.** 2014. [The Hawaiian Freshwater Algae Biodiversity Survey \(2009-2014\): systematic and biogeographic trends with an emphasis on the macroalgae.](#) *BMC Ecology*, 14:28. DOI: 10.1186/s12898-014-0028-2
52. Sharma A and **Presting G.** 2014. [Evolution of Centromeric Retrotransposons in Grasses.](#) *Genome Biology and Evolution*. DOI: 10.1093/gbe/evu096.
51. Campbell MA, **Presting G**, Bennett MS, Sherwood, AR. 2014. Highly conserved organellar genomes in the Gracilariales as inferred using new data from the Hawaiian invasive alga *Gracilaria salicornia* (Rhodophyta). *Phycologia*, 53:109-116.
50. Sharma A, Wolfgruber TK, **Presting G.** 2013. [Tandem repeats derived from centromeric retrotransposons.](#) *BMC Genomics*, 14:142.
49. Sherwood AR, Wang N, Carlile AL, Neumann JM, Wolfgruber TK, **Presting G.** 2012. [The Hawaiian Freshwater Algal Database \(HfwADB\): a laboratory LIMS and online biodiversity resource.](#) *BMC Ecology*, 12:22, DOI:10.1186/1472-6785-12-22.
48. Yakabe LE, Maccree MM, Sudarshana P, McClean AE, Parker SR, Wechter WP, **Presting G**, Marutani-Hert M and Kluepfel DA. 2012. Novel PCR primers for detection of genetically diverse virulent *Agrobacterium tumefaciens* biovar 1 strains. *Journal of General Plant Pathology*, DOI: 10.1007/s10327-012-0364-z.
47. Birchler JA and **Presting G.** 2012. [Retrotransposon insertion targeting: a mechanism for homogenization of centromere sequences on nonhomologous chromosomes.](#) *Genes and Development* 26:638-640.
46. Birchler JA, Gao Z, Sharma A, **Presting G** and Han F. 2011. [Epigenetic aspects of centromere function in plants.](#) *Current Opinion in Plant Biology*, 14:217-222.
45. Schneider KL, Marrero G, Alvarez A and **Presting G.** 2011. [Rapid identification of plant pathogenic bacteria below the species level using a computationally derived DNA marker.](#) *PLoS ONE* 6(4): e18496. DOI:10.1371/journal.pone.0018496.
44. Gent JI, Schneider KL, Topp CN, Rodriguez C, **Presting GG** and Dawe RK. 2011. [Distinct influences of tandem repeats and retrotransposons on CENH3 nucleosome positioning.](#) *Epigenetics & Chromatin*, 4:3 DOI:10.1186/1756-8935-4-3.
43. Sherwood AR, Sauvage T, Kurihara A, Conklin KY and **Presting G.** 2010. [A comparative analysis of COI, LSU and UPA marker data for the Hawaiian florideophyte](#)

[Rhodophyta: implications for DNA barcoding of red algae.](#) *Cryptogamie-Algologie*, 31(4):451-465.

42. Sherwood AR, Kurihara A, Conklin KY, Sauvage T and **Presting G**. 2010. [The Hawaiian Rhodophyta Biodiversity Survey \(2006-2010\): a summary of principal findings.](#) *BMC Plant Biology*, 10:258. DOI:10.1186/1471-2229-10-258.

41. Shi J, Wolf SE, Burke JM, **Presting GG**, Ross-Ibarra J, Dawe RK. 2010. [Widespread Gene Conversion in Centromere Cores.](#) *PLoS Biol* 8(3): e1000327. DOI:10.1371/journal.pbio.1000327.

40. Wolfgruber TK, **Presting G**. 2010. [JunctionViewer: customizable annotation software for repeat-rich genomic regions.](#) *BMC Bioinformatics*, 11:23. DOI:10.1186/1471-2105-11-23.

39. Wolfgruber TK, Sharma A, Schneider KL, Albert PS, Koo D-H, Shi J, Lee H, Gao Z, Han F, Xu R, Allison J, Birchler JA, Jiang J, Dawe RK, **Presting G**. 2009. [Maize centromere structure and evolution: sequence analysis of centromeres 2 and 5 reveals dynamic loci shaped primarily by retrotransposons.](#) *PLoS Genet* 5(11): e1000743. DOI:10.1371/journal.pgen.1000743.



38. Schnable PS, Ware D, Fulton RS, Stein JC, Wei F, Pasternak S, Liang C, Zhang J, Fulton L, Graves TA, Minx P, Reily AD, Courtney L, Kruchowski SS, Tomlinson C, Strong C, Delehaunty K, Fronick C, Courtney W, Rock SM, Belter E, Du F, Kim K, Abbott RM, Cotton M, Levy A, Marchetto P, Ochoa K, Jackson SM, Gillam B, Chen W, Yan L, Higginbotham J, Cardenas M, Waligorski J, Applebaum E, Phelps L, Falcone J, Kanchi K, Thane T, Scimone A, Thane N, Henke J, Wang T, Ruppert J, Shah N, Rotter K, Hodges J, Ingenthron E, Cordes M, Kohlberg S, Sgro J, Delgado B, Mead K, Chinwalla A, Leonard S, Crouse K, Collura K, Kudrna D, Currie J, He R, Angelova A, Rajasekar S, Mueller T, Lomeli R, Scara G, Ko A, Delaney K, Wissotski M, Lopez G, Campos D, Braidotti M, Ashley E, Golser W, Kim H, Lee S, Lin J, Dujmic Z, Kim W, Talag J, Zuccolo A, Fan C, Sebastian A, Kramer M, Spiegel L, Nascimento L, Zutavern T, Miller B, Ambroise C, Muller S, Spooner W, Narechania A, Ren L, Wei S, Kumari S, Faga B, Levy M, McMahan L, Buren PV, Vaughn MW, Ying K, Yeh CT, Emrich SJ, Jia Y, Kalyanaraman A, Hsia AP, Barbazuk WB, Baucom RS, Brutnell TP, Carpita NC, Chaparro C, Chia J, Deragon J, Estill JC, Fu Y, Jeddelloh JA, Han Y, Lee H, Li P, Lisch DR, Liu S, Liu Z, Nagel DH, McCann MC, SanMiguel P, Myers AM, Nettleton DS, Nguyen J, Penning BW, Ponnala L, Schneider KL, Schwartz DC, Sharma A, Soderlund C, Springer NM, Sun Q, Wang H, Waterman M, Westerman R, Wolfgruber TK, Yang L, Yu Y, Zhang L, Zhou S, Zhu Q, Bennetzen JL, Dawe RK, Jiang J, Jiang N, **Presting GG**, Wessler SR, Aluru S, Martienssen RA, Clifton SW, McCombie WR, Wing RA, Wilson RK. 2009. [The B73 maize genome: complexity, diversity and dynamics.](#) *Science*, 326:1112-1115.

37. Wang N, Sherwood AR, Kurihara A, Conklin KY, Sauvage T, **Presting G**. 2009. [The Hawaiian Algal Database: a laboratory LIMS and online resource for biodiversity data.](#) *BMC Plant Biology*, 9:117.



36. Sharma A, Schneider KL and **Presting G**. 2008. [Sustained retrotransposition is mediated by nucleotide deletions and inter-element recombinations.](#) *Proc Natl Acad Sci USA*, 105:15470-15474.

35. Paull RE, Irikura B, Wu P, Turano H, Chen NJ, Blas A, Fellman JK, Gschwend AR, Wai CM, Yu Q, **Presting G**, Alam M, Ming R. 2008. [Fruit development, ripening and quality related genes in the papaya genome.](#) *Tropical Plant Biol.* 1:246–277.

34. Sharma A, **Presting G**. 2008. [Centromeric retrotransposon lineages predate the maize/rice divergence and differ in abundance and activity.](#) *Mol Gen Genomics*, 279:133–147.

33. Sherwood A, Chan YL and **Presting G**. 2008. [Application of universally amplifying plastid primers to environmental sampling of a stream periphyton community.](#) *Mol Ecol Resour*, 8 (5), 1011-1014.



32. Ming R, Hou S, Feng Y, Yu Q, Dionne-Laporte A, Saw JH, Senin P, Wang W, Ly BV, Lewis KLT, Salzberg SL, Feng L, Jones MR, Skelton RL, Murray JE, Chen C, Qian W, Shen J, Du P, Eustice M, Tong E, Tang H, Lyons E, Paull RE, Michael TP, Wall K, Rice D, Albert H, Wang M, Zhu YJ, Schatz M, Nagarajan N, Agbayani R, Guan P, Blas A, Wai CM, Ackerman CM, Ren Y, Liu C, Wang J, Wang J, Na J, Shakirov EV, Haas B, Thimmapuram J, Nelson D, Wang X, Bowers JE, Gschwend AR, Delcher AL, Singh R, Suzuki JY, Tripathi S, Neupane K, Wei H, Irikura B, Paidi M, Jiang N, Zhang W, **Presting G**, Windsor A, Pérez RN, Torres MJ, Feltus FA, Porter B, Li Y, Burroughs AM, Luo M, Liu L, Christopher DA, Mount SM, Moore PH, Sugimura T, Jiang J, Schuler MA, Friedman V, Mitchell-Olds T, Shippen D, dePamphilis CW, Palmer JD, Freeling M, Paterson AH, Gonsalves D, Wang L, Alam M. 2008. [Genome of the transgenic tropical fruit tree papaya \(*Carica papaya* L.\).](#) *Nature*, 452:991-996.

31. Sherwood AR, Vis ML, Entwistle TJ, Necchi O and **Presting G**. 2008. [Contrasting intra- versus inter-specific sequence variation for representatives of the Batrachospermales \(Rhodophyta\): a comparison of two markers.](#) *Phycological Research*, 56:269-279.

30. Umylny B, **Presting G** and Ward WS. 2007. [Evidence of Alu expression in dbEST.](#) *Archives of Andrology*, 53:207-18.

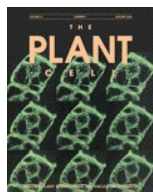
29. Eustice M, Yu Q, Lai CWJ, Moore PH, **Presting G** and Ming R. 2007. [Development and use of microsatellite markers for genetic analysis in papaya.](#) *Tree Genetics and Genomes*, 4:333-341, DOI 10.1007/s11295-007-0112-2.

28. Umylny B, **Presting G**, Efird J and Ward WS. 2007. Near full-length Alu and B1 repeat sequences within protein coding regions and other expressed transcripts. *Journal of Cellular Biochemistry*, 102:110-121, DOI: 10.1002/jcb.21278.
27. Sherwood AR, **Presting G**. 2007. Universal primers amplify a potential DNA barcode region for eukaryotic algae. *Journal of Phycology*, 43:605-608.
26. **Presting G**. 2006. Identification of conserved regions in the plastid genome – implications for DNA barcoding and biological function. *Canadian Journal of Botany*, 84:1434-1443.
25. Luce A, Sharma A, Mollere O, Wolfgruber TK, Nagaki K, Jiang J, **Presting G**, Dawe RK. 2006. Precise centromere mapping using a combination of repeat junction markers and chromatin immunoprecipitation-PCR. *Genetics* 174:1057-61.
24. Jenkins DM, Chami B, Kreuzer M, **Presting G**, Alvarez A, Liaw BY. 2006. Hybridization probe for femtomolar quantification of selected nucleic acid sequences on a disposable electrode. *Anal Chem*. 78:2314-8.
23. Lai CW, Yu Q, Hou S, Skelton RL, Jones MR, Kanako LTJ, Murray J, Eustice M, Agbayani R, Guan P, Moore P, Ming R, **Presting G**. 2006. Analysis of papaya BAC end sequences reveals first insights into the organization of a fruit tree genome. *Mol. Gen. Genomics* 276:1-12.
22. Gabriel DW, Allen C, Schell M, Denny T, Greenberg J, Duan YP, Flores-Cruz Z, Huang Q, Clifford JM, **Presting G**, Gonzalez ET, Reddy J, Elphinstone J, Swanson J, Yao J, Mulholand V, Liu L, Farmerie W, Patnaikuni M, Balogh B, Norman D, Alvarvez A, Castillo JA, Jones J, Saddler G, Walunas T, Zhukov A and Mikhailova N. 2006. Identification of open reading frames unique to a select agent: *Ralstonia solanacearum* race 3 biovar 2. *Mol. Plant Microbe Interactions*. 19:69-79.
21. **Presting G**. 2003. Mapping multiple co-sequenced T-DNA integration sites within the Arabidopsis genome. *Bioinformatics* 19(5):579-586.
20. Sessions A, Burke E, **Presting G**, Aux G, McElver J, Patton D, Dietrich B, Ho P, Bacwaden J, Ko C, Clarke JD, Cotton D, Bullis D, Snell J, Miguel T, Hutchison D, Kimmerly B, Mitzel T, Katagiri F, Glazebrook J, Law M, Goff SA. 2002. A high-throughput Arabidopsis reverse genetics system. *Plant Cell* 14(12):2985-94.



19. Goff SA, Ricke D, Lan T, **Presting G**, Wang R, Dunn M, Glazebrook J, Sessions A, Oeller P, Varma H, Hadley D, Hutchison D, Martin C, Katagiri F, Lange B, Moughamer T, Xia Y, Budworth P, Zhong J, Miguel T, Paszkowski U, Zhang S, Colbert M, Sun W, Chen L, Cooper B, Park S, Wood T, Mao L, Quail P, Wing R, Dean R, Yu Y, Zharkikh A, Shen R, Sahasrabudhe S, Thomas A, Cannings R, Gutin A, Pruss D, Reid J, Tavtigian S, Mitchell J,

Eldredge G, Scholl T, Miller R, Bhatnagar S, Adey N, Rubano T, Tusneem N, Robinson R, Feldhaus J, Macalma T, Oliphant A, Briggs S. 2002. **A Draft Sequence of the Rice Genome (*Oryza sativa* L. ssp. japonica)**. *Science* Apr 5 2002: 92-100.



18. Chen M^a, **Presting G^a**, Barbazuk WB^a, Goicoechea JL, Blackmon B, Fang G, Kim H, Frisch D, Yu Y, Sun S, Higingbottom S, Phimphilai J, Phimphilai D, Thurmond S, Gaudette B, Li P, Liu J, Hatfield J, Main D, Farrar K, Henderson C, Barnett L, Costa R, Williams B, Walser S, Atkins M, Hall C, Budiman MA, Tomkins JP, Luo M, Bancroft I, Salse J, Regad F, Mohapatra T, Singh NK, Tyagi AK, Soderlund C, Dean RA, Wing RA. 2002. An integrated physical and genetic map of the rice genome. *Plant Cell* 14:1-10. ^acontributed equally to this work
17. Wechter WP, Begum D, **Presting G**, Kim JJ, Wing RA, Kluepfel DA. 2002. Physical mapping, BAC-end sequence analysis, and marker tagging of the soilborne nematocidal bacterium, *Pseudomonas synxantha* BG33R. *OMICS – A Journal of Integrative Biology* 6:11-21.
16. Hudakova S, Michalek W, **Presting G**, ten Hoopen R, dos Santos K, Jasencakova Z, Schubert I. 2001. Sequence organization of barley centromeres. *Nucl. Acids Res.* 29:5029-5035.
15. Cheng Z, **Presting G**, Buell CR, Wing RA, Jiang J. 2001. High-resolution pachytene chromosome mapping of bacterial artificial chromosomes anchored by genetic markers reveals the centromere location and the distribution of genetic recombination along chromosome 10 of rice. *Genetics* 157:1749-57.
14. Draye X, Lin YR, Qian XY, Bowers JE, Burow GB, Morrell PL, Peterson DG, **Presting G**, Ren SX, Wing RA and Paterson AH. 2001. Toward integration of comparative genetic, physical, diversity, and cytomolecular maps for grasses and grains, using the sorghum genome as a foundation. *Plant Physiol.* 125:1325-41.
13. Mao L, Wood T, Yu Y, Budiman MA, Woo S, Sasinowski M, **Presting G**, Frisch D, Goff S, Dean R and Wing R. 2000. Rice transposable elements: a survey of 73,000 sequence-tagged connectors. *Genome Res.* 7:982-90.
12. Houben A, Wako T, Furushima-Shimogawara R, **Presting G**, Kunzel G, Schubert I and Fukui K. 1999. The cell cycle dependent phosphorylation of histone H3 is correlated with the condensation of plant mitotic chromosomes. *Plant Journal* 18:675-679.
11. **Presting G**, Malysheva L, Fuchs J and Schubert I. 1998. A Ty3/Gypsy retrotransposon-like sequence localizes to the centromeric region of cereal chromosomes. *Plant Journal* 16:721-728.

10. **Presting G**, Frary A, Pillen KP and Tanksley SD. 1996. Telomere-homologous sequences occur near the centromeres of many tomato chromosomes. *Mol. Gen. Genet.* 251:526-531.
9. Frary A, **Presting G** and Tanksley SD. 1995. Molecular mapping of the centromeres of tomato chromosomes 7 and 9. *Mol. Gen. Genet.* 250:295-304.
8. Ori N, Eshed Y, Paran I, **Presting G**, Aviv D, Tanksley SD, Zamir D and Fluhr R. 1997. The I2C family from the wilt disease resistance locus I2 belongs to the nucleotide binding, leucine-rich repeat family of plant resistance genes. *Plant Cell* 9:521-532.
7. **Presting G**, Smith OPS and Brown CR. 1995. Resistance to potato leafroll virus in potato plants transformed with the coat protein gene or with vector control constructs. *Phytopathology* 85:436-442.
6. **Presting G** and Helgeson JP. 1994. Media and protocols for the isolation of independent mutants and transformants from *Nicotiana plumbaginifolia* protoplasts. *Plant Science* 99:211-221.

Extension Publications

59. Laspisa DJ, Schneider KL, **Presting G**. 2022. Improved Centromere Assemblies for RefGen_v4. bioRxiv 2022.03.30.486462; doi: <https://doi.org/10.1101/2022.03.30.486462>

Commentary/Interview

Provided commentary and perspective for:

Science News on the May 2019 publication from the Barbara Mellone laboratory on the discovery of retrotransposons in *Drosophila* centromeres:
<https://www.sciencenews.org/article/fruit-fly-jumping-gene-chromosome-centromere>

[*The Scientist*](#) on the 2024 *Nature Plants* publication from the Martienssen laboratory.

Leadership Roles (Committees, Boards, Advisory, etc.)

Peer Review for:

Biotechniques
BMC Bioinformatics
BMC Genome Biology (IF=16.8) - 2018
BMC Genomics
BMC Plant Biology

<i>Botany</i>	
<i>Chromosoma</i>	
<i>Chromosome Research</i>	- 2021
<i>Current Opinion in Plant Biology</i> (IF=7.5)	- 2018, 2019
<i>Frontiers in Plant Science</i>	
<i>G3: Genes Genomes Genetics</i>	
<i>Genes</i>	- 2018
<i>Genome Research</i> (IF=10.1)	- 2021
<i>Genome Biology</i>	- 2024
<i>J Biomedicine & Biotechnology</i>	
<i>Journal of Heredity</i>	
<i>Molecular Biology and Evolution</i> (IF=14.8)	- 2019, 2020, 2022, 2023
<i>Nature Communications</i> (IF=11.9)	- 2018, 2019, 2021, 2023
<i>New Phytologist</i> (IF=7.4)	
<i>Peer J</i>	
<i>Plant Cell</i> (IF=8.6)	- 2019, 2020, 2023, 2024
<i>Plant Journal</i>	- 2023
<i>Plant Molecular Biology</i>	
<i>Plant Physiology</i>	
<i>Planta</i>	- 2023
<i>Proceedings of the National Academy of Sciences</i> (IF=9.6)	
<i>Scientific Reports</i>	
<i>the Plant Journal</i>	- 2019 (2), 2020, 2023

Grant Proposal Review:

Panel member for the \$50M **NSF Plant Cyberinfrastructure** iPlant project review - 2012

External reviewer for the **Austrian Science Foundation** (1 year)

Czech Science Foundation (2 years)

German National Science Foundation (3 years)

Panel member for a **Plant Genome Program (NSF)** site visit and project review (1 year)

Panel member for a **Plant Genome Program (NSF)** mid-project review (1 year)

External reviewer for **NSF Plant Genome** program (5 years)

External reviewer for **NSF MCB** program (4 years)

Panel member for the **USDA-CAP** program (panel meeting and reverse site visit) (1 year)

University of Hawaii

Organizer of an “*iPlant Computational Tools and Services workshop Workshop*” on the UH Manoa campus (28 registered attendees) December 2012

Search Committees for:

Chair Plant Biotechnology faculty, Dept. of Molecular Biosciences 2024
 Plant Biochemist faculty, Dept. of Molecular Biosciences 2023
 Office Manager, Dept. of Molecular Biosciences 2023
 Microbiology faculty, Microbiology Dept 2019
 Clinical Microbiology faculty, Microbiology Dept 2019
 Entomology faculty, Dept. of Plant and Environmental Protection Science 2019
 Plant Biochemist faculty, Dept. of Molecular Biosciences 2015
 Soil Microbiologist faculty, Dept. of Tropical Plant and Soil Science 2015
 Insect Vector faculty, Dept. of Plant and Environmental Protection Science 2013
 Plant Breeder faculty, Dept. of Tropical Plant and Soil Science 2011-2012
 Dean of the College of Tropical Agriculture and Human Resources 2009-2010

Other Departmental or Campus Committees:

MBBE Graduate Admissions Committee 2014 - 2024
 MBBE Curriculum Committee 2014 – present
 MBBE Departmental Personnel Committee 2014 - present
 PEPS/TPSS Curriculum Committee Ag Genetics & Genomics 2014 - present
 Cyberinfrastructure Faculty Advisory Committee 2014 – present
 UH Manoa Tenure and Promotion Review Committee 2015
 High Performance Computing Advisory Committee 2005 – 2014
 Greenhouse Committee 2015 - present
 Vice Chancellor for Research UH Undergraduate Student Summer Research Awards
 Selection Committee 2006
 College of Tropical Agriculture and Human Resources Faculty Senate 2023-2024
 2011-2013
 2004-2006
 Secretary of CTAHR Faculty Senate Instruction Committee 2004-2006

Judge for the annual College of Tropical Agriculture and Human Resources Student Symposium Poster (annually from 2004 - 2019) and Oral (annually from 2005 - 2007) Sessions.

Graduate Students

<u>Category</u>	<u>Current Number of Students</u>	<u>Number Graduated (Career)</u>
<i>Chair</i> of Master’s Committees	0	5
<i>Chair</i> of PhD Committees	1	4
Member of Master’s Committees*	0	7
Member of PhD Committees*	6	16

* Includes students enrolled in the University of Hawaii MBBE, ICS, TPSS, Microbiology, PEPS, and Oceanography, as well as the John A. Burns School of

Medicine, and Universität Jena in Germany degree programs.

Grant Support

(PI, co-PI(s), **Hawaii portion of funds = \$6,502,159**)

National Science Foundation, Division of Environmental Biology – 2242142. Discovery and characterization of mesophotic seaweeds in Hawaii: genomic adaptations to low light environment. *Alison Sherwood* and Gernot Presting. Award period: 2023-2026.
\$892,290

National Science Foundation, Plant Genome - 1444624. Characterizing the interplay between maize retrotransposons and the epigenome. *Gernot Presting*. Award period: 2016-2020.
\$1,412,428

National Science Foundation, Plant Genome - 0922703. Functional Genomics of Maize Centromeres. *Kelly Dawe*, Jiming Jiang, James Birchler, Gernot Presting, Jeff Rosslibarra. Award period: 2010-15.
\$1,152,127 (Total: \$5,014,464)

National Science Foundation, DEB Systematic Biology and Biodiversity Inventories - 0841734. Collaborative Research: Biodiversity Survey of Freshwater Algae of the Hawaiian Islands. *Alison Sherwood*, Rex Lowe, J. Patrick Kociolek, Jeffrey Johansen, Gernot Presting. Award period: 2009-2014.
\$499,700 (Total: ~\$905,000)

EPSCoR – REAP. Functional genomics in a Kilauea lave cave microbial mat. *Stuart Donachie*, Gernot Presting, John Berestecky, Mark Brown. Award period: 2007.
\$25,000

EPSCoR – REAP. Characterizing brown algal biodiversity of Hawaiian marine habitats. *Alison Sherwood*, Gernot Presting. Award period: 2007.
\$19,935

Hawaii Coral Reef Initiative. Characterizing green algal biodiversity of Hawaiian reef and estuarine communities. *Alison Sherwood*, Gernot Presting. 2007.
\$85,679

USDA-TSTAR. A DNA barcode database for native and invasive plant species of Hawaii. *Gernot Presting*. 2006-2009.
\$233,686

National Science Foundation, Biodiversity Surveys and Inventories - 0542608. Biodiversity of the Rhodophyta of the Hawaiian Islands. *Alison Sherwood*, Gernot Presting. 2006-2009.
\$599,999

USDA-TSTAR. Genomic barcoding of phytopathogenic bacteria important to Hawaiian agriculture. *Gernot Presting*, Anne Alvarez. 2005-2008.

\$208,525

Maui High Performance Computing Center – Student Engagement Grant. Phylogenetic Profiling of the Arabidopsis Genome. *Gernot Presting*. 2005.

\$25,008

National Science Foundation, Plant Genome - 0421671. Functional Genomics of Maize Centromeres. *Kelly Dawe*, Wayne Parrott, Jiming Jiang, James Birchler, Gernot Presting. Award period: 2004-09.

\$1,140,162 (Total: \$5,602,925)

USDA-Tropical/subtropical agricultural research. Papaya BAC end sequencing. *Gernot Presting*, Ray Ming, Paul Moore. 2004-2007.

\$207,620

Presentations at Conferences

Presting G. 2024. Genetic and Epigenetic Factors That Affect Centromere (Re-)Positioning in Maize. *International Plant and Animal Genome Conference*, January 12-17, San Diego, CA, USA. January 14th.

Presting G. 2022. Genetic and Epigenetic Factors That Affect Centromere (Re-)Positioning in Maize. *International Plant and Animal Genome Conference*, January 8-12, San Diego, CA, USA. January 9th, online.

Presting G. 2021. Timing is Everything – What Ten Thousand Years of Maize Breeding Reveal About Centromere DNA Evolution. *The Socially Distant Centromere Meeting* (online only version of the *Gordon Research Conference on Centromere Biology*), June 15th, online.

Presting G. 2020. A centromere's perspective on genetic recombination. *International Plant and Animal Genome Conference*, January 11-15, San Diego, CA, USA.

Kevin Schneider S., Wolfgruber T., Xie Z., Laspisa D., **Presting G.** 2019. Neocentromeres and the Role of Retrotransposons in Maize Centromere Function. *International Conference of Plant Chromosome Engineering and Functional Genomics for Breeding*, June 3-5, Beijing, China.

Presting G. 2018. The Role of Retrotransposons in Maize Centromeres. *International Plant and Animal Genome Conference*, January 13-17, San Diego, CA, USA.

Presting G. 2017. Neocentromere formation and rapid turnover of centromere repeats are linked to maize domestication. *International Plant and Animal Genome Conference*, January 14-18, San Diego, CA, USA.

Presting G. 2016. Resolving the centromere paradox – microevolution of centromeric DNA repeats. *58th Maize Genetics Conference*, March 17-20, Hyatt Regency Riverfront, Jacksonville, FL, USA.

Presting G. 2015. Impacts of maize domestication and breeding on neocentromere formation. *International Plant and Animal Genome Conference*, January 10-14, San Diego, CA, USA.

Presting G. 2014. The role of centromeric retrotransposons in centromere function. *Gordon Research Conference Centromere Biology Meeting*, July 27 – August 1, Waltham, MA, USA.

Presting G. 2013. Getting Hitched: retrotransposons, chromosome movement and centromere drive. *55th Maize Genetics Conference*, March 14-17, Pheasant Run, St. Charles, IL, USA.

Presting G. 2013. The interplay of centromeric retrotransposons with their host genome. *International Plant and Animal Genome Conference*, January 12-16, San Diego, CA, USA.

Presting G. 2010. Maize centromeres are dynamic loci that are shaped by retrotransposons. *International Plant and Animal Genome Conference*, January 9-13, San Diego, CA, USA.

Presting G. 2009. Evolution of maize centromeres as revealed by their physical maps. *51st Maize Genetics Conference*, March 12-15, Pheasant Run, St. Charles, IL, USA.

Presting G., Lawrence C, Bennetzen J, Fu Y, Uphaus J, Brendel V. 2009. Panel: Community Forum on Gene Annotation: What's Next? Chair: Mike Muszynski. *51st Maize Genetics Conference*, March 12-15, Pheasant Run, St. Charles, IL, USA.

Presting G. 2007. Analysis of papaya BAC end sequences: insights into the organization of a tree fruit genome. *International Plant and Animal Genome Conference*, January 12-17, San Diego, CA, USA.

Lange BM, **Presting G.** 2004. Tools and approaches for surveying the metabolic capabilities of rice. *Second International Symposium of Rice Functional Genomics*, November 15-17, Tucson, AZ, USA.

Lange BM, **Presting G.** 2003. Genomic survey of metabolic pathways in rice. *Annual conference of the Phytochemical Society of North America*, August 10-13, Peoria, IL, USA.

Presting G, Budiman MA, Wood T, Yu Y, Kim HR, Goicoechea JL, Fang E, Blackman B, Jiang J, Woo SS, Dean RA, Frisch D, Wing RA. 2000. A framework for sequencing the rice genome. *Symposium on Rice biotechnology: improving yield, stress tolerance and grain quality, held at the International Rice Research Institute (IRRI), Los Baños, Laguna, The Philippines*, March 27-29.

Presting G. 2000. Comparative Genomics. *Workshop speaker at 42nd Annual Maize Genetics Conference*, March 16-19, Coeur D'Alene, ID, USA.

Presting G, Frisch D, Wood T, Yu Y, Woo S-S, Luo M-Z, Budiman A, Kim HR, Fang E, Blackmon B, Goicoechea JL, Walser S, Farrar K, Higingbottom S, Thurmond S, Dean R, Wing R. 2000. The CUGI rice genome framework project and its application towards development of a sequence ready physical map of chromosome 10. *Plant & Animal Genome VII*, January 9-12, San Diego, CA, USA.

OTHER INVITED ORAL PRESENTATIONS

Presting G. 2015. The role of retrotransposons in centromere function. June 11. *Rutgers University*, New Brunswick, NJ, USA.

Presting G. 2015. The role of retrotransposons in centromere function. May 21. *University of Florida*, Gainesville, FL, USA.

Presting G. 2014. Maize Centromeres. March 12. *Chinese Academy of Sciences*, Beijing, China.

Presting G. 2013. Maize Centromeres. *Interdisciplinary Plant Group Seminar Series at University of Missouri*, April 8, Columbia, MO, USA.

Presting G. 2011. Maize Centromeres - what charting the "final frontier" tells us about genome evolution and epigenetics. *Institute of Biological Chemistry at Washington State University*, October 6, Pullman, WA, USA.

Presting G. 2011. DNA-based Identification of Plant-Associated Bacteria. *Western Region Deans and Directors Meeting – Waves of Change*. July 11, Hilton Waikiki Beach, Honolulu, HI, USA.

Presting G. 2006. Comparative Genomics in Plants and Microbes. *Bioinformatics Colloquium, John A. Burns School of Medicine, University of Hawaii at Manoa*, November 28, Kaka`ako, Honolulu, HI, USA.

Presting G, Sherwood A, Rubinoff D. 2006. DNA barcoding: an introduction and critical discussion. *Departmental Seminar Series, Botany Department, University of Hawaii at Manoa*, November 8, Manoa, Honolulu, HI, USA.

Presting G. 2006. Sequencing the Papaya Genome: What Every Papaya Grower Should Know About the Papaya Sequencing Effort! *42nd Annual Hawaii Papaya Industry Association Conference*, September 22, Honolulu, HI, USA.

Presting G. 2005. Plant Comparative Genomics. *Departmental Seminar Series, MBBE Department, University of Hawaii at Manoa*, November 8, Manoa, Honolulu, HI, USA.

Presting G. 2004. Comparative Plant Genomics. *Departmental Seminar Series, Botany Department, University of Hawaii at Manoa*, November 8, Manoa, Honolulu, HI, USA.

STUDENT ORAL PRESENTATIONS

Keahonui Kam. 2021. Targeting Specificity of Centromeric Retrotransposons. *Aloha 2021 Fall Undergraduate Showcase*, December 10, Honolulu, HI, USA.

Watanabe G, Banasihan J, Hennig F, Yang E, Roberson S, Tello J, Shontell R, Presting G. 2018. Delivering Transgenes to Corn Centromere. *iGEM Jamboree*, October 25-28, Boston, MA, USA.

Shi J, Wolf S, Wolfgruber TK, **Presting G**, Dawe RK. 2009. Recombination within centromere cores. *51st Maize Genetics Conference*, March 12-15, Pheasant Run, St. Charles, IL, USA.

Schneider KL, Marrero G, Alvarez A, **Presting G**. 2009. Comparative Analysis of Whole Bacterial Genomes and Derivation of RIF, a DNA Marker for the Identification of Unknown Bacterial Phytopathogens. *CTAHR Symposium*, April 3-4, Honolulu, HI, USA.
[Runner-up Best PhD oral presentation.](#)

Sharma A, Wolfgruber TK, Schneider KL, **Presting G**. 2009. Characterization of Centromeric Retrotransposons in Corn. *CTAHR Symposium*, April 3-4, Honolulu, HI, USA.

Salazar K, Kwan G, Ruzicka M, Callahan S, Gautz L, **Presting G**. 2009. A BioBrick toolkit for cyanobacteria. *CTAHR Symposium*, April 3-4, Honolulu, HI, USA. [Winner MBBE best undergraduate presentation.](#)

Wolfgruber TK, Sharma A, Schneider K, **Presting G**. 2008. Sequence characteristics of corn centromeres. *CTAHR Symposium*, April 11-12, Honolulu, HI, USA. [Winner best MBBE paper.](#)

Sharma A, Wolfgruber TK, Schneider K, **Presting G**. 2008. Periodic bursts in retrotransposition activity of CRM1 subfamily due to generation of novel recombinant subtypes. *CTAHR Symposium*, April 11-12, Honolulu, HI, USA.

Nakashima M, Morden C, **Presting G**. 2008. Development of a DNA Barcode Database for Endemic, Indigenous, and Non-native Hawaiian Plants. *CTAHR Symposium*, April 11-12, Honolulu, HI, USA.

Wechter P, Levi A, Kluepfel D, **Presting G**. 2007. Microarray analysis: Uses and limitations. *American Society for Horticultural Sciences Southern Region 67th Annual Meeting*, February 3-5, Mobile, AL, USA.

Sherwood AR, **Presting G**. 2006. Universal primers amplify a plastid marker for biodiversity assessment of eukaryotic algae and cyanobacteria. *60th Annual Meeting of the Phycological Society of America*, July 6-12, Juneau, AK, USA.

Ewing, A, **Presting G**. 2006. Elucidation of *Xanthomonas* subspecies relationships using comparative genomics. *CTAHR Symposium*, April 7-8, Honolulu, HI, USA. [Winner best conference paper.](#)

Lai CW, Yu Q, Hou S, Skelton RL, Jones MR, Lewis KLT, Murray J, Eustice M, Agbayani R, Guan P, Moore P, Ming R, **Presting G**. 2006. Analysis of papaya BAC end sequences reveals first insights into the organization of a tree-fruit genome. *CTAHR Symposium*, April 7-8, Honolulu, HI, USA.

Eustice M, Lai CWJ, Yu Q, **Presting G**, Moore P, Ming R. 2006. Variation of microsatellite markers among selected papaya varieties. *CTAHR Symposium*, April 7-8, Honolulu, HI, USA. [Third Prize MS oral presentation.](#)

STUDENT POSTER PRESENTATIONS

Simoné Murguia, Jiani Kaniho and Gernot Presting. 2023. Efficacy of Oxford Nanopore Sequencing Technology For Genotyping. *SURE Symposium*, August 4th, Honolulu, HI, USA.

Laspisa JD, Xie Z, Schneider KL, Presting, G. 2022. H2A.Z and transcription influence neocentromere positioning in *Zea mays*. *64th Annual Maize Genetic Conference*, March 31 - April 3, Union Station, St. Louis, MO, USA.

Laspisa JD, Schneider KL, Presting, G. 2020. Why CR2s are more prominent in domesticated maize than teosinte. *62nd Annual Maize Genetic Conference*, June 25-26, Virtual Meeting due to COVID-19.

Shontell, Ryan H1; Presting, Gernot G. 2019. Understanding centromeric retrotransposons I – identification of protease cut sites and assembly of virus-like particles. *61st Annual Maize Genetic Conference*, March 14-17, Union Station, St. Louis, MO, USA.

Laspisa D, Schneider KL, Presting G. 2019. The landscape of *Zea mays* centromeres and pericentromeres. *61st Annual Maize Genetic Conference*, March 14-17, Union Station, St. Louis, MO, USA.

Schneider KL, Laspisa D, Presting G. 2017. Centromeric Genes of Maize. *59th Annual Maize Genetic Conference*, March 9-12, Union Station, St. Louis, MO, USA.

Laspisa D, Schneider KL, Wolfgruber TK, Jiao Y, Ware D, Maize B73 AGPv4 Consortium, Presting, G. 2017. Improving Maize Centromere Sequences of RefGen V4. *59th Annual Maize Genetic Conference*, March 9-12, Union Station, St. Louis, MO, USA.

Hojatighomi T, Schneider KL, Sharma A, **Presting G.** 2013. A Database of Maize LTRRetrotransposons. *CTAHR/COE Symposium*, April 12-13, Honolulu, HI, USA.
[Runnerup best undergraduate poster presentation.](#)

Schneider KL, Marrero G, Alvarez AM, **Presting G.** 2011. RIFdb: An online database for the classification of plant-associated bacteria using the computationally derived RIF marker. *American Phytopathological Society Meeting*, August 6-10, Honolulu, HI, USA.

Marrero G, Schneider KL, Alvarez AM, **Presting G.** 2011. Assembly of the draft genome of *Xanthomonas axonopodis* pv. *dieffenbachiae* strain V108LRUH1, a bioluminescent strain highly virulent on anthurium. *American Phytopathological Society Meeting*, August 6-10, Honolulu, HI, USA.

Sharma A, Schneider KL, Wolfgruber TK, **Presting G.** 2011. Generating complete physical maps of maize centromeres. *53rd Annual Maize Genetic Conference*, March 17-March 20, Pheasant Run, St. Charles, IL, USA.

Marrero G, Schneider KL, **Presting G.** 2011. Assembly of the draft genome sequence of *Xanthomonas axonopodis* pv. *dieffenbachiae*, causal agent of bacterial blight of anthurium. *CTAHR/COE Symposium*, April 8-9, Honolulu, HI, USA.

Schneider KL, Wolfgruber TK, Sharma A, **Presting G**. 2011. How centromeric repeats influence centromere formation. *CTAHR/COE Symposium*, April 8-9, Honolulu, HI, USA.

Wang N, **Presting G**. 2011. ChimeraBrick: A New Placeholder Standard. *CTAHR/COE Symposium*, April 8-9, Honolulu, HI, USA.

Maroon-Lango CJ, Schneider KL, Turner RS, **Presting G**, Alvarez AM. 2010. *Xanthomonas sacchari* – a pathogen or an endophyte? *American Phytopathological Society Meeting*, August 4-8, Providence, RI, USA.

Wolfgruber TK, Sharma A, Schneider KL, **Presting G**. 2009. Graphic representation of maize centromere 2 using custom annotation software. *American Society of Plant Biology Meeting*, July 18-22, Honolulu, HI, USA.

Sharma A, Wolfgruber TK, **Presting G**. 2009. Identification and characterization of centromeric retrotransposons in maize. *American Society of Plant Biology Meeting*, July 18-22, Honolulu, HI, USA.

Schneider KL, Marrero G, Alvarez AM, **Presting G**. 2009. Comparative analysis of whole bacterial genomes and derivation of RIF, a DNA identification marker for bacterial phytopathogens. *American Phytopathological Society Meeting*, August 6-10, Honolulu, HI, USA.

Schneider KL, Wolfgruber TK, Lee H, Sharma A, Jiang J, **Presting G**. 2009. Delineation of the Functional Maize Centromeres by Chromatin Immunoprecipitation. *American Society of Plant Biology Meeting*, July 18-22, Honolulu, HI, USA.

Wang N, Sherwood AR, Kurihara A, Conklin KY, Sauvage T, **Presting G**. 2009. HADB: The Hawaiian Algal Database. *CTAHR Symposium*, April 3-4, Honolulu, HI, USA.

Wolfgruber TK, Sharma A, Schneider K, Allison JMD, **Presting G**. 2009. Comparison of centromeric DNA sequences between *Zea mays* (maize) chromosomes reveals high sequence variability despite conserved function. *CTAHR Symposium*, April 3-4, Honolulu, HI, USA.

Nakashima M, Wolfgruber T, and **Presting G**. 2009. Understanding Satellite Sequence Evolution in Corn. *CTAHR Symposium*, April 3-4, Honolulu, HI, USA.

Schneider K, Alvarez A, **Presting G**. 2008. DNA markers for identification of the bacterial phytopathogens *Clavibacter*, *Erwinia*, *Ralstonia*, and *Xanthomonas*. *American Phytopathological Society Centennial Meeting*, July 26-30, Minneapolis, MN, USA.

Schneider K, Alvarez A, **Presting G**. 2008. DNA markers for identification of four phytopathogenic bacteria. *CTAHR Symposium*, April 11-12, Honolulu, HI, USA. [Runner-up best PhD poster presentation.](#)

Wolfgruber T, Sharma A, Shi J, Lee H, Schneider K, Allison J, Saski C, Tomkins J, Jiang J, Dawe K, **Presting G**. 2008. Sequence composition of functional maize centromeres. *50th Annual Maize Genetic Conference*, February 27-March 01, Washington DC, USA.

Topp C, **Presting G**, Dawe K. 2008. xChIP combined with deep sequencing to reconcile the functional maize centromere with its DNA sequence. *50th Annual Maize Genetic Conference*, February 27-March 01, Washington DC, USA.

Sharma A, Wolfgruber TK and **Presting G**. 2008. Identification, abundance, activity and phylogenetic relationships of centromeric retrotransposons of maize and rice. *2nd International Conference on Trends in Cellular and Molecular Biology*, January 5-7, Jawaharlal Nehru University, New Delhi, India.

Sherwood AR, Kurihara A, Conklin K, Sauvage T, Wang N and **Presting G**. 2007. DNA barcoding the Hawaiian read algal flora. *Second International Barcode of Life Conference*, September 17-21, Taipei, Taiwan.

Chan Y, Sherwood A and **Presting G**. 2007. Molecular Assessment of Hawaiian stream periphyton diversity using a universally amplifying plastid marker. *Joint Meeting of Phycological Society of America & International Society of Protistologists*, August 5-9, Warwick, RI, USA.

Sharma A, Wolfgruber TK and **Presting G**. 2007. Do centromeric retrotransposons determine chromosome size? *49th Annual Maize Genetics Conference*, March 22-25, Pheasant Run, St. Charles, IL, USA.

Ewing A, Schneider K and **Presting G**. 2007. Evaluation of lateral gene transfer between a plant and a plant pathogenic bacterium. *CTAHR Symposium*, April 5-6, Honolulu, HI, USA.

Schneider K, Ewing A, Alvarez A and **Presting G**. 2007. Identification of a multi-genus genomic DNA barcode in phytopathogenic bacteria. *CTAHR Symposium*, April 5-6, Honolulu, HI, USA.

Sharma A and **Presting G**. 2007. Identification and characterization of centromeric retrotransposons in maize and rice. *CTAHR Symposium*, April 5-6, Honolulu, HI, USA. [Winner, best PhD poster presentation.](#)

Wolfgruber TK, Sharma A and **Presting G**. 2007. Centromeric satellite repeats define individual corn centromeres and undergo local duplication events". *CTAHR Symposium*, April 5-6, Honolulu, HI, USA.

Presting G. 2006. Identification of conserved plastid regions through comparative genomics. *60th Annual Meeting of the Phycological Society of America*, July 6-12, Juneau, AK, USA.

Sherwood A and **Presting G**. 2006. Conservation applications of algal DNA barcodes. *Hawaii Conservation Conference*, July 26-28, Honolulu, HI, USA.

Lai CW, Yu Q, Hou S, Skelton RL, Jones MR, Kanako LTJ, Murray J, Eustice M, Agbayani R, Guan P, Moore P, Ming R, **Presting G**. 2006. Analysis of *Carica papaya* L. BAC end sequences. *Plant and Animal Genome Meeting*, January 14-18, San Diego, CA, USA.

Sharma A, Wolfgruber TK, **Presting G**. 2006. Genetic Mapping of Maize Centromeres. *CTAHR Symposium*, April 7-8, Honolulu, HI, USA.

Schneider K, Ewing A, **Presting G**. 2006. Identification of candidate DNA barcode regions in five plant pathogenic bacteria. *CTAHR Symposium*, April 7-8, Honolulu, HI, USA.

Wolfgruber T, Sharma A, Saski C, **Presting G**. 2006. Fine scale identification and characterization of centromeric regions of the maize genome. *CTAHR Symposium*, April 7-8, Honolulu, HI, USA.

Ewing A, **Presting G**. 2005. Phylogenetic profiling of Arabidopsis. *Albert L. Tester Memorial Symposium*, March 16-18, Honolulu, HI, USA.

Wolfgruber T, **Presting G**. 2005. Functional Genomics of Maize Centromeres. College of Tropical Agriculture Symposium, April 1-2, Honolulu, HI, USA.

Ewing A, **Presting G**. 2005. Phylogenetic profiling of Arabidopsis. College of Tropical Agriculture Symposium, April 1-2, Honolulu, HI, USA. [Runner-up best overall poster presentation.](#)

Lai CW, **Presting G**. 2005. Bioinformatic Analysis of Papaya BAC End Sequences. College of Tropical Agriculture Symposium, April 1-2, Honolulu, HI, USA. [Best MBBE poster presentation.](#)

Eustice M, Moore P, **Presting G**, Ming R. 2005. Microsatellite Discovery in Papaya BAC End Sequences. College of Tropical Agriculture Symposium, April 1-2, Honolulu, HI, USA.

OTHER PRESENTATIONS

Presting G, Schneider KL, Laspisa DJ. 2018. Characterizing the interplay between maize retrotransposons and the epigenome. *NSF Plant Genome Awardee Meeting*, September 6-7, Arlington, VA, USA.

Presting G, Schneider KL, Wolfgruber TK, Sharma A, Xie Z, Nakashima M, Laspisa DJ. 2017. Characterizing the interplay between maize retrotransposons and the epigenome. *NSF Plant Genome Awardee Meeting*, September 7-8, Arlington, VA, USA.

Presting G, Schneider KL, Wolfgruber TK, Sharma A, Xie Z, Nakashima M, Laspisa DJ. 2016. Characterizing the interplay between maize retrotransposons and the epigenome. *NSF Plant Genome Awardee Meeting*, September 8-9, Arlington, VA, USA.

Gabriel D, Allen C, Schell M, Denny T, Huang Q, **Presting G**, Norman D, Flores Z, Reddy J, Duan YP, Elphinstone, Liu L, Farmerie W, Gonzalez E, Patnaikuni M, Balogh B, Alvarez A, Jones J, Mulholand V, Saddler G. 2005. Identification of ORFs unique to a Select Agent: *Ralstonia solanacearum* race 3 biovar 2. American Phytopathological Society.

Dawe RK, Jiang J, Birchler JA, Parrott WA and **Presting G**. 2004. Functional Genomics of Maize Centromeres. *NSF Plant Genome Awardee Meeting*, September 23-24, Arlington, VA, USA.

Manosalva P, **Presting G**, Goff S and Leach J. 2004. Isolation of the bacteria whose sequence contaminated the rice genome sequence. *American Phytopathological Society*, July 31 – August 04, Anaheim, CA, USA.

Chen M, **Presting G**, Barbazuk WB, Goicoechea, JL, Blackmon B, Fang G, Soderlund C, Dean RA, Wing R. 2002. An integrated physical and genetic map of the rice genome. *44th Annual Maize Genetics Conference*, March 14-17, Kissimmee, FL, USA.

Sessions A, Burke E, **Presting G**, Aux G, McElver J, Patton D, Dietrich B, Ho P, Bacwaden J, Ko C, Clarke JD, Cotton D, Bullis D, Snell J, Miguel D, Hutchison D, Kimmerly B, Mitzel T, Glazebrook J, Law M, Goff S. 2002. A high-throughput reverse genetics system for Arabidopsis. *13th International Conference on Arabidopsis Research*, 28 June -2 July, Seville, Spain.

Chen M, **Presting G**, Barbazuk WB, Goicoechea, JL, Blackmon B, Fang G, Higingbottom S, Soderlund C, Dean RA, Wing R. 2002. An integrated physical and genetic map of the rice genome. *Plant & Animal Genome X*, January 12-16, San Diego, CA, USA.

ten Hoopen R, Hudakova S, **Presting G**, Michalek, W, dos Santos, K, Schleker T, Manteuffel R, Schubert I. 2002. DNA and protein components of barley centromeres. *Plant & Animal Genome X*, January 12-16, San Diego, CA, USA.

Blackmon BP, **Presting G**, Goicoechea JL, Fang G-CE, Williams B, Phimphilai D, Phimphilai J, Frisch D, Dean RA, Wing RA. 2001. Physical mapping of rice chromosomes 3s. *Plant & Animal Genome IX*, January 13-17, San Diego, CA, USA.

Fang G-CE, **Presting G**, Goicoechea JL, Blackmon B, Williams B, Phimphilai D, Phimphilai J, Frisch D, Dean RA, Wing RA. 2001. Physical mapping of the rice genome. *Plant & Animal Genome IX*, January 13-17, San Diego, CA, USA.

Kim H, Frisch D, Yu Y, Rambo T, Henry D, Simmons J, Mao L, Thurmond S, Wood T, **Presting G**, Soderlund C, Wing RA. 2001. Physical mapping, shotgun sequencing and annotation of rice (*Oryza sativa* ssp. japonica cv. Nipponbare) chromosome 10p0.0-p3.1. *Plant & Animal Genome IX*, January 13-17, San Diego, CA, USA.

Cheng Z, **Presting G**, Buell CR, Wing RA, Jiang J. 2001. Development of a meiotic pachytene chromosome-based physical map of rice chromosome 10. *Plant & Animal Genome IX*, January 13-17, San Diego, CA, USA.

Bowers, JE, Burow GB, Kaivin C, Draye X, Hooks CA, Lemke C, Marler BS, **Presting G**, Begum D, Blackmon B, Wing RA, Paterson AH. 2001. Development of a BAC based physical map of sorghum. *Plant & Animal Genome IX*, January 13-17, San Diego, CA, USA.

Sasinowska H, Sasinowski M, **Presting G**, Forrester D, Hayes J. 2000. An efficient algorithm for the construction and visualization of physical maps. *Plant & Animal Genome VIII*, January 9-12, San Diego, CA, USA.

Kim HR, Yu Y, **Presting G**, Frisch D, Wing R. 2000. Development of a sequence-ready BAC contig of the rice (*Oryza sativa* ssp. japonica cv. Nipponbare) chromosomes 10p0.0p3.1. *Plant & Animal Genome VIII*, January 9-12, San Diego, CA, USA.

Presting G, Woo S, Sasinowski M, Frisch D, Atkins M, Begum D, Benton J, Bishop J, Boyd C, Bruce-Carver M, Budiman M, Costa R, Fant C, Gaudette B, Gayle A, Goicoechea J, Hester J, Jenkins M, Jian Q, Johnson M, Kaewpipat, K, Kim H, Kingsbury R, Lautenschlaeger A, Lee S, Levy B, Marcoux J, Matheny S, Miller H, Miller J, Phillips K, Phimphilai D, Phimphilai J, Smith S, Thurmond S, Tomkins J, Walser S, WeathersHiggingbottom S, Williams B, Wright E, Yu Y, Dean R, Wing R. 1999. Development of a framework for sequencing the rice genome: Fingerprinting and end sequencing of the CUGI Nipponbare BAC library. *41st Annual Maize Genetics Conference*, March 11-14, Lake Geneva, WI, USA.

Frisch D, Atkins M, Begum D, Bishop J, Blackmon B, Budiman MA, Mao L, Luo M, Miller

H, Tomkins J, Yu Y, Zhu H, **Presting G**, Sasinowski M, Woo S-S, Dean R, Wing R. 1999.

BAC library resource center for agricultural genomics. *41st Annual Maize Genetics Conference*, March 11-14, Lake Geneva, WI, USA.

Frisch D, Presting G, Sasinowski M, Woo S-S, Dean R, Wing R., Staff CUGI. 1999. CUGI: a resource center for the agricultural genomics community. *Plant & Animal Genome VII*, January 17-21, San Diego, CA, USA.

Presting G, Malysheva L, Fuchs J, Schubert I. 1999. A TY3/GYPSY retrotransposonlike sequence localizes to the centromeric regions of cereal chromosomes. *Plant & Animal Genome VII*, January 17-21, San Diego, CA, USA.

Presting G, Malysheva L, Fuchs J, Schubert I. 1998. A novel retrotransposon within the centromeric regions of cereal chromosomes. *Plant & Animal Genome VI*, San Diego, CA, USA.

Frary A, **Presting G**, Tanksley SD. 1995. Molecular mapping of the centromeres of tomato chromosomes 7 and 9. *Plant & Animal Genome III*, San Diego, CA, USA.

Presting G, Tanksley SD. 1995. Most interstitial telomeric repeat sequences of tomato map near centromeres. *Plant & Animal Genome III*, San Diego, CA, USA.