Marcelo Mollinari, Ph.D.

Bioinformatics Research Center • Department of Horticultural Science
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1. Summary

I am a quantitative geneticist specializing in breeding and bioinformatics, driving research to advance specialty crop improvement. My expertise lies in designing and implementing algorithms for genomic analysis in complex family structures, with a particular focus on outcrossing diploid and polyploid crops. Through close collaboration with breeders across multiple species, I develop high-performance tools that streamline genetic analyses, accelerate trait discovery, and enhance predictive breeding. My work is driven by a commitment to delivering innovative, user-friendly solutions that empower breeders to make informed decisions, optimize breeding strategies, and promote sustainable agriculture worldwide.

2. Education

2008-2012 **Ph.D. in Plant Genetics and Breeding**, Department of Genetics, "Luiz de Queiroz" College of Agriculture,University of São Paulo, Brazil. Thesis title: *Development of a model to build genetic maps in autopolyploids, with applications in sugarcane*. Supervisor: Antonio Augusto Franco Garcia

2006-2008 **M.Sc. in Plant Genetics and Breeding**, Department of Genetics, "Luiz de Queiroz" College of Agriculture,University of São Paulo, Brazil. Dissertation title: *Evaluation of algorithms used to order markers on genetic maps* Supervisor: Antonio Augusto Franco Garcia

2001-2005 **Bachelor in Agronomic Engineering**, "Luiz de Queiroz" College of Agriculture, University of São Paulo,Brazil.

3. Professional Experience

2021 - present **Research Assistant Professor**, Bioinformatics Research Center, Department of Horticultural Science, NorthCarolina State University, NC, USA

2018 - 2021 **Senior Research Assistant**, Bioinformatics Research Center, Department of Horticultural Science, NorthCarolina State University, NC, USA

2016 - 2017 **Postdoctoral Fellow**, Bioinformatics Research Center, North Carolina State University, NC, USA Project title: *Genomic tools for sweetpotato improvement.* Supervisor: Zhao-Bang Zeng

2012 - 2015 **Postdoctoral Fellow**, Department of Genetics, "Luiz de Queiroz" College of Agriculture, University of SãoPaulo, Brazil. Project title: *QTL mapping in autopolyploids using SNPs, with applications in sugarcane*. Supervisor: Antonio Augusto Franco Garcia

2014 - 2015 **Visiting Scholar**, Department of Statistics, Purdue University, IN, USA. Project title: *Development of statistical models for QTL mapping in autopolyploids using SNPs, with applications in* *sugarcane.* Supervisor: Rebecca W Doerge

2010 **Internship at Microsoft Research**, Los Angeles, CA, USA. Trainee in eScience Group. Trainee Activities: Use of graphical models in genetic mapping of polyploids, with applications in sugarcane; Study on availability of comparative assembly of the sugarcane genome. Supervisor: David Heckerman

2000 **Computer Support Assistant**, Santa Casa de Misericórdia de São Paulo – School Hospital. São Paulo, Brazil

1998-1999 **Customer Service Representative**, International Business Machines Corporation (IBM) Brasil, São Paulo, Brazil.

4. Scholarships and Fellowships

2018-2022	Bill and Melinda Gates Foundation SweetGAINS
2016-2018	Bill and Melinda Gates Foundation GT4SP
2012-2015	São Paulo Research Foundation -FAPESP(Postdoctoral)
2008-2012	São Paulo Research Foundation - FAPESP (Ph.D.)
2006-2008	Brazilian National Council for Scientific and Technological Development - CNPq (MSc)
2002-2005	Brazilian National Council for Scientific and Technological Development - CNPq (Undergraduate)

5. Grants

In evaluation: *USDA-NIFA: Development of Genomic Tools for Multiparental Outcrossing Diploid and Polyploid Populations* Role: **Project Director**. Budgeted Amount: **$649,232.20**

2023-present *RTB Breeding: A Consolidated Investment*. Role: **Co-investigator**. Award Amount: **$113,876.00** Website: https://www.rtb.cgiar.org

2022-present *USDA-NIFA: A genetics-based data analysis system for breeders in polyploid breeding programs*. Role: **Project Director**. Award Amount: **$634,487.00** Website: https://rb.gy/ik8vy6

2020-present *USDA-SCRI: Tools for Polyploids: Development of a Community Resource*. Role: **Co-investigator**. Award Amount: **$448,335.00**. Website: https://www.polyploids.org

6. Languages

Portuguese	Native
English	Fluent
Spanish	Elementary

7. Programming Skills

Languages: C, C++, Bash, and *Advanced* R, including package development and integration with C++ via Rcpp packages

Software/OS: Linux/MacOS Shell, VS Code, RStudio, SLURM, Mathematica, Git, and Adobe Illustrator.

8. Areas of Research Interest

- Statistical & Quantitative Genetics
- Polyploid Genetics & Plant Breeding
- Haplotype Phasing & Linkage Analysis
- Genomic Selection & QTL Discovery
- Open-Source Software for Genetic Data Analysis.

9. Publications

9.1. Software development

2024 **MAPpoly2** (https://github.com/mmollina/mappoly2) Genetic maps in interconnected diploid and autopolyploid families. (creator)

2024 **MAPpoly** (https://CRAN.R-project.org/package=mappoly) Genetic maps in diploids and autopolyploids (creator)

2022 **VIEWpoly** (https://CRAN.R-project.org/package=viewpoly) Visualization of Genetic Analysis in Polyploids (conceptual lead)

2020 **QTLpoly** (https://CRAN.R-project.org/package=qtlpoly) Random-Effect Multiple QTL Mapping in Autopolyploids (contributor)

2020 **OneMap** (https://CRAN.R-project.org/package=onemap) Genetic mappings in experimental crosses (co-creator)

9.2. Peer-reviewed articles

2024 Wu S, Sun H, Hamilton JP, **Mollinari M**, Gesteira SG, Kitavi M, Yan M, Kreuze J, Yencho GC, Buell R, Fei Z. (2024). Phased chromosome-level genome assembly offers new insights into the origin of hexaploid sweetpotato. *bioRxiv*. https://doi.org/10.1101/2024.08.17.608395. Under review at *Nature Plants*.

2024 Fraher S, Schwarz T, Heim C, de Siqueira Gesteira G, **Mollinari M**, Cuevas H, Laskowski S, Leal-Bertioli SCM, Yencho GC. (2024). Discovery of a major QTL for resistance to the guava root-knot nematode (*Meloidogyne enterolobii*) in 'Tanzania', an African landrace sweetpotato (*Ipomoea batatas*). *Theor. Appl. Genet.*, 137(10), 234. https://doi.org/10.1007/s00122-024-04739-1.

2024 Oh H, Stapleton L, Giongo L, Johanningsmeier S, **Mollinari M**, Mainland CM, Perkins-Veazie P, Iorizzo M. (2024). Prediction of blueberry sensory texture attributes by integrating multiple instrumental measurements. *Postharvest Biology and Technology*, 218, 113160. https://doi.org/10.1016/j.postharvbio.2024.113160.

2024 Gesteira GS, Pereira GS, Zeng ZB, **Mollinari M**. (2024). Genetic maps in sweetpotato. In *The Sweetpotato Genome* (pp. 45-68). https://doi.org/10.1007/978-3-031-65003-1_5.

2024 Pereira GS, da Silva CC, Rosa JRBF, Sobowale OO, de Siqueira Gesteira G, **Mollinari M**, Zeng ZB. (2024). New analytical tools for molecular mapping of quantitative trait loci in sweetpotato. In *The Sweetpotato Genome* (pp. 69-84). https://doi.org/10.1007/978-3-031-65003-1_6.

2024 Zhao D, Sandercock AM, Mejia-Guerra MK, **Mollinari M**, Heller-Uszynska K, Wadl PA, Webster SA, Beil CT, Sheehan MJ. (2024). A public mid-density genotyping platform for hexaploid sweetpotato (*Ipomoea batatas* [L.] Lam). *Genes*, 15(8), 1047. https://doi.org/10.3390/genes15081047.

2024 Zhao D, Sapkota M, Glaubitz J, Bassil N, Mengist M, Iorizzo M, Heller-Uszynska K, **Mollinari M**, Beil CT, Sheehan M. (2024). A public mid-density genotyping platform for cultivated blueberry (*Vaccinium* spp.). *Genet. Resour.*, 5(9), 36-44. https://doi.org/10.46265/genresj.WQZS1824.

2023 Moraes A da CL, **Mollinari M**, Ferreira RCU, Aono A, Lara LAC, Pessoa-Filho M, Barrios SCL, Garcia AAF, Valle CB, Souza AP, Vigna BBZ. (2023). Advances in genomic characterization of *Urochloa humidicola*: exploring polyploid inheritance and apomixis. *Theor. Appl. Genet.*, 136, 238. https://doi.org/10.1007/s00122-023-04485-w.

2023 Zhao D, Mejia-Guerra K, **Mollinari M**, Samac D, Irish B, Heller-Uszynska K, Beil C, Sheehan M. (2023). A public mid-density genotyping platform for alfalfa (*Medicago sativa* L.): A fast and robust genotyping platform for alfalfa breeding. *Genet. Resour.*, 4(8), 55–63. https://doi.org/10.46265/genresj.EMOR6509.

2023 Taniguti CH, Taniguti ML, Amadeu RR, Lau J, Gesteira G de S, Oliveira T de P, Ferreira GC, Pereira G da S, **Mollinari M**, Riera-Lizarazu O, Garcia AAF. (2023). Developing best practices for genotyping-by-sequencing analysis using linkage maps as benchmarks. *GigaScience*, 12, https://doi.org/10.1093/gigascience/giad092.

2022 Taniguti CH, Gesteira G de S, Lau J, Pereira G da S, Zeng Z-B, Byrne DH, Riera-Lizarazu O, **Mollinari M**. (2023). VIEWpoly: a visualization tool to integrate and explore results of polyploid genetic analysis. *J. Open Source Softw.*, 7(74), 4242. https://doi.org/10.21105/joss.04242.

2022 Zeng Z-B, **Mollinari M**, da Silva Pereira G, Olukolu BA, Yencho GC. (2022). Polyploid goes to genomics. *21st Century Pathol.*, 2(2), 113.

2021 Soares NR, **Mollinari M**, Oliveira GK, Pereira GS, Vieira MLC. (2021). Meiosis in polyploids and implications for genetic mapping: A review. *Genes*, 12(10), 1517. https://doi.org/10.3390/genes12101517.

2021 Oloka MB, Pereira G da S, Amankwaah VA, **Mollinari M**, Pecota KV, Yada B, Olukolu BA, Zeng Z-B, Yencho CG. (2021). Discovery of a major QTL for root-knot nematode (*Meloidogyne incognita*) resistance in cultivated sweetpotato (*Ipomoea batatas*). *Theor. Appl. Genet.*, https://doi.org/10.1007/s00122-021-03797-z.

2021 Pereira G da S, **Mollinari M**, Schumann MJ, Clough ME, Zeng Z-B, Yencho CG. (2021). The recombination landscape and multiple QTL mapping in a *Solanum tuberosum* cv. 'Atlantic'-derived F1 population. *Heredity*, https://doi.org/10.1038/s41437-021-00416-x.

2021 Pereira G da S, **Mollinari M**, Qu X, Thill C, Zeng Z-B, Haynes K, Yencho CG. (2021). Quantitative trait locus mapping for common scab resistance in a tetraploid potato full-sib population. *Plant Dis.*, https://doi.org/10.1094/PDIS-10-20-2270-RE.

2020 Gemenet DC, Lindqvist-Kreuze H, Olukolu BA, De Boeck B, Pereira G da S, **Mollinari M**, Zeng Z-B, Yencho CG, Campos H. (2020). Sequencing depth and genotype quality: Accuracy and breeding operation considerations for genomic selection applications in autopolyploid crops. *Theor. Appl. Genet.*, https://doi.org/10.1007/s00122-020-03673-2.

2020 Pereira G da S, Gemenet DC, **Mollinari M**, Olukolu BA, Wood JC, Diaz F, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho CG, Zeng Z-B. (2020). Multiple QTL mapping in autopolyploids: A random-effect model approach with application in a hexaploid sweetpotato full-sib population. *Genetics*, https://doi.org/10.1534/genetics.120.303080.

2020 **Mollinari M**, Olukolu BA, Pereira G da S, Khan A, Gemenet DC, Yencho GC, Zeng ZB. (2020). Unraveling the hexaploid sweetpotato inheritance using ultra-dense multilocus mapping. *G3: Genes, Genomes, Genetics*, https://doi.org/10.1534/g3.119.400620.

2019 Gemenet DC, Pereira GS, De Boeck B, Wood JC, **Mollinari M**, Olukolu BA, Diaz F, Mosquera V, Ssali RB, David M, Kitavi MN, Burgos G, Felde TZ, Ghislain M, Carey E, Swanckaert J, Coin LJM, Fei Z, Hamilton JP, Yada B, Yencho GC, Zeng Z-B, Mwanga ROM, Khan A, Gruneberg WJ, Buell CB. (2019). Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated ß-carotene and starch content in hexaploid sweetpotato (*Ipomoea batatas* [L.] Lam.). *Theor. Appl. Genet.*, https://doi.org/10.1007/s00122-019-03437-7.

2019 **Mollinari M**, Garcia AAF. (2019). Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models. *G3: Genes, Genomes, Genetics*, https://doi.org/10.1534/g3.119.400378.

2016 Costa EA, Anoni CO, Mancini MC, Santos FRC, Marconi TG, Gazaffi R, Pastina MM, Perecin D, **Mollinari M**, Xavier MA, Pinto LR, Souza AP, Garcia AAF. (2016). QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. *Euphytica*, https://doi.org/10.1007/s10681-016-1746-7.

2016 Vigna BBZ, Santos JCS, Jungmann L, Valle CB, **Mollinari M**, Pastina MM, Pagliarini M, Garcia AAF, Souza AP. (2016). Evidence of allopolyploidy in *Urochloa humidicola* based on cytological analysis and genetic linkage mapping. *PLoS ONE*, 11(4): e0153764. https://doi.org/10.1371/journal.pone.0153764.

2015 **Mollinari M**, Serang O. (2015). Quantitative SNP genotyping of polyploids with MassARRAY and other platforms. In Batley J. (Ed.), *Methods in Molecular Biology: Plant Genotyping* (pp. 17). USA: Humana Press. https://doi.org/10.1007/978-1-4939-1966-6_17.

2014 Gazaffi R, **Mollinari M**, Margarido GRA, Pastina MM, Garcia AAF. (2014). A model for quantitative trait loci mapping, linkage phase, and segregation pattern estimation for a full-sib progeny. *Tree Genet. Genomes*, 10, 791-801. https://doi.org/10.1007/s11295-013-0664-2.

2013 Garcia AAF*, **Mollinari M**.*, Marconi TG, Serang OR, Silva RR, Vieira MLC, Vicentini R, Costa EA, Mancini MC, Garcia MOS, Pastina MM, Gazaffi R, Martins ERF, Dahmer N, Sforça DA, Silva CBC, Bundock P, Henry RJ, Souza GM, van Sluys M, Landell MGA, Carneiro MS, Vincentz MAG, Pinto LR, Vencovsky R, Souza AP. (2013). SNP genotyping allows an in-depth characterization of the genome of sugarcane and other complex autopolyploids. *Sci. Rep.*, 3, 3399. https://doi.org/10.1038/srep03399. **Shared first authorship.*

2012 Palhares AC, Rodrigues-Morais TB, Van Sluys M, Domingues DS, Maccheroni W, Jordão H, Souza AP, Marconi TG, **Mollinari M**, Gazaffi R, Garcia AAF, Vieira MLC. (2012). A novel linkage map of sugarcane with evidence for clustering of retrotransposon-based markers. *BMC Genet.*, 13, 51. https://doi.org/10.1186/1471-2156-13-51.

2012 Sabadin PK, Malosetti M, Boer MP, Tardin FD, Santos FG, Guimarães CT, Gomide RL, Andrade CLT, Albuquerque PEP, Caniato FF, **Mollinari M**, Margarido GRA, Oliveira BF, Schaffert RE, Garcia AAF, Eeuwijk FA, Magalhaes JV. (2012). Studying the genetic basis of drought tolerance in sorghum by managed stress trials and adjustments for phenological and plant height differences. *Theor. Appl. Genet.*, 124, 1389-1402. https://doi.org/10.1007/s00122-012-1795-9.

2012 Pastina MM, Malosetti M, Gazaffi R, **Mollinari M**, Margarido GRA, Oliveira KM, Pinto LR, Souza AP, Van Eeuwijk FA, Garcia AAF. (2012). A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. *Theor. Appl. Genet.*, 124, 835-849. https://doi.org/10.1007/s00122-011-1748-8.

2012 Serang O, **Mollinari M**, Garcia AAF. (2012). Efficient exact maximum a posteriori computation for

Bayesian SNP genotyping in polyploids. *PLoS ONE*, 7(2): e30906. https://doi.org/10.1371/journal.pone.0030906.

2011 Marconi TG, Costa EA, Miranda HRCAN, Mancini MC, Cardoso-Silva CB, Oliveira KM, Pinto LR, **Mollinari M**, Garcia AAF, Souza AP. (2011). Functional markers for gene mapping and genetic diversity studies in sugarcane. *BMC Res. Notes*, 4, 264. https://doi.org/10.1186/1756-0500-4-264.

2010 Tarazi R, Sebbenn AM, **Mollinari M**, Vencovsky R. (2010). Mendelian inheritance, linkage, and linkage disequilibrium in microsatellite loci of *Copaifera langsdorffii* Desf. *Conserv. Genet.*, 2, 201-204. https://doi.org/10.1007/s12686-010-9230-5.

2010 Hotta CT, Lembke CG, Domingues DS, Ochoa EA, Cruz GMQ, Melotto-Passarin DM, Marconi TG, Santos MO, **Mollinari M**, Margarido GRA, Crivellari AC, Santos WD, Souza AP, Hoshino AA, Carrer H, Garcia AAF, Buckeridge MS, Menossi M, Sluys M-A, Souza GM. (2010). The biotechnology roadmap for sugarcane improvement. *Trop. Plant Biol.*, 3, 75-87. https://doi.org/10.1007/s12042-010-9050-5.

2009 **Mollinari M**, Margarido GRA, Vencovsky R, Garcia AAF. (2009). Evaluation of algorithms used to order markers on genetic maps. *Heredity*, 103, 494-502. https://doi.org/10.1038/hdy.2009.96.

2009 Oliveira KM, Pinto LR, Marconi TG, **Mollinari M**, Ulian EC, Chabregas SM, Falco MC, Burnquist W, Garcia AAF, Souza AP. (2009). Characterization of new polymorphic functional markers for sugarcane. *Genome*, 52, 191-209. https://doi.org/10.1139/G08-105.

10. Other Information

10.1. Professional service

- Chair of the "Linkage and Deletion Mapping" workshop at the *Plant and Animal Genomics* conference.
- Advisor to a Ph.D. student and committee member for five graduate students in the Department of Horticultural Science at NCSU.
- Member of the NC State Plant Breeding Consortium.
- Member of the National Association of Plant Breeding (NAPB)
- Department of Horticultural Science, NCSU Library Liaison

10.2. Extracurricular Courses

2019 RTB Leadership Training with **Mythodrama**, Bill and Melinda Gates Foundation, Bishoftu, Ethiopia. Funded by Bill and Melinda Gates Foundation

10.3. Selected Posters

2023 Gesteira GS, **Mollinari M**, Pereira G da S, et al. Genetic Mapping in Interconnected Hexaploid Sweetpotato Populations. In: *International Plant & Animal Genome 30 Conference*, San Diego, CA.

2023 Oloka BM, Pereira G da S, **Mollinari M**, et al. Progress in the Implementation of Genomic Selection and Marker-Assisted Breeding in Sweetpotato. In: *International Plant & Animal Genome 30 Conference*, San Diego, CA.

2023 Taniguti CH, Taniguti LM, Lau J, Garcia AAF, **Mollinari M**, Byrne D, Riera-Lizarazu O. Selecting the

Best Bioinformatic Pipeline for Evaluating Diploid and Auto-Tetraploid Garden Rose Genotype-by-Sequencing Data. In: *International Plant & Animal Genome 30 Conference*, San Diego, CA.

2023 Wu S, Sun H, Kitavi M, Hamilton JP, Gesteira GS, **Mollinari M**, Zeng Z-B, Yencho C, Buell R, Fei Z. Advances in the Development of Chromosome-Scale Haplotype-Resolved Genome Assemblies of Hexaploid Sweetpotatoes. In: *International Plant & Animal Genome 30 Conference*, San Diego, CA.

2022 Taniguti CH, Gesteira G de S, Lau J, Pereira G da S, Zeng Z-B, Byrne DH, Riera-Lizarazu O, **Mollinari M.** VIEWpoly: A Visualization Tool to Integrate and Explore Results of Polyploid Genetic Analysis. In: *International Plant & Animal Genome XXIX Conference*, San Diego, CA.

2020 **Mollinari M**, Bode AO, Pereira GS, Gemenet DC, Khan A, Yencho GC, Zeng Z-B. Characterization of Sweetpotato Inheritance Using Ultradense Multilocus Genetic Map. In: *International Plant & Animal Genome XXVIII Conference*, San Diego, CA.

2018 **Mollinari M**, Bode AO, Pereira GS, Gemenet DC, Khan A, Kitavi MN, Ghislain M, Yencho GC, Zeng Z-B. Construction of an Ultradense Genetic Map in Hexaploid Sweetpotato. In: *International Plant & Animal Genome XXVI Conference*, San Diego, CA.

2016 **Mollinari M**, Pereira GS, Shumann M, Yencho C, Zeng Z-B, Garcia AAF. Construction of Genetic Maps in Complex Autopolyploids. In: *International Conference in Quantitative Genetics 5*, Madison, WI.

2014 **Mollinari M**, Garcia AAF, Craig B, Doerge RW. A New Method to Construct Genetic Maps in Complex Autopolyploids Using Quantitative SNP Genotyping. In: *Kansas State Conference on Applied Statistics in Agriculture*, Manhattan, KS.

2012 **Mollinari M**, Marconi TG, Mancini MC, Costa EA, Pinto LR, Souza AP, Garcia AAF. A Novel Method to Construct Genetic Linkage Maps in High Autopolyploid Species Using Hidden Markov Models, with Applications in Sugarcane. In: *International Plant & Animal Genome XX Conference*, San Diego, CA.

10.4. Teaching

2024 **Tools for Genomic Assisted Breeding of Polyploid Crops Workshop**: Introducing MAPpoly2 and Presenting Improvements in QTLpoly, San Diego, CA.

2023 **Theoretical and Practical Aspects of Linkage Analysis in Diploids and Polyploids** – Hosted by Breeding Insight, Cornell University, Ithaca, NY. 30-hour workshop.

2023 **Polyploidy: Importance of Polyploidy, Inheritance Patterns, and Manipulation** – 1 lecture, HS 703: *Breeding Asexually Propagated Crops* – North Carolina State University, Raleigh, NC. Invited by Prof. G. Craig Yencho.

2023 **Tools for Genomic Assisted Breeding of Polyploid Crops Workshop**: MAPpoly and QTLpoly: interconnected sweetpotato families, San Diego, CA.

2022 **Linkage and QTL Mapping in Diploid and Polyploid Species** – 1 lecture in *Advancing Computing Skills in Plant Breeding*, hosted by Plant Breeding Consortium – North Carolina State University, Raleigh, NC. GitHub: https://github.com/mmollina/ACSPB.

2022 **Genotyping, Linkage, and Phasing in Polyploids** – 1 lecture, GN 757: *Statistics for Molecular Quantitative Genetics* – North Carolina State University, Raleigh, NC. Invited by Prof. Zhao-Bang Zeng.

2022 **Tools for Genomic Assisted Breeding of Polyploid Crops Workshop**: MAPpoly and QTLpoly: Use, progress, and case studies, San Diego, CA.

2021 **Polyploidy: Importance of Polyploidy, Inheritance Patterns, and Manipulation** – 1 online lecture, HS 703: *Breeding Asexually Propagated Crops* – North Carolina State University, Raleigh, NC. Invited by Prof. G. Craig Yencho.

2021 **Tools for Genomic Assisted Breeding of Polyploid Crops Workshop**: Overview of Linkage Maps and Haplotype Reconstruction, Genotype Calling, and Map Construction in Polyploid Species (online).

2019 **Polyploid Genetic Data Analysis: From Dosage Calling to Linkage and QTL Mapping** – Short course, 11-13 December, Department of Genetics, "Luiz de Queiroz" College of Agriculture, University of São Paulo, Brazil. Invited by Dr. Guilherme da Silva and Prof. Antonio AF Garcia.

2019 **Genotyping, Linkage, and Phasing in Polyploids** – 2 lectures, GN 757: *Statistics for Molecular Quantitative Genetics*. Invited by Prof. Zhao-Bang Zeng.

2019 **Polyploidy: Importance of Polyploidy, Inheritance Patterns, and Manipulation** – 1 lecture, HS 703: *Breeding Asexually Propagated Crops*. Invited by Prof. G. Craig Yencho.

2017 **Genotyping, Linkage, and Phasing in Polyploids** – 2 lectures, GN 757: *Statistics for Molecular Quantitative Genetics*. Invited by Prof. Zhao-Bang Zeng.

10.5. Talks

2024 **Genomic Challenges in Polyploid Crops: An Overview of Progress So Far**. In: *International Plant & Animal Genome 31 Conference*, San Diego, CA.

2022 **Genetic Models Applied to Polyploid Species** – *Plant Breeding and Genetics Seminar Series*, Cornell University (online).

2021 **Genetic Mapping in Polyploids: From Genotyping to Haplotype Reconstruction**. Universidade Federal de Goiás, Brazil.

2020 **Unraveling Polyploid Inheritance Using Ultra-Dense Multilocus Mapping**. *Computational Genetics Discussion Group* – Roslin Institute, University of Edinburgh (online seminar), Scotland, UK.

2020 **Unraveling Polyploid Inheritance Using Ultra-Dense Multilocus Mapping**. *Genetics & Genomics Initiative Seminar* – North Carolina State University, Raleigh, USA.

2020 **Characterization of Sweetpotato Inheritance Using Ultra-Dense Multilocus Genetic Map**. In: *International Plant & Animal Genome XXVIII Conference*, San Diego, USA.

2019 **Unraveling the hexaploid sweetpotato inheritance using ultra-dense multilocus mapping.** *INTRINSyC Seminar series - North Carolina State University*, Raleigh, North Carolina, USA

2019 **Unraveling the hexaploid sweetpotato inheritance using ultra-dense multilocus mapping.** *Seminar series onplant molecular biology - University of Illinois*, Urbana-Champaign, Illinois, USA

2019 **Genotyping, phasing and map construction in polyploids** *EiB Working Group on Polyploidy Genomics DataManagement and Analysis Meeting - International Potato Center*, Lima, Peru.

2018 **Construction of genetic maps in hexaploid sweetpotato** - *17th Sweetpotato SpeedBreeders' and GenomicsCommunity of Practice Meeting*, Nairobi, Kenya.

2018 **Linkage Analysis and Haplotype Phasing in Sweetpotato**. *Genomic Tools for Sweetpotato Improvement Annual Meeting*, Raleigh, USA.

2018 **Linkage Analysis and Haplotype Phasing in Experimental High Autopolyploid Populations, with Applications in Hexaploid Sweetpotato.** *Plant and Animal Genome Conference XXVI*, San Diego, USA.

2018 **Linkage Analysis and Haplotype Phasing in Experimental High Autopolyploid Populations, with Applications in Hexaploid Sweetpotato** ***Tools for Polyploids Planning Meeting*** - *San Diego Botanical Garden*, San Diego, USA.

2017 **SNP calling, phasing and genetic mapping in autopolyploids.** *Genomic Tools for Sweetpotato Improvement Annual Meeting*, Kampala, Uganda.

2016 **Genetic Mapping in Complex Autopolyploids.** *Genetics Department Retreat, North Carolina State University*,Raleigh, USA.

2016 **Genetic Mapping in Autopolyploids using quantitative SNP genotyping**. *Animal Breeding, Genetics & Genomics Seminar, North Carolina State University*, Raleigh, USA.

2016 **Genetic Mapping in Autopolyploids using quantitative SNP genotyping.** *Ecology, Evolution & Environmentseminar series, The University of Sheffield*, Sheffield, UK.

2015 **Genetic Mapping in Complex Autopolyploids Using Quantitative SNP Genotyping.** *Statistical Bioinformatics Seminar Series - Purdue University*, West Lafayette, Indiana, USA.

2014 **Genetic mapping of sugarcane using genotyping by sequencing - Update.** *SUNLIBB/CeProBIO Meeting*, Ghent, Belgium.

2013 **Constructing genetic linkage maps in complex polyploids using SNPs. Panel discussion.** *59º Brazilian Congress of Genetics*, Águas de Lindóia, São Paulo, Brazil. Members: Bruce Weir (University of Washington), Benilton Carvalho (University of Cambridge), Elias Chaibub Neto (Sage Bionetworks). Chair: AntonioAugusto Franco Garcia (ESALQ/USP)

2013 **Genetic mapping of sugarcane.** *SUNLIBB/CeProBIO Meeting*, Wageningen, Netherlands.

2011 **New approaches for constructing genetic linkage maps in sugarcane, a high polyploid species.** *SUNLIBB/CeProBIOMeeting*, Magdalene College, University of Cambridge, UK.

2009 **Development of an integrated genetic linkage map of sugarcane (*Saccharum* spp.) incorporating double andtriple dose markers.** *55° Brazilian Congress of Genetics*, Águas de Lindóia, São Paulo, Brazil.

10.6. Review Editor in the following scientific journal

- Frontiers in Plant Science

10.7. Ad-hoc Reviewer in the following scientific journals

- Bioinformatics
- BMC Bioinformatics
- BMC Genomics
- Brazilian Journal of Botany
- Briefings in Bioinformatics
- Crop Science
- Euphytica
- Frontiers in Plant Science
- G3 - Genes, Genomes and Genetics
- Genetics
- Journal of Heredity
- Journal of Integrative Plant Biology
- Journal of Statistical Software
- Nature Communications
- Physiological and Molecular Plant Pathology
- PlosONE
- Scientia Agricola
- Scientific Data
- Theoretical and Applied Genetics