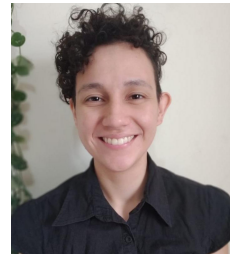


# Cristiane Hayumi Taniguti | CV

- email: [chtaniguti@tamu.edu](mailto:chtaniguti@tamu.edu) or [chaytaniguti@gmail.com](mailto:chaytaniguti@gmail.com)
- webpage: [cristianetaniguti.github.io](https://cristianetaniguti.github.io)
- Programming languages: R, Bash, WDL
- Languages: Portuguese (native), English
- Operational Systems: Unix|Linux, Mac, Windows
- Computer skills: GitHub, L<sup>A</sup>T<sub>E</sub>X, Markdown, RStudio, VS Code, Docker, Emacs, Office 365, Inkscape, Shiny



I am currently working as a Postdoctoral Research Associate in the [Texas A&M University Rose Breeding and Genetics Program](#) at the Horticultural Sciences Department, focusing on developing computational tools for polyploid species genetic analysis. Throughout my academic journey, I have gained diverse research experiences in various areas.

During my undergraduate studies, I engaged in scientific initiation projects in different areas including organic chemistry of fungus mycotoxins, cellular regulation of CNC transcription factors, QTLs studies for fat deposition in mice, differential expression studies in *Anastrepha obliqua* and SNP calling in sugarcane Genotyping-by-Sequencing (GBS) dataset. These experiences provided me with a solid foundation in laboratory techniques such as chromatography, cell cultures, western blot, RNAi and RT-PCR.

In my master, I delved deeper into SNP and genotype calling methods, and I built an integrated genetic map for an outcrossing population from the cross of *Eucalyptus grandis* x *Eucalyptus urophylla*.

For my Ph.D., I concentrated on developing novel methods and algorithms to build genetic maps in highly heterozygous diploid species using markers generated from modern sequencing technologies. This work not only contributed to advancements in OneMap software for building linkage maps but also led to the development of a collection of bioinformatic workflows called Reads2Map. These workflows provide guidance on best practices for performing and comparing different methods for SNP calling, dosage calling, and linkage map building.

In my current postdoctoral research, I have expanded the application of Reads2Map to include polyploid species. Additionally, I am responsible for the development and maintenance of the VIEWpoly package, a Shiny app that facilitates the visualization and integration of genetic analysis results of polyploid species. Furthermore, I have also been working on a new software called Qploidy for aneuploidy identification using array genotyping platform data. As part of my involvement in the [Tools for Polyploids Workshop](#), I contribute to the computational support team.

My other interests include QTL mapping, emerging technologies in molecular biology and sequencing, phenotyping methods, genome selection, and genome-wide association studies. I have collaborated in linkage and QTL mapping studies in rubber trees, roses, miscanthus, cannabis, beans, and eucalyptus. As the maintainer of [OneMap](#), [Reads2Map](#), and [VIEWpoly](#) software, I frequently provide assistance to users conducting linkage mapping in multiple species while continually enhancing the software based on user feedback and evolving research demands.

## ➤➤➤ Education

2017-2021  
(4 years) Ph.D. in Genetics and Plant Breeding

University of São Paulo –  
ESALQ/USP

- Title: Building highly saturated genetic maps with OneMap 3.0: new approaches using workflows
- Advisor: Prof. Antonio Augusto Franco Garcia
- Statistical Genetics Laboratory

2015-2017 (2 years)	Master Degree in Genetics and Plant Breeding	University of São Paulo – ESALQ/USP
<ul style="list-style-type: none"> <li>» Title: Development of an integrated genetic map for a full-sib progeny from crossing between <i>Eucalyptus grandis</i> and <i>Eucalyptus urophylla</i></li> <li>» Advisor: Prof. Antonio Augusto Franco Garcia</li> <li>» Statistical Genetics Laboratory</li> </ul>		
2009 – 2014 (5 years)	Bachelor's Degree in Biotechnology	Federal University of São Carlos – UFSCar
<ul style="list-style-type: none"> <li>» Title: Gene expression of <i>Anastrepha obliqua</i> male tissue libraries</li> <li>» Advisor: Prof. Reinaldo Alvarenga Alves de Brito</li> <li>» Population Genetics and Evolution Laboratory</li> </ul>		

## »»» Experience

2021 - present	Postdoctoral Research Associate	Texas A&M University, Department of Horticultural Sciences
<ul style="list-style-type: none"> <li>» Funded by USDA SCRI grant: "Tools for Genomic-Assisted Breeding in Polyploids" Grant No. 2020-51181-32156</li> <li>» Supervisor: Oscar Riera-Lizarazu and David Byrne</li> </ul>		
2014	Intern	Sugarcane Technology Center – CTC
<ul style="list-style-type: none"> <li>» Topic: SNP calling in sugarcane GBS dataset</li> <li>» Supervisor: Sabrina Chabregas</li> </ul>		
2012 (3 months)	Summer student	McGill University MCGILL
<ul style="list-style-type: none"> <li>» Title: Cellular regulation of CNC transcription factors</li> <li>» Advisor: Prof. Volker Blank</li> <li>» Division of Experimental Medicine</li> </ul>		
2009-2010	Technical training	Accert! Chemistry and Biotechnology
<ul style="list-style-type: none"> <li>» Topic: Studies in commercial important mycotoxin production by <i>Fusarium sp.</i></li> <li>» Supervisor: Rodrigo Facchini Magnani</li> </ul>		

## »»» Publications

Refereed articles for which reprints are available:

Article	<p><b>TANIGUTI, C. H.</b>, TANIGUTI, L. M.; AMADEU, R. R.; LAU, J.; DE SIQUEIRA GESTEIRA, G.; OLIVEIRA, T. D. P.; FERREIRA, G. C.; PEREIRA, G. D. S.; BYRNE, D.; MOLINARI, M.; RIERA-LIZARAZU, O.; GARCIA, A. A. F. Developing best practices for genotyping-by-sequencing analysis in the construction of linkage maps. <b>GigaScience</b>. doi: <a href="https://doi.org/10.1093/gigascience/giad092">https://doi.org/10.1093/gigascience/giad092</a>, 2023.</p>
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- Article LAU, J.; GILL, H.; **TANIGUTI, C. H.**; YOUNG, E.; KLEIN, P. E.; BYRNE D. H.; RIERA-LIZARAZU, O. QTL discovery for resistance to black spot and cercospora leaf spot, and defoliation in two interconnected F1 bi-parental tetraploid garden rose populations. **Frontiers in Plant Science**. doi:10.3389/fpls.2023.1209445, 2023.
- Article HOCHHAUS, T.; LAU, J.; **TANIGUTI, C. H.**; YOUNG, E. L.; BYRNE, D. H.; RIERA-LIZARAZU, O. Meta-Analysis of Rose Rosette Disease-Resistant Quantitative Trait Loci and a Search for Candidate Genes. **Pathogens**. doi: 10.3390/pathogens12040575. 2023.
- Article **TANIGUTI, C. H.**; GESTEIRA, G. S.; LAU, J.; PEREIRA, G. S.; ZENG, Z. B.; BYRNE, D. H.; RIERA-LIZARAZU, O.; MOLLINARI, M. VIEWpoly: a visualization tool to integrate and explore results of polyploid genetic analysis. **Journal of Open Source Software**. doi: 10.21105/joss.04242, 2022.
- Article RAVERDY, R.; LOURGANT, K.; MIGNOT, E.; ARNOULT, S.; BODINEAU, G.; GRIVEAU, Y.; **TANIGUTI, C. H.**; BRANCOURT-HULMEL, M. Linkage Mapping of Biomass Production and Composition Traits in a *Miscanthus sinensis* Population. **BioEnergy Research**, doi: 10.1007/s12155-022-10402-8, 2022.
- Article ALMEIDA, C. P.; PAULINO, J. F. de C. ; BONFANTE, G. F. J. ; PERSEGUINI, J. M. K. C. ; SANTOS, I. L. ; GONÇALVES, J. G. R. ; PATRÍCIO, F. R. A. ; **TANIGUTI, C. H.**; GESTEIRA, G. de S. G.; GARCIA, A. A. F. ; SONG, Q. ; CARBONELL, S. A. M. ; CHIORATO, A. F.; BENCHIMOL-REIS, L. L. Angular Leaf Spot Resistance *Loci* Associated With Different Plant Growth Stages in Common Bean. **Frontiers in Plant Science**, doi: 10.3389/fpls.2021.647043, 2021.
- Article CONSON, A. R. O.; **TANIGUTI, C. H.**; AMADEU, R. R.; ANDREOTTI, I. A. A.; DE SOUZA, L. M.; DO SANTOS, L. H. B.; DE SOUZA, A. P. High-resolution genetic map and QTL analysis of growth-related traits of *Hevea brasiliensis* cultivated under suboptimal temperature and humidity conditions. **Frontiers in Plant Science**, doi: 10.3389/fpls.2018.01255, 2018.
- Article NAKAMURA, A. M.; CHAHAD-EHLERS, S.; LIMA, A. L. A.; **TANIGUTI, C. H.**; SOBRINHO Jr, I.; TORRES, F. R.; DE BRITO, R. A. Reference genes for accessing differential expression among developmental stages and analysis of differential expression of OBP genes in *Anastrepha obliqua*. **Scientific Reports**, doi: 10.1038/srep17480, 2016.
- Available as pre-print:
- Article GAZAFFI, R.; AMADEU, R. R.; MOLLINARI, M.; ROSA, J. R. B. F.; **TANIGUTI, C. H.**; MARGARIDO, G. R. A.; GARCIA, A. A. F. . fullsibQTL: an R package for QTL mapping in biparental populations of outcrossing species. **BioRxiv**, doi: 10.1101/2020.12.04.412262, 2020.

## Software

As principal developer:

- 2023 **TANIGUTI, C. H.**; TANIGUTI, L. M. **Reads2Map**: WDL workflows to build genetic maps from sequencing reads. Available on GitHub: <https://github.com/Cristianetaniguti/Reads2Map>
- 2023 **TANIGUTI, C. H.**. **Reads2MapApp**: Shiny app to evaluate Reads2Map workflows results. Available on GitHub: <https://github.com/Cristianetaniguti/Reads2MapApp>
- 2022 **TANIGUTI, C. H.**; LAU, J. ; ANGELIN-BONNET, O.; GESTEIRA, G. S. ; PEREIRA, G. S. ; BYRNE, D. ; ZENG, Z. B. ; THOMSON, S.; MOLLINARI, M.; RIERA-LIZARAZU, O. **VIEWpoly**: R package to visualize genetic maps and QTL analysis. Available on CRAN and GitHub: <https://github.com/mmollina/viewpoly>
- 2017 MARGARIDO, G. R. A; MOLLINARI, M.; **TANIGUTI, C. H.**; FERREIRA, G.; AMADEU, R. R.; LAU, J.; BROMAN, K.; PREEDY, K.; SCHIFFTHALER, B.; GARCIA, A. A. F. **OneMap**: Construction of Genetic Maps in Experimental Crosses. Responsible for maintaining and update the package since 2017. Package available on CRAN and GitHub: <https://github.com/Cristianetaniguti/onemap>

As collaborator:

- 2023 MOLLINARI, M.; GESTEIRA, G.; **TANIGUTI, C. H.**; LAU, J.; PEREIRA, G. S.; GARCIA, A. A. F.; ZENG, Z. B.; PREEDY, K.; GENTLEMEN, R.; IHAKA, R. **MAPpoly**: Genetic Linkage Maps in Autopolyploids. Available on CRAN and GitHub: <https://github.com/mmollina/MAPpoly>
- 2020 GAZAFFI, R.; AMADEU, R.; **TANIGUTI, C. H.**; MOLLINARI, M.; MARGARIDO, G.; ROSA, J.; BROMAN, K.; GARCIA, A. A. F. **fullsibQTL**: Software for QTL Mapping using a Full-Sib Progeny. Available on GitHub: <https://github.com/augusto-garcia/fullsibQTL>

### »»» Awards

- 2023 Postdoctoral Scholar Travel Award - Texas A&M University
- 2021 Market Ready Prize - Cornell Institute Digital Agriculture Hackathon 2021
- 2018 WikiProject Computational Biology/ISCB award 2018 - International Society for Computational Biology (ISCB) and WikiProject Computational Biology
- 2017 Best Poster Award - Brazilian Association for Bioinformatics and Computational Biology

### »»» Oral presentation in events

- 2023 **TANIGUTI, C. H.**, TANIGUTI, L. M.; AMADEU, R. R.; LAU, J.; DE SIQUEIRA GESTEIRA, G.; OLIVEIRA, T. D. P.; FERREIRA, G. C.; Pereira, G. D. S.; BYRNE, D.; MOLLINARI, M.; RIERA-LIZARAZU, O.; GARCIA, A. A. F. Selecting best bioinformatic pipeline for evaluating diploid and auto-tetraploid garden roses genotyping-by-sequence data. **XXX Plant & Animal Genome Conference**. San Diego (CA), United States.
- 2023 **TANIGUTI, C. H.**, TANIGUTI, L. M.; AMADEU, R. R.; LAU, J.; DE SIQUEIRA GESTEIRA, G.; OLIVEIRA, T. D. P.; FERREIRA, G. C.; Pereira, G. D. S.; BYRNE, D.; MOLLINARI, M.; RIERA-LIZARAZU, O.; GARCIA, A. A. F. Reads2map: Practical and Reproducible Workflows to Build Polyploid Linkage Maps from Sequencing Data. **Tools for Polyploids Workshop**. San Diego (CA), United States.
- 2022 **TANIGUTI, C. H.**, DE SIQUEIRA G. G.; MOLLINARI, M. Genetic data analysis in polyploids: from allelic dosage to QTL mapping. **GVENCK workshop**. Remote, hosted in Piracicaba (SP), Brazil.
- 2022 **TANIGUTI, C. H.**, TANIGUTI, L. M.; AMADEU, R. R.; LAU, J.; DE SIQUEIRA GESTEIRA, G.; OLIVEIRA, T. D. P.; FERREIRA, G. C.; Pereira, G. D. S.; BYRNE, D.; MOLLINARI, M.; RIERA-LIZARAZU, O.; GARCIA, A. A. F. Reads2map: Practical and Reproducible Workflows to Build Linkage Maps from Sequencing Data. **Tools for Polyploids Workshop**. Remote, hosted in College Station (TX), United States.
- 2022 **TANIGUTI, C. H.**; GESTEIRA, G. S.; LAU, J.; PEREIRA, G. S.; ZENG, Z. B.; BYRNE, D. H.; RIERA-LIZARAZU, O.; MOLLINARI, M. VIEWpoly: An Interactive Tool to Visualize, Explore and Integrate Genetic Maps and QTL Analysis with Genomic Information. **XXIX Plant & Animal Genome Conference**. Remote, hosted in San Diego (CA), United States.
- 2020 **TANIGUTI, C. H.**; CORRER, F. H. Plant Biotechnology: from domestication to modern plant breeding. **BiotechLives**. Remote, hosted in Santa Cruz do Sul (RS), Brazil.
- 2019 **TANIGUTI, C. H.**; DIAS, K. O. Talk "Statistical Genetics in Breeding 4.0". **Workshop in Genetics and Plant Breeding (ESALQ/USP)**. Piracicaba (SP), Brazil.

### »»» Teaching and Training Courses

- 2023 MOLLINARI, M.; **TANIGUTI, C. H.**. Building Linkage Map for Inbred Diploid Populations with OneMap. 1 hour course. Part of the course "Theoretical and Practical Aspects of Linkage Analysis in Diploids and Polyploids" presented to **USDA/Breeding Insight group**. Remote, hosted in Ithaca (NY), United States.

- 2023 CORRER, F. H; **TANIGUTI, C. H.**. Linkage and Recombination. 2 hour course. Part of the summer course in Genetics of **Montana State University**. Remote, hosted in Bozeman (MT), United States.
- 2023 **TANIGUTI, C. H.**; ANGELIN-BONNET, O.; GESTEIRA, G. S.; LAU, J.; PEREIRA, G. S.; ZENG, Z. B.; THOMSON, S.; BYRNE, D. H.; MOLLINARI, M.; RIERA-LIZARAZU, O. VIEWpoly + HIDECAN: Usage demonstration of VIEWpoly updates and the integration with HIDECAN package. 1 hour course. **Tools for Polyploids Training Workshop**. Nelson, New Zealand.
- 2023 **TANIGUTI, C. H.**, TANIGUTI, L. M.; AMADEU, R. R.; LAU, J.; DE SIQUEIRA GESTEIRA, G.; OLIVEIRA, T. D. P.; FERREIRA, G. C.; Pereira, G. D. S.; BYRNE, D.; MOLLINARI, M.; RIERA-LIZARAZU, O.; GARCIA, A. A. F. Reads2Map: Usage demonstration in a High-Performance Computing environment. 1 hour course. **Tools for Polyploids Training Workshop**. Nelson, New Zealand.
- 2022 CORRER, F. H; **TANIGUTI, C. H.**. Linkage and Recombination. 2 hour course. Part of the summer course in Genetics of **Montana State University**. Remote, hosted in Bozeman (MT), United States.
- 2022 **TANIGUTI, C. H.**; LAU, J.; GESTEIRA, G. S.; CARAZA-HARTER, M. Computational Support session for SNP and Dosage calling. 2 hours sessions. **Tools for Polyploids Project**. Remote, hosted in College Station (TX), United States.
- 2021 **TANIGUTI, C. H.**; ARAUJO, W.; GODOY, C.; DIAS, K. O. Update on Statistical Tools Applied to Plant Breeding. 8 hours course. **Epagri - Research Center for Family Agriculture**. Remote, hosted in Piracicaba (SP), Brazil.
- 2021 **TANIGUTI, C. H.**; CORRER, F. H; HOSAKA, G. Short course "R introduction and applications in genetics". 4 hours course. **11 Integrated Undergraduate and Graduate Week, São Carlos Institute of Physics**. Remote, hosted in São Carlos (SP), Brazil.
- 2021 **TANIGUTI, C. H.**; CORRER, F. H; HOSAKA, G. Short course "R introduction". 4 hours course. Part of the course for graduate students "Biometrics of Genetic Markers", **Department of genetics, ESALQ/USP**. Remote, hosted in Piracicaba (SP), Brazil.
- 2020 **TANIGUTI, C. H.**; CORRER, F. H. Short course "R introduction and applications in genetics". 4 hours course. **X Four Biotec, Federal University of São Carlos**. Remote, hosted in São Carlos (SP), Brazil.
- 2020 **TANIGUTI, C. H.**. SNP and genotype calling in GBS data - A practical guide. 2 hours course. **Conservation Genetics and Genomics Group, ESALQ/USP**. Remote, hosted in Piracicaba (SP), Brazil.
- 2020 **TANIGUTI, C. H.**; GARCIA, A. L.; PESSOA, V. H. M. Short course "R programming training". 12 hours course. Training organized by extension group **GENT, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.
- 2019 **TANIGUTI, C. H.**; GARCIA, A. A. F. Teaching assistant in the Genetic Marker Biometry course for graduate students. 4 hours course weekly during one semester. **ESALQ/USP**. Piracicaba (SP), Brazil.
- 2018 **TANIGUTI, C. H.**; CORRER, F. H; BATISTA, L.; GARCIA, A. L. "R Introduction Short Course". 6 hours course. **XII Genetics and Plant Breeding Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.
- 2018 **TANIGUTI, C. H.**; CORRER, F. H; GESTEIRA, G. S.; GARCIA, A. L.; AVELAR, A.; HOSAKA, G. "Introduction to R data analysis". 12 hours course. Training organized by the extension group **GVENCK, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.
- 2018 **TANIGUTI, C. H.**; GARCIA, A. A. F. Lecture in the discipline Molecular Biology Applied to Plant Breeding with the talk "Building genetic maps, QTL mapping and applications in Plant Breeding" for graduate students. 4 hours course. **Agronomic Institute of Campinas (IAC)**. Campinas (SP), Brazil.
- 2017 **TANIGUTI, C. H.**; CORRER, F. H. "R Introduction Short Course". 4 hours course. **Plant Ecological Genetics Lab, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

- 2017 **TANIGUTI, C. H.**; KRAUSE, M. "R Introduction and Applications to Genetics and Plant Breeding". 6 hours course. **XI Genetics and Plant Breeding Winter Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.
- 2017 **TANIGUTI, C. H.**; GARCIA, A. A. F. Teaching assistant of the Genetic course for undergrad students. 4 hours course weekly during one semester. **ESALQ/USP**. Piracicaba (SP), Brazil.
- 2016 **TANIGUTI, C. H.**; AMADEU, R. R.; CORRER, F. H.; LARA, L.; QUEZADA, M. "Introduction to the R platform". 4 hours course. **X Genetics and Plant Breeding Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.
- 2015 **TANIGUTI, C. H.**; LARA, L.; QUEZADA, M. "Introduction to R and Genetic Mapping". 4 hours course. **IX Genetics and Plant Breeding Workshop, Department of Genetics, ESALQ/USP**. Piracicaba (SP), Brazil.

## »»» Poster presentations

- Abstract **TANIGUTI, C. H.**; GESTEIRA, G. S. ; LAU, J. ; PEREIRA, G. S. ; BYRNE, D. ; ZENG, Z. B. ; RIERA-LIZARAZU O. & MOLLINARI, M. . VIEWpoly: An interactive tool for mining results from genetic mapping analysis in autopolyploid species. **Advances in Genome Biology and Technology Conference**. San Antonio (TX), United States. Year: 2023.
- Abstract **TANIGUTI, C. H.**; TANIGUTI, L. M. ; GESTEIRA, G. S. ; OLIVEIRA, T. P. ; LAU, J. ; FERREIRA, G. C. ; AMADEU, R. R. ; BYRNE, D. ; RIERA-LIZARAZU O. ; PEREIRA, G. S. ; MOLLINARI, M. & GARCIA, A. A. F.. Comparing genotype calling software performance in Genotyping-by-Sequencing data of outcrossing population based on genetic maps quality. **30th Conference on Intelligent Systems for Molecular Biology**. Madison (WI), United States. Year: 2022.
- Abstract **TANIGUTI, C. H.**; TANIGUTI, L. M. ; GESTEIRA, G. S. ; OLIVEIRA, T. P. ; LAU, J. ; FERREIRA, G. C. ; AMADEU, R. R. ; BYRNE, D. ; RIERA-LIZARAZU O. ; PEREIRA, G. S. ; MOLLINARI, M. & GARCIA, A. A. F. . Reads2Map: Practical and Reproducible Workflows to Build Linkage Maps from Sequencing Data. **XXIX Plant & Animal Genome Conference**. Remote, hosted in San Diego (CA), United States. Year: 2022.
- Abstract **TANIGUTI, C. H.**; GESTEIRA, G. S. ; LAU, J. ; PEREIRA, G. S. ; BYRNE, D. ; ZENG, Z. B. ; RIERA-LIZARAZU O. & MOLLINARI, M. . VIEWpoly: An interactive tool to visualize, explore and integrate genetic maps and QTL analysis with genomic information. **XXIX Plant & Animal Genome Conference**. Remote, hosted in San Diego (CA), United States. Year: 2022.
- Abstract **TANIGUTI, C. H.**; SOUZA, I. C. G. ; ODA, S. ; SIQUEIRA, L. ; GRACA, R. N. ; BENATTI, T. R. ; STAPE, J. L. ; GARCIA, A. A. F. . Development of an integrated genetic map for an Eucalyptus full-sib population considering high error probabilities for low-depth GBS markers. **EUCARPIA Section Biometrics in Plant Breeding**. Ghent, Belgium. Year: 2018.
- Abstract **TANIGUTI, C. H.**; SOUZA, I. C. G. ; ODA, S. ; SIQUEIRA, L. ; GRACA, R. N. ; BENATTI, T. R. ; STAPE, J. L. ; GARCIA, A. A. F. . Development of an integrated genetic map for a full-sib progeny from crossing between *Eucalyptus grandis* and *Eucalyptus urophylla*. **X-meeting - 13<sup>a</sup> International Conference of the Brazilian Association for Bioinformatics and Computational Biology**. Águas de São Pedro (SP), Brazil. Year: 2017.

## »»» Participation in committees

- 2021 ZUCCHI, M. I. ; **TANIGUTI, C. H.** ; MARGARIDO, G. R. A. Participation in qualification exam committee of Aline da Costa Lima Moraes. Molecular-genetics studies in *Urochloa humidicola*: building a high-dense linkage map. State University of Campinas.

## »»» Event co-organization

- 2019 Polyploid Genetic Data Analysis: From dosage calling to linkage and QTL mapping - Department of Genetics, ESALQ/USP, Piracicaba-SP, Brazil
- 2019 Training - Genotype to Phenotype models for Traditional and New Phenotyping data in Plant Breeding - Department of Genetics, ESALQ/USP, Piracicaba-SP, Brazil



2018	II International Meeting on Plant Breeding - Advances in Experimental Design and Statistical Analysis in Genetics and Plant Breeding – Department of Genetics, ESALQ/USP, Piracicaba-SP, Brazil
2017	XI Workshop of Genetic and Plant Breeding – Department of Genetics, ESALQ/USP, Piracicaba-SP, Brazil
2016	X Workshop of Genetic and Plant Breeding – Department of Genetics, ESALQ/USP, Piracicaba-SP, Brazil
2015	IX Workshop of Genetic and Plant Breeding – Department of Genetics, ESALQ/USP, Piracicaba-SP, Brazil
2015	Brazilian edition of the "Tucson Plant Breeding Institute" – Department of Genetics, ESALQ/USP, Piracicaba-SP, Brazil
2010	II Four Biotec – Department of Genetics and Evolution, USFSCar, São Carlos-SP, Brazil
2009	I Four Biotec – Department of Genetics and Evolution, USFSCar, São Carlos-SP, Brazil

### Community service

2022-present	Participation as a mentor in the LGBTQ+ Pride Mentors program in Texas A&M University
2019	Participation in “Domingão do Faustão” live program in open television
2018-2019	Co-fouder of the GENT University extension group and participation in its activities
2018	Scientific communication with society through “Algoritmos nosso de cada dia” text in “Ciência Informativa” blog
2017	Popular Legal Promoters Course – PLPs
2016	Aerial Silk performance at “De última hora” show for get fundings to “Lar Betel-Piracicaba”

### References

<a href="mailto:oscar.riera-lizarazu@ag.tamu.edu">oscar.riera-lizarazu@ag.tamu.edu</a>	Oscar Riera-Lizarazu - Associate Professor at Horticultural Department in Texas A&M University. Relation: current principal advisor
<a href="mailto:augusto.garcia@usp.br">augusto.garcia@usp.br</a>	Antonio Augusto Franco Garcia - Associate Professor at Genetics Department in the University of São Paulo (ESALQ). Relation: Master's and Ph.D. advisor
<a href="mailto:mmollin@ncsu.edu">mmollin@ncsu.edu</a>	Marcelo Mollinari - Research Assistant Professor at North Carolina State University Bioinformatics Research Center. Relation: Ph.D. defense committee member and current collaborator