Marcelo Mollinari, Ph.D.

1. Address

Bioinformatics Research Center
Department of Horticultural Science
North Carolina State University
1 Lampe Drive, Campus Box 7566
Raleigh, North Carolina, 27607
Phone: +1 (919) 515-8884
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2. Personal

Date of Birth: August 03, 1979
Place of Birth: Caieiras, São Paulo, Brazil
Nationality: Brazilian
Google Scholar Citations: http://goo.gl/GW7K0
publons: https://publons.com/researcher/2727941/marcelo-mollinari/
ORCID: http://orcid.org/0000-0002-7001-8498
GitHub: https://github.com/mmollina
e-mail: mmollin@ncsu.edu

3. 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.

4. Professional Experience

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

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

2016 - 2017   Postdoctoral Fellow, Bioinformatics Research Center, North Carolina State University, NC, USAProject 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 São

Paulo, 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 sugar-cane; Study on availability of comparative assembly of the sugarcane genome. Supervisor: David Heckerman

2005   Teaching Assistant: Introduction to Statistics, Alellyx Applied Genomics S.A. Professor: Roland Vencovsky

2004   Teaching Assistant: Statistics Applied to Genetics, Center for Molecular Biology and Genetic Engineering, State University of Campinas. Professor: Antonio Augusto Franco Garcia

2000   Computer Support Assistant, Santa Casa de Misericórdia de São Paulo – School Hostital. SãoPaulo, Brazil

1998-1999   Costumer Service Representative, IBM Brasil, São Paulo, Brazil.

5. Honors

2009   Best work in plant genetics presented by a graduate student at Brazilian Congress of Genetics. Title: *Development of an integrated genetic linkage map of sugarcane (Saccharum spp.) incorporating double and tripledose markers.* 2009.

2005   Honorable work (Undergraduate): *Comparação de algoritmos de ordenação de locos em mapas genéticos usando métodos Monte Carlo* at 13° SIICUSP - International Symposium on Undergraduate Research, São Paulo, Brazil, 2005

6. Scholarships and Fellowships

2018-present   Bill and Melinda Gates Foundation Sweet GAINS
2016-218   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)

7. Grants

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://polyploid.tamu.edu/

8. Languages

Portuguese   Native
English   Fluent

Spanish   Elementary

9. Areas of Research Interest

Statistical Genetics, Quantitative Genetics, Polyploid Genetics, Plant Breeding, Population Genetics, Molecular Breeding and Statistical Computing.

10.Publications

10.1.   Articles

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. *Submitted*

2021   NR Soares, **M Mollinari**, GK Oliveira, GS Pereira, MLC Vieira. Meiosis in Polyploids and Implications for Genetic Mapping: A Review. Genes 12 (10), 1517 (2021) 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, Discovery of a major QTL for root-knot nematode (*Meloidogyne incognita*) resistance in cultivated sweetpotato (*Ipomoea batatas*) *Theor. Appl. Genet.* (2021) doi:10.1007/s00122-021-03797-z

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

2021   Pereira G da S, Mollinari M, Qu X, Thill C, Zeng Z-B, Haynes K, Yencho CG. Quantitative trait locus mapping for common scab resistance in a tetraploid potato full-sib population. *Plant Disease* (2021) doi: 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, YenchoCG, Campos H. Sequencing depth and genotype quality: Accuracy and breeding operation considerations for genomic selection applications in autopolyploid crops. *Theor. Appl. Genet. Genetics* (2020) doi: 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. Multiple QTL mapping in autopolyploids: a random-effect modelapproach with application in a hexaploid sweetpotato full-sib population *Genetics* (2020) doi: 10.1101/622951

2020   **Mollinari M**, Olukolu BA, Pereira G da S, Khan A, Gemenet DC, Yencho GC, Zeng ZB. Unraveling the hexaploid sweetpotato inheritance using ultra-dense multilocus mapping. *G3: Genes, Genomes, Genetics* (2020) doi: 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. 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.* (2019) doi: 10.1007/s00122-019-03437-7

2019   **Mollinari M**, Garcia AA F. Linkage Analysis and Haplotype Phasing in Experimental Autopolyploid Populations with High Ploidy Level Using Hidden Markov Models. G3: Genes, Genomes, Genetics (2019) doi: 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. QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. *Euphytica*. (2016), doi: 10.1007/s10681-016-1746-7.

2016   Vigna BBZ, Santos JCS, Jungmann L, Valle CB, **Mollinari M**, Pastina MM, Pagliarini M, Garcia AAF, SouzaAP. Evidence of Allopolyploidy in *Urochloa humidicola* Based on Cytological Analysis and Genetic Linkage Mapping. *PLoS ONE* 11 (4): e0153764. (2016) doi: 10.1371/journal.pone.0153764

2015   **Mollinari M**, Serang O. Quantitative SNP Genotyping of Polyploids with MassARRAY and Other Plat- forms in Batley, J (Ed.) *Methods in Molecular Biology: Plant Genotyping*, USA: Humana Press. (2015) doi: 10.1007/978-1-4939-1966-6_17

2014   Gazaffi R, **Mollinari M**, Margarido G R A, Pastina MM, Garcia AAF. A model for quantitative trait loci mapping, linkage phase and segregation pattern estimation for a full-sib progeny. *Tree Genet. Genomes*, 10, 791-801. (2014) doi: 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, HenryRJ, Souza GM, van Sluys M, Landell MGA, Carneiro MS, Vincentz MAG, Pinto LR, Vencovsky R, Souza AP. SNP genotyping allows an in-depth characterization of the genome of sugarcane and other complex autopolyploids *Sci. Rep.*, 3, p-3399 (2013) doi: 10.1038/srep03399 *shared the 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. A novel linkage map of sugarcane with evidence for clustering of retrotransposon-based markers. *BMC Genetics*, 13: 51, (2012) 10.1186/1471-2156-13-51

2012   Sabadin, PK; Malosetti, M; Boer, MP; Tardin, FD; Santos, F G; Guimarães, CT; Gomide, RL; Andrade, CLT; Albuquerque, PEP; Caniato, FF; **Mollinari, M**; Margarido, GRA; Oliveira, BF; Schaffert, RE; Garcia, AAF; Eeuwijk, FA; Magalhaes, JV. 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. (2012) 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. A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. *Theor. and Appl. Genet.* 124: 835-849. (2012) 10.1007/s00122-011-1748-8

2012   Serang, O; **Mollinari, M**; Garcia, AAF. Efficient Exact Maximum a Posteriori Computation for Bayesian SNP Genotyping in Polyploids. *PLoS ONE* 7 (2): e30906. (2012) 10.1371/journal.pone.0030906

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

2010   Tarazi R, Sebbenn A M, **Mollinari M**, Vencovsky R. Mendelian inheritance, linkage, and linkage disequilibrium in microsatellite loci of *Copaifera langsdorffii* Desf. *Conservation Genetics*, 2:201-204.(2010) 10.1007/s12686-010-9230-5

2010   Hotta CT, Lembke CG, Domingues DS, Ochoa EA, Cruz GMQ, Melotto-Passarin DM, Marconi TG, SantosMO, **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. The Biotechnology Roadmap for Sugarcane Im-provement. *Tropical Plant Biology* 3: 75-87. (2010) doi: 10.1007/s12042-010-9050-5

2009	**Mollinari M**, Margarido G R A, Vencovsky R, Garcia AAF. Evaluation of algorithms used to order markerson genetic maps. *Heredity* 103: 494-502. (2009) doi: 10.1038/hdy.2009.96
2009	Oliveira KM, Pinto LR, Marconi TG, **Mollinari M**, Ulian EC, Chabregas SM, Falco MC, Burnquist W, GarciaAAF, Souza AP. Characterization of new polymorphic functional markers for sugarcane. *Genome* 52: 191- 209. (2009) doi: 10.1139/G08-105

10.2.   Software

2022	*VIEWpoly 0.1.1*: A Shiny App to Visualize Genetic Maps and QTL Analysis in Polyploid Species (Co-creator). Available at: https://CRAN.R-project.org/package=viewpoly
2022	*MAPpoly 0.3.0*: A software to construct genetic maps in autopolyploids (Creator and Software maintainer). Available at: https://CRAN.R-project.org/package=mappoly
2022	*QTLpoly 0.2.3*: Random-Effect Multiple QTL Mapping in Autopolyploids (Contributor). Available at: https://CRAN.R-project.org/package=qtlpoly
2012	*SuperMASSA*: A graphical Bayesian inference tool for genotyping polyploids (Contributor). Available at: https://bitbucket.org/mmollina/supermassa/src/master/
2012	*OneMap 2.1.2*: R package for constructing genetic maps in experimental crosses: full-sib, RILs, F2 and back-crosses (Creator and Software maintainer from 2013-2017). Available at: https://CRAN.R-project.org/package=onemap

11. Programming Skills

Languages	C, C++, and Advanced R
Software	Maxima, MATLAB, and Maple

12. Other Information

12.1. Extracurricular Courses

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

12.2. Poster presentations

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*
2020	**Mollinari, M**, Bode AO, Pereira GS, GemenetDC, Khan A, Yencho GC, Zeng Z-B. Characterization of Sweet-potato Inheritance Using Ultradense Multilocus Genetic Map. *In: International Plant & Animal Genome XXVIII Conference*
2018	**Mollinari, M**, Bode AO, Pereira GS, GemenetDC, 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*

2016   **Mollinari, M**, Pereira G S, 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, USA.

2014   **Mollinari, M**; Garcia, AAF; Craig B; Doerge R W. 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, USA.

2012   **Mollinari, M**; Marconi, T G; Mancini, M C; Costa E A; Pinto, L R; Souza, A P; 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, USA.

12.3. Teaching

2021   Polyploidy - Importance of polyploidy, inheritance patterns and manipulation - 1 lecture *HS 703 - Breeding Asexually Propagated Crops* invited by Prof. G Craig Yencho. (on-line)

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. (on-line)

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 A F 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

12.4. Talks

2022   MAPpoly and QTLpoly: Use, progress, and case studies. *Second Tools for Genomic Assisted Breeding of Polyploid Crops Workshop* (on-line)

2021   Genetic Mapping in Polyploids: from genotyping to haplotype reconstruction. *Universidade Federal de Goiás, Brazil*

2021   Genotype Calling using SuperMASSA. *First Tools for Genomic Assisted Breeding of Polyploid Crops Workshop* – USDA/SCRI (on-line)

2021   Overview of Linkage maps and haplotype reconstruction. *First Tools for Genomic Assisted Breeding of Polyploid Crops Workshop* – USDA/SCRI (on-line)

2021   Construction of genetic maps in polyploids using MAPpoly. *First Tools for Genomic Assisted Breeding of Polyploid Crops Workshop* – USDA/SCRI (on-line)

2020   Unraveling Polyploid Inheritance Using Ultra-Dense Multilocus Mapping. *Computational Genetics Discussion Group - Roslin Institute - University of Edinburgh* (on-line 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 on plant molecular biology - University of Illinois*, Urbana-Champaign, Illinois, USA

2019   Genotyping, phasing and map construction in polyploids *EiB Working Group on Polyploidy Genomics Data Management 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 & Environment seminar 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   Uso do Programa SuperMASSA para Genotipagem de SNPs em Poliploides. Short course. *7 Brazilian Congress of Plant Breeding*, Uberlândia, Minas Gerais. (In Portuguese)

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: Antonio Augusto 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 and triple dose markers. *55º Brazilian Congress of Genetics*, Águas de Lindóia, São Paulo, Brazil.

12.5. Review Editor in the following scientific journal

- Frontiers in Plant Science

12.6. 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
- Physiological and Molecular Plant Pathology
- PlosONE
- Scientia Agricola
- Scientific Data
- Theoretical and Applied genetics

Reviews can be verified at https://publons.com/researcher/2727941/marcelo-mollinari/ (40 reviews).

13. References

These persons are familiar with my professional qualifications and my character:

Professor Zhao-Bang Zeng
Postdoc supervisor   Phone: 919-515-1942
Bioinformatics Res. Center
Dept. of Horticultural Science
North Carolina State University   e-mail: szeng@ncsu.edu
Raleigh, NC, USA

Professor Rebecca W Doerge
Postdoc supervisor   Phone: 412-268-8156
Dean, MCS / Dept. of Statistics
Carnegie Mellon University   e-mail: rwdoerge@andrew.cmu.edu
Pittsburgh, PA, USA

Professor G. Craig Yencho
Leader of GT4SP and SweetGAINS project   Phone: 919-513-7417
Dept. of Horticultural Science
North Carolina State University   e-mail: craig_Yencho@ncsu.edu

Raleigh, NC, USA

Professor Augusto F Garcia
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University of São Paulo   e-mail: augusto.garcia@usp.br
Piracicaba, São Paulo, Brazil