

ALLEGATO A

UNIVERSITÀ DEGLI STUDI DI MILANO

Procedura di selezione per la chiamata a professore di II fascia da ricoprire ai sensi dell'art. 18, commi 1 e 4, della Legge n. 240/2010 per il settore concorsuale 05/A1 - Botanica,
(settore scientifico-disciplinare BIO/01 - Botanica Generale)
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[Nome e cognome] CURRICULUM VITAE

INFORMAZIONI PERSONALI (NON INSERIRE INDIRIZZO PRIVATO E TELEFONO FISSO O CELLULARE)

COGNOME	BOMBARELY GOMEZ
NOME	AURELIANO
DATA DI NASCITA	[28, December, 1978]

INSERIRE IL PROPRIO CURRICULUM (non eccedente le 30 pagine)

KEYWORDS

Genobotany, Bioinformatics, Genomics, Plant Domestication, Evolution and Systematics, Polyploidy, Genomic Databases, Biodiversity and Populations, Genome2Phenome, Genotyping.

EDUCATION

2002 – 2007 Ph.D. (Biochemistry and Molecular Biology) - *University of Malaga*.

1996 – 2001 B.Sc. (Chemistry) - *University of Malaga*.

APPOINTMENTS

2014 – Present: Assistant Professor, *Department of Horticulture, Virginia Tech*.

2012 – 2014: Research Associate, *Plant Biology Department, Cornell University*. Group Principal Investigator: Prof. Jeffrey J. Doyle.

2008 – 2013: Postdoctoral Research Associate, *Boyce Thompson Institute*. Group Principal Investigator: Dr. Lukas Mueller.

2002 – 2007: Ph.D. Candidate, *Biochem. Mol. Biol. Depart. University of Malaga*. Supervised by Prof. V. Valpuesta and Dr. J.F. Sánchez Sevilla.

2001 – 2002: Graduate student, *Biochem. Mol. Biol. Depart. University of Malaga*. Supervised by Prof. V. Valpuesta and Dr. M.A. Botella.

RESEARCH STATEMENT AND VISION

Vision

World agriculture is facing terrible challenges due to accelerating climate change, global movement of pathogens, and a rapidly-growing human population. The development of new crop varieties may resolve specific problems, but we need to explore different approaches in order to find sustainable solutions. My long-term goal is to contribute to advancing these novel approaches through a better understanding of the changes that occur during plant domestication and their evolutionary consequences. Specifically, my research is focused on unraveling the genetic mechanisms responsible for the increase in phenotypic diversity and the local adaptation that occurs during domestication. Genetic events such as transposon movement, gene conversion, chromosomal reorganization, and gene duplication drive the production of new alleles, but the contribution to phenotypic diversity and local adaptation is unknown. Quantifying the contributions of these genetic events will accelerate the identification of alleles associated with the agronomical traits. This knowledge can also be used to develop fast-evolving crops that are adapted to changing environmental conditions.

Current projects

My laboratory research model is based on two main lines and several local, national and international collaborations. The main lines of research are:

- **Characterization of the origins of phenotypic diversity** during the domestication process using **recently domesticated ornamental crops** as models. One of the main limitations in the study of domestication is the identification of the native populations used in the early stages of domestication of the species. Crops such as maize, rice, wheat, potato, and tomato were domesticated between 4,000 and 12,000 years ago, and identification of the founder population is, in most cases, unlikely. Ornamentals such as begonias, gloxinias, and petunias were domesticated from plants originally collected during early 18th century botanical expeditions. Additionally, these cultivars are easy to grow, and their breeding history has been well documented. In the last three years, we have used the florist's gloxinia (*Sinningia speciosa*) as a model for domestication. We have developed a reference genome sequence with 31,000 annotated genes, and we have collected a biodiversity panel that captures 90% of the cultivated phenotypic diversity, including wild representatives and traditional and modern cultivars. The genetic characterization of the biodiversity panel has revealed two interesting results: (1) the **wild founder population is located in the Rio de Janeiro area**, in agreement with historical records describing the first known collection, and (2) the domestication process involved a **reduction in the genetic diversity in the population**. At the same time, there was an increase in the **phenotypic diversity**. We have also developed a segregating F₂ population from a cross of a wild representative and a domesticated accession to identify alleles associated with unique domesticated traits such as peloric (erect and symmetrical) flowers. Our QTL analysis combined with the re-sequencing of 20 different accessions has identified a **10 bp deletion in the cycloidea gene homolog that is responsible for the peloric flower trait**. We are currently preparing two publications describing these results. My future plan involves searching for the genetic elements associated with the increases in the phenotypic diversity in the domesticated populations using the biodiversity panel and several generations (e.g. F₆) of our F₂ population. Once the elements have been identified, I am planning to study them in popular crops such as tomato or potato and important crops for the Mediterranean basin such as almonds, olives, citruses, grapes and the avocados.
- **Genome Evolution under Adaptation to Arid Environments in *Nicotiana* section *Suaveolentes* (Solanaceae)**. Approximately 40% of *Nicotiana* species are allotetraploids, and this includes the most well-known species *N. tabacum* (a crop) and *N. benthamiana* (a model for plant-pathogen interactions). Polyploid *Nicotiana* species usually have 24 pairs of chromosomes ($2n = 4x = 48$) with a few exceptions in the *Suaveolentes* section in which the number of chromosome pairs range from 16 (in *N. maritima* to 24 in *N. debneyi*). The *Suaveolentes* section is composed of diverse *Nicotiana* species representing a significant radiation in Australia (26 species), the South Pacific (3 species), and Africa (1 species). The geographical distribution in Australia covers different ecological niches from coastal to interior locations and semitropical to arid areas with low annual rainfalls (< 250 mm). The variation in genome architecture within this section of the genus makes the *Suaveolentes* species a unique system in which to study the adaptation of polyploids to arid conditions on a time scale of 10 MY. Currently, I have been funded by Philip Morris International to study the relationship between the evolution of genome architecture and the adaptation to arid areas in these species.

International Collaborative Networks

My research collaborations are aligned with my interests concerning the relationship between genetic and phenotypic diversity. Currently, I am collaborating with more than a dozen groups from different countries including the USA, Spain, France, UK, Ireland, Italy, Switzerland, Brazil, Costa Rica, Iran, and China in many different species (avocadoes, cherimoyas, pawpaws, guavas, mangoes, petunias, begonias, tomatoes, olive trees, *Nicotiana*, saffron, cannabis, sinapis, vanilla, and switchgrass) and fields (plant breeding, molecular biology, population genetics, ecology, and phylogenetics). An example of this network of collaborations is my work with **tropical and semitropical crops**. I am currently coordinating the development of a high quality avocado reference genome using technologies such as PacBio and Illumina sequencing and HiC for pseudomolecule scaffolding. At the same time, I am supporting the genomic needs of three groups working in fruit quality-related traits (IHSM, La Mayora, Spain) and plant-pathogen interactions (UC Riverside, USA and IFAPA, Spain). The IHSM La Mayora interaction is also the source of a collaboration developing genomic tools for cherimoya, in which we are characterizing fruit quality traits and studying the adaptation to cold environments of its close relative, the pawpaw. I am also collaborating with the University of Costa Rica to develop a genome reference sequence for guava and to study fruit traits such as pulp color and ripening.

Future Plans

The development of a successful research program depends upon several factors such as a secure source of funding, assembling a good working team, efficient management of the inevitable setbacks, errors, and pitfalls, and packaging the results into an attractive story that can assure new cycles of funding. Phenotypic biodiversity, local adaptation, and domestication are attractive topics with an important translational component that can address actual agricultural problems. In my case, selection of the system depends on the opportunities to deliver meaningful results and attract different sources of funding. My future plans involve the use of *Sinningia speciosa* as a model in which to apply the results and lessons learned to the most convenient crop depending on funding opportunities; from tropical crops in developing economies to staple food crops in Europe, the USA, and China. My extensive network of colleagues and collaboration will help me to build effective working teams with complementary expertise. The development of my research program will benefit considerably and in many ways from my appointment to the *professori di II fascia* at the *Universita degli studi di Milano*. The *Dipartimento di Bioscienze* has leading experts in the fields of botany, genetics and molecular biology with whom I can develop solid collaborations to explore topics based on their research themes.

PROJECTS

Summary: 8 funded projects of which I served as: PI in 2, Co-PI in 2, External Partner 3 and Consultor 1.

2017

1. **Phillip Morris Products S.A. (International – USA, Switzerland)** “Genome Evolution under Adaptation to Arid Environments in the Suaveolentes section (*Nicotiana* genus)” (\$66,000; 4 months). Role: Principal Investigator.
2. **George Mason University, Mason 4-VA Research Grant Proposal (USA-Local)**. “*Computational Analysis of Microbial Evolution: Building Scaffolds to Teach Next-Generation-Sequencing in the Biology Department, Bioinformatics Concentration*” (\$19,950-USA; 1 year). Role: Consultor.
3. **Harvard Arboretum Genomics Initiative and Sequencing Award (USA-National)**. “*Sequencing the Asimina triloba* (L.) Dun. (*Annonaceae*) genome” (\$10,154-USA; 1 year). Role: Principal Investigator.

2016

4. **European Commission, H2020-EU.1.3.3. MSCA-RISE-Marie Skłodowska-Curie Research and Innovation Staff Exchange (RISE) (European Union-International: Portugal, Italy, Ireland, Australia, USA)**. “*SexSeed*” (Project ID: 690946) (€720,000 for 4 years). Role: External Partner.
5. **Ministry of Economy, Industry and Commerce, Government of Spain (Spain-National)**. “*Development of Omic Strategies for the Management of Verticillium associated disease in olive trees*” (€120,000 for 3 years). Role: External Partner.

2014

6. **European Commission, FP7-PEOPLE-2013-IRSES - Marie Curie Action "International Research Staff Exchange Scheme"** (European Union-International: Italy, Spain, Sweden, USA). “*FruitLook*” (Project ID: 612640) (€203,700 for 4 years). Role: External Partner.
7. **Jaen Local Government and University of Jaen Agreement (Spain-Local)**. “*Olive Genome Sequencing*” (€192,015 for 2 years). Role: External Collaborator/Co-Principal Investigator.

2013

8. **3CPG Priming Grant, Cornell University (USA-Local)**. “*Genome-wide genotypic characterization of a plant polyploidy complex*” (\$8,460 for 1 year). Role: Co-Principal Investigator.
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PROJECT EVALUATION AND ADVISORY ROLES

- *Ad-hoc* project reviewer for US NSF Plant Genome Research Program 2015.
 - *Ad-hoc* project reviewer for the Uruguayan Ministry of Science and Technology FVF 2017.
 - External advisor for the EU Horizon 2020 Research and Innovation Programme, Project – Newcotiana (<https://newcotiana.org/>).
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PUBLICATIONS

Summary: 46 Peer reviewed publications and 1 News & Views publication of which 7 are first author and 2 are corresponding author publications.

Online publication profiles:

Google Scholar (H-index = 21): <http://scholar.google.com/citations?user=9irBJmUAAAAJ>

ORCID: <https://orcid.org/0000-0001-6257-8914>

Submitted or accepted (available under requests)

- Vahedi M, Soorni A, Baba SA, **Bombarely A**, Salami SA. (2018) De novo transcriptome assembly of "Red Gold" stigma and calli: New insights into multiple stigma formation, apocarotenoid biosynthesis and somatic embryogenesis. *BMC Genomics* (Submitted).
- Yan H, **Bombarely A**, Xu B, Wang C, Cheng P, Chen J, Cui C, Zhang XZ, Zhao B, Huang L (2018) SiRNA regulates DNA methylation that interferes gene and lncRNA expression in the heterozygous polyploid switchgrass genome. *Biotechnology for Biofuels* (Accepted, major revisions).
- Bally J, Jung H, Mortimer C, Naim F, Philips JG, Hellens R, **Bombarely A**, Goodin MM, Waterhouse PM (2018) The Rise and Rise of *Nicotiana benthamiana*: A Plant for All Reasons. *Annu. Rev. Phytopathology* (Accepted, in production).

2018

1. **Bombarely A** (2018) Roses for Darwin. *Nature Plants* - News & Views. Published: 15 June 2018. 10.1038/s41477-018-0195-9
2. Blankers T, Oh KP, **Bombarely A**, Shaw KL. (2018) Evolution of the Genomic Architecture in a Rapid Island Radiation: Mapping Chromosomal Rearrangements and Recombination Rate Variation. *Genetics* Early Online June 6, 2018. <https://doi.org/10.1534/genetics.118.300894>
3. Foerster H, **Bombarely A**, Battey JND, Siervo N, Ivanov NV, Mueller LA. (2018) SolCyc: A database hub at the Sol Genomics Network (SGN) for the manual curation of metabolic networks in *Solanum* and *Nicotiana* specific databases. *Database* volume 2018 01/01/2018 bay035 <https://doi.org/10.1093/database/bay035>.
4. Montero-Pau J, Blanca J, **Bombarely A**, Ziarsolo P, Esteras C, Martí-Gómez C, Ferriol M, Gómez P, Jamilena M, Mueller L, Picó B, Cañizares J. (2018). De-novo assembly of zucchini genome: a whole genome duplication associated with the origin of the *Cucurbita* genus. *Plant Biotechnology* 16 (6): 1161-1171
DOI: 10.1111/pbi.12860

2017

5. Soorni A, Fatahi R, Haak D, Salami SA, **Bombarely A**. (2017). Assessment of Genetic Diversity and Population Structure in Iranian Cannabis Germplasm by Genotyping-By-Sequencing Data. *Scientific Reports* 7:15668 doi:10.1038/s41598-017-15816-5
6. Sanchez-Sevilla JF, Vallarino JG, Osorio S, **Bombarely A**, Pose D, Merchante C, Botella MA, Amaya I, Valpuesta V. (2017) Gene expression atlas of fruit ripening and transcriptome assembly from RNA-seq data in octoploid strawberry (*Fragaria × ananassa*). *Scientific Reports* 7:13737 doi:10.1038/s41598-017-14239-6
7. Carlson KD, Fernandez-Pozo N, **Bombarely A**, Mueller LM, Madlung A (2017) Genomic and transcriptomic natural variation in two populations of the allopolyploid *Arabidopsis suecica*. *BMC Genomics* 18 (1), 653; doi: 10.1186/s12864-017-4067-x
8. Villarino G, Hu Q, Scanlon M, Mueller LA, **Bombarely A**, Mattson N. (2017) Dissecting tissue-specific transcriptomic responses from leaf and roots under salt stress in *Petunia hybrida* Mitchell. *Genes* 8(8), 195; doi:10.3390/genes8080195.

9. Zhao C, Lasses T, Bako L, Kong D, Zhao B, Chanda B, **Bombarely A**, Cruz-Ramírez A, Scheres B, Brunner A, Beers E (2017) XYLEM NAC DOMAIN1: A potential angiosperm innovation regulating xylem differentiation through multiple conserved linear motifs interacting with RETINOBLASTOMA-RELATED. **New Phytologist** doi:10.1111/nph.14704.
10. Sherman-Broyles S, **Bombarely A**, Doyle JJ. (2017). Characterizing the allopolyploid species among the wild relatives of soybean: Utility of reduced representation genotyping methodologies. **Journal of Systematics and Evolution** 55: 365–376. doi:10.1111/jse.12268.
11. Edwards K, Fernandez-Pozo N, Drake-Stowe K, Humphry M, Evans A, **Bombarely A**, Allen F, Hurst R, White B, Kernodle S, Bromley J, Sanchez-Tamburrino J.P., Lewis R, Mueller LA (2017) Map-based cloning of homeologous loci implicated in nitrogen utilization efficiency enabled by an improved *Nicotiana tabacum* genome assembly. **BMC Genomics** 18:448. doi:10.1186/s12864-017-3791-6.
12. Zimmers J, Thomas M, Yang L, **Bombarely A**, Mancuso M, Wojciechowski M, Smith J. (2017) Species Boundaries in the *Astragalus cusickii* Complex Delineated using Molecular Phylogenetic Techniques. **Molecular Phylogenetics and Evolution** 114 :93-110. doi:10.1016/j.ympev.2017.06.004.
13. Mizzotti C, Galliani B, Dreni L, Sommer H, **Bombarely A**, Masiero S (2017) ERAMOSIA controls lateral branching in snapdragon. **Scientific Reports** 7:41319 doi:10.1038/srep41319.
14. Soorni A, Haak D, Zaitlin D, **Bombarely A** (2017) Organelle_PBA, a pipeline for assembling chloroplast and mitochondrial genomes from PacBio DNA sequencing data. **BMC Genomics** 18 (1):49 doi:10.1186/s12864-016-3412-9.
15. Jiménez-Ruiz J, Leyva-Pérez MO, Schilirò E, Barroso JB, **Bombarely A**, Mueller LM, Mercado-Blanco J, Luque F (2017) Transcriptomic analysis of the olive (*Olea europaea* L.)-*Verticillium dahliae* interaction during early root infection process. **The Plant Genome** DOI: doi:10.3835/plantgenome2016.07.0060.

2016

16. Frazier TP, Palmer NA, Xie F, Tobias CM, Donze-Reiner T, **Bombarely A**, Childs K, Shu S, Jenkins J, Schmutz J, Zhang B, Sarath G, Zhao B (2016) Identification, Characterization, and Gene Expression Analysis of Nucleotide Binding Site (NB)-Type Resistance Gene Homologues in Switchgrass. **BMC Genomics** 17 (1): 892. doi:10.1186/s12864-016-3201-5.
17. Coate J, Song M, **Bombarely A**, Doyle JJ (2016) Expression-level support for gene dosage sensitivity in three *Glycine* subgenus *Glycine* polyploids and their diploid progenitors. **New Phytologist** 212 (4), 1083-1093. doi:10.1111/nph.14090.
18. **Bombarely A**, Moser M, Amrad A, Bao M, Bapaume L, Barry CS, Bliet M, Boersma M, Borghi L, Bruggmann R, Bucher M, D'Agostino N, Davies K, Druege U, Dudareva N, Egea-Cortines M, Delledonne M, Fernandez-Pozo N, Franken P, Grandont L, Heslop-Harrison JS, Hintzsche J, Johns M, Koes R, Lv X, Lyons E, Malla D, Martinoia E, Mattson NS, Morel P, Mueller LA, Muhlemann J, Nouri E, Passeri V, Qi Q, Reinhardt D, Rich M, Richert-Pöggeler K, Robbins TP, Schatz MC, Schranz E, Schuurink RC, Schwarzacher T, Spelt K, Tang H, Urbanus SL, Vandenbusschen M, Vijverberg K, Villarino GH, Warner RM, Weiss J, Yue Z, Zethof J, Quattrocchio F, Sims TL, Kuhlemeier C (2016) Whole genome sequences of the wild parents of the garden petunia give insights into the evolution of Solanaceae genomes. **Nature Plants** 2: 16074 doi:10.1038/nplants.2016.74.

2015

19. Castro JC, Maddox JD, Cobos M, Requena D, Zimic M, **Bombarely A**, Imán SA, Cerdeira LA, Medina AE (2015) De novo assembly and functional annotation of *Myrciaria dubia* fruit transcriptome reveals multiple metabolic pathways for L-ascorbic acid biosynthesis. **BMC Genomics** 16 (1): 997. doi: 10.1186/s12864-015-2225-6
20. Vallarino JG, Osorio S, **Bombarely A**, Casañal A, Cruz-Rus E, Sánchez-Sevilla JF, Amaya I, Giavalisco P, Fernie AR, Botella MA, Valpuesta V (2015) Central role of FaGAMYB in the transition of the strawberry receptacle from development to ripening. **New Phytologist** 208 (2):482-496. doi:10.1111/nph.13463.

21. Soliman SSM, Greenwood JS, **Bombarely A**, Mueller LA, Tsao R, Mosser DD, Raizada MN (2015) An Endophyte Constructs Fungicide-Containing Extracellular Barriers for Its Host Plant. *Current Biology*. 25 (19):2570-2576. doi:10.1016/j.cub.2015.08.027.
22. Duran I, Csukasi F, Taylor SP, Krakow D, Becerra J, **Bombarely A**, Marí-Beffa M (2015) Collagen duplicate genes of bone and cartilage participate during regeneration of zebrafish fin skeleton. *Gene Expression Patterns* 19 (1): 60-69 doi:10.1016/j.gep.2015.07.004.
23. Strickler SR, **Bombarely A**, Munkvold JD, Menda N, Martin GB, Mueller LA (2015) Comparative genomics and phylogenetic discordance of cultivated tomato and its nearest wild relatives. *PeerJ*. 3, e793. doi:10.7717/peerj.793.
24. Fernandez-Pozo N, Menda N, Edwards JD, Saha S, Tecele IY, Strickler SR, **Bombarely A**, Fisher-York T, Pujar A, Foerster H, Yan A, Mueller LA (2015) The Sol Genomics Network (SGN)—from genotype to phenotype to breeding. *Nucleic Acids Research*. 43 (D1), D1036-D1041; doi: 10.1093/nar/gku1195

2014

25. Kang YJ , Kim S, Kim MY , Lestari P, Kim KH, Ha BK, Jun TH, Hwang WJ, Lee T, Lee J, Shim S, Yoon MY, Jang YE, Han KS, Taeprayoon P, Yoon N, Somta P, Tanya P, Kim KS, Gwag JG, Moon JK, Lee YH, Park BS, **Bombarely A**, Doyle J, Jackson S, Schafleitner R, Srinives P, Varshney R. (2014) Genome sequence of mungbean and insights into evolution within Vigna species. *Nature Communications*. 5: 5443 doi:10.1038/ncomms6443.
26. Menda N, Stricker SR, Edwards JD, **Bombarely A**, Dunham DM, Martin GB, Mejia L, Hutton SF, Havey MJ, Maxwell DP, Mueller LA. (2014) Analysis of introgressions in the genome of a begomovirus-resistant tomato inbred uncovers origins of its wild ancestors. *BMC Plant Biology* 14 (1): 287. doi:10.1186/s12870-014-0287-2.
27. Sherman-Broyles S, **Bombarely A**, Powell AF, Doyle JL, Egan AN, Coate JE, Doyle JJ (2014) The wild side of a major crop: Soybean's perennial cousins from Down Under. *American Journal of Botany* 101:1651-1665. doi:10.3732/ajb.1400121.
28. Sherman-Broyles S, **Bombarely A**, Grimwood J, Schmutz J, Doyle JJ (2014) Complete Plastome Sequences from Glycine syndetika, and Six Additional Perennial Wild Relatives of Soybean. *G3: Genes Genomes Genetics*, g3. 114.012690. doi:10.1534/g3.114.012690.
29. **Bombarely A**, Coate JE, Doyle JJ (2014) Mining transcriptomic data to study the origins and evolution of a plant allopolyploid complex. *PeerJ* 2, e391. doi: 10.7717/peerj.391.
30. Villarino GH, **Bombarely A**, Giovannoni JJ, Scanlon MJ, Mattson NS (2014) Transcriptomic Analysis of Petunia hybrida in Response to Salt Stress Using High Throughput RNA Sequencing. *PloS One* 9 (4), e94651. doi:10.1371/journal.pone.0099146.
31. Jung S, Ficklin S, Lee T, Cheng CH, Blenda A, Zheng P, Yu J, **Bombarely A**, Cho, IH, Yu S, Evans K, Peace C, Abbott A, Mueller LA, Olmstead M, Main D. (2014) The Genome Database for Rosaceae (GDR): Year 10 Update. *Nucleic Acid Research* 42 (D1), D1237-D1244. doi:10.1093/nar/gkt1012

2013

32. Rosli HG, Zheng Y, Pombo MA, Zhong S, **Bombarely A**, Fei Z, Collmer A, Martin GB (2013) Transcriptomics-based screen for genes induced by flagellin and repressed by pathogen effectors identifies a cell wall-associated kinase involved in plant immunity. *Genome Biology* 14 (12): R139. doi:10.1186/gb-2013-14-12-r139.
33. D'Agostino N, Golas T, van der Geest H, **Bombarely A**, Dawood T, Zethof J, Driedonks N, Wijnker E, Bargsten J, Nap JP, Mariani C, Rieu I (2013) Genomic analysis of the native European Solanum species, *S. dulcamara*. *BMC Genomics* 14: 356. doi:10.1186/1471-2164-14-356.
34. Pujar A, Menda N, **Bombarely A**, Edwards JD, Strickler SR, Mueller LA (2013) From manual curation to visualization of the gene families and networks across the Solanaceae plant species. *Database: The Journal of Biological Databases and Curation* 2013, bat028. doi: 10.1093/database/bat028.

35. Doblás VG, Amorim-Silva V, Pose D, Rosado A, Esteban A, Arro M, Azevedo H, **Bombarely A**, Borsani O, Valpuesta V, Ferrer A, Tavares RM, Botella MA (2013) The Arabidopsis SUD1 Gene, encoding a putative E3 Ubiquitin Ligase, is a Positive Regulator of the 3-Hydroxy-3-Methylglutaryl Coenzyme A Reductase Activity. *The Plant Cell*. 25: 728-743. doi:10.1105/tpc.112.108696.

2012

36. Guo S, Zhang J, Sun H, Salse J, Lucas WJ, Zhang H, Zheng Y, Mao L, Ren Y, Wang Z, Min J, Guo X, Murat F, Ham BK, Zhang Z, Gao S, Huang M, Xu Y, Zhong S, **Bombarely A**, Mueller LA, Zhao H, He H, Zhang Y, Zhang Z, Huang S, Tan T, Pang E, Lin K, Hu Q, Kuang H, Ni P, Wang B, Liu J, Kou Q, Hou W, Zou X, Jiang J, Gong G, Klee K, Schoof H, Huang Y, Hu X, Dong S, Liang D, Wang J, Wu K, Xia Y, Zhao X, Zheng Z, Xing M, Liang X, Huang B, Lv T, Wang J, Yin Y, Yi H, Li R, Wu M, Levi A, Zhang X, Giovannoni JJ, Wang J, Li Y, Fei Z, Xu Y (2012) The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions. *Nature Genetics* 45(1): 51-58. doi:10.1038/ng.2470.
37. **Bombarely A**, Edwards KD, Sanchez-Tamburino J, Mueller LA (2012) Deciphering the complex leaf transcriptome of the allotetraploid species *Nicotiana tabacum*: A phylogenomic perspective. *BMC Genomics* 13(1): 187. doi:10.1186/1471-2164-13-406.
38. **Bombarely A**, Rosli HG, Vrebalov J, Moffet P, Mueller LA, Martin G. (2012) A Draft Genome Sequence of *Nicotiana benthamiana* to enhance molecular plant-microbe biology research. *Molecular Plant-Microbe Interactions*. 25(12): 1523-1530. doi:10.1094/MPMI-06-12-0148-TA.
39. Tomato Sequencing Consortium (2012), The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* 485 (7400): 635-641. doi:10.1038/nature11119.
40. Lima-Silva V, Rosado A, Amorin-Silva V, Muñoz-Mérida A, Pons C, **Bombarely A**, Trelles O, Fernández-Muñoz R, Granell A, Valpuesta V, Botella MA (2012) Genetic and genome-wide transcriptomic analyses identify co-regulation of oxidative response and hormone transcript abundance with vitamin c content in tomato fruit. *BMC Genomics* 13 (1), 187. doi:10.1186/1471-2164-13-187.
41. Strickler SR, **Bombarely A**, Mueller LA. (2012) Designing a Transcriptome Next-Generation Sequencing Project for a Non-model Plant Species. *American Journal of Botany* 99 (2): 257-266. doi:10.3732/ajb.1100292.

2011

42. Osorio S, **Bombarely A**, Giavalisco P, Usadel B, Stephens C, Aragüez I, Medina-Escobar N, Botella MA, Fernie AR, Valpuesta V. (2011) Demethylation of oligogalacturonides by FaPE1 in the fruits of the wild strawberry *Fragaria vesca* triggers metabolic and transcriptional changes associated with defence and development of the fruit. *Journal of Experimental Botany*. 62 (8): 2855. doi:10.1093/jxb/erq465.
43. Privat I, Bardil A, **Gomez AB**, Severac D, Dantec C, Fuentes I, Mueller L, Joët T, Pot D, Foucrier S, Dussert S, Leroy T, Journot L, de Kochko A, Campa C, Combes MC, Lashermes P, Bertrand B. (2011) The 'PUCE CAFE' Project: the First 15K Coffee Microarray, a New Tool for Discovering Candidate Genes correlated to Agronomic and Quality Traits. *BMC Genomics*, 12:5. doi:10.1186/1471-2164-12-5.
44. **Bombarely A**, Menda N, Teclé IY, Buels RM, Strickler S, Fischer-York T, Pujar A, Leto J, Gosselin J, Mueller LA. (2011) The Sol Genomics Network (solgenomics.net): growing tomatoes using Perl *Nucleic Acids Research* 39:D1149-D1155. doi:10.1093/nar/gkq866.

2010

45. **Bombarely A**, Merchante C, Csukasi F, Cruz-Rus E, Caballero JL, Medina-Escobar N, Blanco-Portales R, Botella MA, Muñoz-Blanco J, Sánchez-Sevilla JF, Valpuesta V. (2010) Generation and analysis of ESTs from strawberry (*Fragaria xananassa*) fruits and evaluation of their utility in genetic and molecular studies. *BMC Genomics*, 11:503. doi:10.1186/1471-2164-11-503.

46. Edwards KD, **Bombarely A**, Story GW, Allen F, Mueller LA, Coates SA, Jones L. (2010) TobEA: an atlas of tobacco gene expression from seed to senescence *BMC Genomics*, 11:142. doi:10.1186/1471-2164-11-142.

2009

47. Mueller LA, Lankhorst RK, Tanksley SD, Giovannoni JJ, Fei ZJ, van Eck J, Buels R, Mills AA, Menda N, Teele IY, **Bombarely A**, Stack S, Royer SM, Chang SB, Shearer LA, Kim BD, Jo SH, Hur CG, Choi D, Li CB, Zhao JH, Jiang HL, Geng Y, Dai YY, Fan HJ, Chen JF, Lu F, Shi JF, Sun SH, Chen JJ, Yang XH, Lu C, Chen MS, Li CY, Ling HQ, Xue YB, Wang Y, Seymour GB, Bishop GJ, Bryan G, Rogers J, Sims S, Butcher S, Buchan D, Abbott J, Beasley H, Nicholson C, Riddle C, Humphray S, McLaren K, Mathur S, Vyas S, Solanke AU, Kumar R, Gupta V, Sharma AK, Khurana P, Khurana JP, Tyagi A, Sarita, Chowdhury P, Shridhar S, Chattopadhyay D, Pandit A, Singh P, Kumar A, Dixit R, Singh A, Praveen S, Dalal V, Yadav M, Ghazi IA, Gaikwad K, Sharma TR, Mohapatra T, Singh NK, Szinay D, de Jong H, Peters S, van Staveren M, Datema E, Fiers MWEJ, van Ham RCHJ, Philippot M, Frasse P, Regad F, Zouine M, Bouzayen M, Asamizu E, Sato S, Fukuoka H, Tabata S, Shibata D, Botella MA, Perez-Alonso M, Fernandez-Pedrosa V, Osorio S, Mico A, Granell A, Zhang ZH, He J, Huang SW, Du YC, Qu DY, Liu LF, Liu DY, Wang J, Ye ZB, Yang WC, Wang GP, Vezzi A, Todesco S, Valle G, Falcone G, Pietrella M, Giuliano G, Grandillo S, Traini A, D'Agostino N, Chiusano ML, Ercolano M, Barone A, Frusciante L, Schoof H, Jocker A, Bruggmann R, Spannagl M, Mayer KXF, Guigo R, Camara F, Rombauts S, Fawcett JA, Van de Peer Y, Knapp S, Zamir D, Stiekema W. (2009) A snapshot of the emerging tomato genome sequence. *Plant Genome* 2:78. doi:10.3835/plantgenome2008.08.0005.
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CONFERENCES AND INVITED SEMINARS

MEETINGS AND WORKSHOPS MANAGEMENT

2018

- Chair of the *Plant Biodiversity session* at the *International Congress of Genetics* (Foz do Iguaçu, Brazil, September 10-14).
- Chair of the *Challenges to Productivity: Genetics, genomics and biotechnology session* at the Avocado Brainstorming 2018 (Tzaneen, South Africa, May 28 – June 1).

2017

- Co-Chair of the *Nicotiana session* at the *Solanaceae and 2nd Cucurbitaceae Genome Joint Conference* (Valencia, Spain, September 3-6).
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CONTRIBUTED PRESENTATIONS AND WORKSHOPS

My work has been presented in 36 international workshops and conferences.

2018

1. **Bombarely A*** (2018) Development of Community Driven Avocado Genomic Resources. Avocado Brainstorming 2018 (Tzaneen, South Africa, May 28 – June 1).
2. **Bombarely A***, Giudicelli GC, Hasing T, Petzold E, Freitas LB (2018) Petunia domestication through the analysis of the population structure and genetic diversity. *16th World Petunia Days* (Amsterdam, The Netherlands, March 15-18).

2017

3. **Bombarely A*** (2017) The *Nicotiana benthamiana* genome 2.0: from genes to pseudomolecules. *8th Solanaceae and 2nd Cucurbitaceae Genome Joint Conference* (Valencia, Spain, September 3-6) (Oral presentation, * speaker).
4. **Bombarely A*** (2017) Insights of the genome architecture for the species *Begonia conchifolia*. **International Botanical Conference 2017** (Shenzhen, China, July 23-29) (Oral presentation, * Speaker).
5. **Bombarely A*** (2017) Analysis of the Genomes Architectures for *Petunia hybrida* and its Wild Relatives. *Plant & Animal Genome XXV* (San Diego, CA, USA, January 14-18) (Oral Presentation, *Speaker).
6. **Bombarely A***, (2017) Analysis of the *Sinningia speciosa* Diversity under Domestication. *Plant & Animal Genome XXV* (San Diego, CA, USA, January 14-18) (Oral Presentation, *Speaker).

2016

7. **Bombarely A*** (2016) Variation of the *P. hybrida* genome architecture compared with its wild relatives. *The 15th World Petunia Days* (Wittenberg, Germany, October 9-12)(Oral presentation, *Speaker)

2015

8. **Bombarely A***, Moser M, Mueller LA, Johns MA, Schranz ME, Schwarzacher T, Gerats T, Vandenbussche M, Quattrocchio FM, Durareva N, Schuurink RC, Reinhardt D, Robbins TP, Egea-Cortines M, Kuhlemeier C, Sims TL (2015) Evolutionary analysis of *Petunia* genomes *12th Solanaceae Genome Workshop* (Bordeaux, France, October 25-29)(Oral Presentation, *Speaker)
9. **Bombarely A*** (2015) Breaking down the bioinformatic resources used at the *Petunia* Genome Project. *The 14th World Petunia Days* (Murten, Switzerland, April 9-12)(Oral presentation, *Speaker)
10. **Bombarely A**, Zaitlin D (2015) Sequencing the Genome of *Sinningia speciosa* (Lodd.) Hiern, a Reference for the Neotropical Gesneriaceae. *Plant & Animal Genome XXIII* (San Diego, CA, USA, January 10-14)(Poster)
11. **Foester H***, Mueller LA, Fernandez-Pozo N, Bombarely A, Caspi R, Karp PD (2015) Exploring Metabolic Networks: Metacyc and SolCyc as Examples for High-Level Data Curation, Depository and Management Across and within Species. *Plant & Animal Genome XXIII* (San Diego, CA, USA, January 10-14)(Oral presentation, *Speaker)

2013

12. **Bombarely A***, Fernández-Pozo N, Rosli RG, Pombo MA, Lippman ZB, Zaitlin D, Mueller LA, Martin GB. (2013) Genome analysis of the model plant species *Nicotiana benthamiana*. *The 10th Solanaceae Genome Workshop* (Beijing, China, October 13-17) (Oral presentation, * Speaker).
13. Edwards JD*, **Bombarely A***, Mueller LA* (2013) SGN Workshop – from genomes to breeding, *The 10th Solanaceae Genome Workshop* (Beijing, China, October 13-17) (Database workshop, * Speakers).
14. **Bombarely A***, Coate JE, Edwards KD, Mueller LA, Doyle JJ. (2013) Identifying Homoeologues in Allopolyploid Species from NGS Data: Examples from *Nicotiana* and *Glycine* *Plant & Animal Genome XXI* (San Diego, CA, USA, January 12-16) (Oral presentation, *Speaker)
15. Mueller LA, Menda N, Edwards JD, **Bombarely A**, Strickler SR, Teclé IY. (2013) Solgenomics.net: A Platform for Genome Assisted Breeding. *Plant & Animal Genome XXI* (San Diego, CA, USA, January 12-16) (Poster)
16. Main D*, Jung S, Lee T, Ficklin SP, Zhend P, Cheng CH, Ru S, Bleda A, Mueller LA, **Bombarely A**, Layne D, Olmstead M, Chen C, Peace C, Evans KM, Oraguzie N, Gmitter FG, Abbot AG. (2013) Genome Database for *Rosaceae* *Plant & Animal Genome XXI* (San Diego, CA, USA, January 12-16) (Oral presentation, *Speaker).
17. Menda N, Stricker SR, Edwards JD, **Bombarely A**, Mejia L, Hutton S, Scott J, Havey M, Maxwell D, Mueller LA* (2013) Whole Genome Sequencing of a Begomovirus-resistant Tomato Inbred Reveals Introgressions from Wild *Solanum* Species. *Tomato Breeders Roundtable 2013* (Shangri La, Chiang-Mai, Thailand, February 7) (Oral presentation, *Speaker).

2012

18. Sims TL*, **Bombarely A**, Delledonne M, Gerats T, Johns M, Mueller LA, Pezzotti M, Quattrocchio F, Yang B. (2012) Sequencing and Comparison of the Genomes of *Petunia inflata* and *Petunia axillaris*. *Plant & Animal Genome XX* (San Diego, CA, USA, January 14-18) (Oral presentation, *Speaker).
19. Strickler SR*, **Bombarely A**, Munkvold J, Martin GB, Mueller LA. (2012) Comparative Genomics of *Solanum galapaguense*, a Wild Relative of Tomato. *Plant & Animal Genome XX* (San Diego, CA, USA, January 14-18) (Oral presentation, *Speaker).
20. Mueller LA*, Strickler SR, Menda N, **Bombarely A**, Leto J, Buels R, Gosselin J. (2012) Sol Genomics Network (<http://solgenomics.net>): A Resource for Coffee Genomics. *Plant & Animal Genome XX* (San Diego, CA, USA, January 14-18) (Oral presentation, *Speaker).

21. Mueller LA*, Menda N, **Bombarely A**, Teclé IY, Strickler SR, Buels R, Leto J, Gosselin J. (2012) SGN (<http://solgenomics.net>): Of Phenotypes, Genotypes, and Tomatoes. *Plant & Animal Genome XX* (San Diego, CA, USA, January 14-18) (Oral presentation, *Speaker).

2011

22. Mueller LA*, Menda N, **Bombarely A**, Strickler SR, Buels RM, Leto J, Gosselin J. (2011) SGN (<http://solgenomics.net>), a Scalable Platform for Comparative Genomics. *8th Solanaceae and 2nd Cucurbitaceae Genome Joint Conference* (Kobe, Japan, November 28-December 2) (Oral presentation, *Speaker).
23. **Bombarely A**, Edwards KD, Sanchez-Tamburino JP, Mueller LA. (2011) PhygOmics, a Phylogenetic Pipeline for Evolutionary Analysis of High Throughput Sequence Data. *8th Solanaceae and 2nd Cucurbitaceae Genome Joint Conference* (Kobe, Japan, November 28-December 2) (Poster).
24. Mueller LA*, **Bombarely A***, Menda N*. (2011) The Sol Genomics Network Workshop. *8th Solanaceae and 2nd Cucurbitaceae Genome Joint Conference* (Kobe, Japan, November 28-December 2, 2011) (Database workshop, * Speakers)
25. **Bombarely A***, Edwards KD, Coates SA, Mueller LA. (2011) Deciphering the Transcriptome of *Nicotiana tabacum*. *1st Plant Genome Evolution Meeting* (Amsterdam, The Netherlands, September 4-6, 2011) (Oral presentation, *Speaker)
26. **Bombarely A***, Menda N, Teclé I, Strickler S, Fisher-York T, Pujar A, Leto J, Gosselin J, Buels R, Mueller LA* (2011) The Sol Genomics Workshop. *XVIIIth EUCARPIA Meeting - Section Vegetables, Working Group Tomato* (Malaga, Spain, April 11-14) (Database workshop, * Speakers).
27. **Bombarely A***, Menda N, Teclé I, Buels R, Strickler SR, Fisher-York T, Pujar A, Leto J, Gosselin J, Buels R, Mueller LA (2011) Using SGN Resources After the Tomato Genome Sequencing. *Plant & Animal Genome XIX* (San Diego, CA, USA, January 15-19) (Computer Demo, *Speaker).

2010

28. **Bombarely A***, Edwards KD, Coates SA, Mueller LA. (2010) Phylogenomic Analysis of Cultivated Tobacco". *The 7th Solanaceae Genome Workshop* (Dundee, Scotland, September 5-9) (Oral presentation, * Speaker).
29. **Bombarely A***, Menda N, Teclé I, Strickler SR, Fisher-York T, Pujar A, Leto J, Gosselin J, Buels R, Mueller LA* (2010) SGN Workshop. *The 7th Solanaceae Genome Workshop* (Dundee, Scotland, September 5-9, 2010) (Database workshop, * Speakers).
30. **Bombarely A***, Menda N, Teclé I, Strickler SR, Fisher-York T, Pujar A, Leto J, Gosselin J, Buels R, Mueller LA (2010) Sol Genomics Workshop: What SGN can do for you. *XIVth EUCARPIA Meeting on Genetics and Breeding of Capsicum & Eggplant* (Valencia, Spain, August 30-September 1) (Database workshop, * Speaker).
31. **Bombarely A**, Edwards KD, Menda N, Teclé I, Pujar A, York T, Mills A, Gosselin J, Buels R, Coates SA, Mueller LA. (2010) SEDM, Expression Data Module for The SOL Genomic Network Database. *Plant & Animal Genome XVIII* (San Diego, CA, USA, January 9-13) (Poster).
32. Mueller LA, Teclé I, Pujar A, **Bombarely A***, Buels R, Menda N. (2010) Community Curation Software at the SOL Genomic Network (solgenomics.net) *Plant & Animal Genome XVIII* (San Diego, CA, USA, January 9-13, 2010) (Poster and Computer Demo) (*Speaker).

2009

33. **Bombarely A***, Menda N, Teclé I, Fisher-York T, Pujar A, Mills A, Gosselin J, Buels R, Mueller LA. (2009) SGN Workshop. *Plant Biology 2009* (Honolulu, HA, USA, July 18-22, 2009) (Database Workshop, *Speaker).

2008

34. Pujar A, **Bombarely A***, Mueller LA. (2008) SolCyc, the SGN database for biochemical pathways. *The 5th Solanaceae Genome Workshop* (Cologne, Germany, October 12-16) (Oral Presentation, * Speaker).

2004

35. Amaya I, **Bombarely A**, Cruz E, Stephens C, Botella MA y Valpuesta V. (2004) Identificación y Análisis de Genes Implicados en la Biosíntesis de Vitamina C en *Arabidopsis thaliana* a partir de Ácido D-Galacturónico. *VII Reunión de Biología Molecular de Plantas* (Benalmádena, Spain, June 3-5) (Poster).

2003

36. Agius F, **Bombarely A**, Botella M.A, Valpuesta V, Amaya I* (2003) Modification of Vitamin C Content in Plants by Overexpression of GalUR, a D-Galacturonate Reductase gene from Strawberry. *7th International Conference of Plant Molecular Biology* (Barcelona, Spain, June 23-28) (Oral Presentation, *Speaker).
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INVITED ACADEMIC SEMINARS

I have been invited to present my work in 18 academic seminars in international research institutions, universities and botanical gardens.

2018

2018-06-19 University of Crete, Research Center, Rethymnon, Greece "Biodiversity, Genomics and Intellectual Property Rights"

2017

2017-11-23 Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil "Genome Evolution and Phenotypic Diversity Under the Plant Domestication Process using *Sinningia speciosa* as Model".

2017-09-26 University of British Columbia (UBC), Vancouver, Canada "Genome Evolution and Phenotypic Diversity Under the Plant Domestication Process using *Sinningia speciosa* as Model".

2017-09-21 University of Puget Sound, Tacoma, WA, USA "Genomic Exploration of the Plant Domestication Process through XVIII Century Floral Crops".

2017-03-07 Universiteit van Amsterdam (UvA), Amsterdam, Netherlands "Study of the Plant Evolution and Domestication using 18th Century Floral Crops".

2017-03-01 Institute for Conservation & Improvement of Valentian Agrodiversity (COMAV), Valencia, Spain "Evolution of the Genome Architecture in the Solanaceae Family".

2017-02-28 Instituto de Biología Molecular y Celular de Plantas (IBMCP), Valencia, Spain "Study of the Plant Evolution and Domestication using 18th Century Floral Crops".

2017-02-27 Centre for Research in Agricultural Genomics (CRAG), Barcelona, Spain "Study of the Plant Evolution and Domestication using 18th Century Floral Crops".

2017-02-17 Royal Botanical Gardens, Edinburgh (RBGE), Edinburgh, UK "Study of the Plant Evolution and Domestication using 18th Century Floral Crops".

2017-01-20 University of California, CA, Riverside, USA. "Evolution of the Genome Architecture in the Solanaceae Family".

2016

2016-10-27 École Normale Supérieure (ENS) de Lyon, Lyon, France. “Study of the Plant Evolution and Domestication using 18th Century Floral Crops”.

2016-06-09 Università degli Studi di Milano (UNIMI), Milan, Italy. “Evolution of the Genome Architecture in the Solanaceae Family”.

2015-10-23 University of Malaga (UMA), Malaga, Spain. “Study of Plant Domestication using Genomics and Bioinformatics”.

2015

2015-04-13 University of Bern, Switzerland. “Genomic Landscapes for the *Nicotiana* genus, a model for polyploid evolution”

2015-03-27 University of Kentucky, Lexington, KY, USA. “Genomic Landscapes for the *Nicotiana* genus”.

2015-03-17 North Carolina State University, Raleigh, NC, USA. “Unraveling the Petunia genome, model system and ornamental crop”.

2014

2014-11-24 Boyce Thompson Institute, NY, USA. “Unravelling the origin and evolution of the *Glycine* polyploid complex using genome reduced representation methodologies”.

2014-10-07 Kew Royal Botanical Gardens, UK. Unravelling the origin and evolution of the *Glycine* polyploid complex using genome reduced representation methodologies

EDITORIAL AND PEER REVIEW ACTIVITY

Editorial role

- Editor for *Genes* (ISSN 2073-4425, <http://www.mdpi.com/journal/genes>), Plant Genetics and Genomic Section (since 2017).
- Editor for *BMC Genomics* (ISSN 1471-2164, <https://bmcgenomics.biomedcentral.com/>), Plant genomics Section (since 2018).

Reviewer role

As a reviewer, I have revised 76 manuscripts in my career. A summary of my reviewer activity including the journals and the number of manuscripts is detailed in the following paragraph.

BMC Evolutionary Biology (1); BMC Genomics (9); BMC Plant Biology (3); Communication Biology (2); Current Genomics (1); Electrophoresis (1); Food Chemistry (2); Frontiers in Molecular Biosciences (1); Frontiers in Plant Science (9); Functional and Integrative Genomics (1); Genome Biology and Evolution (2); Genome Research (1); GigaScience (2); Journal of Experimental Botany (1); Journal of the American Society for Horticultural Science (1); Journal of Zhejiang University-SCIENCE B (1); Molecular Biology Reports (1); Molecular Genetics and Genomics (1); Molecular Phylogenetics and Evolution (1); Molecular Plant-Microbe Interactions (1); Molecules (2); Nature Genetics (2); Nature Plants (2); Plant Cell Reports (1); Plant Genome (1); Plant Journal (1); Plant Methods (2); Plant Molecular Biology (1); Plant Physiology (1); Plant Physiology and Biochemistry (5); Plant Signalling and Behaviour (1); PLoS Genetics (1); PLoS ONE (7); Science (1); Scientific Reports (5); Theoretical and Applied Genetics (1);

TEACHING EXPERIENCE

Teaching Statement

One of the reasons you are reading this teaching statement relates to the lessons that I have learned from my own teachers and mentors. Teaching is the act of communicating knowledge to the students, but it is also an exercise in understanding and empathy toward the people who attend the class. Teaching can be a challenge depending on the message that you want to transmit, the number of people in the classroom, and the type of media and time available for the class. Teaching modes also vary depending on who is receiving the message. Teaching strategies used in an undergraduate class are not the same as those for a graduate class or for a PhD student that you are mentoring. In the last six years, I have taught three courses in the botanic field of plant genomics and bioinformatics for graduate students, several invited lectures for undergraduates (University of Pudget Sound, USA) and at the graduate level (UNIMI, Italy), and two genomic data analysis workshops for students of plant sciences in different institutions (UNIBE, Switzerland and UFRGS, Brazil). I have also mentored five visiting doctoral and two masters-level students, and I presently supervise two Ph.D. students and one undergraduate student at Virginia Tech. For all of these students, my goal is the same: the class or the mentorship should provide them with some valuable, useful tools that they can use in their future careers. It may be a piece of knowledge (e.g. types of DNA for a genomics class) or the development of a skill (e.g. write a script to perform a phylogenetic analysis for a bioinformatics practice), but it can also be an inspirational lecture (e.g. about the green revolution or the work of Barbara McClintock), moral support (e.g. after a failed experiment), a good professional suggestion, or help writing a cover letter for a job application. Good teaching requires preparation but also flexibility; for example, a course needs to follow the syllabus and the class activities have to be well prepared, but at the same time, they should be able to change to meet the students' needs. Finally, putting all these ideas together, I can define how I like my classes to be in three words: useful, educational, and entertaining.

Teaching History

2018

- **Regular academic course: Plant Genomics** CSES 5844, CRN 20406 Spring Semester 2018. 4 credits course co-taught with Prof. Saghai Maroof, Dr. David Haak and Dr. Song Li. Virginia Tech (Blacksburg, VA, USA). January 19th – May 4th, 2018.

2017

- **Workshop:** Postgraduate program in Genetics and Molecular Biology – “**Genomic Data Analysis**” Universidade Federal do Rio Grande do Sul (Porto Alegre, Brazil). Oct 24th – Oct 26th, 2017.
- **Invited lecture:** Molecular Biology – “**Genome Assembly and Annotation**”. University of Pudget Sound (Tacoma, WA, USA). Sept 22th, 2017.

2016

- **Invited lecture:** Corso di Strategie Riproductive (BIOEVO) – “**An evolutionary perspective of plant reproduction and domestication**”. Universita Degli Studi di Milano (Milan). Oct 10th and Nov 2nd, 2016.
- **Regular academic course: Introduction to Genomic Data Science** ALS 4984/5984 Fall Semester 2016 3 credits course co-taught with Dr. Song Li. Virginia Tech (Blacksburg, VA, USA). Aug 26th -Dec 9th, 2016
- **Workshop:** CUSO, Plant Bioinformatics – “**Genomic & transcriptomic Analysis**” University of Bern (Bern, Switzerland). Sept 5th – Sept 7th, 2016.
- **Regular academic course: Plant Genomics** CSES 5844, CRN 20406 Spring Semester 2016.4 credits course co-taught with Prof. Saghai Maroof, Dr. David Haak and Dr. Song Li. Virginia Tech (Blacksburg, VA, USA). January 25th – May 2nd, 2016.

2015

- **Regular academic course: Introduction to Applied Genomic Analysis** ALS 4984/5984 Fall Semester 2015. 3 credits course co-taught with Dr. David Haak and Dr. Song Li. Virginia Tech (Blacksburg, VA, USA). Aug 26th - Dec 9th, 2015.

2014

- **Workshop: 1st Latham Bioinformatics Course.** Fall Semester 2014. Organized by Dr. Aureliano Bombarely, Dr. David Haak and Dr. Song Li. Virginia Tech (Blacksburg, VA, USA). November 3rd – January 19th, 2014 (<https://vtplantbioinfocourse.wordpress.com/>).

2013

- **Workshop: 2nd BTI Bioinformatics Course: Basic Linux, Basic R. Data Mining.** Organized by Mueller Laboratory Group. Boyce Thompson Institute (Ithaca, NY, USA). Mar 19th - May 21st, 2013 (<http://btiplantbioinfocourse.wordpress.com/>).
- **Workshop: Bioinformatics and Genomics Workshop.** Organized by Dr. Sarah Shaack. Reed College (Portland, OR, USA) April 13th – 14th, 2013.

2012

- **Workshop: Curso de Biotecnología: Análisis de RNAseq (Biotechnology Course: RNAseq Analysis)** Organized by Dr. Luz-Stella Barrero. Corpoica (Bogota, Colombia). Nov. 26th – 27th, 2012 (Class language: Spanish).
- **Workshop: 1st BTI Bioinformatics Course: Basic Linux, Basic R.** Organized by Mueller Laboratory Group. Boyce Thompson Institute (Ithaca, NY, USA). Feb 22nd - Apr 23th, 2012. (<http://btiplantbioinfocourse.wordpress.com/>).

2011

- **Workshop: Curso de Bioinformática de la Estación Experimental de La Mayora (1st Bioinformatics Course of “Estación Experimental La Mayora”).** Organized by Dr. Jose Reina Pinto. La Mayora (Algarrobo-Costa, Malaga, Spain). Dec. 2011. (Class language: Spanish).

Teaching experience as graduate student

- **Regular academic course: Laboratory Teaching Assistant, Biotechnology.** Academic year 2003-2004. University of Malaga (Malaga, Spain).
 - **Regular academic course: Laboratory Teaching Assistant, Molecular Biology.** Academic year 2002-2003. University of Malaga (Malaga, Spain).
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Students and Postdoctoral Researchers Mentoring

Student Supervision

1. Elijah Rinaldi (Undergraduate Research: 2017-2018): Undergraduate research project; “Characterization of the genetic diversity of the species *Asimina triloba* in the states of Virginia and North Carolina”.
2. Haidong Yan (PhD supervisor: 2017-2020): Molecular Plant Science PhD program at Virginia Tech (Blacksburg, VA, USA). Research project: “Evaluation of the Phenotypic Diversity Driven by the Repetitive Element Dynamics”.
3. Tomas Hasing (PhD supervisor: 2015-2018): Molecular Plant Science PhD program at Virginia Tech (Blacksburg, VA, USA) with the project: “Genomic Analysis of the Domestication of the ornamental species, *Sinningia speciosa*”.
4. Mario Fenech-Torres (Ms. Co-supervisor: 2014-2015): Co-supervision for master student for the Biotechnology program at University of Malaga (Malaga, Spain) with the project “Evolutionary analysis of the Vitamin C biosynthesis in plants”.

Short Term Student Supervision

1. Suzanne Laliberte (Mentor: Summer 2017): VTREEL Program (Blacksburg, VA) with the project: “Analysis of the transcriptomic response to salt stress in *Petunia*”.
2. Adrian Pena (Mentor: Spring 2017): Molecular Plant Science PhD rotation program at Virginia Tech (Blacksburg, VA) with the project “Development of a Pipeline to Call Variants from SRA data”.
3. Morgan Shock (Mentor: Fall 2016): Molecular Plant Science PhD rotation program at Virginia Tech (Blacksburg, VA) with the project “Genome Size Estimation by Flow Cytometry on the *Sinningia* genus”.
4. Karl Compton (Mentor: Spring 2016): Molecular Plant Science PhD rotation program at Virginia Tech (Blacksburg, VA) with the project “Identification of the homolog genes for the ABC model in 150 sequenced plant species”.
5. Marco Mechan (Mentor: Fall 2014): Molecular Plant Science PhD rotation program at Virginia Tech (Blacksburg, VA) with the project “Identification of the diploid origins in *Nicotiana tabacum*”.
6. Benjamin Gordon (Mentor: Summer 2011): Summer internship at Boyce Thompson Institute (Ithaca, NY) with the project “Plant-Pathogen database design”.
7. Jessica Jeffrey (Mentor: Summer 2011): Summer internship at Boyce Thompson Institute (Ithaca, NY) with the project “GenBank .tpf file tool”.
8. Dean Bobo (Mentor: Summer 2010): Summer internship at Boyce Thompson Institute (Ithaca, NY) with the project “Tomato expression at SGN database”.
9. Vera Kutsenko (Mentor: Summer 2010): Summer internship at Boyce Thompson Institute (Ithaca, NY) with the project “Sequence assembly file parsing”.
10. Waleed Haso (Mentor: Summer 2009): Summer internship at Boyce Thompson Institute (Ithaca, NY) with the project “*In silico* PCR tool”.
11. Mallory Freeberg (Summer 2008): Summer internship at Boyce Thompson Institute (Ithaca, NY) with the project “UTR sequencing analysis”.

PhD Student Committees

1. Merve Kiremit (Supervisor: Prof. Bingyu Zhao), Virginia Tech, Blacksburg, VA, USA (2018-2020).
2. Vivian Bernal (Supervisor: Prof. Jim Westwood), Virginia Tech, Blacksburg, VA, USA (2017-2019).
3. Zhibo Wang (Supervisor: Prof. Bingyu Zhao), Virginia Tech, Blacksburg, VA, USA (2016-2018).
4. Chenming Cui (Supervisor: Dr. David Haak), Virginia Tech, Blacksburg, VA, USA (2015-2018).
5. Marco Mechan (Supervisor: Prof. Boris Vinatzer), Virginia Tech, Blacksburg, VA, USA (2015-2018).
6. John Herlihy (Supervisor: Prof. John McDowell), Virginia Tech, Blacksburg, VA, USA (2015-2018).
7. Parker Laimbeer (Supervisor: Prof. Richard Veilleux), Virginia Tech, Blacksburg, VA, USA (2014-2018).
8. Jaime Jimenez Ruiz (Supervisor: Prof. Francisco Luque), University of Jaen, Spain (2010-2014).

Hosted Visiting Scholars

1. Mr. James Friel (Ms. Student, National University of Ireland (NUI), Galway, Ireland; Oct. 2017 – Apr. 2018). Project: “RNA-Seq analysis of the Arabidopsis triploid block”.
 2. Dr. Antonio J. Manzaneda Avila (Associate Professor, University of Jaen, Spain; Sept. – Dec. 2017). Project: “Analysis of the Population Structure of the species *Sinapis alba* in Southern Spain”.
 3. Dr. Silvia Manrique Urpi (Postdoctoral Researcher, UNIMI, Italy; Apr. – Dec. 2017). Project: “Study of the Interaction between MADS Box Proteins and Epigenetic Regulators in *Arabidopsis thaliana*”.
 4. Ms. Lisa Rotasperti (Ph.D. Student, UNIMI, Italy; Jun. – Aug. 2017). Project: “Analysis of the Fruit Development using RNA-Seq data in *Arabidopsis thaliana*”.
 5. Ms. Giovanna Giudicelli (Ph.D. Student, Universidade Federal do Rio Grande do Sul, Brazil; May. – Aug. 2017). Project: “Analysis of the Population Structure of the species *Petunia axillaris* in Brazil”.
 6. Ms. Alicia Talavera Juez (Ph.D. Student, IHSM La Mayora, Spain; May – Sept. 2017). Project: “Sequencing and Assembly of the Tropical Crop *Annona cherimoya*”.
 7. Ms. Pietro Gramazio (Ph.D. Student, COMAV, Spain; Sept. – Nov. 2016). Project: “Analysis of the Genome Re-sequencing of Seven *Solanum melogena* accessions and its wild relative *S. incanum*”.
 8. Ms. Aboozar Soorni (Ph.D. Student, University of Teheran, Iran; Feb. – Aug. 2016). Project: “Analysis of the Genetic Structure of the species *Cannabis sativa* in Iran”.
 9. Ms. Luisa Martinez Martinez (Ph.D. Student, University of Jaen, Spain; May. – Aug. 2015). Project: “Transcriptomic Analysis of the allopolyploid species *Brachypodium hybridum* under Drought Stress”.
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SKILLS AND COURSES

LANGUAGES

- Spanish (Native proficiency)
- English (Full professional proficiency)
- Italian (Basic proficiency)

MEMBERSHIPS

- American Society of Plant Biology (since 2009).
- Botanical Society of America (since 2017).
- Genetics Society of America (since 2017).
- Society for Experimental Biology (since 2017).

COMPUTER SKILLS

- Operating systems: MS-Windows, Linux (Debian, Ubuntu, Red Hat), Mac OS X
- Programming languages: Perl, Python (Basic Knowledge).
- Statistical computing skills: R and Bioconductor.
- Relational Database Programs: MySQL, Postgres, Microsoft Office Access, SRS Visual Administrator.
- Code repository software: SVN and Git.
- Expertise in sequence assembly, mapping and annotation software, biological databases, transcriptomics analysis, phylogenetic analysis and population genetics software.

RELEASED CODE

- **CPAN: R::YapRI** (Yet Another Perl R Interface, <http://search.cpan.org/~bombarely/R-YapRI-0.09/>)
 - **GenoToolBox** (Perl scripts for genomic data manipulation, <https://github.com/aubombarely/GenoToolBox>)
 - **Organelle_PBA** (Tool for long read plastid genome assembly, https://github.com/aubombarely/Organelle_PBA)
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ADDITIONAL STUDIES

- Pedagogical Competence Certificate (*Certificado de Aptitud Pedagógica (C.A.P.)*) for 180 hours (2001-2002).
- Research aptitude verification for Advanced Studies Certificate in the field of Biochemistry and Molecular Biology (*Suficiencia Investigadora acreditada por Certificado-Diploma de Estudios Avanzados en el área de conocimiento de Bioquímica y Biología Molecular*)

ATTENDED COURSES AND WORKSHOPS

- Computational Molecular Evolution (2013). Organized by Prof. Anders Gorm Pedersen from Technical University of Denmark. Online at Coursera. June 24 - September 12, 2013.
- Genotyping-By-Sequencing (GBS) (2012). Organized by CBSU at Cornell University (Ithaca, NY, USA). Sept 13-14, 2012.
- Postdoc Leadership Development Program (2011-2012). Organized by Postdoctoral Studies Program at Cornell University (Ithaca, NY, USA). October 10, 2011 to April 12, 2012.
- Managing Conflict in the Workplace (2011). Organized by Human Services Coalition of Tompkins County (Ithaca, NY, USA) October 21, 2011.
- Reference genome based sequence variation (SNP and INDEL) detection workshop (2011). Organized by CBSU at Cornell University (Ithaca, NY, USA). May 23-25, 2011.
- Advanced R (2011). Organized by CISER at Cornell University (Ithaca, NY, USA). March 10, 2011.
- CAUG2010, Celera Assembler User Group training (2010). Organized by J. Craig Venter Institute (Rockville, MD, USA). August 26-27, 2010.
- Parallel Computing on Ranger workshop (2010). Organized by CAC at Cornell University (Ithaca, NY, USA). May 19-20, 2010
- Introduction to R (2010). Organized by CISER at Cornell University (Ithaca, NY, USA). February 25, 2010.
- Microarray data processing course. (2003). Organized by Integromics S.L. and the University of Málaga (Malaga, Spain). November 27-29, 2003.
- Complementary formation course: Functional Genomics. Microarrays, proteomic and metabolomic. (2001). Organized by the International University of Andalucía (La Rávida, Spain).
- II Seminar Molecular Biology of Cancer. Fundamentals and Perspectives (2001) (*II Curso teórico-práctico Biología Molecular del Cáncer. Fundamentos y perspectivas*). Organized by the department of Biochemistry and Molecular Biology, University of Malaga. (Malaga, Spain). July 9-20, 2001.

Data

26/06/18

Luogo

Blacksburg, VA, USA