



TO MAGNIFICO RETTORE OF UNIVERSITA' DEGLI STUDI DI MILANO

ID CODE 4856

I the undersigned asks to participate in the public selection, for qualifications and examinations, for the awarding of a type B fellowship at **Dipartimento di Bioscienze**

Scientist- in - charge: Prof. Aureliano Bombarely

Noe Fernandez-Pozo

CURRICULUM VITAE

PERSONAL INFORMATION

Surname	Fernandez Pozo
Name	Noe
Date of birth	03.06.1980

LAST POSITION

Appointment	Structure
Research Assistant	University of Marburg

EDUCATION AND TRAINING

Degree	Course of studies	University	year of achievement of the degree
Degree	Biology	University of Malaga	2007
PhD	Molecular and Cell Biology	University of Malaga	2012
Master	Molecular and Cell Biology	University of Malaga	2009
Others - Training course	CMS web Schulung im Content-Management-System	University of Marburg	2020
Others - Training course	Genotyping by sequencing GBS Workshop	Cornell University	2013
Others - Training course	Introduction to R software for data analyzing	University of Malaga	2011
Others - Training course	Workshop: Introduction to the new Integromics Biomarker Discovery 3.0 software of TIBCO Spotfire	Bioinformatics Andalusian Platform (PAB) and Universidad of Málaga, Spain	2010



Others - Training course	Statistical Microarray Analysis Using R & Bioconductor	Imperial College, London	2009
Others - Training course	Bioinformatics Tools Advanced Use Workshop	Bioinformatics Andalusian Platform (PAB) and Universidad of Málaga	2008
Others - Training course	Multidisciplinary databases (Web of knowledge and Scopus)	University of Malaga	2007
Others - Training course	Citing index and impact factor	University of Malaga	2007

REGISTRATION IN PROFESSIONAL ASSOCIATIONS

Date of registration	Association	City
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FOREIGN LANGUAGES

Languages	level of knowledge
Spanish	Native speaker
English	Fluent
German	Basic

AWARDS, ACKNOWLEDGEMENTS, SCHOLARSHIPS

Year	Description of award
2020	Invited speaker at the Virtual Black Forest Summer School 2020.
2019	Awarded ¥600,000 by the Goho Life Science International Foundation for the organization of a Bioinformatics workshop in Hokkaido University, Japan
2019	Invited speaker at the Plant Science Seminar, Hokkaido University IGP HU International Graduate Program, September 19th 2019. Sapporo, Japan.
2016	Invited speaker at SEARCA, University of the Philippines Los Baños (UPLB), Los Baños, Laguna, Philippines.
2011	Invited speaker at Ciclo de conferencias en la semana de San Alberto de Asociación Calopterix. Universidad de Málaga, Málaga, Spain.

TRAINING OR RESEARCH ACTIVITY

description of activity	
07.2017 - 12.2020	Research Assistant at University of Marburg, Germany. Plant Cell Biology. Rensing Lab. Research: Evolution of plants, with special focus in the transition from water to land.



08.2014 05.2017	-	Research Associate at Boyce Thompson Institute, Cornell University, Ithaca, NY, USA. Mueller Lab. Research: Study of Solanaceae species and development of bioinformatics tools and the Sol Genomics Network.
08.2012 08.2014	-	Postdoctoral Researcher at Boyce Thompson Institute, Cornell University, Ithaca, NY, USA. Mueller Lab. Research: Study of Solanaceae species and development of bioinformatics tools and the Sol Genomics Network.
09.2007 06.2012	-	PhD Student at Department of Molecular Biology and Biochemistry at University of Malaga. Claros Lab. Research: Bioinformatic analysis of pine transcriptome.

PROJECT ACTIVITY

Year	Project
2021-2024	Reference: Programa de ayudas a la captación de talento «Emergia» (Under revision). Title: Development of bioinformatic resources for genomic, phenotypic and transcriptomic analyses of subtropical fruit crops. Funding body: Junta de Andalucía, Consejería de Economía, Conocimiento, Empresas y Universidad. Secretaría General de Universidades, Investigación y Tecnología. Call: EMERGIA PI: Dr. Noe Fernandez-Pozo. Institution: CSIC IHSM Duration: 2021 - 2024. Amount to be funded: 160,000.00 € Role: Principal Investigator (PI). Status: Under review (delayed by covid-19).
2020-2023	Reference: DFG Ausschreibung Nr. 44 for software sustainability (Under revision). Title: SUsustainable Bloinformatics TOols (SUBITO). Funding body: DFG. Call: Nr. 44 for software sustainability. PI: Dr. Noe Fernandez-Pozo. Institution: University of Marburg. Duration: 2020 - 2023. Amount to be funded: 179,493.00 € Role: Principal Investigator (PI). Status: Under review (delayed by covid-19).
2020-2022	Reference: DFG SEQ1005. Title: CharKeyS: Charophyte key genome sequencing. Funding body: DFG. Call: Sequencing Costs in Projects. PI: Prof. Dr. Stefan A. Rensing. Institution: University of Marburg. Duration: 2020 - 2022 Amount funded: 509,963.00 € Role: Co-PI.
2020-2023	Reference: DFG priority programme 2237. Title: MADland - Molecular Adaptation to Land: plant evolution to change. Funding body: DFG. Call: Priority programme. PI: Prof. Dr. Stefan A. Rensing. Institution: University of Marburg. Duration: 2020 - 2023. Amount funded: 6,219,000.00 € Role: Researcher, coordination team. Web: https://madland.science
2017-2021	Reference: H2020-MSCA-ITN-2017 Marie Skłodowska-Curie Actions European Training Networks n°764965. Title: EpiDiverse, European Training Network. Funding body: EU Horizon 2020 and Marie Skłodowska-Curie. Call: European Training Network (ETN). Coordinated by: Dr. Koen Verhoeven. Institution: NIOO-KNAW. Duration: 01/09/2017 - 31/08/2021. Amount funded: 3,784,150.00 € Role: PI, co-supervisor of PhD student. Web: https://epidiverse.eu
2014-2017	Reference: ERA-CAPS SeedAdapt. Title: SeedAdapt: dimorphic fruits, seeds and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments. Funding body: ERA-CAPS call: Joint calls. PI: Gerhard Leubner Institution: UK Royal Holloway University of London. Duration: 2014 - 2017 Amount funded: 1,750,073.00 € Role: Researcher.
2015-2020	Reference: Accession: 1005600, Project: Ks603372, Grant: 2015-70016-23028, Proposal: 2014-10154. Title: Developing an infrastructure and product test pipeline to deliver novel therapies for citrus greening disease Funding body: USDA NIFA Call: SCRI Citrus Disease Research and Extension Program. PI: Prof. Dr. Susan J. Brown Institution: Kansas State University. Duration: 01/03/2015 - 29/02/2020 Amount funded: \$ 3,734,480.00 Role: Researcher.
2014-2020	Reference: NSF grant IOS 1339287. Title: High Resolution Functional Genomics of Fleshy



	Fruit Development and Environmental Responses. Funding body: National Science Foundation (NSF) Call: Plant Genome Research Project. PI: Prof. Dr. Jocelyn Rose. Institution: Cornell University. Duration: 01/09/2014 - 31/08/2020 Amount funded: \$ 4,696,930.00 Role: Researcher
2009-2015	Reference: NSF grant IOS 0820612. Title: Tomato Chromosome 1 and 10 Sequencing, Coordination and Bioinformatics for the International Solanaceae Genome Initiative. Funding body: National Science Foundation (NSF) Call: Plant Genome Research Resource. PI: Prof. Dr. James Giovannoni. Institution: Cornell University. Duration: 01/06/2009 - 31/05/2015 Amount funded: \$ 10,407,225.00 Role: Researcher
2011-2014	Reference: NSF grant IOS 1025642. Title: Leveraging Genomics Resources and Wild Species of Tomato to Identify New Sources of Disease Resistance. Funding body: National Science Foundation (NSF). Call: Plant Genome Research Project. PI: Prof. Dr. Alan Collmer. Institution: Cornell University. Duration: 04/03/2011 - 14/04/2014 Amount funded: \$ 4,187,897.00 Role: Researcher.
2010-2013	Reference: PLANT-KBBE 2009, PLE2009-0016. Title: SUSTAINPINE, Genomic tools in maritime PINE for enhanced biomass production and SUSTAINable forest management. Funding body: MICINN and FP7-PLANT-KBBE Call: 2009 PI: Prof. Dr. Francisco M. Cánovas Ramos. Institution: Universidad de Málaga. Duration: 2010-2013 Amount funded: 832,601.00 € Role: Researcher, coordination team and web master. Web: www.scbi.uma.es/sustainpine/index.html
2011-2013	Reference: CVI-6075 (Proyecto de Excelencia de la Junta de Andalucía). Title: Desarrollo de herramientas bioinformáticas para los estudios genómicos y transcriptómicos a partir de datos de secuenciación de lecturas cortas de alto rendimiento para las especies que no tienen un organismo modelo de referencia (NEOGEN) . Funding body: Junta de Andalucía. Duration: 2011-2013. PI: M. G. Claros. Institution: Universidad de Málaga. Role: Researcher
2006-2009	Reference: AGR-663 (Proyecto de Excelencia de la Junta de Andalucía). Title: Estudios de genómica funcional en plantas de interés forestal. Funding body: Junta de Andalucía. Duration: 2006-2009. PI: Francisco M. Cánovas. Institution: Universidad de Málaga. Role: Researcher
2008	Reference: BIO2007-29814-E (MEC). Title: Participación en la primera fase de la iniciativa internacional para la secuenciación del genoma de pino. Funding body: MEC. Duration: 2008. PI: Francisco Cánovas. Institution: Universidad de Málaga. Role: Researcher

PATENTS

Patent

CONGRESSES AND SEMINARS

Date	Title	Place
September 11th-13th, 2020.	Noe Fernandez-Pozo and Fabian Haas. The MAdLand RNA-seq pipeline and the PEATmoss online expression atlas. Oral communication.	MAdLand Black Forest Workshop 2020. Online + Black Forest Highlands, Germany.
May 11th 2020.	Noe Fernandez-Pozo and Fabian Haas. NGS data processing (Quality checks and mapping). Oral communication.	Invited speaker at the Virtual Black Forest Summer School 2020. Germany.



February 27th 2020.	Noe Fernandez-Pozo. Bioinformatic Web Tools for Gene Expression Analysis and Transcription Factor Annotation. Oral communication.	IBBMDS Symposium on Interdisciplinary Bioinformatics and Biomedical Data Science. University of Marburg, Marburg, Germany.
December 19th 2019.	Noe Fernandez-Pozo. PEATmoss (Physcomitrella Expression Atlas Tool): a gene expression atlas and bioinformatics tools for <i>Physcomitrella patens</i> adaptable and customizable for any species and expression data. Oral communication.	Avances en Biología Molecular por Jóvenes Investigadores en el Extranjero. CNB, Madrid, Spain.
September 19th 2019	Noe Fernandez Pozo. <i>Physcomitrella patens</i> Genomic and Bioinformatic Resources. Oral communication.	Invited speaker at the Plant Science Seminar, Hokkaido University IGP HU International Graduate Program. Sapporo, Japan.
July 2019	N Fernandez-Pozo, FB Haas, ..., K Barry, J Schmutz, LA Mueller, SA Rensing PEATmoss (Physcomitrella Expression Atlas Tool): a unified gene expression atlas and gene model lookup database for <i>Physcomitrella patens</i> . Oral communication.	IAB IMOSS SEB Conference. Royal Botanical Garden (CSIC) Madrid, Spain.
February 2018	N Fernandez-Pozo. A unified expression atlas web tool for the plant model <i>Physcomitrella patens</i> . Oral communication.	31st Conference Molecular Biology of Plants (MBP 2018). Dabringhausen, Germany.
October 2017	N Fernandez-Pozo. The Chara genome: implications for plant terrestrialization. Oral communication.	Third working group meeting COST Action FA1406 "PHYCOMORPH" Programme. COST Association Premises, Brussels, Belgium.
September 2016	N Fernandez-Pozo. SGN Workshop: Bioinformatics Tools. Oral communication.	13th Annual Solanaceae Conference, SolGenomics: From Advances to Applications. Davis, California.
September 2016	N Fernandez-Pozo, KD Edwards, ..., RS Lewis, LA Mueller. A new <i>Nicotiana tabacum</i> chromosome level genome reference sequence enables map-based cloning. Poster 304-TU	13th Annual Solanaceae Conference, SolGenomics: From Advances to Applications. Davis, California.
January 2016	N Fernandez-Pozo. The Sol Genomics Network: Bioinformatics tools for genomics and breeding. Oral communication.	Invited speaker at SEARCA, University of the Philippines Los Baños (UPLB), Los Baños, Laguna, Philippines.
October 2015	N Fernandez-Pozo. SGN Workshop: Bioinformatics Tools. Oral communication.	12th Solanaceae Conference. Bordeaux, France.
November 2014	N Fernandez-Pozo, HG Rosli, GB Martin and LA Mueller. User-friendly web tool to design virus-induced gene silencing (VIGS) constructs for functional genomics. Oral communication.	11th Solanaceae Conference Arraial D' Ayuda, Bahia, Brazil.
November 2014	N Fernandez-Pozo. SGN Workshop: Sequence Analysis Tools. Oral communication.	11th Solanaceae Conference, Arraial D' Ayuda, Bahia, Brazil.
2014	N Fernandez-Pozo. SGN Workshop: Sequence Analysis Tools. Oral	Workshop W708 at International Plant and Animal Genome Conference XXII 2014, San



	communication.	Diego, CA, USA.
2014	N Fernandez-Pozo, HG Rosli, GB Martin, LA Mueller. The SGN VIGS Tool: User-Friendly Software to Optimize Virus-Induced Gene Silencing (VIGS). Poster P1044.	International Plant and Animal Genome Conference XXII 2014, San Diego, CA, USA.
November 16th 2011	N Fernandez-Pozo. Bioinformática, otra forma de hacer biología. Oral communication.	Invited speaker at Ciclo de conferencias en la semana de San Alberto de Asociación Calopterix. Universidad de Málaga, Málaga, Spain.
October 2010	N Fernandez-Pozo, D Guerrero-Fernandez, ..., FM Canovas, MG Claros. GENote v. B: a web tool prototype for annotation of unfinished sequences in non-model eukaryotes.	Xth Spanish Symposium on Bioinformatics. Torremolinos, Spain.
September 2010	N Fernandez-Pozo, D Guerrero, ..., FR Canton, FM Canovas, MG Claros EuroPineDB: una base de datos con metadatos de secuencias de tres especies de pino europeas. Poster PoR81.	XXXIII Conference of the Spanish Society of Biochemistry and Molecular Biology. Cordoba, Spain.

PUBLICATIONS

Books
Pombo MA, Rosli HG, Fernandez-Pozo N , Bombarely A. (2020). <i>Nicotiana benthamiana</i> , A Popular Model for Genome Evolution and Plant-Pathogen Interactions. Springer Nature. Book chapter in: Ivanov N., Sierro N., Peitsch M. (eds) <i>The Tobacco Plant Genome. Compendium of Plant Genomes</i> . Springer, Cham. https://doi.org/10.1007/978-3-030-29493-9_14
Mueller LA, Fernandez-Pozo N . (2016). <i>Tomato Databases</i> . Book chapter in <i>The Tomato Genome</i> . Edited by Springer Berlin Heidelberg. Pages 245-255. Print ISBN: 978-3-662-53387-1, Online ISBN: 978-3-662-53389-5
Claros MG, Bautista R, Guerrero-Fernández D, Benzerki H, Seoane P, Fernández-Pozo N . (2014). Book chapter: Why assembling plant genome sequences is so challenging. <i>The Role of Bioinformatics in Agriculture</i> . Apple Academic Press. ISBN: 9781771880039

Articles in reviews
Fernandez-Pozo N , Metz T, Chandler J, Gramzow L, Merai Z, Maumus F, Scheid O, Theissen G, Schranz ME, Leubner-Metzger G, Rensing SA. (2020). <i>Aethionema arabicum</i> genome annotation using PacBio full-length transcripts provides a valuable resource for seed dormancy and Brassicaceae evolution research. <i>Plant J.</i> doi:10.1111/tpj.15161.
Fernandez-Pozo N , Haas FB, ..., Coates JC, Barry K, Schmutz J, Mueller LA, Rensing SA (2020) PEATmoss (<i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant J.</i> , 102(1): 165.
Haas FB, Fernandez-Pozo N , Meyberg R, Perroud PF, Göttig M, Stingl N, Saint-Marcoux D, Langdale J, Rensing SA. (2020). Single nucleotide polymorphism charting of <i>P. patens</i> reveals accumulation of somatic mutations during in vitro culture on the scale of natural variation by selfing. <i>Frontiers in Plant Science</i> , 11, 813.
Li FW, Nishiyama T, Waller M, Frangedakis E, Keller J, Li Z, Fernandez-Pozo N , ..., Rensing SA, Villarreal JC, Weijers D, Wicke S, Wong GKS, Sakakibara K, Szövényi P. (2020). <i>Anthoceros</i> genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 6(3): 259.
Jiménez-Ruiz J, Ramírez-Tejero J, Fernández-Pozo N , ..., Navarro F, Barroso J, Beuzón C, Valpuesta V,



Bombarely A, Luque F. (2020). Transposon Activation is a Major Driver in the Genome Evolution of Cultivated Olive Trees (*Olea europaea* L.). *Plant Genome*. 13:e20010.

Kreutz C, Can NS, Schulze-Bruening R, Meyberg R, Merai Z, **Fernandez-Pozo N**, Rensing SA. (2020). A Blind and Independent Benchmark Study for Detecting Differentially Methylated Regions in Plants. *Bioinformatics*, 36 (11): 3314. As co-PI, supervisor of Can NS.

Sun G, Bai S, ..., **Fernandez-Pozo N**, Czyrt A, Sun H, Rensing SA, Huang J. (2020). Are fungi-derived genomic regions related to antagonism toward fungi in mosses? *New Phytologist*, 228: 1169.

Treves H, Siemiatkowska B, Luzarowska U, Murik O, **Fernandez-Pozo N**, Moraes TA, Erban A, Armbruster U, Brotman Y, Kopka J, Rensing SA, Szymanski J, Stitt M. (2020). Multi-omics analysis reveals mechanisms of complete resistance to extreme illumination levels in a green alga isolated from desert soil crusts. *Nature Plants*, 6(8): 1031.

Wilhelmsson PKI, Chandler JO, **Fernandez-Pozo N**, Graeber K, Ullrich KK, Arshad W, Khan S, Hofberger JA, Buchta K, Edger PP, Pires JC, Schranz ME, Leubner-Metzger G, Rensing SA. (2019) Usability of reference-free transcriptome assemblies for detection of differential expression: a case study on *Aethionema arabicum* dimorphic seeds. *BMC genomics*, 20 (1): 95.

(Shinozaki Y, Nicolas P, **Fernandez-Pozo N**)*, Ma Q, ..., Catalá C, Fei Z, Mueller LA, Giovannoni JJ, Rose JKC. (2018). High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. *Nature communications*, 9 (1), 364. *Equal contribution.

De Clerck O, Kao SM, Bogaert KA, ..., **Fernandez-Pozo N**, ..., Rensing SA, Van Der Straeten D, Vardi A, Sterck L, Vandepoele K, Van de Peer Y, Wichard T, Bothwell JH. (2018). Insights into the evolution of multicellularity from the sea lettuce genome. *Current Biology*, 28 (18), 2921-2933.

Fernandez-Pozo N, Zheng Y, Snyder S, Nicolas P, Shinozaki Y, Fei Z, Catala C, Giovannoni JJ, Rose JKC, Mueller LA. (2017). The Tomato Expression Atlas. *Bioinformatics*, 33 (15), 2397-2398.

Edwards KD, **Fernandez-Pozo N**, Drake-Stowe K, Humphry M, Evans AD, Bombarely A, Allen F, Hurst R, White B, Kernodle SP, Bromley JR, Sanchez-Tamburrino JP, Lewis RS, Mueller LA. (2017). A reference genome for *Nicotiana tabacum* enables map-based cloning of homeologous loci implicated in nitrogen utilization efficiency. *BMC Genomics*, 18:448

Carlson KD, **Fernandez-Pozo N**, Bombarely A, Pisupati R, Mueller LA, Madlung A. (2017). Natural variation in stress response gene activity in the allopolyploid *Arabidopsis suecica*. *BMC Genomics*, 18:653

Schwizer S, Kraus CM, Dunham DM, Zheng Y, **Fernandez-Pozo N**, Pombo MA, Fei Z, Chakravarthy S, Martin GB. (2017). The Tomato Kinase Pti1 Contributes to Production of Reactive Oxygen Species in Response to Two Flagellin-Derived Peptides and Promotes Resistance to *Pseudomonas syringae* Infection. *Mol. Plant Microbe Interact*. 30 (9), 725-738.

Saha S, Flores M, Hosmani P, **Fernandez-Pozo N**, Brown S, Mueller L. (2017). Citrusgreening.org - A systems biology resource for vector biologists. *Phytopathology*, 107(2s): 11. <http://dx.doi.org/10.1094/PHYTO-107-2-S2.5>.

Bombarely A, Moser M, ..., **Fernandez-Pozo N**, ..., Zethof J, Quattrocchio F, Sims TL, Kuhlemeier C. (2016). Insight into the evolution of the Solanaceae from the parental genomes of *Petunia hybrida*. *Nature Plants*, 2, article number 16074.

Osorio-Guarin JA, Enciso-Rodriguez FE, González C, **Fernandez-Pozo N**, Mueller LA, Barrero LS. (2016). Association analysis for disease resistance to *Fusarium oxysporum* in cape gooseberry (*Physalis peruviana* L). *BMC Genomics*, 17:248.

Seoane-Zonjic P, Cañas RA, Bautista R, Gómez-Maldonado J, Arrillaga I, **Fernandez-Pozo N**, Claros MG, Canovas FM, Avila C. (2016). Establishing gene models from the *Pinus pinaster* genome by combining gene capture with BAC sequencing. *BMC Genomics*, 17:148.

Fernandez-Pozo N, Rosli HG, Martin GB, Mueller LA. (2015). The SGN VIGS Tool: User-friendly software to design virus-induced gene silencing (VIGS) constructs for functional genomics. *Molecular plant*, 8 (3), 486-488.



<p>Fernandez-Pozo N, Menda N, Edwards JD, Saha S, Teclé 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. <i>Nucleic acids research</i>, 43 (D1), D1036-D1041.</p>
<p>Tzin V, Fernandez-Pozo N, Richter A, Schmelz EA, Schoettner M, Schäfer M, Ahern KR, Meihls LN, Kaur H, Huffaker A, Mori N, Degenhardt J, Mueller LA, Jander G. (2015). Dynamic maize responses to aphid feeding are revealed by a time series of transcriptomic and metabolomic assays. <i>Plant physiology</i>, 169 (3), 1727-1743.</p>
<p>Pombo MA, Zheng Y, Fernandez-Pozo N, Dunham DM, Fei Z, Martin GB. (2014). Transcriptomic analysis reveals tomato genes whose expression is induced specifically during effector-triggered immunity and identifies the Epk1 protein kinase which is required for the host response to three bacterial effector proteins. <i>Genome Biology</i>, 15, 492.</p>
<p>Canales J, ..., Fernandez-Pozo N, ..., Miguel C, Cervera MT, Cantón FR, Plomion C, Harvengt L, Avila C, Gonzalo Claros M, Cánovas FM. (2014). De novo assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. <i>Plant biotechnology journal</i>, 12 (3), 286.</p>
<p>Benzekri H, ..., Fernandez-Pozo N, ..., Claros MG, Manchado M. (2014) De novo assembly, characterization and functional annotation of Senegalese sole (<i>Solea senegalensis</i>) and common sole (<i>Solea solea</i>) transcriptomes: integration in a database and design of a microarray. <i>BMC genomics</i>, 15:952.</p>
<p>Singh DK, Calviño M, Brauer EK, Fernandez-Pozo N, Strickler S, Yalamanchili R, Suzuki H, Aoki K, Shibata D, Stratmann JW, Popescu GV, Mueller LA, Popescu SC. (2014). The tomato kinome and the tomato kinase library ORFeome: novel resources for the study of kinases and signal transduction in tomato and solanaceae species. <i>Mol. Plant Microbe Interact.</i> 27(1), 7.</p>
<p>Claros MG, Bautista R, Guerrero-Fernandez D, Benzerki H, Seoane P, Fernandez-Pozo N. (2012). Why assembling plant genome sequences is so challenging. <i>Biology 1 (2)</i>, 439.</p>
<p>Fernández-Pozo N, Canales J, ..., Cervera MT, Soto A, Ordás R, Cantón FR, Avila C, Cánovas FM, Claros MG. (2011) EuroPineDB: a high-coverage web database for maritime pine transcriptome. <i>BMC Genomics</i>, 12:366.</p>
<p>Falgueras J, Lara AJ, Fernández-Pozo N, Cantón FR, Pérez-Trabado G, Claros MG. (2010). SeqTrim: a high-throughput pipeline for pre-processing any type of sequence read. <i>BMC Bioinformatics</i>, 11:38.</p>

OTHER INFORMATION

Supervision, mentoring and training

<p>PhD thesis. Epigenome-wide association studies. Student: Sultan Nilay Can. EpiDiverse, European Training Network. University of Marburg. 03/04/2018 - In progress.</p>
<p>Master thesis. <i>Physcomitrella patens</i> genome annotation. Student: Viktor Kratz. Master in Systems Biology and Bioinformatics. University of Giessen. 01/02/2019 - 30/08/2019. 5 months.</p>
<p>Bachelor thesis. Genome annotation of <i>Aethionema arabicum</i>. Student: Timo Metz. BSc. Vertiefungsmodul. University of Marburg. 16/10/2017 - 28/09/2018. 1 year.</p>
<p>Praktikum from the Master in Systems Biology and Bioinformatics. Student: Viktor Kratz. Project: Development of bioinformatics tools for <i>P. patens</i>. University of Giessen, Germany, 24/09/2018 - 06/12/2018.</p>
<p>Praktikum from the Master in Systems Biology and Bioinformatics. Student: Alexander Klingenberger. Project: Analysis pipeline for the expression of <i>P. patens</i> sporophyte mRNA data. University of Giessen, Germany, 09/10/2017 - 31/01/2018.</p>
<p>Praktikum from the Master in Systems Biology and Bioinformatics. Student: Ralf Schulze Bruening. Project: Comparison of DMR callers. University of Giessen, Germany, 06/11/2017 - 31/01/2018.</p>



Praktikum from the Master in Systems Biology and Bioinformatics. Student: Sven Foerster. Project: Physcomitrella patens V3-Genom-Verbesserung mit Hilfe von Oxford Nanopore MinION long-reads. University of Giessen, Germany, 01/12/2017 - 31/01/2018.
Mentor at the BTI Summer School 2016. Intern: Phillip Jander. Project: Iochroma cyaneum Gene Family Analysis. Boyce Thompson Institute, Ithaca, NY, US. 16/06/2016 - 12/08/2016.
Mentor at the BTI Summer School 2016. Intern: Matthew. Project: Building a genomic resource for a major African staple crop: the Cassava Expression Atlas. Boyce Thompson Institute, Ithaca, NY, US. 16/06/2016 - 12/08/2016.
Mentor at the BTI Summer School 2015. Intern: Jonathan Gomes Selman. Project: Extending CRISPR design software features for tomato protein kinase silencing. Boyce Thompson Institute, Ithaca, NY, US. 08/06/2015 - 07/08/2015.
Mentor at the BTI Summer School 2014. Intern: Javon R. Mullings. Project: Multi Gene Analysis Tool for Virus Induced Gene Silencing. Boyce Thompson Institute, Ithaca, NY, US. 02/06/2014 - 07/08/2014.
Supervisor of 3 bioinformatics PhD students, 2 bioinformatics scientific researchers, 5 master students and 1 bachelor student at Rensing Lab.

Organization of international conferences, summers schools and Workshops

MAdLand Black Forest Workshop 2020. Online + Black Forest Highlands, Germany. September 11th-13th, 2020. https://4science.de/madland
MAdLand Kickoff meeting. Online + Black Forest Highlands, Germany. September 14th-16th, 2020. https://4science.de/madland
Virtual Black Forest Summer School (vBFSS2020). Hosted virtually using Zoom webinars. May 11th-12th, 2020. https://4science.de/BFSS2020
EpiDiverse Annual Meeting Online. Hosted virtually using Zoom. May 13-15, 2020.
32nd Conference Molecular Biology of Plants (MBP 2019). Dabringhausen, Germany. 18/02/2019 - 21/02/2019.
Bioinformatics Workshop. Hokkaido University, Sapporo, Japan. 11/09/2019 - 18/09/2019.
Black Forest Workshop 2018. The 1st Black Forest Flagellated Plant Workshop. Black Forest Highlands, Germany. 17/09/2018 - 20/09/2018. https://plantco.de/BFW2018
Black Forest Summer School 2017. Next generation sequencing and phylogenetics. Black Forest Highlands, Germany. 24/09/2017 - 27/09/2017. https://plantco.de/BFSS2017
Bioinformatics Workshop Series 3: Genome Database and Mining. University of the Philippines Los Baños (UPLB). 14/01/2016 - 15/01/2016.
Sol Genomics Network Workshop. At the 13th Solanaceae Conference, 2016, Davis, CA, US. 09/2016.
Sol Genomics Network Workshop. At the 12th Solanaceae Conference, 2015, Bordeaux, France. 10/2015.
Sol Genomics Network Workshop. At the 11th Solanaceae Conference, 2014, Arraial D' Ayuda, Bahia, Brazil. 11/2014.
Sol Genomics Network Workshop. PAG Conference XXII 2014, W708, San Diego, CA, US. 01/2014
BTI Plant Bioinformatics Course 2017. Boyce Thompson Institute, Ithaca, NY, US. 14/03/2017 - 09/05/2017.
BTI Plant Bioinformatics Course 2016. Boyce Thompson Institute, Ithaca, NY, US. 15/03/2016 - 17/05/2016.
BTI Plant Bioinformatics Course 2015. Boyce Thompson Institute, Ithaca, NY, US. 17/03/2015 -



05/05/2015.
BTI Plant Bioinformatics Course 2014. Boyce Thompson Institute, Ithaca, NY, US. 25/2/2014 - 15/04/2014.
BTI Plant Bioinformatics Course 2013. Boyce Thompson Institute, Ithaca, NY, US. 19/03/2013 - 07/05/2014. https://btiplantbioinfocourse.wordpress.com
Microarray analysis course. Plataforma Andaluza de Bioinformática (PAB). Malaga, Spain. 2010.

Memberships of reviewer boards and scientific societies

Review editor on the editorial board of Frontiers in Plant Science (plant development and evo-devo section).
Member of the reviewer board of the International Journal of Molecular Sciences (IJMS), from the MDPI publisher.
Member of iMOSS, the international molecular moss science society.
Treasurer of 4Science e.V., a non profit association for the organization of scientific events. 2018-2020.

Teaching experience

Bioinformatics Workshop. Hokkaido University, Sapporo, Japan. Full workshop (only teacher), 11/09/2019 - 18/09/2019. 40 hours of teaching.
Bioinformatics: NGS, phylogeny and genome annotation. MSc. Aufbaumodul Molecular Cell Biology and Evolution of Plants. Master in Molecular and Cellular Biology. Winter semester, 30/11/2020 - 13/01/2021. University of Marburg, Germany. 40 hours.
Bioinformatics: NGS, phylogeny and genome annotation. MSc. Aufbaumodul Molecular Cell Biology and Evolution of Plants. Master in Molecular and Cellular Biology. Winter semester, 18/11/2019 - 13/12/2019. University of Marburg, Germany. 40 hours.
Bioinformatics: NGS, phylogeny and genome annotation. MSc. Aufbaumodul Molecular Cell Biology and Evolution of Plants. Master in Molecular and Cellular Biology. Winter semester, 19/11/2018 - 14/12/2018. University of Marburg, Germany. 40 hours.
Bioinformatics: NGS, phylogeny and genome annotation. MSc. Aufbaumodul Molecular Cell Biology and Evolution of Plants. Master in Molecular and Cellular Biology. Winter semester, 20/11/2017 - 15/12/2017. University of Marburg, Germany. 40 hours.
Bioinformatics: NGS and genome annotation. AM Molekulare Zellbiologie der Pflanzen. Biology (B.Sc.) degree. Summer semester, 13/04/2020 - 28/05/2020. University of Marburg, Germany. 10 hours.
Bioinformatics: NGS and genome annotation. AM Molekulare Zellbiologie der Pflanzen. Biology (B.Sc.) degree. Summer semester, 10/04/2019 - 06/07/2019. University of Marburg, Germany. 10 hours.
Bioinformatics: NGS and genome annotation. AM Molekulare Zellbiologie der Pflanzen. Biology (B.Sc.) degree. Summer semester, 04/04/2018 - 06/07/2018. University of Marburg, Germany. 10 hours.
Bioinformatics: Next Generation Sequencing (NGS) and genome annotation Marburg School of Microbiology workshop, 03/09/2018 - 07/09/2018, University of Marburg, Germany. 4 hours.
Phytozome, CoGe and TAPscan: plant comparative genomics web tools Black Forest Workshop 2018. 17/09/2018 - 20/09/2018. Black Forest Highlands, Germany.
NGS data processing and differential expression analysis. Black Forest Summer School 2017 (BFSS2017), Next generation sequencing and phylogenetics. 24/09/2017 - 27/09/2017. Black Forest Highlands, Germany.
Mapping: short read alignment to a reference. Black Forest Summer School 2017 (BFSS2017), Next



generation sequencing and phylogenetics. 24/09/2017 - 27/09/2017. Black Forest Highlands, Germany.
Introduction to UNIX command-line. (2013 - 2017, 5 times). BTI Plant Bioinformatics Course, 2013 - 2017. Boyce Thompson Institute, Ithaca, NY, US. 20 hours in total.
BLAST and other command-line tools. BTI Summer School 2016. Boyce Thompson Institute, Ithaca, NY, US. 4 hours.
Bioinformatics Workshop Series 3: Genome Database and Mining. University of the Philippines Los Baños. Full workshop (only teacher). 14/01/2016 - 15/01/2016. 16 hours.
Introduction to UNIX command-line (2013 - 2016, 4 times). BTI Summer Schools 2013 - 2016. Boyce Thompson Institute, Ithaca, NY, US. 16 hours in total.
Introduction to Perl (2013 - 2016, 4 times). BTI Summer Schools, 2013 - 2016. Boyce Thompson Institute, Ithaca, NY, US. 16 hours in total.
Introduction to Perl. Cornell University, Ithaca, NY, US. 2014. 4 hours.
Two color microarrays analysis using Bioconductor. PAB Microarray analysis course. Malaga, Spain. 2010.

Development of genomic databases and bioinformatic tools

The Tomato Expression Atlas (http://tea.solgenomics.net/)
PEATmoss (The Physcomitrella Expression Atlas Tool) (https://peatmoss.online.uni-marburg.de/)
The SGN VIGS Tool (https://vigs.solgenomics.net/)
EuroPineDB, SustainPineDB (http://www.scbi.uma.es/pindb/)
OliveTreeDB (https://genomaolivar.dipujaen.es/)
<i>Aethionema arabicum</i> DB (https://plantcode.online.uni-marburg.de/aetar_db/)
The Sol Genomics Network (https://solgenomics.net/)

Researcher IDs

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Research Summary

<p>I am an expert in bioinformatics with more than 13 years of experience. From 2012 to 2017, I worked as a researcher at the Boyce Thompson Institute in Cornell University, where I learnt from some of the best plant scientists in the world. I have investigated and developed resources for many species of great interest for agriculture and forestry, such as tomato, potato, pepper, cassava, pine, olive tree, and for evolution and basic science, such as <i>N. benthamiana</i>, <i>P. patens</i> and many others. I participated in several millionaire projects in the USA and Germany to study citrus greening disease, to deeply understand tomato fruit ripening, to investigate plant-pathogen interactions in tomato, and to learn about how plants evolved to adapt from water to land, among others. I have created bioinformatics tools and databases such as The Tomato Expression Atlas, PEATmoss, The SGN VIGS Tool, EuroPineDB, <i>Aethionema arabicum</i> DB and OliveTreeDB, and highly contributed to the development, improvement and expansion of the Sol Genomics Network, SeqTrim, SoleaDB, The Citrus Expression Network and others. Among my bioinformatics skills, I have broad experience with NGS, data processing, assembly, annotation, gene expression, RNA-seq, comparative genomics, transcriptomics, genetic variation analysis, phylogeny and epigenetics. This is reflected in 43 publications, including 32 SCI articles, 30 of</p>



them in the first quartile. I have publications as first author in prestigious journals such as Nature communications, Bioinformatics, Nucleic Acids Research and Plant Journal, including 2 of them labeled as highly cited publications by the Web of Science.

As a research assistant at the University of Marburg, I supervised Bachelor, Master and PhD students. I am a PI in EpiDiverse, a European Training Network where I am co-directing a PhD student, and a PI in CharKeyS, a project granted by DFG to develop non-model streptophyte algae of interest for evo-devo studies. I am involved in MAdLand, a 6 million euros project with more than 20 research groups, where PEATmoss, the expression atlas and bioinformatics tools I developed, have a key role to analyze and host the generated data. Additionally, I submitted a grant proposal to the DFG (German Research Foundation) as main PI to further develop this tool.

My goal in the near future is to investigate and create resources for species of interest for South European agriculture, where the Mediterranean countries are top crop producers and have unique climatic conditions to develop subtropical crops such as avocado and mango. I would like to apply my experience in bioinformatics to support breeding and to research about important traits and mechanisms in crops such as resistance to stresses, fruit ripening, gene regulation and genetic variation/diversity.



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Declarations given in the present curriculum must be considered released according to art. 46 and 47 of DPR n. 445/2000.

The present curriculum does not contain confidential and legal information according to art. 4, paragraph 1, points d) and e) of D.Lgs. 30.06.2003 n. 196.

Place and date: Málaga, 20 of January of 2021

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