CV: LILIANA M. CANO

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Area of expertise
Genome analyses of plant pathogens; gene expression analyses during plant-pathogen interactions. Evolutionary and functional analyses of pathogen effector proteins.

Research interest
I am interested in understanding how effectors secreted by microbes can reprogram host physiology and achieve colonization. My research aims in using genomics to identify pathogen effectors together with functional analyses to elucidate their biochemical activity and for the development of new approaches for breeding disease resistant crop plants. My research topics fall within the scope of effector biology and plant immunity. These include effector specialization, gene expression of effectors during infection, activation of effectors by plant immune receptors and modulation of host pathways by effectors.

Education
2007-2011	PhD in Plant-microbe interactions, The Sainsbury Laboratory (TSL)/ Department of Biological Sciences, University of East Anglia (UEA), Norwich, UK.
2001-2002	Diploma in Molecular Biology and Genetics, University of Pamplona (UP), Pamplona, Colombia.
1998-2004	BSc in Engineering (Biotechnology), Francisco de Paula Santander University (UFPS), Cucuta, Colombia.

Professional experience
2016- Present	Assistant Professor in Citrus Pathology, Dept. of Plant Pathology, University of Florida, Indian River Research and Education Center (IRREC), Fort Pierce, FL, USA.
2014-2015	Postdoc, Dept. of Plant Pathology, North Carolina State University (NCSU), Raleigh, NC, USA.
2012-2014	Postdoc, The Sainsbury Laboratory (TSL), Norwich, Norfolk, UK.
2007-2011	PhD, The Sainsbury Laboratory (TSL)/University of East Anglia (UEA), Norwich, Norfolk, UK.
2006-2007	Visiting scientist, Dept. of Plant Pathology, The Ohio State University (OSU), Ohio Agricultural Research and Development Center (OARDC), Wooster, Ohio, USA.
2004-2006	Research scientist, Dept. of Entomology, National Coffee Research Center (CENICAFE), Chinchina, Caldas, Colombia.
2003-2004	Undergraduate research assistant, Dept. Cassava Genetics, International Center for Tropical Agriculture (CIAT), Cali, Valle, Colombia.
Oct-Dec2002	Undergraduate intern, Dept. of Biopesticidal Formulation, Live Systems Technology S.A. (LSTSA), Bogota, Cundinamarca, Colombia.

Teaching and training experience
- Training and mentoring of students and postdocs at The Sainsbury Laboratory and North Carolina State University. Unix/Linux basics, bioinformatics in plant-microbe interactions.
- Course PP502 on plant disease methods and diagnosis at Dept. of Plant Pathology, North Carolina State University. Shared lecture on plant pathogen effectors.

Awards
2015	Oomycete Molecular Genetics Network OMGN 2015 Travel award. USA.
2011	Excellence in Science Communication Student Prize from John Innes Center (JIC) Foundation, UK.
2010	Daiwa Adrian Prize (collaboration in use of genomics to understand plant-pathogen interactions), Japan-UK.
2009	Young Presenter Prize - EMBO at The Comparative Genomics of Eukaryotic Microorganisms Conference, Spain.
2006	Hernan Alcaraz Viecco Presenter Prize from Colombian Society of Entomology (SOCOLEN), Colombia.

Professional activities
Member of the American Phytopathological Society (APS). Member of the Oomycete Molecular Genetic Network (OMGN).

Peer-review science journal activities
Associate Editor of Molecular Plant Microbe Interactions (MPMI). Reviewer for: Physiological and Molecular Plant Pathology (PMPP). PLoSONE, New Phytologist, Frontiers in Plant Science - Section Plant-Microbe Interaction and Phytopathology.

Bioinformatics and laboratory skills
- Knowledge of cell and molecular biology techniques (DNA and RNA extraction, CDNA synthesis, PCR, RT-PCR, qPCR, cloning, virus induced silencing, protein purification and western blot, and others)
- Extensive work in plant pathology (infection assays using bacteria, oomycetes and fungi).
- Working with high performance computing clusters using Unix/Linux platform.
- Skills in regular expressions and programming using Perl, statistical analysis and graphical visualization with R.
- Familiar with commercial and open-source computational tools, public genome browsers and databases.
- Genome assembly and transcriptome and gene expression analysis using RNAseq.
- Detection of polymorphisms in plant and pathogens genomes such single nucleotide polymorphisms (SNPs) and copy number variations (CNVs).
- Effector gene annotation, phylogenetics and evolutionary analysis of effector gene families.
- Transient expression of pathogen effectors *in planta* and co-inmunoprecipitation assays.
- MS/MS analysis for the identification of pathogen effector and host protein complexes using Scaffold
- Subcellular localization of pathogen proteins with fluorescent tags.

Oral presentations
2015   Speaker: Embracing effector discovery in the hop downy mildew pathogen. ***American Phytopathological Society (APS) Annual Meeting****. Pasadena, USA

2015   Speaker: Embracing effector discovery in the hop downy mildew pathogen. ***Oomycete Meeting Genetic Network (OMGN).*** Asilomar, USA.

2014   Speaker: Genome analyses of filamentous plant pathogens. ***Plant Pathology Society of North Carolina Meeting (PPSNC)****. Raleigh, USA.

2013   Speaker: Genome sequencing and expression profiling of emerging strains of *Phytophthora infestans*. ***Pathogen-informed strategies for sustainable broad-spectrum crop resistance. COST Action FA1208.*** Birnam, Scotland.

2011   Speaker: The Secrets of Crop Killers: Evolution and Function of Filamentous Pathogen Effectors. Chemical & Biological Terrorism Defense. **Gordon Research Conferences.** Los Angeles, USA.

2011   Speaker: Comparative pathogenomics of emerging clones of *Phytophthora infestans*. Concurrent session I: Fungal effectors at the ***26th Fungal Genetics Conference (FGC).*** Asilomar, USA.

2010   Speaker: Comparative genome analysis of a strain from the UK blue 13 clonal lineage of *P. infestans* reveals significant genetic and expression polymorphisms in effector genes. ***Oomycete Meeting Genetic Network (OMGN).*** Toulouse, France.

2009   Speaker: Effector evolution of a protease inhibitor EPIC1 in the *Phytophthora infestans* species cluster. ***Comparative Genomics of Eukaryotic Microorganisms EMBO Conference.*** San Feliu de Guixols, Spain.

2009   Speaker: Exploring transcriptome sequencing to study effector evolution in *Phytophthora ipomoeae* and *Phytophthora mirabilis*. ***XX Molecular Biology of Plant Pathogens (MBPP).*** Somerville College, University of Oxford. Oxford, UK.

2009   Speaker: Transcriptome sequencing of *P. ipomoea* and *P. mirabilis* to understand effector evolution in the *Phytophthora infestans* species cluster. ***Oomycete Meeting Genetic Network (OMGN).*** Asilomar, USA

2008   Speaker: Exploring transcriptome sequences to understand effector evolution in the *P. infestans* species cluster. ***Oomycete Meeting Genetic Network (OMGN).*** Birnam, Scotland

2007   Speaker: Full-Length cDNA Sequences for Genome Annotation in *Phytophthora infestans*. ***Oomycete Meeting Genetic Network (OMGN).*** Asilomar, USA.

2005   Speaker: Genetic diversity of ants of the genus *Acropyga* from the Central Andean region of Colombia. ***XXXII Congress of the Colombian Society of Entomology (SOCOLEN).*** Pereira, Colombia

Research publications [Researcher ID: D-2093-2013, N= 37, h-index: 20]

1. Yoshida K, Saunders, DGO, Mitsuoka C, Natsume S, Kosugi S, Saitoh H, Inoue Y, Chuma I, Tosa Y, **Cano LM,** Kamoun S and Terauchi R: Host specialization of the blast fungus *Magnaporthe oryzae* is associated with dynamic gain and loss of genes linked to transposable elements. ***BMC Genomics*** **2016** 17:370.

2. Belhaj K, **Cano LM**, Prince DC, Kemen A, Yoshida K, et al: Arabidopsis late blight: infection of a nonhost plant by Albugo laibachii enables full colonization by *Phytophthora infestans*. ***Cell Microbiol*** **2016.**

3. Pitino M, Armstrong CM, **Cano LM** and Duan Y: Transient Expression of *Candidatus* Liberibacter Asiaticus Effector Induces Cell Death in *Nicotiana benthamiana*. ***Frontiers in Plant Science.***

4. Kasuga T, Bui M, Bernhardt E, Swiecki T, Aram K, **Cano LM**, et al: Host-induced aneuploidy and phenotypic diversification in the Sudden Oak Death pathogen *Phytophthora ramorum*. ***BMC Genomics*** **2016** 17:385.

5. Oliva RF, **Cano LM**, Raffaele S, Win J, Bozkurt TO, et al: Recent expansion of the RXLR effector gene *Avrblb2* is maintained in global populations of *Phytophthora infestans* indicating different contributions to virulence. ***Mol Plant Microbe Interact*** **2015** (8):901-12.

6. Sharma R, Xia X, **Cano LM**, Evangelisti E, Kemen., et al: Genome analyses of the sunflower pathogen *Plasmopara halstedii* provide insights into effector evolution in downy mildews and *Phytophthora.* ***BMC Genomics*** **2015** 16(1):741.

7. Bozkurt TO, Belhaj K, Dagdas YF, Chaparro-Garcia A, Wu CH, **Cano LM**, Kamoun S: Rerouting of Plant Late Endocytic Trafficking Toward a Pathogen Interface. ***Traffic*** **2015** 16(2):204-226.

8. Solovyeva I; Schmuker A, **Cano LM**, et al: Evolution of *Hyaloperonospora* effectors: ATR1 effector homologs from sister species of the downy mildew pathogen *H. arabidopsidis* are not recognised by RPP1(WsB). ***Mycological Progress*** **2015** 14:53.

9. Dong S, Stam R, **Cano LM**, et al: Effector specialization in a lineage of the Irish potato famine pathogen. ***Science*** **2014** 343(6170):552-555.

10. **Cano LM*,** Raffaele S*, Haugen RH, et al: Major transcriptome reprogramming underlies floral mimicry induced by the rust fungus *Puccinia monoica* in *Boechera stricta*. ***PLoS ONE*** **2013** 8(9):e75293. *These authors contributed equally to this work.

11. Cooke* DE, **Cano* LM,** Raffaele S, et al: Genome analyses of an aggressive and invasive lineage of the Irish potato famine pathogen. ***PLoS Pathog*** **2012,** 8:e1002940. *These authors contributed equally to this work**.**

12. Saunders DGO, Win J, **Cano LM,** et al: Using hierarchical clustering of secreted protein families to classify and rank candidate effectors of rust fungi. ***PLoS ONE*** **2012,** 7:e29847. **Recommended by Faculty of 1000.**

13. Raffaele* S, Farrer* RA, **Cano* LM,** et al: Genome evolution following host jumps in the Irish potato famine pathogen lineage. ***Science*** **2010,** 330:1540-1543. *These authors contributed equally to this work. **Recommended by Faculty of 1000.**

14. Rietman H, Bijsterbosch G, **Cano LM,** et al: Qualitative and quantitative late blight resistance in the potato cultivar Sarpo Mira is determined by the perception of five distinct RXLR effectors. ***Mol Plant Microbe Interact*** **2012,** 25:910-919.

15. van Damme M, **Cano LM,** et al: Evolutionary and functional dynamics of oomycete effector genes. In ***Effectors in Plant–Microbe Interactions.*** **Wiley-Blackwell; 2011:** 101-120

16. Bozkurt TO, Schornack S, Win J, Shindo T, Ilyas M, Oliva R, **Cano LM,** et al: *Phytophthora infestans* effector AVRblb2 prevents secretion of a plant immune protease at the haustorial interface. ***Proc Natl Acad Sci U S A*** **2011,** 108:20832-20837.

17. Vleeshouwers VG, Raffaele S, Vossen JH, Champouret N, Oliva R, Segretin ME, Rietman H, **Cano LM,** et al: Understanding and exploiting late blight resistance in the age of effectors. ***Annu Rev Phytopathol*** **2011,** 49:507-531.

18. Raffaele S, Win J, **Cano LM,** Kamoun S: Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of *Phytophthora infestans*. ***BMC Genomics*** **2010,** 11:637.

19. Haas BJ, Kamoun S, Zody MC, Jiang RH, Handsaker RE, **Cano LM,** et al: Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*. ***Nature*** **2009,** 461:393-398.

20. Bozkurt TO, Belhaj K, Dagdas YF, Chaparro-Garcia A, Wu C-H, **Cano LM**, Kamoun Sclose, 2014, Rerouting of plant late endocytic trafficking towards a pathogen interface. ***Traffic.*** ISSN: 1398-9219

21. Kosugi S, Natsume S, Yoshida K, MacLean D, **Cano L**, Kamoun S, Terauchi R: Coval: Improving Alignment Quality and Variant Calling Accuracy for Next-Generation Sequencing Data. ***PLoS ONE*** **2013** 8(10): e75402.

22. Yoshida K, Schuenemann VJ, **Cano LM,** Pais M, Mishra B, et al.: The rise and fall of the *Phytophthora infestans* lineage that triggered the Irish potato famine. ***eLife*** **2013,** 2:e00731.

23. Pais M, Win J, Yoshida K, Etherington GJ, **Cano LM,** et al: From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. *Genome Biol* **2013,** 14:211.
24. Fekih R, Takagi H, Tamiru M, Abe A, Natsume S, Yaegashi H, Sharma S, Sharma S, Kanzaki H, Matsumura H, Saitoh H, Mitsuoka C, Utsushi H, Uemura A, Kanzaki E, Kosugi S, Yoshida K, **Cano LM**, Kamoun S, Terauchi R. MutMap+: genetic mapping and mutant identification without crossing in rice*. PLoS ONE* **2013** 8, e68529.
25. Takagi H, Abe A, Yoshida K, Kosugi S, Natsume S, Mitsuoka C, Uemura A, Utsushi H, Tamiru M, Takuno S, Innan H, **Cano LM**, Kamoun S, Terauchi R. QTL-seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of DNA from two bulked populations. *Plant J* **2013** 74, 174-183.
26. Takagi H, Uemura A, Yaegashi H, Tamiru M, Abe A, Mitsuoka C, Utsushi H, Natsume S, Kanzaki H, Matsumura H, Saitoh H, Yoshida K, **Cano LM**, Kamoun S, Terauchi R. MutMap-Gap: whole-genome resequencing of mutant F2 progeny bulk combined with de novo assembly of gap regions identifies the rice blast resistance gene Pii. *New Phytol* **2013** 200, 276-283.
27. Lamour KH, Mudge J, Gobena D, Hurtado-Gonzales OP, Schmutz J, Kuo A, Miller NA, Rice BJ, Raffaele S, **Cano LM,** et al: Genome sequencing and mapping reveal loss of heterozygosity as a mechanism for rapid adaptation in the vegetable pathogen *Phytophthora capsici*. *Mol Plant Microbe Interact* **2012,** 25:1350-1360.
28. Abe A, Kosugi S, Yoshida K, Natsume S, Takagi H, Kanzaki H, Matsumura H, Yoshida K, Mitsuoka C, Tamiru M, Innan H, **Cano LM,** Kamoun S, Terauchi R: Genome sequencing reveals agronomically important loci in rice using MutMap. *Nat Biotechnol* **2012,** 30:174-178.
29. Gilroy EM, Breen S, Whisson SC, Squires J, Hein I, Kaczmarek M, Turnbull D, Boevink PC, Lokossou A, **Cano LM,** et al: Presence/absence, differential expression and sequence polymorphisms between *PiAVR2* and *PiAVR2-like* in *Phytophthora infestans* determine virulence on R2 plants. *New Phytol* **2011,** 191:763-776.
30. Schornack S, van Damme M, Bozkurt TO, **Cano LM,** et al: Ancient class of translocated oomycete effectors targets the host nucleus. *Proc Natl Acad Sci U S A* **2010,** 107:17421-17426.
31. Levesque CA, Brouwer H, **Cano L,** et al: Genome sequence of the necrotrophic plant pathogen *Pythium ultimum* reveals original pathogenicity mechanisms and effector repertoire. *Genome Biol* **2010,** 11:R73.
32. Oliva R, Win J, Raffaele S, Boutemy L, Bozkurt TO, Chaparro-Garcia A, Segretin ME, Stam R, Schornack S, **Cano LM,** et al: Recent developments in effector biology of filamentous plant pathogens. *Cell Microbiol* **2010,** 12:1015.
33. Schornack S, Huitema E, **Cano LM,** et al: Ten things to know about oomycete effectors. *Mol Plant Pathol* **2009,** 10:795-803.
34. Oh SK, Young C, Lee M, Oliva R, Bozkurt TO, **Cano LM,** et al: In planta expression screens of *Phytophthora infestans* RXLR effectors reveal diverse phenotypes, including activation of the *Solanum bulbocastanum* disease resistance protein Rpi-blb2. *Plant Cell* **2009,** 21:2928-2947.
35. van Damme M, Schornack S, **Cano LM,** et al: Interactions between *Phytophthora infestans* and Solanum. In *Oomycete Genetics and Genomics.* **John Wiley & Sons, Inc.; 2008:** 287-302
36. Win J, Morgan W, Bos J, Krasileva KV, **Cano LM,** et al: Adaptive evolution has targeted the C-terminal domain of the RXLR effectors of plant pathogenic oomycetes. *Plant Cell* **2007,** 19:2349-2369.
37. Lopez-Nunez JC, **Cano L**, Gongora-B CE, Stock SP: Diversity and evolutionary relationships of entomopathogenic nematodes (Steinernematidae and Heterorhabditidae) from the Central Andean region of Colombia. *Nematology 2007*, 9:333-341.

Referees

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