

# Liliana M Cano

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

9,925  
citations

109321

35  
h-index

182427

51  
g-index

64  
all docs

64  
docs citations

64  
times ranked

7736  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lessons learned about the biology and genomics of <i>Diaphorina citri</i> infection with <i>Candidatus Liberibacter asiaticus</i> by integrating new and archived organ-specific transcriptome data. <i>GigaScience</i> , 2022, 11, .	6.4	5
2	Draft Genome Sequence Resource of the Citrus Stem-End Rot Fungal Pathogen <i>Lasiodiplodia theobromae</i> CITRA15. <i>Phytopathology</i> , 2021, 111, 761-764.	2.2	9
3	In Planta Localization of Endophytic <i>Cordyceps fumosorosea</i> in Carrizo Citrus. <i>Microorganisms</i> , 2021, 9, 219.	3.6	5
4	Draft genome sequence resource for the orange rust pathogen of sugarcane <i>Puccinia kuehnii</i> . <i>Phytopathology</i> , 2021, , PHYTO01210008A.	2.2	1
5	Effect of Propagation Systems and Indole-3-Butyric Acid Potassium Salt (K-IBA) Concentrations on the Propagation of Peach Rootstocks by Stem Cuttings. <i>Plants</i> , 2021, 10, 1151.	3.5	4
6	In Vitro Effects of Leaf Extracts from <i>Brassica rapa</i> on the Growth of Two Entomopathogenic Fungi. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 779.	3.5	2
7	The Effector Repertoire of the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> . <i>Frontiers in Genetics</i> , 2020, 11, 910.	2.3	9
8	First Report of <i>Gilbertella persicaria</i> Causing Postharvest Soft Rot of Strawberry Fruit in Florida. <i>Plant Disease</i> , 2020, 104, 2736.	1.4	4
9	Reinterpretation of <i>sperm pump</i> or <i>sperm syringe</i> function with notes on other male internal reproductive organs in the Asian citrus psyllid, <i>Diaphorina citri</i> (Hemiptera: Liviidae). <i>Arthropod Structure and Development</i> , 2020, 54, 100915.	1.4	0
10	<i>Quercus</i> leaf extracts display curative effects against <i>Candidatus Liberibacter asiaticus</i> that restore leaf physiological parameters in HLB-affected citrus trees. <i>Plant Physiology and Biochemistry</i> , 2020, 148, 70-79.	5.8	16
11	Evaluation of High-Resolution Melting for Rapid Differentiation of <i>Phytophthora</i> Hybrids and Their Parental Species. <i>Plant Disease</i> , 2019, 103, 2295-2304.	1.4	6
12	Temporal and spatial detection of <i>Candidatus Liberibacter asiaticus</i> putative effector transcripts during interaction with Huanglongbing-susceptible, <i>tolerant</i> , and <i>-resistant</i> citrus hosts. <i>BMC Plant Biology</i> , 2019, 19, 122.	3.6	38
13	nQuire: a statistical framework for ploidy estimation using next generation sequencing. <i>BMC Bioinformatics</i> , 2018, 19, 122.	2.6	128
14	Asian citrus psyllid stylet morphology and applicability to the model for inter-instar stylet replacement in the potato psyllid. <i>Arthropod Structure and Development</i> , 2018, 47, 542-551.	1.4	5
15	Bioinformatic characterisation of the effector repertoire of the strawberry pathogen <i>Phytophthora cactorum</i> . <i>PLoS ONE</i> , 2018, 13, e0202305.	2.5	40
16	Gene expression polymorphism underpins evasion of host immunity in an asexual lineage of the Irish potato famine pathogen. <i>BMC Evolutionary Biology</i> , 2018, 18, 93.	3.2	41
17	Genomics analysis of <i>Aphanomyces</i> spp. identifies a new class of oomycete effector associated with host adaptation. <i>BMC Biology</i> , 2018, 16, 43.	3.8	62
18	Arabidopsis late blight: infection of a nonhost plant by <i>Albugo laibachii</i> enables full colonization by <i>Phytophthora infestans</i> . <i>Cellular Microbiology</i> , 2017, 19, e12628.	2.1	44

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19	Improved annotation of the insect vector of citrus greening disease: biocuration by a diverse genomics community. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	62
20	Transient Expression of Candidatus Liberibacter Asiaticus Effector Induces Cell Death in Nicotiana benthamiana. Frontiers in Plant Science, 2016, 7, 982.	3.6	93
21	Host-induced aneuploidy and phenotypic diversification in the Sudden Oak Death pathogen Phytophthora ramorum. BMC Genomics, 2016, 17, 385.	2.8	55
22	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.	2.8	157
23	Genome analyses of the sunflower pathogen Plasmopara halstedii provide insights into effector evolution in downy mildews and Phytophthora. BMC Genomics, 2015, 16, 741.	2.8	135
24	A Recent Expansion of the RXLR Effector Gene <i>Avrblb2</i> Is Maintained in Global Populations of <i>Phytophthora infestans</i> Indicating Different Contributions to Virulence. Molecular Plant-Microbe Interactions, 2015, 28, 901-912.	2.6	44
25	Evolution of Hyaloperonospora effectors: ATR1 effector homologs from sister species of the downy mildew pathogen H. arabidopsidis are not recognised by RPP1WsB. Mycological Progress, 2015, 14, 1.	1.4	3
26	Rerouting of Plant Late Endocytic Trafficking Toward a Pathogen Interface. Traffic, 2015, 16, 204-226.	2.7	103
27	Effector Specialization in a Lineage of the Irish Potato Famine Pathogen. Science, 2014, 343, 552-555.	12.6	179
28	Whole-genome resequencing of mutant F2 progeny bulk combined with <i>de novo</i> assembly of gap regions identifies the rice blast resistance gene <i>Pii</i> . New Phytologist, 2013, 200, 276-283.	7.3	196
29	From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. Genome Biology, 2013, 14, 211.	8.8	64
30	QTL-seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of DNA from two bulked populations. Plant Journal, 2013, 74, 174-183.	5.7	1,065
31	The rise and fall of the Phytophthora infestans lineage that triggered the Irish potato famine. ELife, 2013, 2, e00731.	6.0	339
32	Major Transcriptome Reprogramming Underlies Floral Mimicry Induced by the Rust Fungus Puccinia monoica in Boechera stricta. PLoS ONE, 2013, 8, e75293.	2.5	25
33	MutMap+: Genetic Mapping and Mutant Identification without Crossing in Rice. PLoS ONE, 2013, 8, e68529.	2.5	267
34	Coval: Improving Alignment Quality and Variant Calling Accuracy for Next-Generation Sequencing Data. PLoS ONE, 2013, 8, e75402.	2.5	58
35	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. PLoS Pathogens, 2012, 8, e1002940.	4.7	321
36	Qualitative and Quantitative Late Blight Resistance in the Potato Cultivar Sarpo Mira Is Determined by the Perception of Five Distinct RXLR Effectors. Molecular Plant-Microbe Interactions, 2012, 25, 910-919.	2.6	162

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37	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	2.6	264
38	Genome sequencing reveals agronomically important loci in rice using MutMap. <i>Nature Biotechnology</i> , 2012, 30, 174-178.	17.5	1,087
39	Using Hierarchical Clustering of Secreted Protein Families to Classify and Rank Candidate Effectors of Rust Fungi. <i>PLoS ONE</i> , 2012, 7, e29847.	2.5	235
40	<i>Phytophthora infestans</i> effector AVRblb2 prevents secretion of a plant immune protease at the haustorial interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20832-20837.	7.1	285
41	Understanding and Exploiting Late Blight Resistance in the Age of Effectors. <i>Annual Review of Phytopathology</i> , 2011, 49, 507-531.	7.8	369
42	Presence/absence, differential expression and sequence polymorphisms between <i>PiAVR2</i> and <i>PiAVR2-like</i> in <i>Phytophthora infestans</i> determine virulence on <i>R2</i> plants. <i>New Phytologist</i> , 2011, 191, 763-776.	7.3	142
43	Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of <i>Phytophthora infestans</i> . <i>BMC Genomics</i> , 2010, 11, 637.	2.8	188
44	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.	2.1	108
45	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 1015-1015.	2.1	11
46	Ancient class of translocated oomycete effectors targets the host nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17421-17426.	7.1	326
47	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. <i>Science</i> , 2010, 330, 1540-1543.	12.6	440
48	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	9.6	391
49	In Planta Expression Screens of <i>Phytophthora infestans</i> RXLR Effectors Reveal Diverse Phenotypes, Including Activation of the <i>Solanum bulbocastanum</i> Disease Resistance Protein Rpi-blb2. <i>Plant Cell</i> , 2009, 21, 2928-2947.	6.6	376
50	Ten things to know about oomycete effectors. <i>Molecular Plant Pathology</i> , 2009, 10, 795-803.	4.2	185
51	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
52	Diversity and evolutionary relationships of entomopathogenic nematodes (Steinernematidae and Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	17
53	Adaptive Evolution Has Targeted the C-Terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes. <i>Plant Cell</i> , 2007, 19, 2349-2369.	6.6	315
54	2021-2022 Florida Citrus Production Guide: Decay Control of Florida Fresh Citrus. <i>Edis</i> , 0, , .	0.1	0

#	ARTICLE	IF	CITATIONS
55	Interactions between <i>Phytophthora infestans</i> and <i>Solanum</i> . , 0, , 287-302.		1
56	2020â€“2021 Florida Citrus Production Guide: Decay Control of Florida Fresh Citrus. Edis, 0, , .	0.1	0