Sergio M. Latorre, PhD

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Experience

2021 – Present **Research fellow. Department of Genetics, Evolution and Environment. University College London. UK**
Research fields: *Population Genomics; Ancient DNA; Pathogens and host plant interactions*

2016 – 2020 **Ph.D. in Biology. Max Planck Institute for Biology & University of Tuebingen**
Thesis title: *Phylogenomic and population history inference using ancient DNA.*
http://dx.doi.org/10.15496/publikation-52143

Education

2011 – 2014 **M.Sc. in Microbiology. Universidad Nacional de Colombia**
Thesis title: Identification of arsenic resistance genes in the metagenome of Bogotá river*
** Meritorious award*

2005 – 2010 **B.Sc. in Agronomic Engineering. Universidad Nacional de Colombia**

Courses

2018. Apr 21 – 27 **Population Genomics: background and tools**
Sponsored by ELIXIR Italy Training. Naples, Italy.

2016. Oct 17 – 19 **Population genomic data analysis**
Sponsored by Adaptomics SPP1529. Hohenheim, Germany.

Skills

Computational
- Experience with the most relevant biological databases as well as parsing their formats (FASTA/FASTQ, SAM/BAM/CRAM, GFF, GENBANK, VCF, PED, among others).
- Broad expertise in scripting code in *Python, R* and *Bash*.
- Knowledge of specific packages for genomics and data analysis like *Biopython, Dendropy, NumPy, Pandas, Matplotlib, Scikit-learn*.
- Use of *Git* as a version-control system to release and share code with the community standards.
- Experience in creating and managing *Conda* environments and *Docker* containers to increase science reproducibility.
- Experience in summarizing complex data through meaningful and comprehensive graphical pieces to increase the impact of science communication.

Research
- Expertise using whole genome information to interrogate questions related with population genomics, demographic histories and phylogenomics in a wide variety of biological systems.
- Use of combined genomic datasets from contemporary, historical and ancient samples for different evolutionary analyses.

Skills (continued)

Laboratory
- Ample experience in DNA isolation from contemporary and historical samples of a diversity of organisms and tissues (e.g. plants, associated microorganisms and insects).
- Experience on DNA quantification, DNA quality assessment, DNA library preparation and general sample preparation protocols for *Next Generation Sequencing* platforms.
- Specific experience of experiment design and work in clean laboratory facilities.
- General background in basic and standard microbiology laboratory procedures.

Languages
Strong reading, writing and speaking competencies for Spanish and English. Intermediate level for French and Italian. Basic level for German.

Field experience

2018 Mar
Plants and associated microbiota field sample and documentation
Pathodopsis project. Central Spain.

2017 Oct
Herbaria sampling and documentation
Staatliches Museum für Naturkunde. Stuttgart, Germany.

2017 Sep
Herbaria sampling and documentation
University of Tuebingen. Tuebingen, Germany.

2015
Field experience as Agronomist with rural communities
Parques Nacionales Naturales de Colombia. Colombia.

2013
Field experience as Agronomist with rural communities
Instituto Colombiano de Desarrollo Rural (INCODER). Colombia.

Student supervision and training

Oct 2002 – Present
Bioinformatic methods for phylogenetic analyses.
Supervision and training Master student Jiajun Cui, University College London.

Jun – Jul 2022
Bioinformatic methods to process and authenticate ancient DNA genomic sequences.
Supervision and training Master student Mattias Sherman, University College London.

Sep 2021 – Jul 2022
Bioinformatic methods to detect parallel evolution in pathogenic clonal lineages.
Supervision and training Master student Eva Morisot, University College London.

Mar 2019
Molecular methods and protocols to work with herbaria inside clean laboratory facilities.
Training of visiting PhD student Julia M. Kreiner, University of Toronto.

Oral and poster presentations

2023. Mar 5 – 8
Poster presentation: Historical herbarium genomes reveal century-long genetic continuity of a clonal lineage of the rice blast fungus in Europe
16th European Conference on Fungal Genetics - ECFG 2023. Innsbruck, Austria.

2022. Aug 16
Oral presentation: Detecting parallel adaptation in clonal lineages of a plant pathogenic fungus
Congress of the European Society for Evolutionary Biology - ESEB 2022. Prague, Czech Republic.

Oral and poster presentations (continued)

2021. Aug 31 — **Invited speaker: Genetic history of the rice blast fungus**
Workshop: The reconstruction of human history through an interdisciplinary approach. University of Zurich. Zurich, Switzerland.

2020. Nov 06 — **Oral presentation: Population history of rice-infecting pathogen *Magnaporthe oryzae***
UCL Genetics Institute Seminar. London, UK.

2019. Jun 21 – 25 — **Poster presentation: Population history of rice-infecting *Magnaporthe oryzae* populations**
Evolution 2019. American Society of Naturalists; Society for the Study of Evolution; Society of Systematic Biologists. Providence (RI), USA.

2018. Aug 19 – 22 — **Poster presentation: Estimating methylation levels in historic plant specimens**
Evolution 2018. European Society for Evolutionary Biology; American Society of Naturalists; Society for the Study of Evolution; Society of Systematic Biologists. Montpellier, France.

2016. Nov 04 — **Oral presentation: Detecting Methylation in Ancient Plant Genomes**
Meeting StEvE 2016. Evolution and Ecology Research School Tuebingen. University of Tuebingen. Tuebingen, Germany.

Research Publications

Latorre, S.M; Were, V.M; Foster, A.J; Langner, T; Malmgren, A; Harant, A; Asuke, S; Reyes-Avila, S; Gupta, D.R; Jensen, C; Ma, W; Mahmud, N.U; Mehebub, Md.S; Mulenga, R.M; Muzahid, A.N.Md; Paul, S.K; Rabby, S.M.F; Raha, A.A.M; Ryder, L; Shrestha, R; Sichilima, S; Soanes, D.M; Singh, P.K; Bentley, A.R; Saunders, D.G.O; Tosa, Y; Croll, D; Lamour, K.H; Islam, T; Tembo, B; Win, J; Talbot, N.J; Burbano, H.A; Kamoun, S. (2023). **Genomic surveillance uncovers a pandemic clonal lineage of the wheat blast fungus.** ***PLOS Biol***. https://doi.org/10.1371/journal.pbio.3002052

Kreiner, J; **Latorre, S.M**; Burbano, H.A; Stinchcombe, J.R; Otto, S.P; Weigel, D; Wright, S.I. (2022). **Rapid weed adaptation and range expansion in response to agriculture over the past two centuries.** ***Science***. https://doi.org/10.1126/science.abo7293

Latorre, S.M; Langner, T; Malmgren, A; Win, J; Kamoun, S; Burbano, H.A. (2022). **SNP calling parameters have minimal impact on population structure and divergence time estimates for the rice blast fungus.** ***bioRxiv***. https://doi.org/10.1101/2022.03.06.482794

Lang, PLM; Erberich, J.M; Lopez, L; Weiß, C.L; Amador, G; Fung, H.F; **Latorre, S.M**; Lasky, J.R; Burbano, H.A; Expósito-Alonso, M; Bergmann, D. (2022). **Century-long timelines of herbarium genomes predict plant stomatal response to climate change.** ***bioRxiv***. https://doi.org/10.1101/2022.10.23.513440

Latorre, S.M; Burbano, H.A. (2021). **The emergence of wheat blast in Zambia and Bangladesh was caused by the same genetic lineage of *Magnaporthe oryzae*.** ***Zenodo***. https://doi.org/10.5281/zenodo.4605959

Langner, T; Harant, A; Gomez-Luciano, L.B; Shrestha, R.K; Malmgren, A; **Latorre, S.M**; Burbano, H.A; Win, J; Kamoun, S. (2021). **Genomic rearrangements generate hypervariable mini-chromosomes in host-specific isolates of the blast fungus.** ***PLoS Genetics***. https://doi.org/10.1371/journal.pgen.1009386

Shirsekar, G; Devos, J; **Latorre, S.M**; Blaha, A; Queiroz-Dias, M; González-Hernando, A; Lundberg, D.S; Burbano, H.A; Fenster, C.B; Weigel, D. (2021). **Multiple Sources of Introduction of North American *Arabidopsis thaliana* from across Eurasia.** ***Molecular Biology and Evolution***. https://doi.org/10.1093/molbev/

Win, J; Harant, A; Malmgren, A; Langner, T; Shrestha, R; **Latorre, S.M**; Were, V; Talbot, N.J; Burbano, H.A; Picco, A.M; Kamoun, S. (2020). **Large scale genome assemblies of *Magnaporthe oryzae* rice isolates from Italy.** ***Zenodo***. https://doi.org/10.5281/zenodo.4326823

Latorre, S. M; Lang, P.L; Burbano, H.A; Gutaker, R.M. (2020). **Isolation and analyses of DNA from historical and ancient plant tissues.** ***Current Protocols in Plant Biology***. https://doi.org/10.1002/cppb.20121

Lang, P.L; Weiß, C.L; Kersten, S; **Latorre, S. M**; Nagel, S; Nickel, B; Meyer, M; Burbano, H.A. (2020). **Hybridization ddRAD-sequencing for population genomics of nonmodel plants using highly degraded historical specimen DNA.** ***Molecular Ecology Resources***. https://doi.org/10.1111/1755-0998.13168

Latorre, S.M; Reyes-Avila, C.S; Malmgren, A; Win, J; Kamoun, S; Burbano, H.A. (2020). **Differential loss of effector genes in three recently expanded pandemic clonal lineages of the rice blast fungus.** ***BMC Biology***. https://doi.org/10.1186/s12915-020-00818-z

Latorre, S.M; Herrmann, M; Paulsen, M; Rödelsperger, C; Dréau, A; Röseler, W; Sommer, R.J; Burbano, H.A. (2020). **Museum phylogenomics of extinct *Oryctes* beetles from the Mascarene Islands.** ***bioRxiv***. https://doi.org/10.1101/2020.02.19.954339

Alonso, D.L; **Latorre, S.M.**; Castillo, E; Brandão, P.F. (2014). **Environmental occurrence of arsenic in Colombia: A review.** ***Environmental pollution***. https://doi.org/10.1016/j.envpol.2013.12.009

References

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