

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*
- 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*, *Dropy*, *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; Meheub, 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. (2022). **A pandemic clonal lineage of the wheat blast fungus.** *bioRxiv*. <https://doi.org/10.1101/2022.06.06.494979>

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/msab268>

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; Rödelberger, 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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