

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; Evolutionary Biology; Ancient DNA; Pathogens and host plant interactions*

Jan 2024 – Present 📌 **Selection Committee for the "GGLatAm2024" initiative. Get Genome Genomics for all. UK**

Education

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>

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**

Skills

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 and design of bayesian and frequentist statistics in the context of genomic and evolutionary analyses.
- Use of dimensionality reduction and machine learning methods to understand and extract relevant features from complex genomic datasets.
- Use of combined genomic datasets from contemporary, historical and ancient samples for different evolutionary analyses.

Computational 📌

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

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.

Awards

- 2023
- **Innovation & Impact Awards 2023**
Winner: Improving global crop disease diagnosis to reduce economic loss and improve food security. University of East Anglia, UK.

Teaching experience and supervision

- Jan 2024 – Present
- **Course: Methods in Ecology and Evolution 23/24.** Design and delivering lectures as well as marking, University College London.
 - **Methods for phylogenetic analyses in bacterial populations.** Supervision and training PhD student Jiajun Cui, University College London.
- Sep 2022 – Sep 2023
- **Course: Methods in Ecology and Evolution 22/23.** Assistance leading computational workshops with students, University College London.
 - **Course: Plant Ecology and Evolution 22/23.** Assistance leading journal club discussions with students attending the course, 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
- **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.

Complementary education and experience

- Apr 21 – 27 2018
- **Population Genomics: background and tools.** Sponsored by ELIXIR Italy Training. Naples, Italy.
- Mar 2018
- **Plants and associated microbiota field sample and documentation.** Pathodopsis project. Central Spain.
- Sep – Oct 2017
- **Herbaria sampling and documentation.** Staatliches Museum für Naturkunde, Stuttgart and University of Tuebingen, Germany.
- Oct 17 – 19 2016
- **Population genomic data analysis.** Sponsored by Adaptomics SPP1529. Hohenheim, Germany.

Peer-reviewed publications

11. Barragan, A.C*; **Latorre, S.M***; Malmgren, A; Harant, A; Win, J; Sugihara, Y; Burbano, H.A; Kamoun, S; Langner, T. (2024). Multiple Horizontal Mini-chromosome Transfers Drive Genome Evolution of Clonal Blast Fungus Lineages. *Molecular Biology and Evolution*. <https://doi.org/10.1093/molbev/msae164> ***Contributed equally**
10. 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. (2024). Century-long timelines of herbarium genomes predict plant stomatal response to climate change. *Nature Ecology & Evolution*. <https://doi.org/10.1038/s41559-024-02481-x>
9. **Latorre, S.M**; Were, V.M; Foster, A.J; Langner, T; et al; 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 Biology*. <https://doi.org/10.1371/journal.pbio.3002052>
8. Backman, T; **Latorre, S.M**; Symeonidi, E; Muszyński, A; Bleak, E; Eads, L; Martinez-koury, P.I; Som, S; Hawks, A; Gloss, A.D; Belnap, D.M; Manuel A.M; Deutschbauer, A.M; Bergelson, J; Azadi, P; Burbano, H.A; Karasov, T. (2022). A phage tail-like bacteriocin suppresses competitors in metapopulations of pathogenic bacteria. *Science*. <https://doi.org/10.1126/science.ado0713>
7. 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>
6. 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>
5. 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 *Ara-bidopsis thaliana* from across Eurasia. *Molecular Biology and Evolution*. <https://doi.org/10.1093/molbev/msab268>
4. **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>
3. 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>
2. **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>
1. 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>

Preprints

4. **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>
3. Barragan, A.C; **Latorre, S.M**; Mock, P.G; Harant, A; Win, J; Malmgren, A; Burbano, H.A; Kamoun, S; Langner, T. (2022). Wild grass isolates of *Magnaporthe* (Syn. *Pyricularia*) spp. from Germany can cause blast disease on cereal crops. *bioRxiv*. <https://doi.org/10.1101/2022.08.29.505667>
2. 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>

Preprints (continued)

1. **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>