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**

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.

Oct 2002 – Present **Methods for phylogenetic analyses in bacterial populations.** Supervision and training Master 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.

Complementary education and experience (continued)

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.

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.

Peer-reviewed publications

8. **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

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 *Arabidopsis 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

7. 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. ***bioRxiv***. https://doi.org/10.1101/2024.02.13.580079 ***Contributed equally***

6. Backman, N; **Latorre, S.M**; Eads, L; Som, S; Belnap, D; Manuel A.M; Burbano, H.A; Karasov, T. (2022). A weaponized phage suppresses competitors in historical and modern metapopulations of pathogenic bacteria. ***bioRxiv***. https://doi.org/10.1101/2023.04.17.536465

Preprints (continued)

5. **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

4. 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

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

1. **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