

# PAULA RUIZ RODRÍGUEZ

## PERSONAL DATA

Date of Birth: 1997-10-22

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## CURRENT INSTITUTION

**2020-Present** | Research support technician at Pathogenomics group at the Institute for Integrative Systems Biology (I2SysBio) led by researcher Dra. Mireia Coscollá Devís. Bioinformatic and evolutionary analysis of *Mycobacterium tuberculosis* pathogenesis. Bioinformatic and evolutionary analysis of SARS-CoV-2 genomic sequences.

## EDUCATION

**2015-2019** | University of Valencia, Bachelor's in Biology (Valencia, Spain)

**2019-Present** | University of Valencia, Master's Degree in Bioinformatics (Valencia, Spain)

**Languages:** Spanish, English, Catalan

## RESEARCH EXPERIENCE

**2020-Present** | Collaboration in the SeqCOVID consortium led by researchers Dr. Iñaki Comas Espadas, Dra. Mireia Coscollá Devís and Dr. Fernando González-Candelas. <https://seqcovid.csic.es/>. Bioinformatic and evolutionary analysis of SARS-CoV-2 genomic sequences. SARS-CoV-2 diversity analysis. Phylogenetic reconstructions of SARS-CoV-2.

**2018-Present** | Collaboration in the Pathogenomics group at the Institute for Integrative Systems Biology (I2SysBio) led by researcher Dra. Mireia Coscollá Devís. <https://www.uv.es/pathogenomic>. Final Project of Bachelor's in Biology: Antigenic Variation in *Mycobacterium tuberculosis*. Score: 9.4/10. Bioinformatic and evolutionary analysis of genomic sequences of epitopes in *Mycobacterium tuberculosis*.

**2016-2017** | Collaboration in the EpiMol group at Joint Research Unit «Infección y Salud Pública» FISABIO-Universitat de València and the Institute for Integrative Systems Biology, I2SysBio (CSIC-UV) led by researcher Dr. Fernando González-Candelas. <http://epimol.uv.es/>. Bioinformatic analysis of viral sequences of HIV.

## AWARDS & HONORS

**2020-02-03** | Honorable mention in the 15th edition of the Ciutat d'Algemesi Scientific-Technical Award: Antigenic Variation in *Mycobacterium tuberculosis* (Valencia, Spain).

**2016-05-17** | MOTIVEM 3rd Edition: Awards for the Motivation of Entrepreneurship in the Classroom. Extremofilm Project. Project to curb car pollutant emissions by bacterial filters (University of Valencia Awards, Valencia, Spain).

## PUBLICATIONS

Coscollá, M., Gagneux, S., Menardo, F., Loiseau, C., **Ruiz-Rodriguez, P.**, Borrell, S., Otchere, I. D., Asante-Poku, A., Asare, P., Sánchez-Busó, L., Gehre, F., Sanoussi, C. N., Antonio, M., Affolabi, D., Fyfe, J., Beckert, P., Niemann, S., Alabi, A. S., Grobusch, M. P., ... Brites, D. (2021). *Phylogenomics of Mycobacterium africanum reveals a new lineage and a complex evolutionary history*. *Microbial Genomics*, 7(2). <https://doi.org/10.1099/mgen.0.000477>

**Ruiz-Rodriguez, P.** et al. (2021). *Evolutionary and phenotypic characterization of spike mutations in a new SARS-CoV-2 Lineage reveals two Variants of Interest*. Preprint at MedRxiv Cold Spring Harbor Laboratory. <https://doi.org/10.1101/2021.03.08.21253075>

López, M. G., Chiner-Oms, Á., de Viedma, D. G., **Ruiz-Rodriguez, P.**, ... Coscollá M., González-Candelas, F. Comas, I. (2020). *The first wave of the Spanish COVID-19 epidemic was associated with early introductions and fast spread of a dominating genetic variant*. Preprint at MedRxiv Cold Spring Harbor Laboratory. <https://doi.org/10.1101/2020.12.21.20248328>

Alm, E., Broberg, E. K., Connor, T., Hodcroft, E. B., Komissarov, A. B., Maurer-Stroh, S., Melidou, A., Neher, R. A., O'Toole, Á., & Pereyaslov, D. (2020). *Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020*. *Eurosurveillance*, 25(32). <https://doi.org/10.2807/1560-7917.es.2020.25.32.2001410>

Hodcroft, E. B., Zuber, M., Nadeau, S., Vaughan, T. G., Crawford, K. H. D., Althaus, C. L., Reichmuth, M. L., Bowen, J. E., Walls, A. C., Corti, D., Bloom, J. D., Veesler, D., Mateo, D., Hernando, A., Comas, I., González Candelas, F., Stadler, T., & Neher, R. A. (2020). *Emergence and spread of a SARS-CoV-2 variant through Europe in the summer of 2020*. Preprint at MedRxiv Cold Spring Harbor Laboratory. <https://doi.org/10.1101/2020.10.25.20219063>

## ORAL COMMUNICATIONS

**2021-04-13** | 2<sup>nd</sup> National Multidisciplinary Congress Covid-19. "Emergence of Adaptive Mutations of the Spike In SARS-CoV-2". Virtual Congress, Spain. **Paula Ruiz-Rodriguez** et al.

**2020-02-05** | VIII Congress of Biomedical Research. "Genetic variability of *Mycobacterium tuberculosis* antigens". University of Valencia (Valencia, Spain). **Paula Ruiz-Rodriguez** and Mireia Coscollá.

**2020-02-06** | VII Congress of the Spanish Society of Evolutionary Biology. "Phylogenomics and Antigenic Variation in *Mycobacterium tuberculosis*". Spanish Society of Evolutionary Biology (Seville, Spain). Mireia Coscollá and **Paula Ruiz-Rodriguez**.

## POSTER COMMUNICATIONS

**2019-10-05** | II Conference of investigating researchers of Fisabio Foundation. “Deciphering the immune system: Antigenic Variation in *Mycobacterium tuberculosis*”. Fisabio Foundation (Valencia, Spain). Mireia Coscollá and **Paula Ruiz-Rodriguez**.

**2019-09-19** | MycoPorto. “Antigenic Variation through genomic analysis in *Mycobacterium tuberculosis*”. MycoNET (Porto, Portugal). **Paula Ruiz-Rodriguez** and Mireia Coscollá.

**2019-04-23** | III National Congress for Young Researchers in Biomedicine. “Clinical case: Effectiveness in the diagnosis of antiphospholipid syndrome by line immunoassay”. CONBIOPREVAL (Valencia, Spain). **Paula Ruiz-Rodriguez**.

## INTERESTS

Genetics, Evolution, Next Generation Sequencing, Bioinformatics, Genetic Diversity, Microbiology, *Mycobacterium tuberculosis*, SARS-COV-2, Phylogenies, Immune System, Python, Programming.

## SKILLS ACQUIRED

Great skills acquired in the management of genomic sequences of microbial pathogens, advanced use of programming languages both in Python and R working with pipelines. Knowledge in bioinformatic analysis of RNA-seq and DNA chips using R. Experience in clusters (Prince Felipe and I2SysBio cluster) and Linux environments, activities that involve use of the queuing system. Experience in databases in SQL and NoSQL languages (MongoDB) based on the Java programming language, through knowledge of query statements and database creation, experience in MariaDB, Labkeyserver, MongoDB. Experience in evolutionary analysis such as the generation of alignments, phylogenetic reconstructions, selection analysis, diversity analysis, among others. Advanced knowledge in illustration programs such as Adobe Photoshop, Illustrator, Inkscape, applied in the production of scientific graphics and creation of scientific illustrations, both in raster and vector images. Experience and knowledge in 3D modeling with programs such as Autodesk Fusion, Blender, experience in laminating 3D models which translates into their preparation for 3D printing, and experience in 3D printing. Experience and knowledge in methodologies for management and execution of research projects using Agile and Slurm. Experience in production and scientific communication in pathogen genomics.

## MOTIVATION

My current research is focused on the world's two deadliest pathogens: *Mycobacterium tuberculosis* and SARS-COV-2. For the study of *M. tuberculosis*, my research has focused on the bioinformatic analysis of antigenic diversity, studying the nucleotide diversity of both T-cell and B-cell epitopes to decipher the differences between the different MTBC ecotypes. For the SARS-COV-2 study, my research is part of the SeqCOVID consortium where I perform diversity analysis in Spanish sequences both defining frequencies of mutations of interest and analyzing possible mutations of interest, as well as developing phylogenetic analysis of Spanish sequences. My interest in being part of this course resides in the importance and passion that I have developed for bioinformatics. I am currently studying in the second year of my master's degree in which the applications that the field of bioinformatics can offer to that of evolutionary biology are not fully developed, another field in which I am widely interested. Overall, I process great interest in phylogenetic analyses and everything that derives from them. This course could be very useful for the research that I carry out since for both research areas I have data that can be exploited, generating new knowledge, and completing the analyses carried out in both lines of research, reaching more complete and complex conclusions.