PhD. PALOMA PEREZ-BELLO GIL

Personal Information

I am a highly experienced plant genomics researcher specializing in bioinformatics and the analysis of any kind of NGS data. My expertise includes whole-genome sequencing (WGS), bisulfite sequencing (BS-seq), mRNA-seq, small RNA-seq, nanopore, ddRAD-seq and Duplex-seq. I have extensive experience working with various sequencing platforms, including Illumina, Nanopore and Ion Torrent.

I am particularly skilled in developing and implementing custom bioinformatics pipelines to analyze complex biological datasets. My ability to quickly learn and apply new techniques allows me to adapt to emerging sequencing technologies and analytical challenges.

I consider I have good interpersonal and communication skills, and I have demonstrated the ability to work independently, and as part of a team.

Education & training

- **Postdoctoral Researcher in University of Udine** 2022-2024

  As part of the LIFE Seedforce project (LIFE20 NAT/IT/001468), which aims to improve the conservation status of 29 endangered native plant species by assessing genetic diversity within and between populations analysing ddRAD seq data. https://lifeseedforce.eu/en/

- **Postdoctoral Researcher in Joint Research Centre of the European Commission (Ispra, Italy)** 2021-2022

  Development of an NGS-based system for double strand DNA sequencing of short regions of plant mutants in collaboration with the University of Udine and the Joint Research Centre of the European Commission, (ISPRA, Italy)

- **PhD Student in Molecular Biology at IGA Technology (Udine, Italy)** 2018-2023

  As part of the PhD program in Molecular Biology in SISSA (Scuola Internazionale Superiore di Studi Avanzati), (Trieste, Italy). “Dynamics of DNA methylation variation in the clonally propagated perennial tree *Populus nigra* cv. ‘italica’”

- **Postgraduate Diploma in Bioinformatics Analysis** 2017-2018

  Universidad Pablo de Olavide, (Seville, Spain) (750h)

- **MSc. Environmental, Industrial and Nutritional Biotechnology** 2016-2018

  Universidad Pablo de Olavide, (Seville, Spain). MSc thesis: “Horizontal method for the detection, enumeration, and serotyping of *Salmonella* in food; Transition to the reference standard UNE-EN ISO 6579-1:2017”

- **Internal student in Plant Biology and Ecology** 2014-2015

  Universidad de Sevilla, (Seville, Spain)

- **BSc. Biology** 2009-2015

  Universidad de Sevilla, (Seville, Spain) BSc. Thesis: “Study about the spatial distribution of Holm oak Lepidoptera larvae defoliators”

Job-related skills

- Expertise in bioinformatics analysis of data generated by NGS techniques, with experience in sequencing platforms such as Illumina, Nanopore, and Ion Torrent

- Proficient in analyzing large-scale biological datasets, including WGS, BS-seq, mRNA-seq, small RNA-seq, Nanopore sequencing, ddRAD-seq, and Duplex-seq

- Experienced in working within supercomputing environments, utilizing multiple processors and job scheduling systems

- Skilled in developing and executing bioinformatics pipelines using Bash, Perl, R, and AWK to solve complex biological problems

- Experienced in DNA and RNA extraction, as well as NGS library preparation

Experience

Co-supervisor BSc thesis “Analisi genetiche per la salvaguardia delle specie a rischio di estinzione all’interno del progetto seedforce” April 2023-Dec 2023

Early Stage Researcher as part of EPIDIVERSE. MSCA-ITN European Training Network at IGA Technology Services srl August 2018-2021

Epidiverse is a Marie Skłodowska-Curie Innovative Training Network aimed at the study of epigenetic variation in wild plant species. https://epidiverse.eu/

I developed my work as an Early-Stage Researcher (ESR) at the Institute of Applied Genomics (IGA-Technology), a company that offers wide range of sequencing and bioinformatics services for industry and academia. https://igatechnology.com. My experience as an ESR allowed me to acquire interdisciplinary skills not only in bioinformatics, but also in molecular biology and ecology.

Production and operations department manager September 2017-May 2018

Innoagral Laboratory. Hesperides Biotech Group. https://www.innoagral.com

Courses

Science Communication and Entrepreneurship 18-22 January 2021

Course focused on the development of transferable skills in the realm of science communication, industrial transition and entrepreneurship. University of Udine, (Udine, Italy)

Plant Ecological Epigenetics 10-13 May 2020

Virtual Black Forest Summer School on Plant Ecological Epigenetics

Plant phenotyping in Marburg University August 2019

Phenotyping of ecologically related properties in *Populus nigra* and relate them to epigenetic determinants. Marburg University, (Marburg, Germany)

Course of Bioinformatics for Epigenetic analysis **February-May 2019**

Course of Bioinformatics for Epigenetic analysis (30 hrs) from the Master program of Molecular Biotechnology. University of Udine, (Udine, Italy)

Bioinformatics for Genome and Epigenome Analysis **5-16 November 2018**

Training in bioinformatics analysis of whole-genome bisulfite sequencing (WGBS) data, including the detection of differentially methylated regions (DMRs). EcSeq, (Leipzig, Germany)

Epigenetics: on the top of genetics **4-7 September 2018**

Basic analysis of epigenetic data produced by NGS. IGA-Technology, (Udine, Italy)

Languages

- Spanish (Native)
- English (B2)
- Italian (B1)

Publications and Conferences

Introduction to Ecological Plant Epigenetics. Free online learning platform on ecological plant epigenetics. https://epidiverse.gitbook.io/project/-MfxkdBDZggX_vc_sG5l

Díez Rodríguez, B., Peña-Ponton, C., Pérez-Bello Gil, P., Bettea, J., Lena, L., Mackenbacha, T., Wullea, S., De Paoli, E., Koen, V., Heera, K., & Opgenoortha, L. (2022). An uncommon garden experiment: microenvironment has stronger influence on phenotypic variation than epigenetic memory in the clonal Lombardy poplar. BioRxiv

Peña-Ponton, C., Diez-Rodriguez, B., Perez-Bello, P., Becker, C., McIntyre, L. M., van der Putten, W. H., De Paoli, E., Heer, K., Opgenoorth, L., & Verhoeven, K. J. F. (2024). High-resolution methylome analysis uncovers stress-responsive genomic hotspots and drought-sensitive transposable element superfamilies in the clonal Lombardy poplar. Journal of Experimental Botany. https://doi.org/10.1093/jxb/erae262

Rodríguez, B. D., Galanti, D., Nunn, A., & Peña-ponton, C. (2022). Epigenetic variation in the Lombardy poplar along climatic gradients is independent of genetic structure and persists across clonal reproduction. BioRxiv, 11.
ddRAD sequencing of the Endangered Species *Primula palinuri* Petagna Reveals High Levels of Inter-Population Diversity. Scientific Reports (Already submitted and approved)

A duplex sequencing approach for high-sensitivity detection of genome-edited plants (Already submitted)

Talk in Epidiverse Conference 2021 in Seville, Spain. "An emerging relation between epimutations, gene body methylation and gene expression in a clonally propagated perennial tree".
https://www.youtube.com/watch?v=43VA9UbbNaA&t=124s&ab_channel=EpiDiverse

2nd Price Poster in CYBO Conference 2025 Genova, Italy.
https://conferenceyoungbotanists.com/cybo-2025/cybo-2025-prizes