

GONZALO VILLARINO PIZARRO

SCIENTIFIC CONSULTANT | PLANT BIOTECHNOLOGY | INTEGRATED DATA

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Aargau, Switzerland
Swiss, Chilean & American citizen

English & Spanish (native)
German (A1)

[GitHub ↗](#) | [ORCID ↗](#)
[Portfolio ↗](#)

PROFESSIONAL PROFILE

Plant biologist and scientific consultant with 15+ years connecting genomics, genome editing, phenotyping, experimental data, and reproducible R/Python to support R&D decisions.

CORE EXPERTISE

Plant biotechnology	Experimental strategy	Quantitative biology	Scientific integration
Genomics & genome editing Phenotyping & transcriptomics	Design, controls & validation Biological interpretation	R, Python & mixed-effects ML, QC & visualization	Cross-functional R&D Publications, patents & reporting

PROFESSIONAL EXPERIENCE

2025 - 2026 SENIOR SCIENTIST / DATA SCIENTIST - *Puregene AG, Switzerland*

- Initiated a cannabis genome-editing platform across breeding and laboratory teams.
- Developed reproducible R/Python workflows for experimental-data QC, modeling, visualization, and reporting.
- Applied statistical and machine-learning methods to complex experimental datasets across research teams.
- Translated evidence into practical R&D decisions while maintaining strict confidentiality.

2019 - 2024 RESEARCH SCIENTIST - *Salk Institute for Biological Studies, USA*

- Discovered WRKY47 as a regulator of root periderm development and became co-inventor on the finding.
- Led plant genomics, RNA-seq, genome-editing, imaging, and machine-learning phenotyping work.
- Collaborated with academic and industry partners to translate discoveries into applied biotechnology.
- Led PAT, a first-author high-throughput phenotyping study using automated microscopy and UNet++.

2016 - 2018 POSTDOCTORAL RESEARCHER - *Yale University, USA*

- Developed and optimized CRISPR/Cas9 protocols for plant genome editing and molecular validation.
- Studied epigenetics, histone modification, DNA replication, DNA repair, and genome stability.

2014 - 2016 NSF POSTDOCTORAL FELLOW - *North Carolina State University, USA*

- Engineered a FACS-based system for high-resolution, cell-type-specific transcriptomic profiling.
- Integrated molecular biology, imaging, bioinformatics, and developmental biology.

SELECTED SCIENTIFIC IMPACT

International patent application

Co-inventor, Compositions and Methods for Increasing Periderm in Plant Roots.
WO2023164515A2 (WIPO/PCT) ↗

First-author ML phenotyping paper

PAT: a quantitative, large-scale method for periderm measurement using deep-learning segmentation.
Plant Phenomics (2024) | DOI 10.34133/plantphenomics.0156 ↗

Cross-domain scientific work

Plant genomics, genome editing, phenotyping, experimental data, and reproducible computation.

EDUCATION

2008 - 2014	PH.D., PLANT SCIENCES- <i>Cornell University, Ithaca, NY, USA</i> Molecular biology genomics/transcriptomics Mattson Lab
2003 - 2007	B.S., PLANT SCIENCES- <i>Pontifical Catholic University of Valparaiso, Chile</i>

SELECTED PUBLICATIONS

[Complete record on Google Scholar ↗](#)

2026 JOURNAL OF CANNABIS RESEARCH ACCEPTED
Genome-Wide SNP Genotyping and Chemotype Profiling of Commercial Swiss CBD Hemp Flowers
Cannabis genomics SNP genotyping chemotype profiling Swiss CBD hemp
2024 PLANT PHENOMICS
PAT: A Quantitative and Large-Scale Screening Method for Periderm Measurements
Deep learning phenotyping automated microscopy Arabidopsis
2022 SCIENCE
The histone H3.1 variant regulates TONSOKU-mediated DNA repair during replication
Chromatin biology DNA replication genome stability
2021 THE PLANT CELL
H3.1K27me1 maintains transcriptional silencing and genome stability by preventing GCN5-mediated histone acetylation
Epigenetics chromatin transcriptional silencing
2019 DEVELOPMENT
miR167 limits anther growth to potentiate anther dehiscence
CRISPR/Cas9 reproductive development Arabidopsis
2016 PLANT PHYSIOLOGY
Transcriptomic Signature of the SHATTERPROOF2 Expression Domain Reveals the Meristematic Nature of Arabidopsis Gynoecial Medial Domain
RNA-seq FACS reproductive meristems
2016 NATURE PLANTS
Insight into the evolution of the Solanaceae from the parental genomes of Petunia hybrida
Comparative genomics Solanaceae evolution crop biology

SELECTED METHODS & CAPABILITIES

Plant biotechnology	CRISPR/Cas9, molecular validation, RNA-seq, GWAS-ready phenotypes, crop R&D
Experimental systems	Arabidopsis, Petunia, Solanaceae, crop species, controlled experiments, microscopy
Assay development	Tecan-based luciferase reporter assays, microplate readouts, qPCR, optimization
Quantitative analysis	R, Python, mixed-effects models, multivariate analysis, machine learning
Reproducible workflows	Data QC, version control, documented code, visualization, reporting
Scientific leadership	Cross-functional R&D, mentoring, publications, patents, external collaboration

SELECTED RECOGNITION

2024	Published international patent application, WO2023164515A2
2022	Promoted from Research Assistant III to Research Scientist, Salk Institute
2018	Faculty University Grants Program, San Diego State University