

Leen Nanchira Abraham

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PROFESSIONAL PROFILE

I am a computational biologist with a solid background in managing and analyzing large-scale multi-omics datasets, specializing in transforming complex data into actionable insights that support plant breeding and host–pathogen interaction research. I excel in interdisciplinary environments and recognized for my clear communication, collaborative approach, and enthusiasm for mentoring and problem-solving across diverse teams. As I continue to grow in the field of data science, I am eager to apply my expertise, contribute to innovative research, and help drive meaningful, data-informed solutions.

WORK EXPERIENCE

POST DOCTORAL RESEARCHER – Institute of plant sciences, University of Köln (2022 - present)

Project 1: Contribution of epigenetic regulation to complex trait heritability in plant populations

Modelling non-additive effects of epigenetic variation within and between population for genomic prediction using Bayesian regression models and machine learning.

- Designed and analyzed large-scale experiments integrating DNA methylation and RNA-seq data from ~800 *Arabidopsis lyrata* samples to quantify trait heritability using Bayesian regression models.
- Predicted fitness related traits from DNA methylation in the gene body using supervised (PCA) and unsupervised (gradient boosting classifier) learning approaches.
- Developed and applied a ML (Random forest) models to identify genomic and regulatory features predictive of genetic variance in plant populations.
- Built reproducible multi-omics data processing workflows using R, Python, and Bash to ensure data quality and analysis transparency.
- Implemented FAIR-compliant data management strategies to support reproducibility and data sharing in large-scale genomic studies.
- Published [peer-reviewed research papers](#) and presented findings at international conferences.

Project 2: Whole-Genome Assembly Using Long-Read Sequencing in Arabidopsis lyrata

Generated a chromosome-level genome assembly of *Arabidopsis lyrata* individuals using PacBio long-read sequencing. This work improved genome continuity and accuracy, providing a high-resolution reference for studying genetic and epigenetic variation in natural populations.

PHD RESEARCHER – Laboratory of evolutionary genetics, University of Neuchatel, switzerland (2017 to 2022)

Project: Genome-wide multi-omics analyses of gene regulation in a fungal pathogen population

Investigated the association of genetic variation in cis-regulatory elements on gene expression and epigenetic variation within a wheat fungal population using genome-wide association mapping (**eQTL mapping**).

- Developed and implemented computational pipelines for NGS data processing, variant calling, transcriptome and epigenome analysis, eQTL mapping, and GWAS.

- Designed research projects, overseeing experimental design, data generation (Illumina, RNA-seq, ChIP-seq), and downstream analysis to ensure high-quality, reproducible findings.
- Performed functional characterisation of identified eQTLs associated with host-pathogen interactions
- Applied advanced data visualization and statistical modeling to transform complex datasets into actionable insights for research and publication.

JUNIOR RESEARCH FELLOW – Institute of plant biology, ETH, ZURICH AND CTCRI INDIA (2014- 2017)

Project: Indo - Swiss Cassava Network Project on the development of mosaic virus resistant cassava in Indian farmer preferred cultivars

- Successfully managed highly collaborative projects between ETH Zurich and research institute in India, fostering strong international partnerships. (1 year research visit at ETH Zurich for transfer of technology to India)

TECHNICAL SKILLS

- Programming & Data Science: **Advanced proficiency in R bash and Python (NumPy, Pandas, Matplotlib, Scikit)** for data analysis
- Machine learning and statistical methods: **Random Forest, gradient boosting classifier ,logistic regression, and linear mixed models for genetic association studies**; trait heritability using **Bayesian regression models(stan)** of plant research and breeding applications.
- Cloud computing: **Proficient with High-Performance Computing (HPC)**, Linux environments, and job schedulers (**SLURM**); experienced in handling large-scale genomics datasets.
- Version Control: **Git/GitHub for code management** and collaborative development.
- NGS & Genomics: Analyzed large scale population level Whole Genome Sequencing (WGS), RNA-seq (STAR, DEseq2, HISAT2), Whole Genome Bisulfite Sequencing (WGBS) for variant calling (GATK), structural variant detection and genome assembly.
- Bioinformatics Pipeline Development: Design and automation of reproducible **workflows** using **Bash, Python,R and Snakemake**
- Quantitative Genetics & Genomic Analysis: **GWAS, eQTL mapping**
- Training & Support: **Mentoring students and colleagues** in bioinformatics tools and pipelines; troubleshooting workflows.
- Molecular Biology: Advanced proficiency in DNA/RNA extraction, NGS library prep (Illumina TruSeq), general molecular biology techniques.

SELECTED PUBLICATIONS ([Google Scholar link](#))

- **Abraham, L.N.**, Croll, D. Genome-wide expression QTL mapping reveals the highly dynamic regulatory landscape of a major wheat pathogen. 2023. BMC Biol 21, 263. <https://doi.org/10.1186/s12915-023-01763-3>
- **Abraham L.N.**, Oggenfuss U, Croll D. Population-level transposable element expression dynamics influence trait evolution in a fungal crop pathogen. 2024. mBio 15:e02840-23. <https://doi.org/10.1128/mbio.02840-23>

EDUCATION

- DOCTOR OF PHILOSOPHY (Ph.D.) IN BIOLOGICAL SCIENCES, 2022; University of Neuchâtel, Switzerland
- BACHELOR'S & MASTER OF SCIENCE IN BIOTECHNOLOGY 2024: Kerala Agricultural University, India

AWARDS

- Jean Georges Baer Prize, University of Neuchâtel – Awarded for PhD thesis (1000 CHF).
- Mobility Grant (2021), University of Neuchâtel – Funded a 6-month research stay at the University of Birmingham for the functional characterization of eQTL in pathogen populations (~55K CHF).

CONTRIBUTIONS TO INTERNATIONAL CONFERENCES

- Oral presentation in Asilomar fungal genetics conference-2022, California, US, entitled “Genetic and epigenetic variants underpinning within-species transcriptional polymorphism in a major fungal pathogen”
- Oral presentation in 15th European Conference on fungal genetics (ECFG 2020), Rome, entitled “Genome-wide expression analysis to map regulatory polymorphisms in a major fungal pathogen.”

ADDITIONAL INFORMATION

Languages: English (Fluent), German (B1-Middle level proficiency), Malayalam (Native)

Nationality: India

REFERENCES

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