

PERSONAL INFORMATION

1.1 Personal data

Abu Bakar Siddique

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Date of birth: 19th Oct 1985. Nationality: Bangladeshi. Family: Married and two children.

ResearcherID: R-1776-2018. ORCID: <https://orcid.org/0000-0002-3178-523X> . URL for website: <https://www.slu.se/en/profilepages/s/abu-siddique/>

1.2 Current employment

Bioinformatician (Bioinformatiker), from **2024-06-01**, Department of plant biology, SLU - Swedish University of Agricultural Sciences, Uppsala, Sweden.

1.3 Previous employments

- **Research Engineer** (Forskningsingenjör), from **2022-02-15** to **2024-05-31**, Department of plant biology, SLU - Swedish University of Agricultural Sciences, Uppsala, Sweden.
- **Senior research engineer** (Senior forskningsingenjör), from **2022-01-06** to **2022-02-15**, Department of Ecology and Environmental Sciences, Umeå University, Umeå, Sweden.
- **Post-doc** research fellow (Forskare), from **2020-01-06**, Department of Ecology and Environmental Sciences, Umeå University, Umeå, Sweden.
- **Post-doc** research fellow (Forskare), **2018-07-09** to **2019-10-31**, Dept of Virology, Institute Of Plant Molecular Biology, Biology Centre CAS, Ceske Budejovice, Czech Republic.
- **PhD-student** (Doktorand), **2013-12-01** to **2017-05-31**, Institute of Botany and Landscape Ecology, Ernst-Moritz-Arndt Universität (Greifswald University), Greifswald, Germany.
- **Research assistant** (Forskningsassistent), **2012-07-01** to **2012-09-30**, Department of Plant physiology, UPSC, Umeå University, Sweden.

Family leave approx. nine months after PhD studies (2017-2018).

EDUCATION

2.1 University degrees

- Dr. rer. nat. (**PhD**), Molecular Ecology, 2017, *Greifswald University*, Germany.
- **Master** of Science (Two Year) in Ecology, 2013, Umeå University, Sweden.
- **Master** of Science (One and half Year) in Plant Pathology, 2010, Sher-e-Bangla Agricultural University, Bangladesh.
- **Bachelor** of Science (Four Years) in Agricultural Sciences, 2008, Sher-e-Bangla Agricultural University, Bangladesh.

3. QUALIFICATIONS

3.1 Funding from research councils

- STSM (short scientific mission) in the COST Action FA1405, 2017. 3k SEK.
- Travel grant: 10 000 euro, 2014-2019.

3.2 Accomplishments

- **7** amplicon, **4** metagenomics & **8** RNASeq HTS data analysis and downstream analysis.

- Developed a cheap metabarcoding pipeline and efficient data analysis for fungal metabarcoding data (led by Dr. M. Unterseher).
- Mentored one PhD student, co-supervised two master's students, three undergrads and one exchange-graduate student, culminating in one publication.
- Received seven travel grants (about \$10,000 awarded), leading to attendance at seven international conferences.
- Selected for the Master program (Tuition Free) at Umeå University.
- Achieved experience in mycovirus identification, characterization, gene expression.
- Participated in planning seminars, programs, content; solicited, wrote the last minutes in (PREI Umea, Sweden).

4. FIELD OF RESEARCH

Metagenomics and Metabarcoding: Pattern and processes of leaf inhabiting mycobiome; plant-fungi-insect interaction; fungal metagenomics. **Environmental DNA:** biomonitoring through metagenomics. **Mycovirus:** Interactions between fungi and viruses in mixed infections and viral gene expression in fungi.

5. ADDITIONAL QUALIFICATIONS

5.1 Active participation in international conferences and workshops

Scientific Presentations

2018, COST Action FA1405 (annual meeting). St Julians, Valletta, Malta.

2016, DGFM (German Mycological Society) meeting. Bernried, Germany.

2015, Screening of endophyte functions and diversity. Budapest, Hungary.

Poster Presentations

2020, OIKOS. Nordic Oikos 2020, in Iceland (presented by Edvin Karlsson)

2019, COST FA 1405 final meeting. Thessaloniki, Greece.

2014, DGFM (German mycological society), Mettlach-Orscholz, Saarland, Germany.

2014, The 10th International Mycological Congress, Bangkok, Thailand (presented by Martin Unterseher).

2012, KBC days, UPSC, Umeå, Sweden.

Workshops

2020, Introduction to Python, NBIS, Sweden.

2020, Introduction HPC2N and Linux, Umeå University, Sweden.

2019, Presentation skill, Presentation skill for young scientists, Biology Centre, Ceske Budejovice, Czech Republic.

2017, Training School, Title: Ecological Network Analysis of multispecies interactions, organized by the department of biology and biotechnology, School of Agriculture, IPB, Braganca, Portugal.

2016, Academic writing, Graduate academy, Ernst Moritz Arndt University Greifswald, Germany.

2015, Fungal metabarcoding; Institute of Botany & Landscape Ecology, Ernst Moritz Arndt University Greifswald, Germany.

Conference (as a participant)

2021, Biodiversity Genomics 2021, Virtual conference.

2020, Biodiversity Genomics 2020, Virtual conference.

5.2 Reviewer

British Ecological Society (BES), PLOS One (Biology), Frontiers in microbiology

5.3. Societal Membership

Board Member - Umeå Postdoc Society: <https://umeapostdocsociety.se/orgaboard/>

5.4 Network

World: IMC (International Mycological Congress), Biodiversity Genomics.

European network: **COST Actions** FA1405 & FA1103, **DGFM** (German mycological society), IMS

5.5 Supervision

Teaching/Training:

PhD course:

- Analysis of High-Throughput Sequencing RNA-Seq Data (PhD course)
- Genome-wide predictions in breeding: genotype-phenotype associations and genomic selection (PhD course)
- Data handling and high-quality illustrations for publications (PhD course)

Lab courses, protocols, academic writing

Supervising: one PhD student in project works, three Master's students in their thesis (co-supervisor) & two bachelor students.

5.6 Language:

Fluent in **English**, basic in **Swedish** and German; native **Bengali**.

6 LABORATORY AND ANALYTICAL SKILLS

6.1 Wet lab:

- eDNA: Shotgun sequences, amplicons
- **Fungi:** Metabarcoding, cultivation, **Sanger sequencing, high-throughput sequencing** (Illumina), fungal Screening: **DNA** extraction, PCR, Illumina library preparation, Illumina sequencing (HTS) data analysis, gel-electrophoresis, image-J analysis, bioanalyzer, blue Pippin for extracting size-selective DNA amplicons, Nanodrop quantification (DNA), centrivup, vortex, heatblock, permanent fungal culturing.
Bacteria: Experienced with laboratory techniques including culturing, nucleic acid extraction, PCR and RT-PCR, gel electrophoresis, cloning, primer design, bacteria cell culture, and reagent preparation.
- **Virus:** Identification, characterization, gene expression: Virus isolation, dsRNA and total **RNA extraction**, RT-PCR, Real-time PCR, Plasmid ligation, Bacterial transformation, cloning, Screening, molecular identification, Phylogeny, protoplast infection, fungal inoculation, gene expression.
- **Others:** Sample collection from the field, designing the experiment, spectrophotometry, duallex measurement (chlorophyll, flavonoid and nitrogen content estimation of the leaf), disease management by biological control agent.

6.2 Dry lab:

- **Bioinformatics:** **a)** expert bioinformatician in metagenomics (metabarcoding, shotgun, longreads), RNASeq HTS data analysis, metatranscriptomics **b)** expert in DADA2 & QIIME pipeline for amplicon sequence analysis **c)** expert in handling NGS data (Shotgun eDNA, amplicons ITS & 16S), **c)** experienced in mapping (bwa, HISAT2, bbmap) and post-filtering, **d)** experienced in Kraken2 DB building & classification, **e)** expert BLAST search and identification, **e)** FunGuild functional classification
- **Phylogeny:** MEGA, MAFFT, MrBayes, RAxML,
- **Raw data submission:** in SRA, ENA repository, Zonodo repository.
- **Analytical language:** **Bash, Python:** Bioinformatics, **R:** CRAN packages, VEGAN techniques
- **Workflow manager:** Nextflow, snakemake,
- **Programming:** **R:** **Qurato**, mar presentation, shiny.
- **R, RStudio & statistics:** Data analysis with base R & Tidyverse (vectorization, data uploading, tidying and wrangling, ggplot), Multivariate data analysis, GLM, GMM, GAM, PERMANOVA, ANOVA, t-test, chi-squared test, Ecological network analysis, Bipartite analysis, alpha & beta diversity analysis, taxonomy, JMP statistics.
- **Version control:** git and github
- **Computer cluster** (virtual machines): 5 years experienced of NAISS, PDC-Dardel, UPPMAX, HPC2N.
- **Microsoft packages:** Office, Excel, PowerPoint, Outlook, OneDrive, OneNote. GIMP image editor.

6.3 Related Experience:

- Collecting and processing large-scale scientific data, including experience with the **Linux/UNIX environment, conda environment, aptainer, command lines, shell scripting, slurm and high-performance computing.**
- applying statistical and mathematical methods to biological problems
- Experience in **Python, R, or similar programming languages**
- Experience in **genome-wide genotype data** and/or next-generation sequencing data
- Capacity for coordinating and supporting effective teamwork
- Proven track record showing continuous scientific productivity in peer-reviewed journals
- Independent thinking and analytical aptitude for devising innovative scientific or technical solutions
- Experience in experimental design and planning of experiments
- Experience in handling multi-omics data

7. PUBLICATIONS

7.1 Peer-Reviewed Publications

1. **Siddique AB**, Biella P, Unterseher M, Albrechtsen BR. **2021**. Mycobiomes of Young Beech Trees Are Distinguished by Organ Rather Than by Habitat, and Community Analyses Suggest Competitive Interactions Among Twig Fungi. *Front Microbiol*, 12.
2. **Siddique AB**. **2020**. Viruses of endophytic and pathogenic forest fungi. *Virus Genes*. <https://doi.org/10.1007/s11262-020-01763-3>

3. Karel P, **Siddique AB**. 2019. Mycoparasitic and opportunistic fungus is inhabited by a mycovirus. Archive of Virology. <https://doi.org/10.1007/s00705-019-04359-x>
4. Albrechtsen BR, **Siddique AB**, Decker VH, Unterseher M, Robinson KM. 2018. Both plant genotype and herbivory shape aspen endophyte communities. Oecologia. Mar 1:1-11. <https://doi.org/10.1007/s00442-018-4097-3>
5. Unterseher M, Karunarathna SC, Cruz GR...., **Siddique AB**,.... et al. 2018. Mycobiomes of sympatric *Amorphophallus albopathus* (Araceae) and *Camellia sinensis* (Theaceae) – a case study reveals clear tissue preferences and differences in diversity and composition. Mycol Progress. <https://doi.org/10.1007/s11557-018-1375-8>.
6. **Siddique AB**, Khokon AM & Unterseher M. 2017. What do we learn from cultures in the omics age? High-throughput sequencing and cultivation of leaf-inhabiting endophytes from beech (*Fagus sylvatica* L.) revealed complementary community composition but similar correlations with local habitat conditions. MycoKeys 20: 1-16. <https://doi.org/10.3897/mycokeys.20.112655>
7. **Siddique AB** & Unterseher M. 2016. A cost-effective and efficient strategy for Illumina sequencing of fungal communities: A case study of beech endophytes identified elevation as main explanatory factor for diversity and community composition. Fungal Ecology, 20, 175-185. <https://doi.org/10.1016/j.funeco.2015.12.009>
8. Unterseher M, **Siddique AB**, Brachmann A, & Peršoh D. 2016. Diversity and composition of the leaf mycobiome of beech (*Fagus sylvatica*) are affected by local habitat conditions and leaf biochemistry. PloS One, 11(4), e0152878. <https://doi.org/10.1371/journal.pone.0152878>

7.2 Manuscript in Review

- Nasif SO, Siddique AB, Islam MM, Hassan O, Deepo DM, **Siddique AB***. The role of fungal endophytes in sustainable agriculture: potential growth promoters, inhibitors, biofertilizers, growth regulators, biocontrol agents, stress alleviators and bioremediators. **CROP Protection (submit 01-05-2021)**.
- Md Mazharul Islam^{1†}, Deen Mohammad Deepo^{1†}, Saifullah Omar Nasif^{2†}, Abu Bakar Siddique^{3†}, Md Abu Bakar Siddique⁴, Oliul Hassan⁵, **Abu Bakar Siddique⁶** and Ki-Byung Lim^{1*}. Polyploidization: An Overview of Breeding Roles, Cytogenetics, and Crop Interactions. **Euphytica (submission 30-03-2021)**.

7.3 Manuscript in Preparation

- Unterseher M, **Siddique AB** et al. The phyllosphere mycobiome of European beech (*Fagus sylvatica*) show strong seasonal turnover, which differs between introduced and naturally growing trees (manuscript under preparation).
- Edvin Karlsson^{1,2*}, Alexis Sullivan³, Daniel Svensson⁴, Daniel Bellieny³, **Abu Bakar Siddique³**, Jose Antonio Villegas³, Anna-Mia Johansson¹, Håkan Grahn², David Sundell², Björn Brindefalk⁶, Anita Norman⁵, Andreas Sjödin², Navinder J Singh⁵, Tomas Brodin⁵, Mats Forsman² and Per Stenberg^{2,3*} Airborne eDNA captures the diversity and dynamics of a subarctic ecosystem across three decades.

7.4 Thesis and Short Projects

- 2017. PhD cumulative thesis: "Leaf-inhabiting mycobiomes under different environmental conditions – local habitat conditions, leaf biochemistry and seasonal variations drive fungal community dynamics". Supervisor: Dr. Martin Unterseher, PD, Institut für Botanik und Landschaftsökologie, Ernst-Moritz-Arndt Universität Greifswald, Greifswald, Germany. [Link](#).
- 2013. Master thesis: "The role of endophytic fungi in aspen leaves in the presence and absence of beetle damage". Supervisor: Benedicte Albrechtsen, Associate Professor, Department of Plant Physiology, Umeå University, Sweden. [Link](#).
- 2010. M Sc. Thesis: "Efficacy of *Trichoderma* and some botanicals in controlling leaf blight of mustard and disease variability of pathogen" Supervisor: Prof. Dr. Abu Bakar, Project Director, Pulse and Oil Seed Division in Bangladesh Agricultural Research Institute (BARI), Gajipur, Bangladesh
- 2011. Short project on 'Evolution of plant reproductive diversity: why and how selfing evolves from out crossing' Dept. of Ecology and environmental science, Umeå, Sweden.
- 2012. Course project entitled 'Molecular technique for endophytes identification in aspen' at UPSC, Umeå, Sweden.
- 2012. Short project on *Arabidopsis* transformation at UPSC, Umeå, Sweden.

- Conducted advanced data analyses primarily on meta'omic data (metagenomics, meta transcriptomics, transcriptomic data).
- Developed and share pipelines and workflows for advanced data analyses.
- Trained students and researchers in bioinformatics.
- Engaged in continuous development and improvement of the reproducibility.
- Assist with bioinformatic analyses for projects run at the University.
- Conducted own research, including application for external research funding.

QUALIFICATIONS

- Extensive experience (equivalent to 5+ years) with analysis of prokaryotic & eukaryotic metagenomic DNA data (e.g. identification, assembly, binning, mapping, annotation)
 - Experience with population genomic analyses (e.g. admixture, PCA, F-branch statistics).
- Merits.

Experience in workflow development with, for example, Nextflow or Snakemake

- Experience in using AI when performing bioinformatics tasks
- Experience in working with high-performance computer systems such as those provided by NAISS (naiss.se)
- Experience in teaching bioinformatics methods
- Experience in working with collaborative projects and code sharing (e.g. git and GitHub)
- Experience in combining genomic data with big data retrieved from large biodiversity/climate data repositories (e.g. GBIF) You are a person who plans, organizes and prioritizes your work in an effective manner.