

Mathu Malar C

Date of Birth: 25th December, 1989; Sex: Female
4, Raja S C Mullick Road, Jadavpur, Kolkata – 700032, West
Bengal, India.
+91-8444878357 (mobile);
mmadhubioinfo@gmail.com
<https://github.com/madhubioinfo>

Current Position:

Senior Research Fellow (PhD candidate) at Indian Institute of Chemical Biology Kolkata (IICB Kolkata) – Jadavpur, West Bengal, India.

PhD (Biological Sciences); Oct, 2013 - present

Expected time of completion: September 2018

Dissertation title: Development of efficient sequence assembly pipelines for high-throughput genome sequencing

Thesis Adviser: Dr. Sucheta Tripathy

(<https://sites.google.com/site/suchetalab/>)

Educational Background:

Bharathidasan University (BDU, Tamil Nadu) – Tiruchirapalli, Tamil Nadu, India.

-M.Sc (Bioinformatics); 2010 - 2012

[Cumulative GPA secured:7.41/10.0]

Acharya Arts and Science College, Pondicherry University – Pondicherry, UT, India.

-B.Sc (Bioinformatics); 2007 - 2010

Sacred Heart Convent Anglo Indian Higher Secondary School - Villupuram, Tamil Nadu, India (2007)

Awards and Competitive Fellowships:

Awarded **DST INSPIRE (AORC)** at 2013.

Awarded the **1st Rank** along with a First Class medallion in MSc. in Bharathidasan University.

DST-SERB travel award from Government of India for presenting the poster at **ECCB16** conference at Hague, Netherlands.

Travel award from **SCIGENOME** for presenting poster at NGBT16 Cochin, Kerala.

USDA NIFA travel award grant entitled "Meeting: 18th Annual Oomycete Molecular Genetics Meeting" at Shandong China.

Publications in Journals:

- Draft Genome Sequence of Filamentous Marine Cyanobacterium *Lyngbya confervoides* Strain BDU141951 **Chandrababunaidu MM**, Sen D, Tripathy S. Genome Announc. 2015March.
- Draft Genome Sequence of *Tolypothrix boutellei* Strain VB521301. Genome Announc. 2015 Feb **Chandrababunaidu MM**, Singh D, Sen D, Bhan S, Das S, Gupta A, Adhikary SP, Tripathy S.
- Tricking *Arthrrium malaysianum* into Producing Industrially Important Enzymes Under 2-Deoxy D-Glucose Treatment. Mukherjee S, **Chandrababunaidu MM**, Panda A, Khowala S, Tripathy S. Front Microbiol. 2016.
- EumicrobeDBLite: a lightweight genomic resource and analytic platform for draft oomycete genomes. Panda, A., Sen, D., Ghosh, A., Gupta, A., **Mathu Malar C.**, Prakash Mishra, G., Singh, D., Ye, W., Tyler, B. M. and Tripathy, S. Molecular plant pathology (2016).

- Characterization of phenotypic variation and genome aberrations observed among *Phytophthora ramorum* isolates from diverse hosts Marianne Elliott , Jennifer Yuzon , **Mathu Malar C** , Sucheta Tripathy , Mai Bui , Gary A. Chastagner , Katie Coats , David M. Rizzo , Matteo Garbelotto and Takao Kasuga BMC Genomics (2018)

Manuscripts in Review/Preparation:

- Tree pathogen *Phytophthora plurivora* has a compact ‘two speed’ genome (Ramesh Vettukuri*[†], Sucheta Tripathy*[†], **Mathu Malar C**[†] et al) [Joined First Author **Revision in Genome Biology and Evolution**]
- Genome plasticity in cultured *Leishmania donovani*: Comparison of early and late passages (Roma Sinha#, **Mathu Malar C**#, Raghwan Kumar# et al) [**Revision in Frontiers in Microbiology**] # Joint First Author
- Haplotype-phased genome assembly of virulent *Phytophthora ramorum* isolate facilitated by long-read sequencing uncovers genome plasticity (**Mathu Malar C**, Jennifer Yuzon et al) [**For submission in BMC Biology**] Joint First Author
- Hybrid Genome assembly of *P. ramorum* Pr102 using long reads and short reads (**Mathu Malar C**, Jennifer Yuzon et al) [**Manuscript in Preparation**] Joint First Author

Technical Skills:

Operating System: Windows, UNIX.

Programming Language: Shell scripting, R, Perl, Python (Beginner)

Genome assembly expertise, Genome analysis includes Comparative genomics, Visualization of Genomes, Transcriptomics, Differential Expression analysis, haplotype Phasing, variant calling, copy Number variant analysis.

Presentations at Conferences:

- Presented a poster entitled “Benchmarking the genome assembly of *Phytophthora ramorum* using third generation sequencing technology” at ECCB2016 Den Hague, Netherlands, 2016.
- Presented a talk entitled “Improving the genome assemblies of two strains of *Phytophthora ramorum*” in the 3rd international Symposium on “*Phytophthora*: Taxonomy, Genomics, Pathogenicity, Resistance and Disease Management”, Indian Institute of Horticultural Research, Bengaluru, 2015.
- Presented a talk and poster on “Efficient computational contamination removal approaches for improving prokaryotic genome assembly” at NGBT, 2016, Cochin, India.
- Presented a talk entitled “Diploid genome assembly works better when Pacbio long reads are supplemented with Illumina reads: *P. ramorum* assembly a case study” at OMGN18, Shandong Agricultural University, China, 2018.
- **Languages:**

English (proficient), Hindi and Tamil (both native).

List of Referees:

Dr. Sucheta Tripathy, Principal Scientist, Dept. of Structural Biology and Bioinformatics, Indian Institute of Chemical Biology, Kolkata, India. (tsucheta@gmail.com; tsucheta@iicb.res.in).

Dr. Nahid Ali, Senior Scientist, Dept. of Infectious Diseases, Indian Institute of Chemical Biology, Kolkata, India. (nali@iicb.res.in)

Dr. Takao Kasuga, Molecular Geneticist, Lecturer / Sr Lecturer, UC Davis, USA (tkasuga@gmail.com, tkasuga@ucdavis.edu)

Dr. Ramesh Vettukuri, Senior Researcher, Swedish University of Agricultural Sciences (SLU), Alnarp (Ramesh.vetukuri@slu.se)