POOJA SETHIYA

PhD Candidate, Faculty of Health Sciences, University of Macau
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RESEARCH INTEREST

Understanding strategies adopted by pathogens upon host-pathogen confrontation by genomics and bioinformatics approach.

RESEARCH EXPERIENCE

❖***PhD Candidate*** **University of Macau, Macau**
Supervisor**: Prof. Chris, Koon Ho Wong**

1. **Understanding transcriptional regulation in human pathogenic fungi**
   - Gene expression profile analysis (using public microarray data, in-house RNASeq, and RNA Pol II ChIPSeq data) to understand the adaptability of pathogenic fungi, *C. glabrata* to oxidative environment [**Github**].
   - Unveiling response of *C. glabrata* to prolonged stress conditions (RNASeq) and temporal transcription regulation mediated by Hsf1 (Hsf1 ChIPSeq and RNA Pol II ChIPSeq) in *C. albicans* under heat stress.
   - Integrated genomics approach to classify genes according to their transcript stability in *C. glabrata* upon macrophage infection.
   - Effect of antifungal drugs on the growth of pathogenic fungi (*C. glabrata* and *C. albicans*) under different environmental conditions.
   - Deciphering antisense transcription events from strand-specific RNASeq data in pathogenic fungi.

   Developed R-packages
   - **growkar:** An R-package to visualize and analyze growth curve data.
   - **fastaR:** An R-package for easy manipulation of fasta sequences useful in whole-genome analysis.

2. **Spore biology in filamentous fungi**
   - A computational framework was developed to analyze NGS data from multiple platforms (ChIPSeq- RNA Pol II, Histone marks, Transcription factors; RNASeq and Ribosome Profiling) to understand the molecular basis of spores in *A. nidulans*, *A. fumigatus,* and *T. marneffei*.

Developed R-package

- **FungalSporeAnalysis**: An R-package containing functions required for ChIPSeq data visualization and reproducibility of the fungal spore data analysis.

❖ ***Junior Research Fellow*** **National Chemical Laboratory, India**
Supervisor: **Dr. Narendra Kadoo**

1. **Whole-genome transcriptome analysis of agricultural crops**
   Aug 2014-Nov 2015
   - RNASeq analysis of grapes under hormonal stress conditions was performed using a genome-based alignment approach.
   - Transcriptional response of Chickpea in interaction with plant fungal pathogen *Fusarium oxysporum f.sp. cicer* was studied by *de novo* transcriptome analysis.
   - Non-coding RNA mediated regulation of gene expression was carried out in flax plant by identification of miRNA from small RNA library using tools like mirdeep2, small RNA workbench.
   - Assisted in analysis of fungal infected Chickpea transcriptome data obtained using SAGE library.

❖ ***Postgraduate dissertation*** **Bioinformatics Centre, University of Pune, India**
Supervisors:
1. **Dr. Narendra Kadoo,**
2. **Sanjay Londhe**

1. **Computational prediction of miRNA and its targets in plant pathogenic fungi**
   Dec 2013-Jun 2014
   - A prediction pipeline was developed to screen miRNAs and their targets from genomes of a large number of plant pathogenic fungi.
   - Understanding plant-pathogen interaction by microRNA-mediated trans-kingdom gene regulation in fungi and their host plants.

❖ ***Undergraduate dissertation*** **National Centre for Cell Science(NCCS), India**
Supervisor: **Dr. Yogesh Shouche**
Mentor: **Dr. Snehit Mhatre**

1. **Screening of heavy metal resistant bacterial isolates from alkaline lake ecosystem**
   Dec 2011-May 2012

- Soil and water samples from hypersaline meteorite crater lake, Lonar were screened by Minimum Inhibitory Count test (MIC) under heavy metal stress. Resistant isolates were characterized by 16S rRNA sequencing.

❖ ***Student's awardee (Pune Inter College Consortium)*** **NCCS, India**
Supervisor: **Dr. Yogesh Shouche**

1. **Phylogenetic analysis of gut microbiota, comparing diabetic and non-diabetic individuals.**
June 2010-Jan 2011
   - 16S rRNA based phylogenetic analysis was performed using stool samples to determine bacterial population dominance in diabetic and non-diabetic individuals.

EDUCATION

University of Macau **Macau, SAR**
Ph.D. (Biomedical Sciences) **May-2021**

University of Pune **Pune, India**
Master of Science (Bioinformatics) **2014**

University of Pune **Pune, India**
Bachelor of Science (Biotechnology) **2012**

PUBLICATIONS

1. **P Sethiya**, MN Rai, R Rai, C Parsania, K Tan and KH Wong, "Transcriptomic analysis reveals global and temporal transcription changes during *Candida glabrata* adaptation to an oxidative environment."*Fungal Biol.*, Dec. 2019.

2. J Yan, P Bhadra, A Li, **P Sethiya**, L Qin, HK Tai, KH Wong, SWI Siu, "Deep-AmPEP30: Improve Short Antimicrobial Peptides Prediction with Deep Learning." *Molecular Therapy-Nucleic Acids*, 2020.

3. F Wang, **P Sethiya**, K Tan, KH Wong, "Fungal spore experience before dormancy matters." (Manuscript in revision: Nature Microbiology)

4. C Parsania, **P Sethiya**, KH Wong, "**FungiExpresZ**: An R-shiny package to analyze and visualize fungal gene expression data." (Manuscript under preparation)

SKILLS

PROGRAMMING

- Currently using R and RMarkdown. I have experience of working with shell scripting and Perl.

R-PACKAGES

- For day-to-day programming, tidyverse packages and tidydata philosophy is been heavily used
  - **Bioconductor packages:**
    - GenomicRanges, IRanges, GenomicFeatures, Biostrings, rtracklayer, AnnotationHub, ComplexHeatmap, EnrichedHeatmap
  - **Core R-packages**
    - Base R, tidyverse (dplyr, tibble, tidyr, tidytext, rlang, purrr, readr, stringr, rlang, ggplot2, broom), Seqinr, UpSetR, usethis,
    - Package development: devtools, roxygen,
    - Isolated and reproducible environment: packrat, renv
  - **Documentation**
    - Rmarkdown, Knitr, kableExtra
  - **Reproducible Research by Rmarkdown**
    - FungalSporeAnalysis, CgOxidativeStress

VERSION CONTROL

- GitHub, GitKraken

DATABASE AND WEB DEVELOPMENT

- MySQL, PHP

OPERATING PLATFORMS

- Mac, Linux, proven experience of working on high-performance computing, Windows

SEQUENCING TECHNOLOGIES

- Proven experience in analyzing NGS data such as
  - RNASeq (by Tuxedo protocol, Trinity, DESeq2, htseq-count and Picard)
  - small RNA (by mirDeep2, small RNA workbench)
  - ChIPSeq (by MACS2, HOMER, deepTools)
  - Ribosome Profiling (by riboseqR, RiboProfiling)
  - Sanger sequencing data (by GeneMapper)

LABORATORY SKILLS

- DNA extraction, gel electrophoresis, Realtime-PCR, fungal transformation, monitoring fungal growth by MIC, MBC and growth curve assay, ChIP-sequencing, library preparation, and routine molecular biology techniques

OTHER SCIENTIFIC ACTIVITIES

- **Speaker** at **RNA-SIG'18** (Integrative RNA Biology track of **ISMB 2018** meeting), Chicago, IL, USA(July-2018)
- Presented poster in Macau Biomedical Sciences Symposium at the Faculty of Health Sciences, University of Macau, Macau SAR (Jun-2018, Jun-2019)
- Presented poster on Science day at the National Chemical Laboratory, NCL, Pune, India (Feb-2015)
- Online certification of courses offered by **Datacamp**
- Online certification of courses offered by **Coursera** (Computing for Data Analysis-87%, Bioinformatic Methods I-100%)
- **Summer intern:** Structural analysis of proteins (May-2013 offered by **Indian Institute of Technology Madras, India**) under the guidance of **Dr. Athi Nagnathan**

AWARDS AND CERTIFICATES

- **Teaching assistance** in designing and conducting **bioinformatics course** for undergrad students at the Faculty of Health Sciences, University of Macau, Macau (2016-2020)
- **Yatri** at **Jagriti Yatra**; a 15-day national odyssey journey, aimed to awaken the spirit of entrepreneurship (social and economic) among youths of India (2014)
- Qualified Graduate Aptitude Test in Engineering (**GATE**)-2014
- Awarded with **G.N Ramachandran Fellowship** (July-December 2012 and July 2013 – May 2014)
- Awarded with **DBT Fellowship** (Dept. of Biotechnology, Govt. of India) (January – June 2013)
- Received **postgraduate scholarship** from **Lila Poonawalla Foundation** (2012-2014)
- **Student's coordinator** for departmental fest (Chimera) at Fergusson College, Pune (2011)
- Selected in Pune Inter College Consortium (PICC) program, funded by the **J.N. TATA Scholarship** Trust (2010)
- International English Language Test System (**IELTS**), Band Score 7.0 (2012)
- Level-1 and Level-2, **German Language exam** at **Max Muller Bhavan(**MMB), Pune
- Keen interest in **photography**, **painting, and calligraphy**.