Faculty CV

Name

Vivek

Designation

Assistant Professor

Email

vivek22@uohyd.ac.in

Phone/mobile number

+91 40 2313 4720 (Off.)

Lab/Office room number

F75B (old BIF lab)

Profile photo (1 photo upto 10 MB)

profile_Vivek - vi...

Add File

Links of Personal webpage/Google scholar/LinkedIn etc.

Google scholar: https://scholar.google.com/citations?hl=en&user=RtCoXB4AAAAJ&sortby=pubdate
Personal webpage: https://sites.google.com/uohyd.ac.in/computational-genomics-lab

Broad areas of research (only keywords)

Gene discovery for plant dev. traits, Gut Microbiome for human health

Professional Experience

Assistant Professor, University of Hyderabad (Since July 2018)
Ramalingaswami Fellow, ICRISAT, Hyderabad (Jan 2017 - June 2018)
Research Associate/Guest faculty at JNU/Indraprastha University New Delhi (2016)
Postdoctoral Fellow in C4 Rice project at International Rice Research Institute (IRRI) (2010-2015)
Visiting Scientist, ICRISAT, Hyderabad (June 2008 - Dec 2009)

Education/Training

Ph.D. (Bioinformatics) at Jawaharlal Nehru University, New Delhi (2008)
Advanced PG Diploma in Bioinformatics at Jawaharlal Nehru University, New Delhi (2003)
M. Sc. in Medical Toxicology, Hamdard University, New Delhi (2002)
B. Sc. in Zoology, Delhi University, New Delhi (1999)

Detailed research interests (Upto 2 paragraphs or 10 bullet points)

Some of the research problems that my group is currently working on are below.

[1] Taxonomic/Functional characterization of gut microbiota for nutrition and diseases:
Behaviour of native gut microbiota in case of malnutrition has not been thoroughly investigated. So our hypothesis is whether altered abundance/composition of microbes contribute to the prevalence of deficiency of essential micronutrients? Several gut microbes may have metabolic capability for biosynthesis of some of the essential micronutrients, but they fail to do so due to lack of either one or a few genes. Such microbes can potentially be engineered or complemented in the form of pairs for in vivo or in vitro micronutrient production. Overall, through this project we want to make discoveries for exploiting gut microbes for addressing the prevalent deficiency of essential B-vitamins. This may also lead to the development of new probiotic formulations.

Members involved: Nisha Chandel (JRF, UoH), Priyansh Patel (JRF, ICMR-NIRTH), Dr Anil Verma & Dr Suyash Srivastave (Co-PIs, ICMR-NIRTH)
Funding: UoH-Institute of Eminence

[2] Trait discovery related to C4 anatomy/biochemistry
Driven by the challenge of food insecurity, some global projects are already underway to develop future crops by modifying the C3 photosynthetic pathway to C4 type, as the latter provides higher yield/biomass with reduced inputs. The major hurdle to these efforts has been incomplete knowledge of the genomic changes needed to operate the C4 pathway. Attempts based on gene expression studies limit only to the genes and thus miss the regulatory elements involved, and also provide list of genes too long to be implementable. In order to discover the missing genetic components as well as to address the limitations of current approach, I would like to take an alternate approach involving evolutionary insights and changes in transcriptome.

Members involved: Angeo Saji (Current), Manoj Kumar Chevella (Past)
Funding: DBT-Ramalingaswami grant

[3] Integration of omics data for knowledge mining of genes and genome annotation improvement: The availability of draft genomes of the majority of crops has boosted forward genetics research for various agroeconomic traits. However, such studies often lead to multiple candidate genes, and narrowing down to causal gene becomes a challenging task. The challenges increase when the candidates happen to be partially annotated or even without annotation. To address these challenges we have developed a one-stop web-application, namely KYCg, that not only provides functional details from as many sources, but also makes use of public transcriptome data to predict functional information of the uncharacterized ones.

Members involved: Gopikrishnan (current), Hitesh Thakur, Pulkit Srivastava and Prasad Gandham (Past)

[4] Genomics of Fe uptake/transport/storage
Members involved: Padhma Preiya

Selected publications (upto 5)

1. Gandham, P., Vadla, N., Saji, A., …, Thakur V. Genome assembly, comparative genomics, and identification of genes/pathways underlying plant growth-promoting traits of an actinobacterial strain, Amycolatopsis sp. (BCA-696). Sci Rep 14, 15934 (2024). https://doi.org/10.1038/s41598-024-66835-y
ISSN: 2045-2322 | IF: 4.4 | Citation:

2. Chandel N, Maile A, Shrivastava S, Verma AK, Thakur V. Establishment and perturbation of human gut microbiome: common trends and variations between Indian and global populations. Gut Microbiome. 2024;5:e8. https://doi.org/10.1017/gmb.2024.6 ISSN: 2632-2897 | IF: NA | Citation: 0

3. Chandel, N.,Gorremuchu, J.P., & Thakur, V. (2024). Antimicrobial resistance burden, and mechanisms of its emergence in gut microbiomes of Indian Population. Front. Microbiomes Sec. Omics Approaches Volume 3 - 2024 | https://doi.org/10.3389/frmbi.2024.1432646
ISSN: 2813-4338 | IF: NA | Citation: 0

4. Chandel N, Somvanshi PR, Thakur V. Characterisation of Indian gut microbiome for B-vitamin production and its comparison with Chinese cohort. British Journal of Nutrition. 2024;131(4):686-697. https://doi.org/10.1017/S0007114523002179 ISSN: 0007-1145 | IF: 3.6 | Citation: 4

5. Danila F, Thakur V, et al. “Bundle sheath suberisation is required for C4 photosynthesis in a Setaria viridis mutant" Communications Biology 4, 254 (2021) https://doi.org/10.1038/s42003-021-01772-4 ISSN: 2399-3642 | IF: 6.3 | Citation: 6

6. Rizal G*, Thakur V*, Dionora J*, Karki S, Wanchana S, Acebron K, Larazo N, Garcia R, Mabilangan A, Montecillo F, Danila F, Mogul R, Pablico P, Leung H, Langdale JA, Sheehy J, Kelly S, Quick, WP (2015) Two forward genetic screens for vein density mutants in sorghum converge on a cytochrome P450 gene in the brassinosteroid pathway. The Plant Journal 84(2):257. (Cover article) (*: equal author) IF: 6 | Citation: 23

Selected projects (upto 5)

1 Discovery of missing components of gene regulatory network underlying C4 pathway/anatomy translational research. DBT-Ramalingaswami scheme. 5 yrs (5/1/2017- 4/6/2022). 88 lakhs. PI. Ongoing

2 Evaluation of change in micronutrients content in rice grains with variation in rice yield, and prediction of genes/alleles involved in the underlying process. DST-CRG. 3 years. 99.5 lakhs. PI. Submitted.

3. Characterization of human gut microbiota for micronutrient production and exploring metabolic potential for its enhancement. UoH-IoE. 3 years (30/8/2021-29/8/2024). 39.5 lakhs. PI. Ongoing

4. “DBT-Centre for Microbial Informatics (CMI)”-BIC at University of Hyderabad. DBT. 5 years (29/9/2021-28/9/2026). 179.4 lakhs. Co-PI

5. Allele mining for the epigenetic regulator NGR5 and the yield associated genes (GID1 and GRF4) and their modulation using multiple genomic and molecular approaches to enhance rice yield under low nitrogen conditions. ICAR-NASF. 3 years (Aug 2022- July 2025). 147.8
Co-PI. Sanctioned

Selected patents (a paragraph or upto 5 bullet points)

None

Current PhD scholars and broad research topics

Name	Joined As	Area of research
Nisha Chandel	Ph.D. program	B-vitamin Biosynthetic potential of gut microbiome
Padhma Preiya	Ph.D. program	Gene regulatory network for Fe and Zinc level in plants
Angeo Saji	Ph.D. program	Regulators of development of dense vein patterning in C4