Curriculum Vitae

Dr. Medha L. Upasani
(Dr. Medha R. Dange)

Educational Qualification

- Ph.D. Biotechnology, Savitribai Phule Pune University, 2008-2017
- M.Sc. Microbiology, Savitribai Phule Pune University, 2006-2008
- B.Sc. Microbiology, Savitribai Phule Pune University, 2003-2006

Significant Achievements

- Qualified Graduate Aptitude Test in Engineering (GATE) in 2008 in Life Sciences with score 422, percentile 95.26 and all India Rank 623.
- Cleared national level examination (for PhD) for Indian Institute of Science, India (in 2008) and National Institute of Immunology, India (in 2008).
- Awarded Junior Research Fellowship and Lectureship through nationwide exam (NET) conducted by Council of scientific and Industrial Research (CSIR), India (Dec. 2007 and also Jun. 2008) to undertake Ph.D.
- First rank in University of Pune in B.Sc. Microbiology (2006, 86%) and M.Sc. Microbiology (2008, GPA-5.92/6).
- 14th rank in Nasik divisional board in HSC, 2002.

Teaching Experience: ~ 09 years

- **Assistant Professor (Consolidated), Department of Microbiology, MES Garware college, Pune (July 2018- April 2019):**
  Subjects taught include, theory and practicals in Basic techniques in Microbiology, Medical Microbiology at undergraduate level.

- **Assistant Professor (1 year post), Department of Microbiology, Savitribai Phule Pune University (September 2016- July 2017):**
  Conducted theory lectures in Molecular biology, Immunology, Bioinformatics and practicals in ecology at postgraduate level.

- **Assistant Professor (CHB), Department of Microbiology, MES Garware college, Pune (July 2016- September 2016):**
  Subjects taught include, theory and practicals in Basic techniques in Microbiology, Medical Microbiology and genetics at undergraduate level.

- **Assistant Professor (CHB), Department of Microbiology, H.V. Desai College, Pune (December 2014- April 2015):**
  Subjects taught include, theory and practicals in Basic techniques in Microbiology, Industrial Microbiology and genetics at undergraduate level.

- **Conducted Few Biology practicals in IISER, Pune in 2008.**

Research Experience

Research work during Ph.D. : 9 years [2008-2017]

Ph.D. Topic: Molecular characterization of chickpea-*Fusarium oxysporum* f. sp. *ciceri* interaction

Summary: Chickpea is an important source of dietary proteins, especially for the vegetarian population and is the most abundantly grown legume in India which contributes to 70% of the world production of this legume

crop (FAOSTAT, 2014). Fusarium wilt, caused by *Fusarium oxysporum* Schlenchtend.: Fr. f. sp *ciceris* (Foc) (Padwick) Matuo and Sato, is one of the most destructive diseases of chickpea throughout the world and a major limiting factor of chickpea productivity. Foc is a root pathogen, which causes blockage of xylem vessels upon infection, preventing the uptake of water from the soil finally resulting in severe wilt and death of plants. The present thesis work was planned to characterize the chickpea-Foc interaction at molecular level using approaches like Confocal Laser Scanning Microscopy, quantitative reverse transcription PCR and transcriptome profiling using LongSAGE.

1. Differential colonization of Foc in chickpea cultivars

Possible mechanism of invasion of Foc in wilt resistant and susceptible chickpea cultivars was studied using CLSM of eGFP-transformed Foc 2. The transformant D4 having the highest and uniform GFP fluorescence and virulence comparable to that of wild type was selected for studying the *in planta* pathogen progression. Attachment and germination of fungal spores on to epidermal cells within 3 dpi followed by fast penetration of root epidermis, cortex and xylem of the susceptible cultivar by 4 dpi. These processes were, however, impeded in the resistant cultivar. The transformed Foc 2 could be detected throughout the inspected plant parts during disease progression in susceptible inoculated cultivar (JGI), particularly with increasing fungal load. However, the pathogen could be seen only in root cortex region of inoculated resistant cultivar with very few mycelia escaping to vascular tissue. Quantification of fungal colonization in various tissues of the resistant and susceptible chickpea cultivars by qPCR uncovered four distinct phases of Foc proliferation in susceptible cultivar In phase 1 (0 hpi) high amount of fungal DNA was observed in both the cultivars, indicating adherence and germination of the fungal spores. Phase 2 (16 hpi-4 dpi) was marked by the decrease in the fungal DNA suggesting the degradation of a fraction of the hyphae due to autophagy. This could be attributed to the fact that, before the pathogen colonizes the plant to the extent that it can derive nutrients from the host, it undergoes intracellular degradation to supply nutrients to the non-assimilating fungal structures. Steep increase in fungal DNA was observed in phase 3 (4 dpi—14 dpi) indicating widespread colonization of the fungus in JGI compared to that in DVI. During this phase, JGI also showed the typical wilting symptoms like flaccidity of leaves, drooping of petioles etc. Lastly, the phase 4 (14 dpi—28 dpi) was marked by decrease in fungal DNA content in JGI. This indicated that the fungus proliferated massively in JGI till nutrients from the host were available (phase 3), resulting in high mycelial mass and pathogen DNA. After the nutrients from the host were exhausted (due to wilting), the pathogen switched to conidiation, leading to reduced mycelial mass and as a result, pathogen DNA. Alternatively in DVI, successful activation of defense responses early in the infection process (before phase 3) might have restricted the fungal proliferation throughout the course of infection.

2. Gene expression dynamics of chickpea and Foc during the interaction

Expression of chickpea defense related genes revealed differential response of the cultivars to Foc challenge. Expression of chitinase and glucanase intensified only in the late stages of disease in susceptible inoculated cultivar while these genes were steadily expressed right from the beginning in resistant inoculated cultivar suggesting clever programming of plant itself to oppose the pathogen establishment. While the expression of β-glucosidase, glucan endo β-1,3 glucosidase and glycosyltransferase elevated at initial stage of colonization are indicative of their role in defense against the pathogen. Similarly phenylalanine ammonia lyase, Chalcone synthase and isoflavone reductase, three key enzymes of phenylpropanoid pathway expressed very high in resistant inoculated cultivar. Interestingly, these genes expressed high in susceptible control plants compared to susceptible inoculated ones indicating the effect of Foc virulence in shutting down the defense gene expression in the cultivar. Several other genes like WRKY, chaperonin, Pathogenesis related proteins, metallothionein and NBS-LRR were observed to be expressed more in resistant inoculated cultivar highlighting their role in defense mechanism. Quantitative real time expression of Foc genes were assessed in both chickpea cultivars during the disease progression. Good concurrence was observed in the expression of genes with the pathogen proliferation phases obtained prior. Expression of genes involved in fungal morphogenesis, signaling, plant cell wall degradation in susceptible inoculated cultivar was in accordance with the colonization pattern. Many of these genes expressed least and at later stage of disease progression in resistant inoculated cultivar. The genes like chitin synthase, glucanosyltransferase, G protein β subunit and mitochondrial carrier protein, which play important role in fungal growth and morphogenesis, were expressed significantly during the initial colonization period, when the pathogen tried to establish in the host

environment. This was followed by the decrease in expression of these genes pertaining to autophagy phase. The last phase was again the rise in expression revealing successful invasion and further proliferation of pathogen in the susceptible host. This rise was significantly high in JGI compared to that in DVI as the pathogen could colonize to great extent only in JGI.

3. Transcriptomic outcome of chickpea-Foc interaction

Transcriptome analysis of chickpea-Foc interaction revealed several chickpea defense related genes and Foc virulence related genes with differential as well as unique expression in both the cultivars. The comparison of four LongSAGE libraries in the present study elucidated key factors involved in chickpea resistance mechanisms upon Foc inoculation. Mercator term assignment and protein-protein interaction network analysis revealed important biological processes like protein, hormone metabolism, signaling and biotic-abiotic stress that might be playing a role in successful defense in resistant chickpea cultivar. In addition, certain transcripts related to tetrapyrrol synthesis, aquaporins and actin depolymerization factor, observed to be up-regulated in susceptible cultivar upon Foc challenge, could be associated with susceptibility based on literature evidences. On the other hand, comparative analysis of transcriptomes of both cultivars challenged by Foc revealed a large number of Foc genes expressed only in JGI (533). Only five Foc genes (three of which were uncharacterized) were expressed only in DVI substantiating the strong defense strategy of the cultivar. Blast2GO analysis and comparison with PHI database revealed a complete Foc metabolism functional only in susceptible inoculated cultivar. All the differentially expressed genes of Foc were up-regulated in susceptible and down-regulated in resistant inoculated cultivar.

Publications

Papers in peer reviewed journals :

1. **Medha L. Upasani**, Gurjar GS, Kadoo NY, Gupta VS (2016) Dynamics of Colonization and Expression of Pathogenicity Related Genes in *Fusarium oxysporum* f.sp. *ciceris* during Chickpea Vascular Wilt Disease Progression. **PLoS ONE** 11(5): e0156490. doi:10.1371/journal.pone.0156490
2. **Medha L. Upasani,** Bhakti M Limaye, Gayatri S. Gurjar, Sunitha Manjari K, Rajendra R. Joshi, Narendra Y. Kadoo, Vidya S. Gupta1(2017) Chickpea-*Fusarium oxysporum* interaction transcriptome reveals differential modulation of plant defense strategies. (**Nature Scientific reports,** DOI:10.1038/s41598-017-07114-x)
3. **Medha L. Upasani**, Meenakshi B. Tellis, Gayatri S. Gurjar, Narendra Y. Kadoo (2017) Transcriptional Regulations in chickpea-*Fusarium* interaction. (Under Preparation)

Book Chapters :

4. Gurjar G, Mishra M, Kotkar H, **Medha L. Upasani**, Pradeep Kumar, Tamhane V, Kadoo N, Giri A and Gupta V (2009) Major biotic stresses of chickpea and strategies for their control. In: **Pests and Pathogens: Management Strategies**. Editors: - D.V. Reddy, P.N. Rao, K.V.Rao @ 2010 BS Publications ISBN: 978-81-7800-227-9.

Posters Presented in Conferences:

1. **Medha L. Upasani,** Bhakti M Limaye, Gayatri S. Gurjar, Sunitha Manjari K.,Rajendra R. Joshi, Narendra Y. Kadoo, Vidya S. Gupta. Chickpea-*Fusarium* interaction transcriptome reveals differential modulation of plant defense and fungal virulence strategies. 'Accelerating Biology 2017: Computing Life' organized by The Centre for Development of Advanced Computing(CDAC) at YASHADA, Pune in January 2017.
2. **Medha L. Upasani**, Gayatri S. Gurjar, Bhakti M. Limaye, Amit k Singh, Sunitha Manjari K, Dr. Rajendra R. Joshi, Dr. Vidya Gupta, Dr. Narendra Kadoo. Oral Presentation. Transcription dynamics of chickpea-Fusarium interaction explored using serial analysis of gene expression studies. 'Accelerating Biology 2014: Computing Life' organized by The Centre for Development of Advanced Computing(CDAC) at YASHADA, Pune in February 2014.
3. **Medha L. Upasani,** Dr. Narendra Kadoo, Dr. Vidya Gupta. Molecular analysis of chickpea-*Fusarium oxysporum* f.sp. *ciceris* interactions for improving chickpea productivity. Science Day organized by CSIR-National Chemical Laboratory, Pune on 26 Feb. 2013.
4. **ML Upasani,** SM Channale, Murugesan K, M Gupta, M Sarangdhar, NY Kadoo and VS Gupta. Analysis of Chickpea-*Fusarium* Interactions using Molecular Approaches. National Symposium on 'Molecular

Approaches for Management of Fungal Diseases of Crop Plants' organized by Indian Institute of Horticultural Research, Bangalore in December,2010.

5. **Medha Upasani,** Arun Kancharla, Narendra Kadoo, Vidya Gupta. Serial Analysis of Gene Expression-A molecular approach to analyze plant-pathogen interactions for improving chickpea productivity. Science Day organized by CSIR-National Chemical Laboratory, Pune on 26 Feb. 2010.

6. **M Upasani,** A Kancharla, N Kadoo and V Gupta. Best Student Poster Award. Serial Analysis of Gene Expression-A molecular approach to analyze plant-pathogen interactions for improving chickpea productivity. 50th Annual Conference of Association of Microbiologists of India, held at National Chemical Laboratory, Pune, India during December 15-18, 2009.

Extra-curricular Activities

- I am a fifth year student of Hindustani classical music and have scored distinctions in all four exams of Gandharva Mahavidyalaya, Pune, Maharashtra, India. I was one of the participants in an extra-ordinary classical music concert named 'Anternaad' held in January, 2010 in Pune by Shree Shree Ravi Shankar, founder of "The Art of Living". The event has been recorded in Guinness book of World Records.

- I have successfully completed two exams of Yoga from 'Bharatiya Yoga Vidya Dham', Nasik, Maharashtra, India and regularly practice the Pranayama and meditation early morning.

Personal Information

Name:	**:**	Medha Laxmikant Upasani (Medha Rahul Dange)
Gender	**:**	Female
Birth Date	**:**	30th March 1986
Marital Status	**:**	Married
Nationality	**:**	Indian
Languages known	**:**	English, Hindi, Marathi
Permanent Address	**:**	P2-18, Krishna kamal HSG, Pashan-sus road,Pune-411002, MH, India
Contact No	**:**	+91 9420690968/9860488395
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Strength	**:**	An achiever by nature, I have an ability to pursue things till my satisfaction and would like to benefit others through my knowledge.

Place: Pune
Date : 7th December 2018 **Dr. Medha R. Dange**