CURRICULUM VITAE

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4. CURRENT POSITION AND ADDRESS FOR COMMUNICATION:

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5. PREVIOUS EMPLOYMENT HISTORY:

Tenure	Institute/Organization	Position held
Jan., 2000 – Oct., 2005	Bose Institute, Kolkata, India	Research fellow
Dec., 2005 – May, 2008	US Environmental Protection Agency, Corvallis, Oregon, USA	National Research Council Postdoctoral Associate
June, 2008 – Sept., 2009	Virginia Polytechnic Institute and State University, Virginia USA	Postdoctoral Associate
Oct., 2009 – Sept., 2012	Helmholtz Zentrum Munchen, Germany	Alexander von Humboldt Fellow

6. LIST OF PUBLICATIONS:

6A. RESEARCH PAPERS

1. Das M and Pal A (2005)[a] *In vitro* regeneration of *Bambusa balcooa* Roxb.: factors affecting changes of morphogenetic competence in the axillary buds. **Plant Cell, Tissue and Organ Culture** 81: 109- 112. JIF: 1.243

2. Das M and Pal A (2005)[b] Clonal propagation and production of genetically uniform regenerants from axillary meristems of adult bamboo. **Journal of Plant Biochemistry and Biotechnology** 14: 185- 188 JIF: 0.323

3. Das M, Bhattacharya S and Pal A (2005) Generation and Characterization of SCARs by Cloning and Sequencing of RAPD Products: A Strategy for Species-Specific Marker Development in Bamboo. **Annals of Botany** 95(5): 835–841. JIF: 3.388

4. Bhattacharya S*, **Das M***, Bar R and Pal A (2006) Morphological and Molecular Characterization of *Bambusa tulda* with a Note on Flowering. **Annals of Botany** 98(3): 529-535 *equal contribution. JIF: 3.388

5. Das M, Bhattacharya S, Basak J and Pal A (2007) Phylogenetic relationships among the bamboo species as revealed by morphological characters and polymorphism analyses. **Biologia Plantarum** 51(4): 667-672. JIF: 1.656

6. Das M*, Bhattacharya S, Singh P, Filgueiras TS and Pal A (2008) Bamboo taxonomy and diversity in the era of molecular markers. **Advances in Botanical Research** 47: 225-268 *corresponding author. JIF: 1.333

7. Bhattacharya S, Ghosh JS, **Das M** and Pal A (2009) Morphological and molecular characterization of *Thamnocalamus spathiflorus* subsp. *spathiflorus* at population level. **Plant Systematics and Evolution** 282: 13-20. JIF: 1.41

8. Das M, Reichman JR, Haberer G, Welzl G, Aceituno FF, Mader MT, Watrud LS, Pfleeger TG, Gutiérrez R, Schäffner AR and Olszyk D (2010) A composite transcriptional signature differentiates responses towards closely related herbicides in *Arabidopsis thaliana* and *Brassica napus*. **Plant Molecular Biology** 72(4-5):545-56. JIF: 4.149

9. Wickett, NJ., Loren AH, Wafula EK, **Das M**, Huang K, Wu B, Timko MP., Yoder J, Westwood J and dePamphilis CW (2011) Expression of the chlorophyll synthesis pathway in a non-photosynthetic plant revealed by the transcriptomes of above ground structures from three parasitic plants from the family Orobanchaceae. **Current Biology** 21: 2098-2104. JIF: 10.025

10. Westwood JH, dePamphilis CW, **Das M**, Fernández-Aparicio M, Honaas LA, Timko MP, Wickett NJ and Yoder JI (2012) The Parasitic Plant Genome Project: New Tools for Understanding the Biology of *Orobanche* and *Striga*. **Weed Science** 60: 295-306 JIF: 1.528

11. Zhang Y, Fernandez-Aparicio M, Wafula E, **Das M**, Jiao Y, Wickett NJ, Honaas LA, Ralph PA, Wojciechowski MF, Timko MP, Yoder JI, Westwood JH, and dePamphilis CW (2013) A horizontally acquired legume gene, albumin 1, in the parasitic plant *Phelipanche aegyptiaca* and related species. **BMC Evolutionary Biology** 13: 48 JIF: 3.5

12. Das M, Haberer G, Schäffner AR (2013) Gene expression patterns can identify functional orthologs and modes of gene function evolution in plants. **Plant Physiology** (in preparation) JIF: 6.5

6B. POSTER PRESENTATIONS IN CONFERENCES

1. Pal A, **Das M,** Bhattacharya S and Basak J. Validation of DNA-based markers for critical assessment of bamboo diversity. 7th International Congress of Plant Molecular Biology, The International Society for Plant Molecular Biology, Barcelona, Spain, June 23-28, 2003.

2. Das M and Pal A. Influence of physiological age and position of the nodal explants on in vitro regeneration of *Dendrocalamus strictus* from field grown culms. National Symposium on Biotechnology, Society of Plant Tissue Culture Association of India, University of Rajasthan, Jaipur, India. 2003.

3. Das M, Schaeffner AR, Mader MT, Reichman JR, Watrud LS, Pfleeger T and Olszyk D. Global expression profiling as a tool to develop molecular markers linked to herbicide stress in *Arabidopsis*. Plant Biology and Botany. American Society of Plant Biology (ASPB), Chicago, Illinois, USA, July 7-11, 2007.

4. Pal A, Bhattacharya S, Ghosh JS, Mitra A and **Das M.** Molecular markers: A trendy approach for bamboo identification. National Seminar on Recent Advances in Plant Sciences, Acharya Nagarjuna University, Andhra Pradesh, India, 2007.

5. Das M, Mader MT, Haberer G, Reichman JR, Aceituno FF, Watrud LS, Pfleeger TG, Gutiérrez R, Olszyk DM, Schäffner AR. *Arabidopsis* transcriptional responses differentiating closely related chemicals (herbicides) and cross-species extrapolation to *Brassica*. 19th International Conference on *Arabidopsis* Research. Montreal, Canada, July 23-27, 2008.

6. Olszyk D, **Das M**, Lee EH, Pfleeger T, Plocher M. Comparison of Brassicaceae species for phytotoxicity testing. Annual meeting of Agronomy, Crop and Soil Science. Houston, Texas, USA, October 5-9, 2008.

7. dePamphilis C, Wickett N, Westwood J, Timko M, Yoder J, **Das M**, Gowda B, Gunathilake P, Honaas L, Huang K, Lis K, Sheaffer L, Stromberg V, Wall K, Wu B. The Parasitic Plant Genome Project II: Large-scale EST sequencing of *Triphysaria, Striga*, and Orobanchaceae. 10th World Congress on Parasitic Plants. Kusadasi, Turkey, June 8-12, 2009.

8. Das M, Haberer G, Schäffner A.R.. How to identify functional orthologs in Brassicaceae? 7th Tri-National Arabidopsis Meeting. Salzburg, Austria, September 15-18, 2010.

9. Westwood, JH., Fernandez-Aparicio M, **Das M**, Alford S, Stromberg V, Wickett NJ, Huang K, Wu B, Yoder JI., Timko MP, dePamphilis C. The Evolution of Weediness in Parasitic Plants of the Orobanchaceae. Plant and Animal Genome Conference. San Diego, CA, USA, January 15-19, 2011.

10. Das M, Haberer G, Schäffner AR. Dissecting genomes of *Arabidopsis thaliana* and *A. lyrata* to identify rules of functionally related ortholog identification in plants. Botaniker Tagung. Berlin, Germany, September 18-23, 2011.

6C. INVITED TALKS

1. The Parasitic Plant Genome Project: New Insight Into Parasitic Weed Biology And Evolution. Plant and Animal Genome XVII Conference, Town & Country Convention Center, San Diego, California, USA, January 10-14, 2009.

2. How to identify functional orthologs in Brassicaceae? Network Meeting of the Alexander von Humboldt Foundation. University of Ulm, Germany, October 5-7, 2010.

7. SYNOPSIS OF MY MAJOR RESEARCH CONTRIBUIONS

(A) Resolving bamboo taxonomy and diversity at the molecular levels

A total of 1400 species of bamboo are grouped under the sub-family Bambusoideae within the family Poaceae. Due to infrequent flowering, taxonomy has traditionally been dependent on morphological characters. Therefore taxonomic delineation at lower levels often lack sufficient resolution. I have successfully utilized the power of DNA molecular markers to resolve many fundamental and applied questions related to bamboo taxonomy and diversity:

(i) Phylogenetic relationships amongst the woody bamboo species that has been in the center of controversy for a long time were resolved by the allelic polymorphism data (Das et al., 2007).

(ii) Two species-specific sequence characterized amplified regions (SCARs) were identified in *B. balcooa* and *B. tulda* to allow for their proper identification, in order to avoid unintentional adulteration that affects the quality and quantity of paper pulp production (Das et al., 2005). This is the first report of any species-specific marker development in bamboo.

(iii)I have also utilized the power of DNA molecular markers to study bamboo genetic diversity at the population level (Das et al., 2008, Bhattacharya et al., 2009).

(B) An orthologous transcriptional signature differentiates responses towards closely related herbicides in *Arabidopsis thaliana* and *Brassica napus* (Das et al., 2010)

Herbicides contain structurally diverse chemicals designed to inhibit targets in susceptible weeds, and, thus, help reduce crop yield losses. In spite of their enormous economic importance, not many studies have been conducted to reveal the molecular basis of plant herbicide interactions. Here genome-wide expression profiling was used to compare effects of five related, amino acid biosynthesis inhibiting herbicides on *Arabidopsis thaliana* and *Brassica napus*. Besides providing enhanced molecular insights regarding the effects of these herbicides, the study has two novel outcomes and impacts:

a) A composite transcriptional signature could be identified that allowed differentiating and classifying the response to herbicides, which contain active ingredients targeting the same enzyme (acetolactate synthase) or even possessing the same chemical backbone (sulfonylurea).

b) Despite complications in the establishment of *A. thaliana* and *Brassica* orthologous relationsships due to the genome triplication in the *Brassica* lineage, a set of *Brassica napus* genes could be identified that retained the ability to correctly classify the interaction with these related herbicides.

Thus, a complex, transcriptional signature could be successfully transferred from the model plant to a related, agronomically important crop species. Its ability to classify the correct herbicidal exposures highlights future implications of such transcript based signatures in

environmental studies such as non-target movement of herbicides, or in a broader perspective in analogous analyses of the impact of chemicals on organisms.

(C) The evolution of parasitism in plants (Parasitic Plant Genome Project, http://ppgp.huck.psu.edu/)

The Parasitic Plant Genome Project (PPGP) has sequenced transcriptomes of three parasitic species and a non-parasitic relative in the Orobanchaceae with the goal of understanding genetic changes associated with parasitism. The species studied includes all nutritional types: facultative hemiparasites (photosynthetic), obligate hemiparasites (photosynthetic heterotrophic), and holoparasites (non-photosynthetic). The data are now being analyzed to answer many unaddressed questions related to the evolution of plant parasitism.

(a) Study of the transcriptomes of above ground structures from three parasitic plants (Wickett et al., 2011)
Easily-collected above-ground tissues (Stages 5 and 6) were the first into the analysis pipeline and provide insights into parasite evolution, specifically that the transition from photosynthetic to non-photosynthetic nutritional ability is accompanied by a loss (or absence of expression) of genes associated with light harvesting and photosynthesis (Wickett et al. 2011). Our results show surprising conservation of both gene expression and amino acid sequence in the chlorophyll biosynthesis pathway of a non-photosynthetic parasitic plant, suggesting that this pathway may be maintained in non-photosynthetic organisms for functions unrelated to photosynthesis.

(b) Why parasitic plants make their own strigolactone? (Das et al., 2013, in preparation)
Another evolutionary step toward obligate parasitism is an increased sophistication in mechanisms for locating a host. *Striga* and *Orobanche* seeds are very small and contain limited nutrient reserve. Therefore seed germination occurs only when they can detect the presence of host roots by sensing minute quantities of specific chemicals known as strigolactones (SLs) released by host roots. Since parasite seed germination depends on detecting exogenous strigolactones, it has been assumed that parasites do not produce their own strigolactones. However, our data indicate that *Striga* and *Orobanche* contain and express genes for all known enzymatic steps in the synthesis of strigolactones. Furthermore, expression analysis of key biosynthetic genes suggest that *Striga* and *Orobanche* require their own strigolactones, but have modified regulation of strigolactone biosynthesis to serve developmentally specific needs in host recognition.

(D) Investigating the ability of gene expression data to identify functional orthologs across species when Bioinformatic methods are limiting

Identification of functionally equivalent genes across genomes is necessary for accurate transfer of experimental knowledge from well-characterized organisms to others. This relies on automated approaches such as OrthoMCL, InParanoid, KOG, which usually work well for one-to-one homologous situation. However, this strategy does not always work accurately for plants. Due to the occurrence of extensive gene/genome duplication quite often for one query gene the prediction ends up with multiple hologous genes in the other genome and it is not clear which

one among them is the functional ortholog. Here I am testing the power of gene expression data to distinguish between orthologs and paralogs in such one-to-many situations. By designing whole transcriptome microarray for Arabidopsis thaliana and A. lyrata, I am studying the expression patterns of the duplicated genes under salt, drought and UV stressed conditions. The overall expression similarity/divergence was measured by Corelation analyses and was used to distinguish between orthologous and paralogous genes. In six selected cases this was further validated by complementing *A. thaliana* KO mutant lines with *A. lyrata* homologs, which were predicted as functional homolog by correlation analyses. My study indicates the power of gene expression data to identify functional homologs across genomes when traditional Bioinformatic methologies are limiting.

8. Research areas and group members

- Functional and comparative genomics in Brassicaceae
- Gene duplication and evolution of novel stress genes
- Evolution of parasitism in plants
- Molecular markers and genetic diversity in bamboo
- Flower induction in tropical tree bamboos

Name of Group members:

Mr. Prasun Biswas (CSIR-UGC JRF awardee), April, 2013-

Topic of research: Identification and molecular characterization of genes regulating flower induction in tree bamboo