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IN MEMORIAM

Gopi Krishna Podila

In memoriam

Robin Sen

Many of you may by now have heard of the tragic and untimely death of Professor Gopi Krishna Podila on Friday, 12th February 2010. Gopi's passing has been deeply mourned by his family in the USA, India and the UK and by students, professional colleagues and friends. His life's work, encompassing over 100 peer-reviewed papers, books and patents, span the key disciplines of plant molecular genetics, forest biotechnology and plant-microbe interactions to which he had made seminal contributions from early on in his scientific career.

Gopi was born 14th September 1957 in Guntur, Andhra Pradesh, India, the youngest of four brothers. He studied biology, soil microbiology and plant pathology at Ngarjuna University graduating with a first class degree and Masters. He moved to the USA in 1982 and took a further Masters degree in plant pathology from Louisiana State University in 1983 that was awarded a Gold medal. A Ph.D in Molecular biology from Indiana State University in 1987 was followed by postdoctoral research in the laboratory of Professor Pappachan Kolattukudy at Ohio State University on cutinase gene expression in early leaf—*Fusarium solani* f. sp. *pisi* interactions that was published in *Science* and *Nature* (Podila et al., 1988; Dickman et al., 1989). Gopi then moved north in September 1990 to take up an associate professorship in the Department of Biological Sciences, Michigan Technological University where he maintained collaboration with Pappachan Kolattukudy on the molecular basis of early fungal–plant pathogenesis (e.g., Podila et al., 1993, 1995) and established an active forest biotechnology research group investigating genetic transformation and herbicide/insecticide resistance gene expression in aspen (*Populus tremuloides*) (Akkapeddi et al., 1994; Podila 1996). Working with Dr. David Karnosky and colleagues at the USDA Forest Service, his group had made significant contributions to understanding antioxidant and defence/lignin synthesis gene expression in ozone-exposed aspen (e.g., Karnosky et al., 1998b; Wurstmann et al., 2001).

It was while at Michigan Tech in the mid-90s that Gopi embarked on a genomics programme aimed at elucidating root symbiotic ectomycorrhiza development in forest trees. Initially, he worked on developing transformation systems for recalcitrant ectomycorrhizal fungi using *Paxillus involutus* as a model (Bills et al., 1995). His expertise relating to early infection gene expression analysis was put to good use in the application of first generation genomics (differential display) that enabled publication of one of the earliest studies highlighting differential gene expression in *Laccaria bicolor* during pre-symbiotic association with the roots of *Pinus resinosa* (Kim et al. 1998, 1999). At that time, Gopi visited Dr. Francis Martin, INRA, Nancy, France on a three-month invited sabbatical and, I understand, it was then that both established the goal to sequence *L. bicolor* as a model ectomycorrhizal fungus. Gopi visited other laboratories working on the mycorrhizal symbiosis in Europe, including our group at the University of Helsinki, Finland in 2000. Gopi provided me with crucial support that resulted in funds for a Scots pine—*Suillus bovinus* nitrogen assimilation genomics project (Juuti et al., 2004). I particularly remember his exciting presentation on the characterisation of an early symbiosis related *ras* gene expressed in *L. bicolor* (Lbras) during symbiosis development. The in situ localisation of the Lbras encoded protein to the fungal Hartig net was particularly novel and mammalian

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cell complementation studies unequivocally proved the fungal gene to be a functional homolog of a mammalian *ras* gene controlling cell cycling and tumour formation (Sundram et al., 2001).

In 2002, Gopi Podila was elected chair of the Department of Biological Sciences at the University of Alabama, Huntsville, an appointment which crucially gave him access to state-of-the-art genomics facilities and the biotechnology industry. Research on characterising aspen developmental genes and encoding protein functioning, e.g., MADS-box genes, and differential gene expression in ectomycorrhizas of the *L. bicolor*-red pine model system continued apace in utilising high-throughput microarrays (e.g., Sceske et al., 2007; Gupta et al., 2005). Together with Dr. Francis Martin, Gopi was instrumental in securing funds for their earlier dream goal, the genome-sequencing programme of *L. bicolor* and, additionally, the model arbuscular mycorrhizal fungus, *Glomus intraradices,* at the US Department of Energy's Joint Genome Institute (JGI) at Walnut Creek, California (Lammers et al., 2004). This initiative complemented the *Populus* genome-sequencing project (Tuskan et al., 2006) and is of critical importance as *Populus* species can host both ectomycorrhizal and arbuscular mycorrhizal symbioses involving these ‘model’ mycorrhizal fungal species (Martin et al., 2004). It is a measure of the resolve of both co-ordinators and their collaborators that the 65-megabase *L. bicolor* genome sequence was completed and reported on in under 40 months. The project identified 20,000 protein-encoding gene sequences, large numbers of transposons and repeated sequences (Martin et al., 2008). Detection of highly expressed small secretory proteins (SSPs) in proliferating hyphae of the fungus during early colonisation of the root further highlighted Gopi's insightful early symbiosis gene expression work more than a decade earlier at Michigan Tech University.

Most recently, Gopi's group has developed high efficiency/throughput *Agrobacterium tumefaciens* and *A. rhizogenes* transformation protocols for *Populus* (Cseke et al., 2007) and carried out a transcriptomic comparison of two *Populus* genotypes with differing CO_2 response physiology (Cseke et al., 2009a). Although similar with respect to photosynthetic efficiency, stomatal conductance and leaf area index, differential carbon partitioning were identified, based on transcriptome analysis, during early and late growth seasons in the two genotypes exposed to elevated CO_2 at the Aspen FACE experimental site. In collaboration with Dr. Mike Miller at the Argonne National Laboratory, microarray-based transcriptomics experiments on >2,300 genes have also been carried out to assess multi-trophic impacts of elevated ozone and CO_2 alone and in combination on five *Populus* genotypes and their arbuscular mycorrhizal symbiont, *G. intraradices.* Increased arbuscular mycorrhizal fungal lipid metabolism was identified under elevated ozone and CO_2 exposure suggesting a shift to resting activity (Miller and Podila, 2008). The group has respectively collaborated with German and French partners on characterisation the regulation of copper and cadmium metalothioneins in the ectomycorrhizal fungus *Hebeloma cylindrosporum* (Ramesh et al., 2009) and cold stress induced enolase genes in the necrotrophic plant pathogen, *Botrytis cinerea* (Pandey et al. 2009). Gopi, in collaboration with Dr. Maria Davis, Dr. Ron Orlando and co-workers, has been recently applying proteomics to characterise secretory proteins from *B. cinerea* in mock-infecting media. A high number of SignalP motifed extracellular proteins were predicted and secretory transport proteins, peptidases and pathogenicity factors were identified that are crucial for early plant infection and host colonisation (Shah et al., 2009).

Gopi Podila and Robin Sen seen enjoying a summer's evening by the harbour in Helsinki, Finland.

Over the last 15 years, Gopi has championed both the fields of tree and mycorrhiza genomics not only in his primary publications but in numerous reviews and book chapters (e.g., Podila, 1996; Pandey et al., 2007; Podila et al., 2009). In particular, he has emphasised the importance of trees as a crucial carbon sequestration resource and as a sustainable source of biofuels in climate change management and mitigation (e.g., Karnosky et al., 1998b; Cseke at al., 2009b). The five patents to his name relate to application of a plant reproductive tissue promoter, PrAGI, in production of reproductively debilitated or sterile plants (Podila et al, 2005), imidazolinone herbicide resistance in transgenic trees (Karnosky et al., 2002), *Agrobacterium* mediated transformation system to generate plants with altered lignin composition (Chiang et al., 1999a), genetic engineering of wood colour in plants (Chiang et al., 1999b) and MADS-box transgenics to control reproduction and development of trees (Podila et al., 2004).

Gopi Podila was an editorial board member of the *Journal of Plant Interactions*, *New Phytologist*, *Symbiosis* and *Physiology and Molecular Biology of Plants.* He was also an active council member for the *International Symbiosis Society.* He will be dearly remembered by the many undergraduate, postgraduate and postdoctoral students that were lucky enough to have known Gopi as a mentor and friend. One of his Masters students, Rena Webb, was quoted in the Huntsville Times as saying that "he really is the nicest man I've ever known. You don't feel like a graduate student, you feel part of a family" Gopi K. Podila is survived by his wife, Vani Podila, and their two daughters, Bindu and Anila.

Robin Sen

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References cited in the article are included in Electronic Supplementary Materials.