

SIGNIFICANT RESEARCH CONTRIBUTIONS

The main contribution has been in the area of **development of new genic and genomic microsatellite markers in a range of crops** and **use of these markers to understand genetic diversity pattern, phylogenetic relationship, variety identification and gene mapping** as briefly outlined below:

➤ **Development of New Concepts and Designing of Novel Sequence-based Robust Molecular Markers**

- Developed **two new concepts** and designed **a large number of genic microsatellite markers** namely, **“UGMS”** (UniGene derived MicroSatellite) in five cereal species (rice, wheat, maize, sorghum and barley), sugarcane, *Brassica* and *A. thaliana*, and **“GNMS”** (Genic Non-coding MicroSatellite) from different regulatory (5'UTRs and promoters) and non-coding (3'UTRs and intronic) sequence components of protein coding rice genes [*Parida et al. (2006) Theor. Appl. Genet. 112:808-817 & Parida et al. (2009) BMC Genomics 10:140*].
- Developed a total of **25,318 including 5,985 hypervariable class I UGMS markers** in **nine different plant species** including rice (12,212), wheat (1,542), maize (1,372), sorghum (917), barley (971), sugarcane (961), *Brassica* (2,721) and *Arabidopsis thaliana* (4,622) and placed them in public domain for unrestricted use **which would extend the accessibility of such gene based functional microsatellite markers to researchers for many genetic studies in these crop species for wider genome coverage** [*Parida et al. (2006) Theor. Appl. Genet. 112:808-817, Parida et al. (2010) BMC Plant Biology 10:251 & Parida et al. (2010) Genome 53:55-67*].
- Designed **17,966 novel GNMS markers** from different regulatory and non-coding sequence components in 18,935 predicted **protein coding rice genes including 14,308 putative promoter sequences** which were bin mapped on the 12 rice chromosomes [*Parida et al. (2009) BMC Genomics 10:140*].
- Genetic analysis has been hindered in sugarcane because of its complex polyploid genome and lack of sufficiently informative markers. In this context, a larger set of **1,315 including 567 hypervariable class I informative genomic microsatellite markers designated as “SEGMS” (Sugarcane Enriched Genomic MicroSatellite) markers developed** from the enriched genomic libraries of two high sugar containing and red rot resistant Indian sugarcane commercial varieties namely, Co7201 and Co86011 **would be of immense use for various marker-based genotyping applications in sugarcane** [*Parida et al. (2009) Theor. Appl. Genet. 118:327-338*].
- Detected and validated the **SNPs and InDels** in important **sugar pathway and disease resistance genes** through **cloned amplicons sequencing** and **DHPLC analysis** and using a cost-efficient CAPS genotyping assay and developed **CAPS markers** which can be of immense use for various **marker-assisted genetic improvement of sugar content and disease resistance in sugarcane** [*Parida et al. (2011) Mol. Genet. Genomics (In Press)*].

- Identified a large number of **SNPs and InDels** in coding and regulatory sequence components of **stress-responsive rice genes** by **whole genome resequencing** and **transcriptome sequencing** of commercially important Indian rice varieties [*Parida et al. (2011) Theor. Appl. Genet. (In Press)*].

➤ **Comparative Mapping and Genome Analysis**

- Identified “**UGMS-COS (Conserved Orthologous Set)**” markers which would be very useful to breeders and geneticists, especially for minor or underfunded crop species belonging to grass family and large genome amphidiploid dicot species like *B. juncea* and *B. carinata* where no such sequence information is available [*Parida et al. (2006) Theor. Appl. Genet. 112:808-817* & *Parida et al. (2010) Genome 53:55-67*].
- Identified a set of **236 sugarcane UGMS-COS markers syntenic to rice and wheat chromosomes** which would be useful for **transferring information about genes from model species rice to large and complex genome crop species** like wheat and sugarcane and **for understanding their genetic and taxonomic complexities** [*Parida et al. (2006) Theor. Appl. Genet. 112:808-817*].
- **Comparative physical mapping** of *Brassica* UGMS markers on *A. thaliana* genome identified about **85% Brassica unigenes as single copy and retained collinearity/ conserved primordial gene order with A. thaliana genome**, which would **guide cloning of genes in the cultivated Brassica species using the positional information of candidate genes for A. thaliana** [*Parida et al. (2010) Genome 53:55-67*].
- Demonstrated the usefulness of **112 orthologous and paralogous “CNMS” (Conserved Non-coding MicroSatellite) markers** identified in the putative rice promoter sequences **for comparative genome mapping and understanding of evolutionary and gene regulatory complexities** among rice and other members of grass family [*Parida et al. (2009) BMC Genomics 10:140*].
- Identified a large number of **genomic STMS and UGMS markers** polymorphic between *Brassica* species and genera which would be **useful in transfer of the target genomic regions of related Brassica species like B. carinata** possessing various traits of agricultural importance such as *Alternaria* and white rust resistance **to the genetic background of B. juncea by marker-assisted selection** [*Yadava et al. (2009) J. Plant Biochem. Biotech. 18:29-36*].

➤ **Mapping of Genomes and Genes**

- Mapped a **major locus for fertility restoration in Basmati restorer line PRR78** to a short marker interval of 0.8 cM and a physical interval of 163.6 kb **on long arm of rice chromosome 10** and developed a **sequence tagged site (STS) marker and a GNMS marker** based on a **pentatricopeptide repeat (PPR) motif containing candidate gene** present in the targeted marker interval which would be of **use in efficient marker assisted selection for fertility restoration in hybrid breeding program for WA-CMS in rice** [*Ngangkham et al. (2010) Mol. Breed. 26:275-292*].

- Constructed a UGMS and GNMS marker based **framework physical map of rice genome** and a UGMS marker based **bin-map of wheat genome** which would provide invaluable information for **targeted mapping of genes for useful agronomic traits, comparative genomics** and **sequencing of gene-rich regions of the genome** [Parida et al. (2006) *Theor. Appl. Genet.* 112:808-817 & Parida et al. (2009) *BMC Genomics* 10:140].
- Evaluated the **genomic Sequence Tagged MicroSatellite (STMS) markers** first time for **molecular mapping of the *Brassica juncea* genome** and **constructed a microsatellite marker based Indian mustard genome map** [Koundal et al. (2008) *J. Plant Biochem. Biotech.* 17:69-72].

➤ **DNA Fingerprinting and Variety Identification**

- Developed **DNA fingerprinting** for **germplasm characterization and variety identification** in rice, sugarcane and *Brassica* and **economically important horticultural crops** like ash gourd and bitter gourd and in a northwestern Himalayan region medicinal herb *Podophyllum hexandrum* [Parida et al. (2010) *BMC Plant Biology* 10:251, Yadava et al. (2009) *J. Plant Biochem. Biotech.* 18:29-36, Verma et al. (2007) *Scientia Hort* 113:231-237 and Naik et al. (2010) *Physiol. Mol. Biol. Plants* 16:1-13].
- Developed **Molecular Bar Codes** of commercially important Indian Basmati rice **varieties** based on DNA fingerprints using a set of informative GNMS markers for their **utility in Basmati trade and commerce** [Parida et al. (2009) *BMC Genomics* 10:140].
- Demonstrated the efficiency of **five mitochondrial gene specific CAPS markers** for **testing the purity of Pusa6A parental lines** during seed production of Pusa Rice Hybrid 10 which would be of **immense use in marker assisted production of pure hybrid rice seeds in India** [Ngangkham et al. (2010) *Mol. Breed.* 26:275-292].
- Studied **morphological and genetic variation among different isolates of rice blast fungus (*Magnaporthe grisea*)** collected from Chhattisgarh region [Sonah et al. (2009) *Indian Phytopath.* 62:469-477].

➤ **Studying Genetic Diversity Pattern and Establishing Phylogenetic Relationships**

- Demonstrated the **utility of SEGMS and UGMS markers** for **assessment of molecular genetic diversity** and **establishing phylogenetic relationships** among sugarcane species, Indian sub-tropical and tropical varieties and related genera.
- Resolved and analyzed the **allelic variants precisely** for a set of **fluorescent dye labeled UGMS markers** in sugarcane genotypes and five cereal species **using the automated fragment analysis** system which suggested the utility of designed markers for various **high-throughput genotyping applications in sugarcane** and **revealed a broad genetic base of the Indian varieties in respect of functionally relevant regions of the large and complex sugarcane genome** [Parida et al. (2010) *BMC Plant Biology* 10:251].

- A set of rice GNMS markers revealed **functional genetic diversity** and clearly established **molecular phylogenetic relationships** among domesticated traditional and evolved long and short-grained aromatic, *indica* and *japonica* rice cultivar groups, thereby suggesting their **utility in defining varietal identity in commerce** [*Parida et al. (2009) BMC Genomics 10:140*].
- Demonstrated the utility of SNPs validated in stress-responsive rice genes by Illumina GoldenGate assay in assaying **wider level of natural genetic diversity, understanding the diversity pattern, evaluating the degree of admixture and establishing strong population genetic structure** among different existing domesticated rice cultivars and wild species accessions.

➤ **Genetic association analysis**

- Demonstrated **large-scale validation** and **high-throughput genotyping** of SNPs from stress-responsive rice genes in a set of domesticated rice cultivars and wild species accessions using the **Illumina GoldenGate assay** and utilized large number of such validated useful SNP alleles/haplotypes for **candidate-gene based association analysis** of **important stress-tolerance traits in rice** [*Parida et al. (2011) Theor. Appl. Genet. (In Press)*].