

Hybrid Rice Breeding in India



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Ongoing hybrid rice research activities

- ❖ Genetic improvement of maintainers and development of CMS lines
- ❖ **Exploitation of inter sub-specific heterosis in rice**
- ❖ Development and Evaluation of three line hybrids
- ❖ **Breeding of parental lines and Hybrids suited to Aerobic and salinity/alkalinity Conditions**
- ❖ Molecular breeding for Disease Resistance, Fertility Restoration and Wide Compatibility in Rice

Enhancement of heterosis-different approaches

- ❖ Improvement of parental lines
- ❖ Exploitation of inter sub-specific heterosis

Breeding Approaches for Good Quality Restorers

- ❖ R x R cross
- ❖ R x PR cross
- ❖ PR x PR cross
- ❖ A x R cross
- ❖ A x PR cross followed by selective mating
- ❖ Three way cross approach involving three different restorers

Development of Restorers

Cross	Number of lines		Freq. of R (%)
	Developed	Tested	
R x R	350	150	63
R x R x R	160	105	58
R x PR	480	250	41
R x (PR x R)	140	90	52
R x (PR x PR)	135	80	39

Promising R-line



Restorers released as varieties

Akshaydhan



Varadhan



Pusa Sugandh-2



PUSA SUGANDH-3





One promising NPT plant



Promising NPT restorer plants in the segregating progenies

Development of maintainers

Type of cross	Number of lines		Freq. of B (%)
	Developed	Tested	
$B_1 \times B_2$	405	200	65
$B_1 \times PM$	150	75	40
$B_1 \times (B_2 \times B_3)$	135	60	56
$B_1 \times (PM \times B_2)$	120	70	48
$B_1 \times (PM_1 \times PM_2)$	115	55	41
$B_1 \times PM // PM$	126	40	35

Promising B-line



Development of CMS lines

Maintainer Line	CMS line	Days to maturity	Stigma Exsertion (%)		Out crossing (%) on A line
			B line	A Line	
MI. 15-1-8-1-3	DRR 4A	126	32	84	62
MI. 15-4-3-1-1-4	DRR 5A	132	30	86	65
MI. 15-5-5-2-3	DRR 6A	140	36	79	59
SC₅ 113-1	DRR 8A	131	24	80	57
MI. 15-1-10-1-1	DRR 9A	132	34	85	69

Promising CMS Lines

Centre	CMS lines
Hyderabad	DRR-4A, DRR-5A, DRR-6A, DRR-9A
Maruteru	APMS 6A, 8A, 9A
Delhi	Pusa 3A, Pusa 6A (Basmati), Pusa 5A
Cuttack	CRMS 31A, CRMS 32A
Coimbatore	COMS 23A, COMS 29A, COMS 30 A, COMS 31A

Gene pools developed

Population	No. of lines	
	Added	Developed
Restorer Population		
DRCP 140	12	125
DRCP 102	10	115
DRCP 103	14	110
Maintainer population		
DRCP 104	08	70
DRCP 105	10	90



MARS - Marker assisted recurrent selection strategy is being adopted To identify restorer and maintainer lines possessing resistance to biotic stresses from the elite breeding lines developed



Line with good stigma exertion

A hybrid with NPT background



A promising restorer line in the *indica japonica* background

Grain quality improvement breeding - progress

Hybrids with medium slender grain type

DRRH-3



27P11



Breeding of parental lines and Hybrids suited to Aerobic and salinity/alkalinity Conditions

Diverse parental lines, CMS lines and INGER nurseries for aerobic and upland rice screened under direct seeded aerobic (dry plot), alternate wetting and drying and normal transplanted irrigated conditions.

CR 2707-185-16-1-1-1, APO, B644F-MR-6-0-015, IR84887-B-152-CRA-121-1, IR82639, UPLRI 7, CR 691-5812, KRH 2, APMS 6B, DRRH 3 performed well under direct seeded conditions

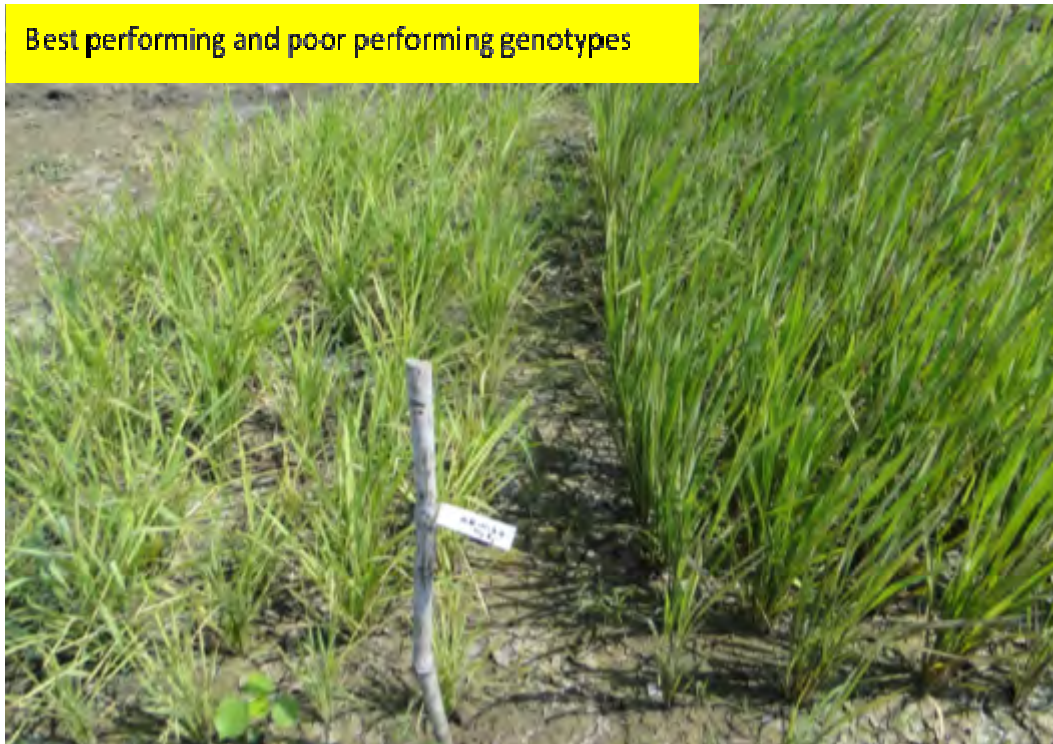
FL 478, DRR 9B, RPHR 1005, APMS 6B, DRRH 3, NVSR 6029 were found tolerant screening under nutrient salt solution for seedling stage



Direct seeded aerobic rice



Best performing and poor performing genotypes

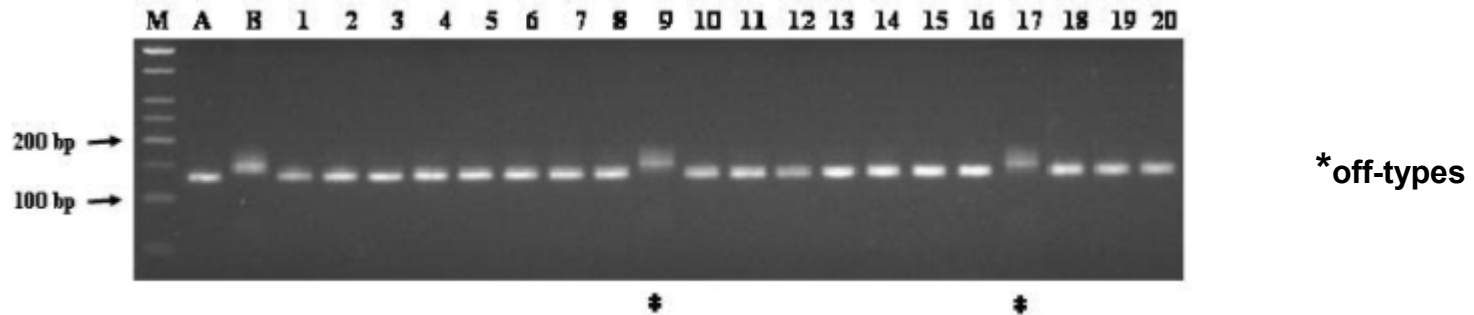


Development of molecular tools for enhancing hybrid rice breeding efficiency

- **Assessment of genetic purity of rice hybrids and their parental lines**
- **Screening of genotypes/varieties for *Rf* and *WCG* Genes**
- **Incorporation of biotic stress resistance in parental lines of released hybrids**

A mitochondrial SSR marker (drrcms) based assessment of genetic purity of WA-CMS lines

CMS purity testing – IR58025A



A Mitochondrial Repeat Specific Marker for Distinguishing Wild Abortive Type Cytoplasmic Male Sterile Rice Lines from their Cognate Isogenic Maintainer Lines

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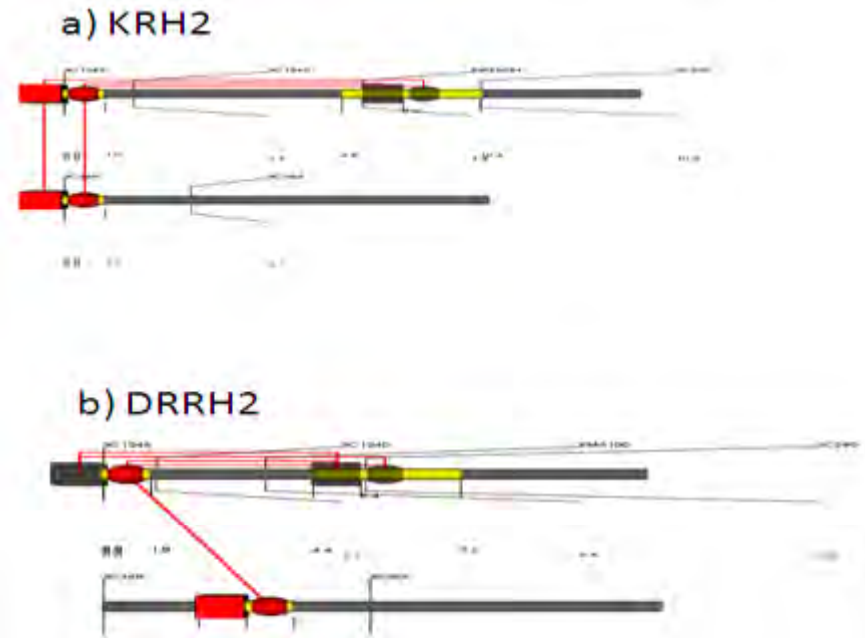
Published in *Crop Sci.* 47:207–211 (2007).

Mapping of fertility restorer genes for WA-CMS system of rice and its validation

Two reported Rf loci were fine mapped and their interaction was studied

Rf3 locus:
23-31%

Rf4 locus:
41-43%



Validation of Rf linked markers

Selection accuracy (%) for combinations of markers for *Rf3* and *Rf4* loci

	<i>Rf3</i>	RG140/ <i>pvuI</i> *	DRRM-RF3-6	DRRM-RF3-10	DRRM-RF3-5	RM10315	RM10318
		47.3	50.0	57.3	48.4	44.8	44.9
<i>Rf4</i>							
RM6100*	74.7	79.5	81.0	81.0	82.6	80.2	77.2
TMPPR3*	85.2	85.4	88.4	91.9	91.9	86.2	74.8
DRRM-RF4-10	81.0	84.2	85.3	88.4	86.0	84.2	73.0
DRCG-RF4-14	86.8	86.1	89.4	91.9	91.9	87.4	75.4
DRCG-RF4-8	85.2	82.6	89.4	91.9	91.9	87.4	75.4

*Reported markers

Amplification patterns of restorer and maintainer lines with the linked markers – *Rf4* and *Rf3* (201 rice lines)

The newly developed microsatellite markers were compared with earlier reported markers (RM6100 and RG140) for their selection efficiency of *Rf* genes among 180 rice lines (known restorers and maintainers)

Selection accuracy (%) for combinations of markers for *Rf3* and *Rf4*

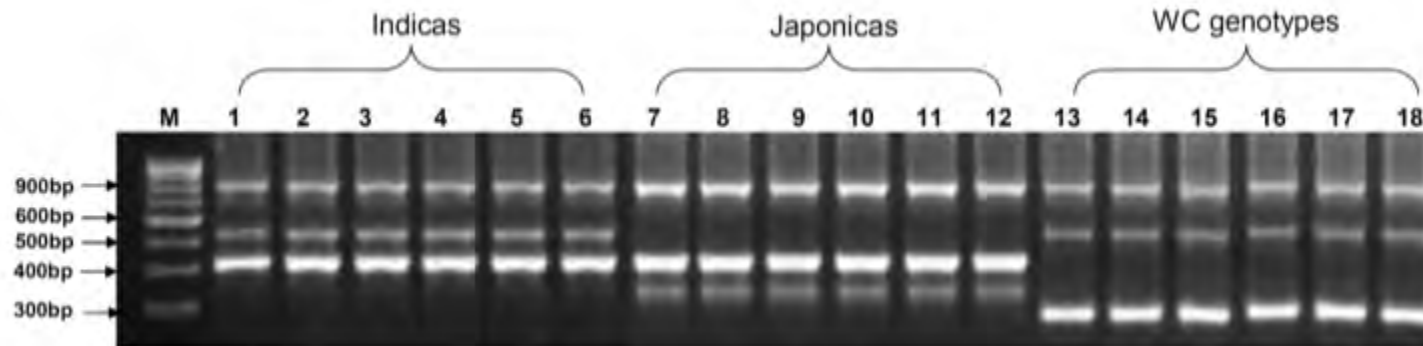
		Chr1- <i>Rf3</i>			
		STS- RG140	RM- <i>Rf3</i> -2	STS-RG140 + RM- <i>Rf3</i> -2	
Chr10 – <i>Rf4</i>			47.3	56.2	71.2
	RM6100	78.4	88.4	93.4	94.6
	RM- <i>Rf4</i> -5	86.8	92.8	92.2	96.4
	RM6100+RM-<i>Rf4</i>-5	93.4	97.6	97	97.6

When the markers flanking *Rf3* and *Rf4* were deployed in combination– Excellent selection efficiency (97.6%).

Rf4 – major locus, *Rf3* – minor locus

We are presently analyzing the candidate genes present in the *Rf4* and *Rf3* region in addition to analysis of additional QTLs for *Rf* trait.

A functional marker for the major wide compatibility gene locus S_5



The marker can clearly distinguish WC genotypes from others.....

Mol Breeding (2010) 26:719–727
DOI 10.1007/s11032-010-9482-5

SHORT COMMUNICATION

Development and validation of a PCR-based functional marker system for the major wide-compatible gene locus S_5 in rice

R. M. Sundaram · K. Sakthivel · A. S. Hariprasad · M. S. Ramesha ·
B. C. Viraktamath · C. N. Neeraja · S. M. Balachandran ·
N. Shobha Rani · P. Revathi · P. Sandhya · Y. Hari

Mol Breeding (2010) 26:719–727 (2010)

Short Communication

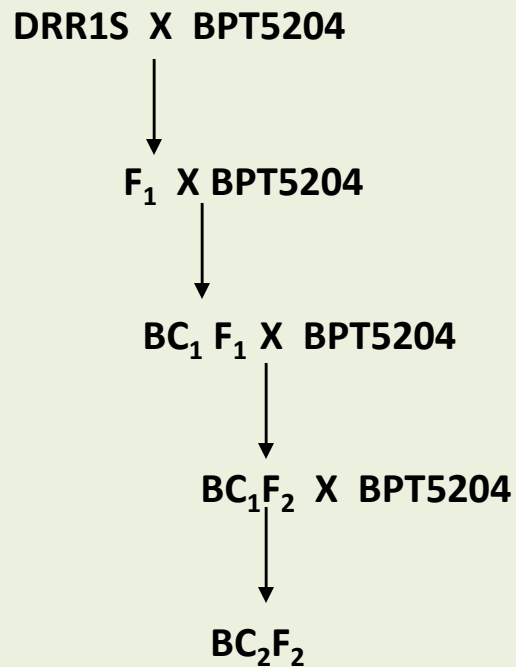
Molecular screening for the presence of wide compatibility gene S_5 neutral allele in the parental lines of hybrid rice

P. Revathi¹, Arun Kumar Singh, R. M. Sundaram, P. Senguttavel, K. B. Kemparaju, K. S. Ganaprasad and B. C. Viraktamath

Genotypes with neutral allele at S₅ locus identified

Genotypes	No. of lines screened	No. of lines identified to possess neutral allele at S ₅ locus
Cultivars	154	11
IRRI germplasm lines	207	47
Aromatic rice genotypes	37	12
Restorer lines	157	36
Breeding lines	17	06
Total	572	112

Introgression of the TGMS gene(s) present in DRR1S into Samba Mahsuri (BPT 5204)



MAS using flanking SSR marker i.e., RMDrrtms3 & RMDrrtms24

Selection criteria: Grain type and yield like Samba Mahsuri + TGMS trait

Introgression of bacterial blight (*Xa21*) & blast (*Pi-k^h*) R genes into hybrid rice parental lines

BK49-77 – An Introgression line of KMR-3R, with good grain quality, complete fertility restoration, high yield and BB resistance



Plant Breeding
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doi:10.1111/j.1439-0523.2011.01881.x

Marker-assisted improvement of a stable restorer line, KMR-3R and its derived hybrid KRH2 for bacterial blight resistance and grain quality

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PRR 78 with *xa13+Xa21*



PRR 78 with *Pikh* and *PiZ5*



Pusa 6B with *xa13+Xa21*



Pusa 6B with *Piz5* and *Pi-kh*



Marker-based prediction of grain yield heterosis

- **EST-SSRs:** Significantly high positive correlation with grain yield heterosis ($r = 0.83$) as compared to genomic SSRs ($r = 0.42$)
- A set of 10 'key' informative EST-SSR markers have been identified (RMES2-1, RMES3-2, RMES5-1, RMES6-1, RMES8-1, RMES9-2, RMES10-1, RM151, RM168 and RM169) highly useful for prediction of grain yield heterosis.
- These informative EST-SSR markers can be used for preliminary sorting of parental lines in order to identify heterotic cross combinations

Short Communication

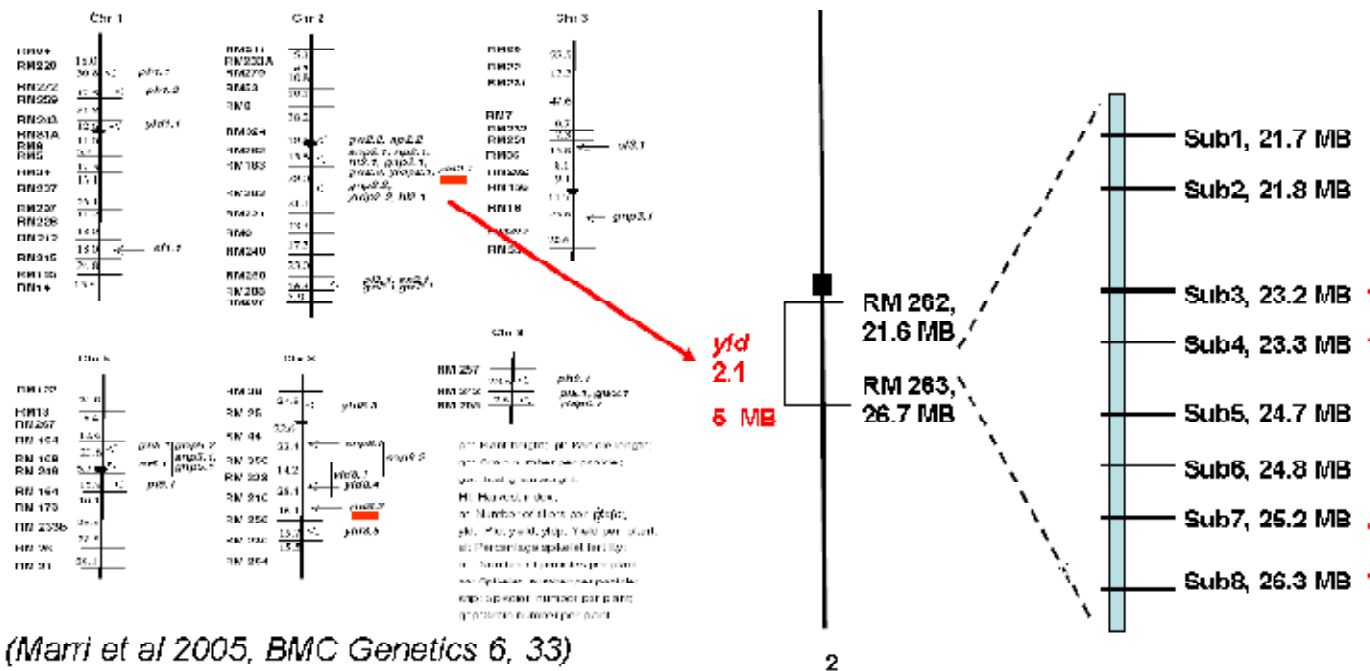
Prediction of heterosis for grain yield in rice using 'key' informative EST-SSR markers

I. JAIKISHAN^{1,*}, P. RAJENDRAKUMAR^{1,*}, M. S. RAMESHA¹, B. C. VIRAKTAMATH¹, S. M. BALACHANDRAN¹,
C. N. NEERAJA¹, K. SUJATHA¹, K. SRINIVASA RAO¹, P. NATARAJKUMAR¹, Y. HARI¹, K. SAKTHIVEL¹,
A. S. RAMAPRASAD¹ and R. M. SUNDARAM^{1,2,*}

Introgression of yield enhancing QTLs from wild rice into and parental lines

yld2.1 narrowed to two yield sub QTLs for fine mapping

MABC for 3 generations, marker analysis of 504 BC3F1 plants and derived BC3F2



Ref: Swamy and Sarla (2008) Biotech Adv. 26: 106-120

**Increased grain number in KMR3-IL50
with *yld2.1* subQTL3-4**



Constraints

- ❖ **Yield stagnation - Marginal heterosis - unattractive**
- ❖ **Narrow genetic base - a major concern**
- ❖ **Diversified consumer preferences – Meeting the grain quality requirements**
- ❖ **Few hybrids in late duration & early groups**
- ❖ **Limited choice of hybrids for unfavorable ecologies**
- ❖ **Susceptibility of parental lines to major pests & diseases**
- ❖ **Lack of molecular markers for identification of maintainers like *Rf* genes in case of restorers**

Future Strategies

- **Use of *I/J* derived parental lines for enhancing level of heterosis.**
- **Incorporation of resistance to major diseases in parental lines.**
- **Incremental improvement of parental lines.**



THANK YOU