

Genetic Diversity of Rice in India

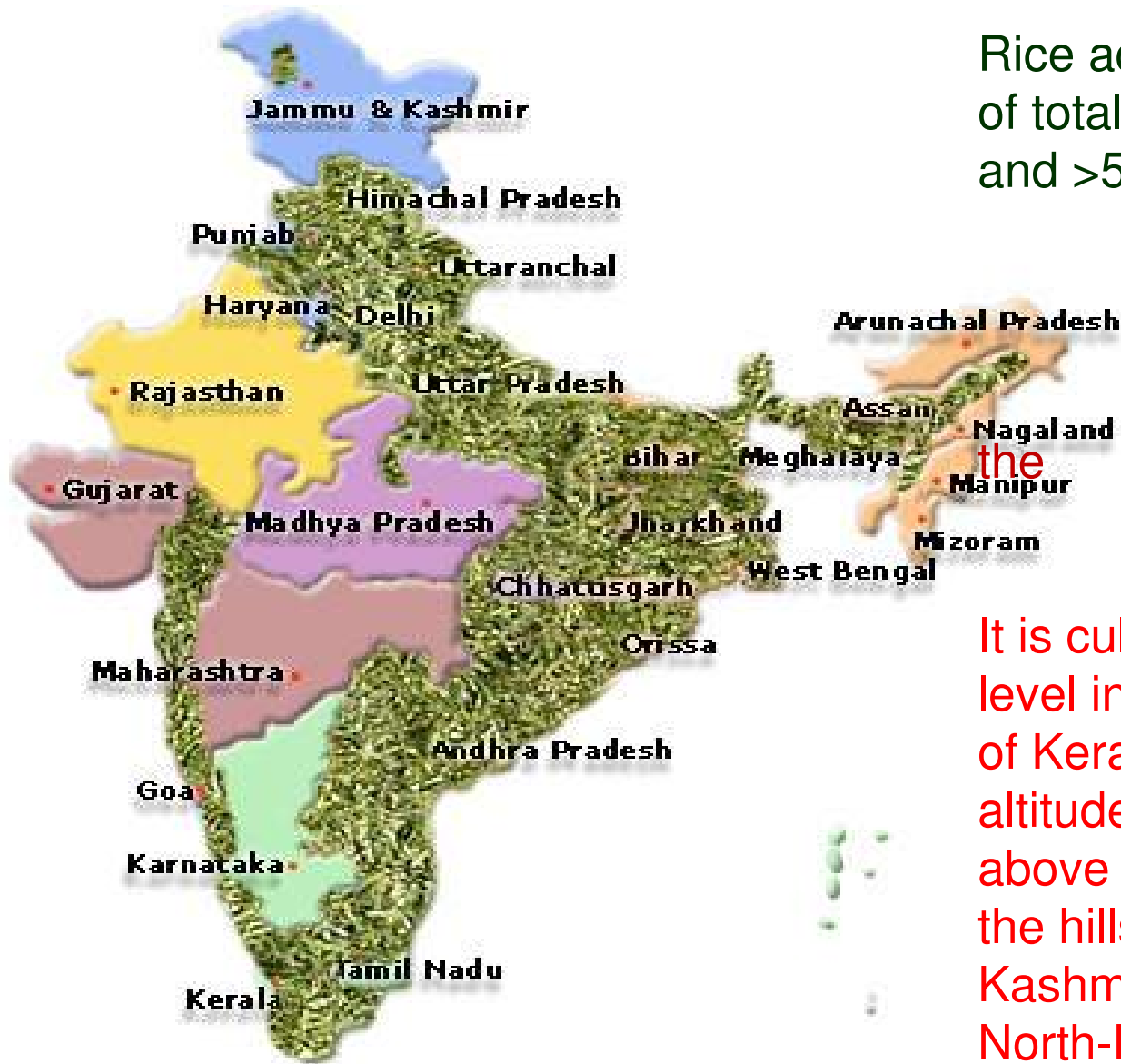
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Rice accounts for about 42% of total food grain production and >55% of diet in India

Rice is considered to have originated in the Himalayan foot-hills

It is cultivated below the sea level in the Kuttanad district of Kerala state as well as at altitude of 2000 meters above the mean sea level in the hills of Jammu & Kashmir, Uttarakhand and North-Eastern States.

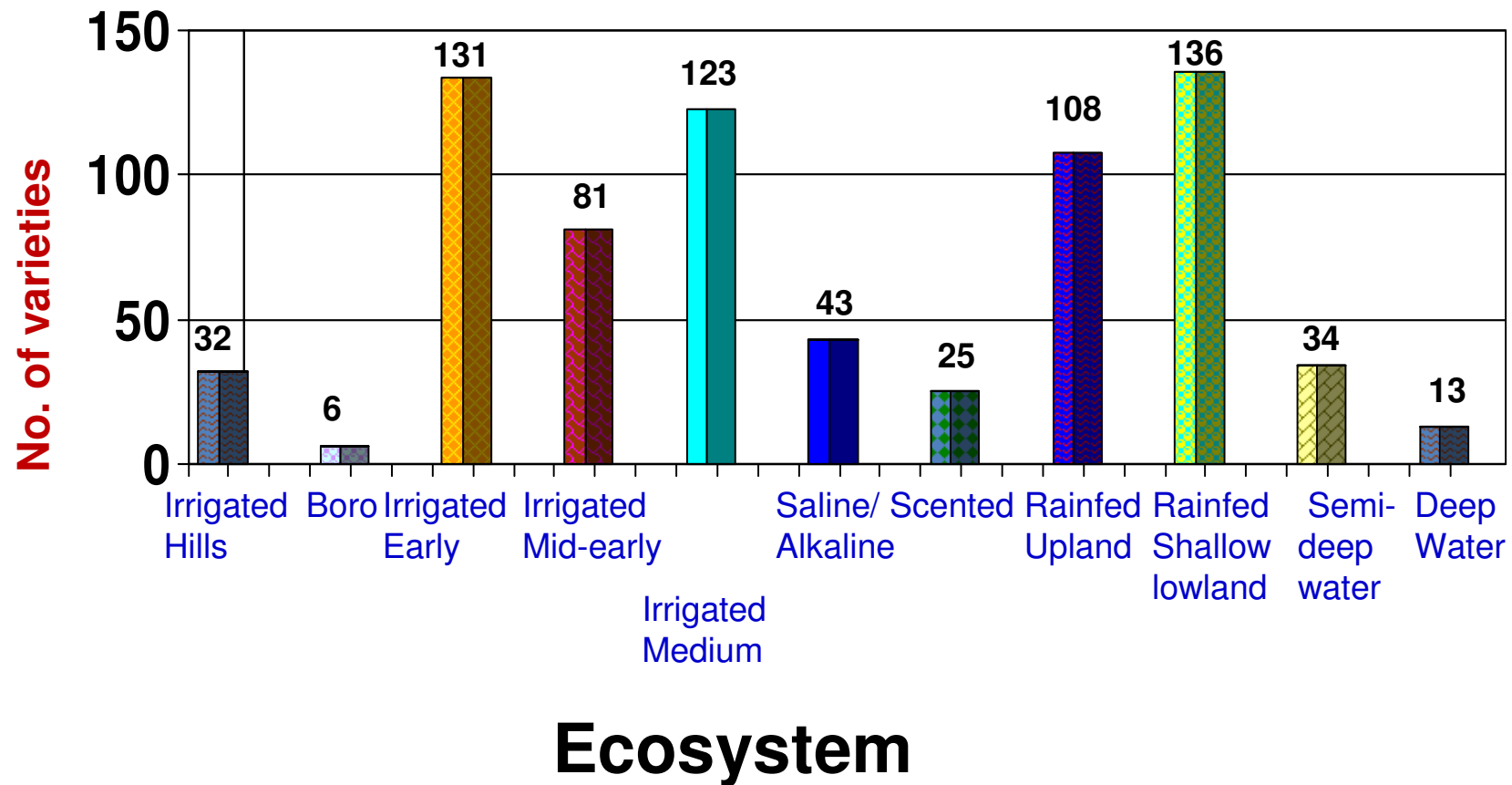
RICE GROWING AREAS IN INDIA



Rice diversity consists of landraces, improved cultivars, hybrids, closely related wild relatives adapted to varied agro-ecological conditions, viz., altitude, temperature, rainfall, soil-type etc. and possessing varied agro-morpho-physiological characteristics

No. of accessions is estimated to range from 75,000 to 1,00,000 including duplicates (~30%)

Rice varieties released in India by ecosystem during 1969-2005 (732)



Rice Varieties Developed for Fragile Ecosystem

S. No.	Ecosystem	Total Varieties Released	Prominent Varieties
1.	Rainfed Upland (RUP)	123	N22, Vandana, AAUDR-1, Birsa Vikash Dhan 10, Birsa Vikash Dhan 12, CR Dhan 40
2.	Rainfed Shallow Lowland (RSL)	126	CR Sugandh Dhan 3
3.	Semi Deep Water (SDW)	14	Jalmagna, Jal Lahari, Barh Avarodhi, Hansaswari
4.	Deep Water (DW)	15	
5.	Irrigated Saline and Alkaline Soils (IRSA)	27	CSR23, CSR27, CSR30, CSR36, Amalmana
6.	Aerobic (ARB)	2	MAS 946-1, Rasi

Field View of 500 Rice Varieties Grown During *Kharif* 2009 at IARI



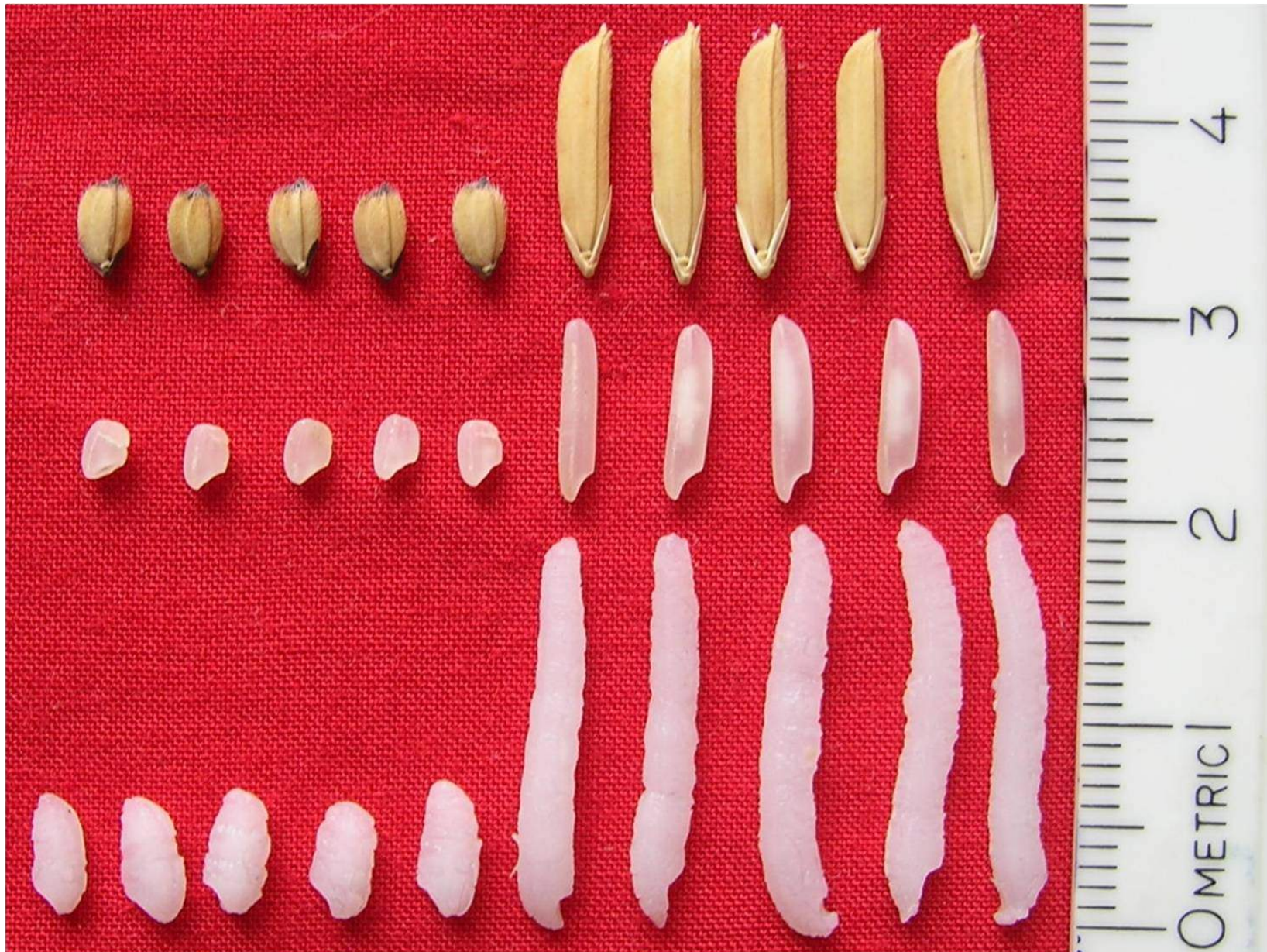
Close View of Rice Varieties Grown During *Kharif* 2009 at IARI



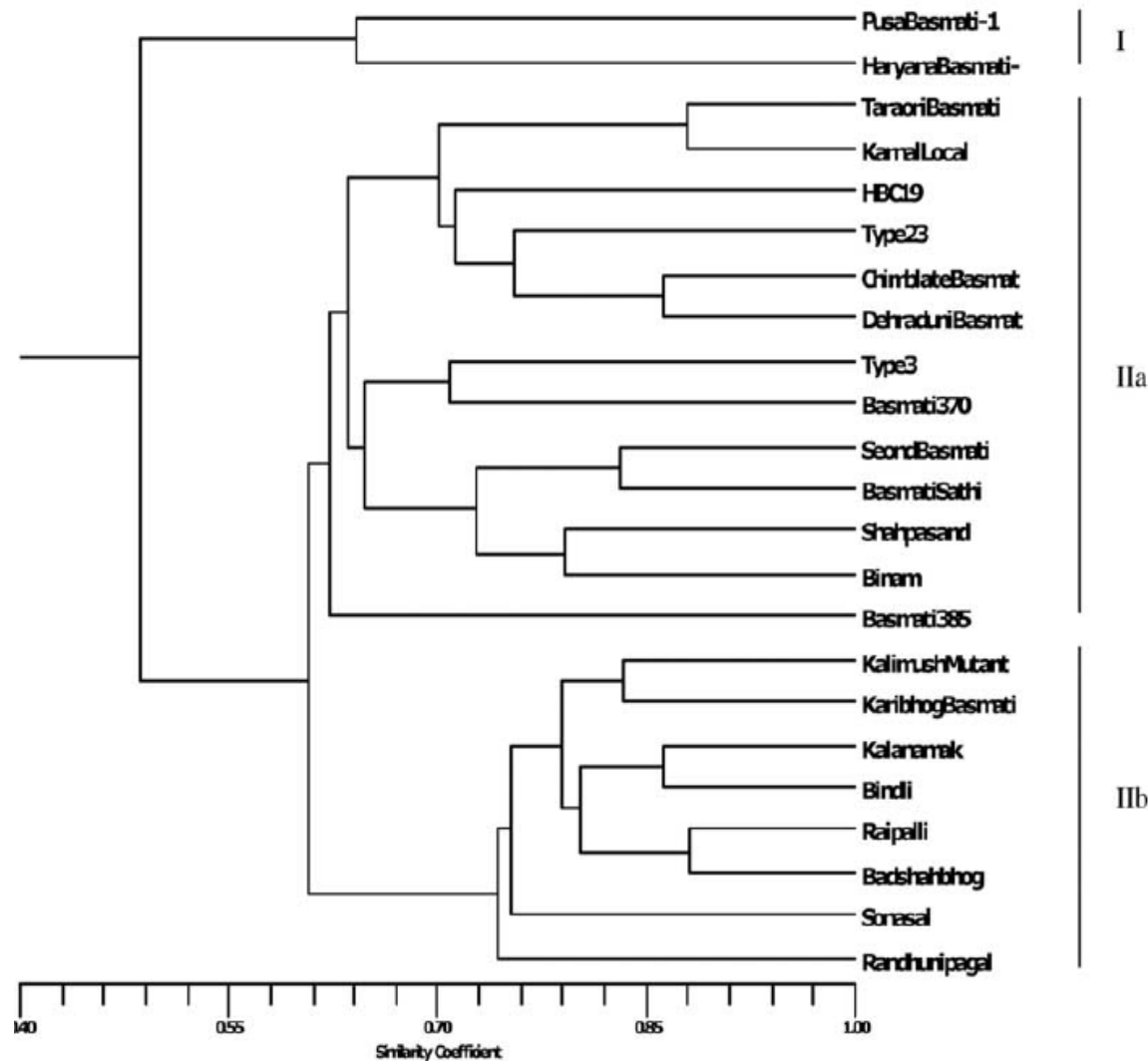
Variation in Panicle Length, Grain Number and Grain Density



Aromatic Rice Varieties of India



Between Variety Diversity: The Aromatic Group



- 55 RM series of STMS markers distributed across 12 rice chromosomes used
- Forty-one of these (74.5%) showed polymorphism
- The PIC varied from 0.083 to 0.665 with an average of 0.338.
- All the varieties could be differentiated from each other at a low probability of identical match by chance (0.07×10^{-13}).

I. Dendrogram depicting the classification of the aromatic rice varieties based on UPGMA and Sequential Agglomerative Hierarchic (SAHN) clustering. The major clusters and sub-clusters are marked on the right side of the dendrogram.



Between Variety Diversity: The Tall Landraces

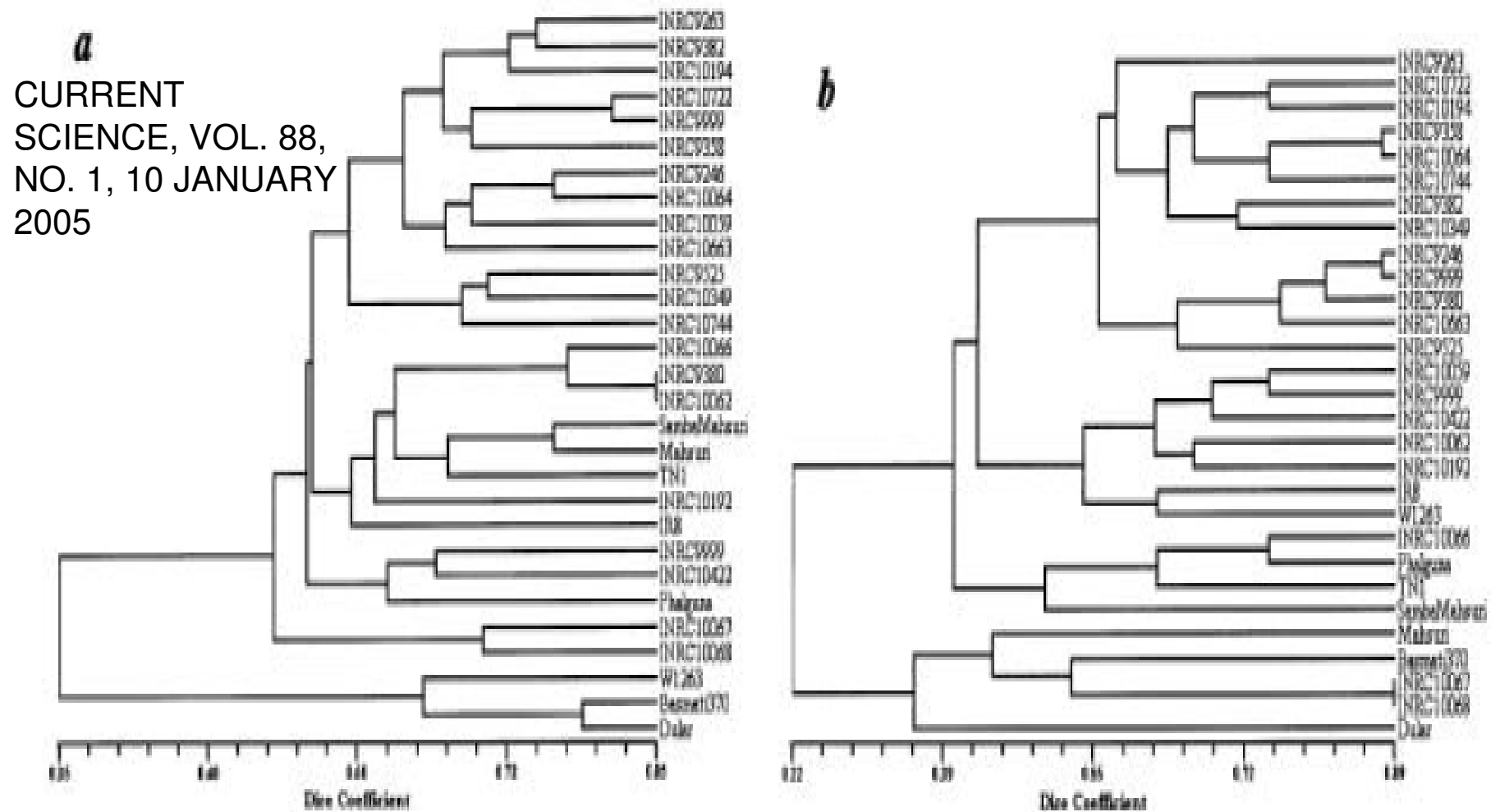
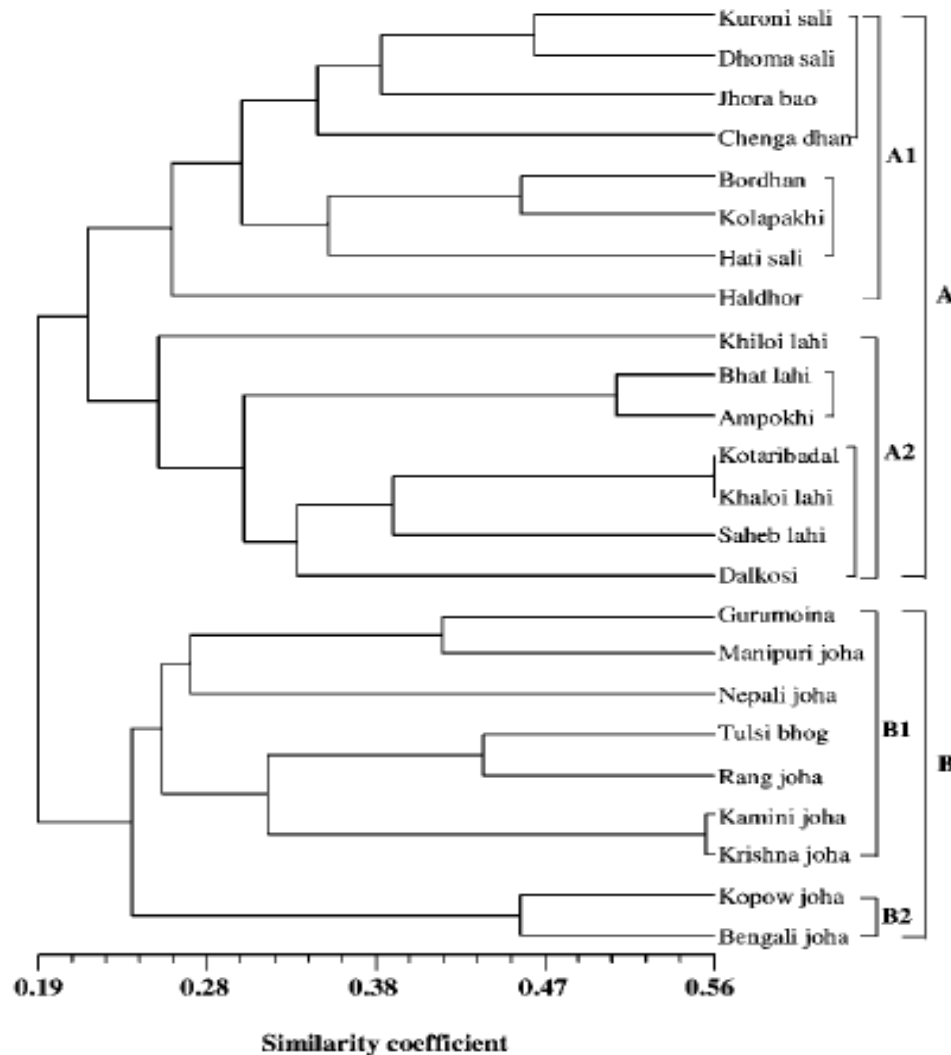


Figure 1. Dendrogram generated by UPGMA-based analysis. (a) Gene-derived SSRs and (b) other SSRs. Tall landraces are represented by INRC accession numbers, W1263, Basmati 370 and Dular. Semi-dwarf varieties are represented by IR8, TN1, Phalguna, and semi-tall varieties are represented by Mahsuri and SambaMahsuri.

Mean no. of alleles/marker in 29 accessions– 4.3/5.88

Between Variety Diversity: The Assam Rice Collection

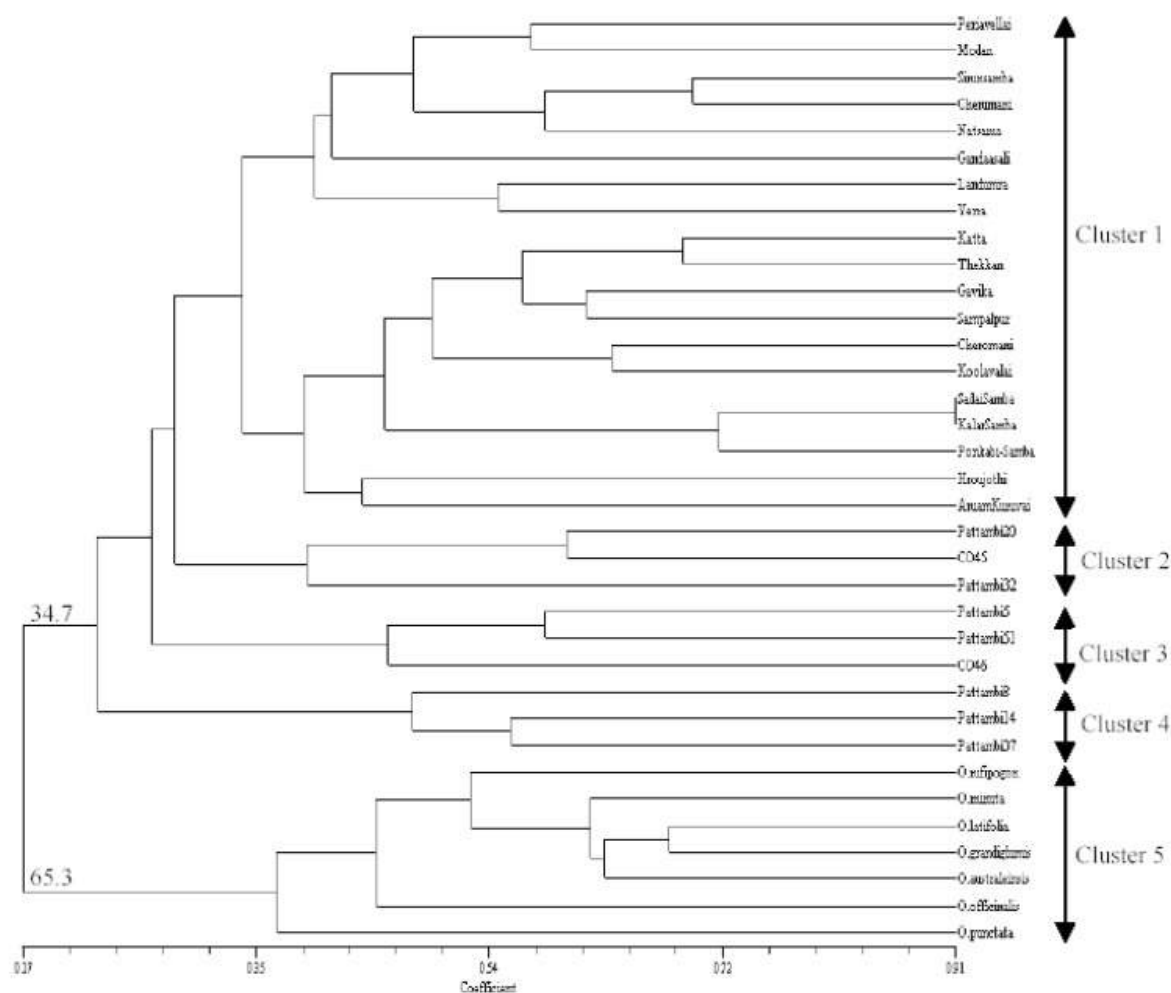


- Diversity among 24 traditional low land rice genotypes quite high
- Similarity ranged from 0.10 to 0.56
- Classification based on molecular data fairly represented the farmer's classification as *Sali* (coarse or bold-grain), *Lahi* (medium slender grain) and *Joha* (scented fine-grain).

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Figure 4. Dendrogram showing clustering of 24 Assam rice cultivars constructed using UPGMA based on Jaccard's similarity coefficient obtained from ISSR analysis.

Genetic Diversity Among Rice Accession from Kerala and Tamil Nadu

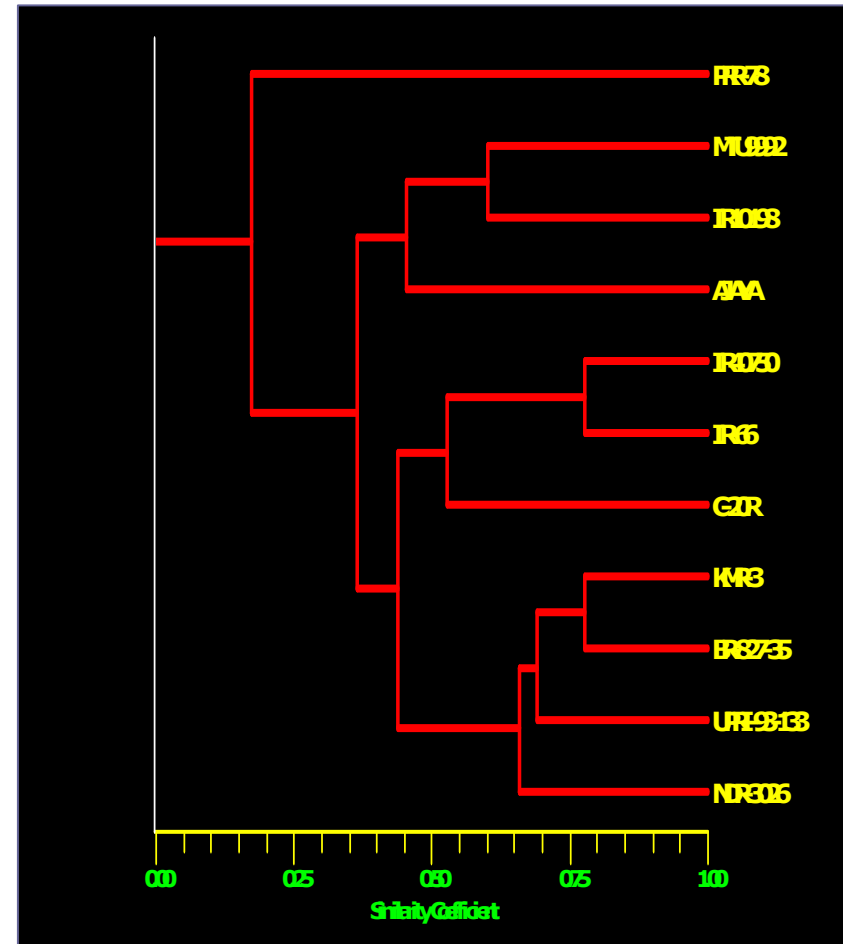


35 rice accessions, included 19 landraces, 9 cultivars and 7 wild relatives mostly from Kerala and Tamil Nadu states.

The allelic richness computed based on 25 STMS markers for the clusters indicated that genetic diversity was the highest among wild relatives (0.436), followed by landraces (0.356), and the lowest for cultivars.

Genetic Diversity Among Indian Rice Restorers Lines

<i>Hybrids</i>	<i>CMS Lines</i>	<i>Restorer Lines</i>
PRH-10	Pusa 6A	PRR-78
APHR 2	IR- 62829A	MTU-9992
CORH 1	IR- 62829A	IR-10198
CNRH 3	IR- 62829A	AJAYA
DRRH 1	IR- 58025A	IR-40750
KRH 2	IR- 58025A	KMR-3
PSD 1	IR- 58025A	UPRI-93-133
CORH 2	IR- 58025A	C20R
ADTRH 1	IR- 58025A	IR-66
SAHYADRI	IR- 58025A	BR 827-35
NSD 2	IR- 58025A	NDR-3026



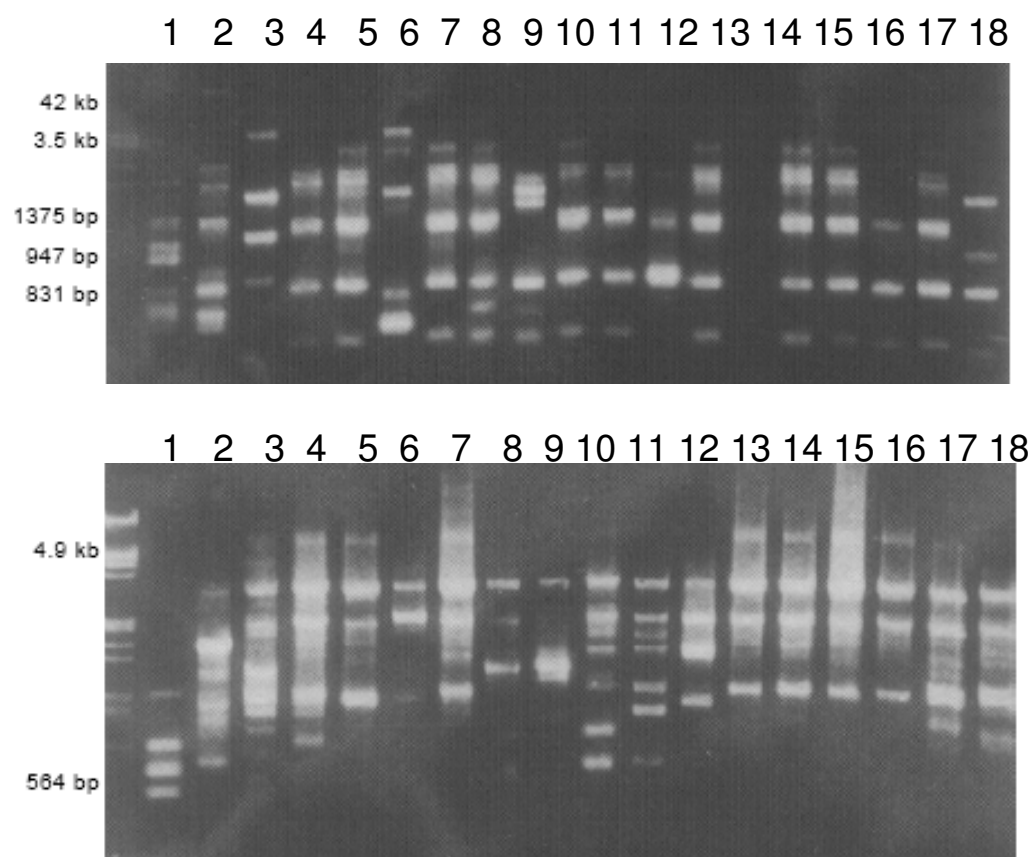
A set of four markers (RM 206, RM 216, RM 258 and RM 263) differentiated all the 11 hybrids from each other



Euphytica 136: 257–264, 2004.

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Hansraj – Same Name, Genetically so Different?

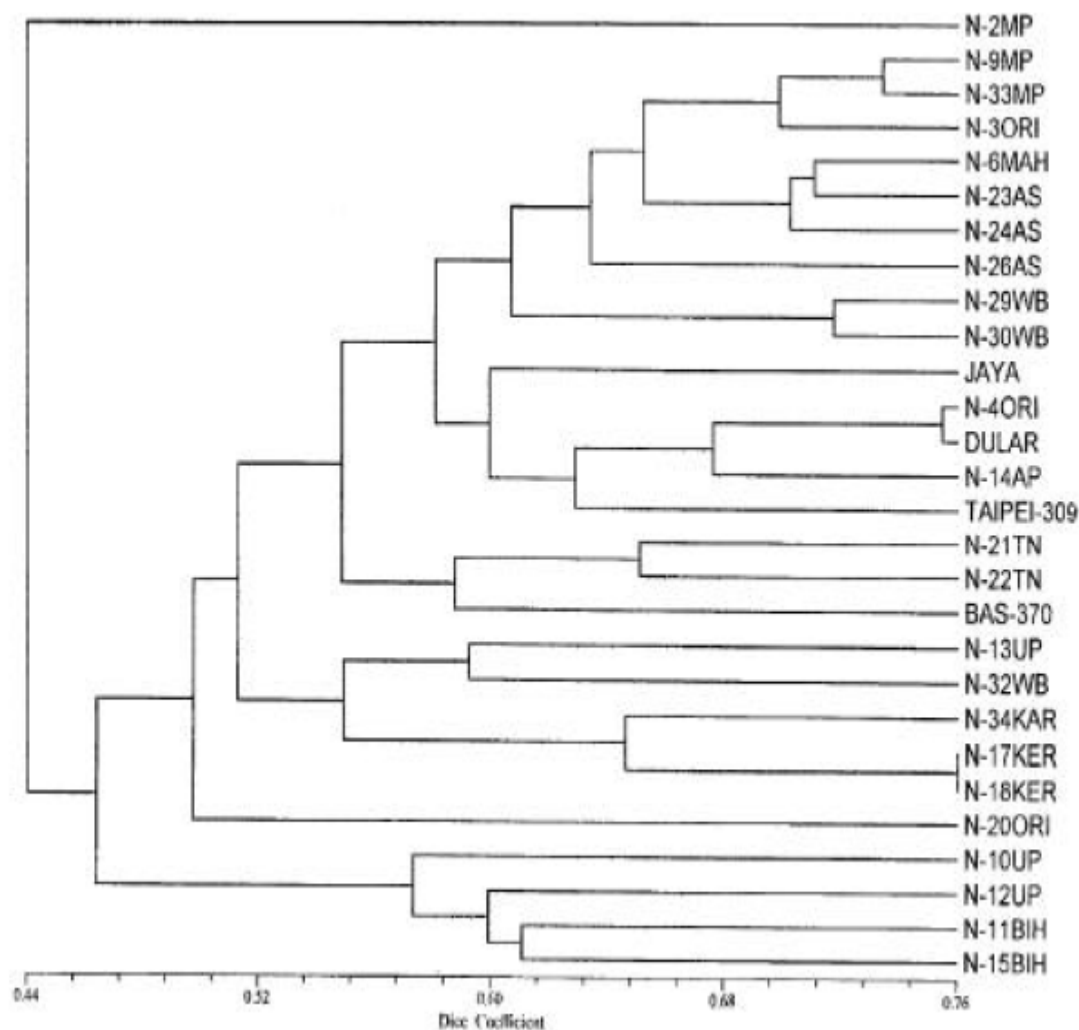


RAPD analysis of genetic variability in Indian scented rice germplasm (*Oryza sativa* L.)

P. Raghunathachari*, V. K. Khanna***[†], U. S. Singh[#] and N. K. Singh*

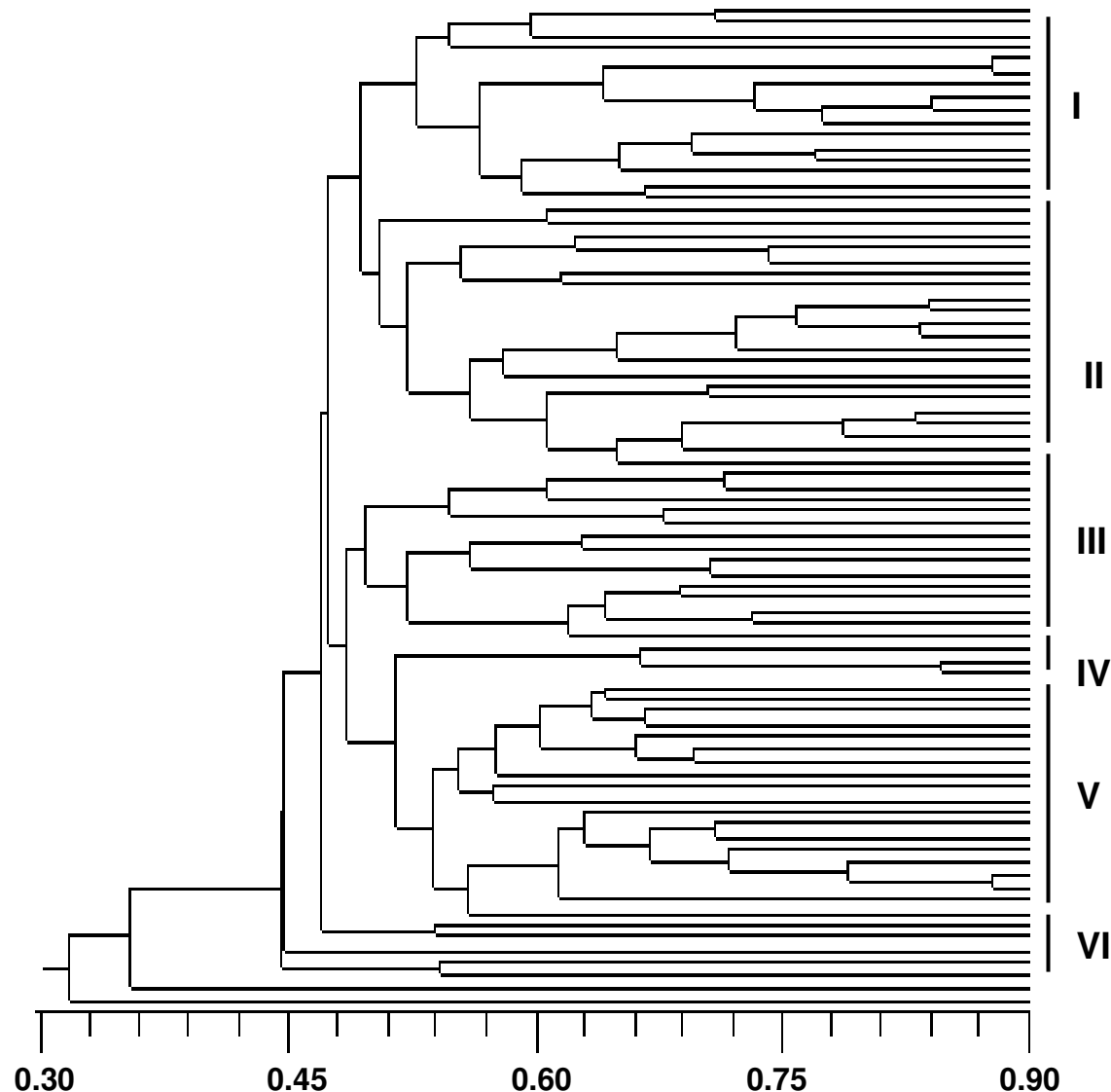
- | | | |
|----|---|------------------------|
| 1 | - | Chota Hansraj 27 |
| 2 | - | Hansraj 43 (Nagina 12) |
| 3 | - | Hansraj 111 |
| 4 | - | Hansraj 102 |
| 5 | - | Hansraj 115 |
| 6 | - | Hansraj 108 |
| 7 | - | Hansraj 103 |
| 8 | - | Hansraj N 109 |
| 9 | - | Hansraj 45 |
| 10 | - | Desi Hansraj 106 |
| 11 | - | Hansraj 101 |
| 12 | - | Hansraj 107 |
| 13 | - | Chota Hansraj 107 |
| 14 | - | Hansraj 110 |
| 15 | - | Desi Hansraj 114 |
| 16 | - | Desi Hansraj 105 |
| 17 | - | KH-7 |
| 18 | - | Pakistani Basmati. |

ISSR and SSR markers delineate geographically diverse *Oryza nivara* accessions and reveal rare alleles



- Genetic diversity among 24 accessions of *O. nivara* from 11 states of India and four *O. sativa* varieties one each from Glaszmann's isozyme groups I, II, V and VI were analysed
- Diversity ranged from 0.19 – 0.67 among 24 *nivara* accessions

Overall Genetic Diversity in Indian Rice Varieties



- Based on 55 STMS markers distributed across 12 chromosomes
- Considerable diversity exists among the released varieties
- Relationships correspond more to pedigree than the target ecosystem
- Traditional landraces and their selections played significant role in combination with the semi-dwarf introductions from IRRI

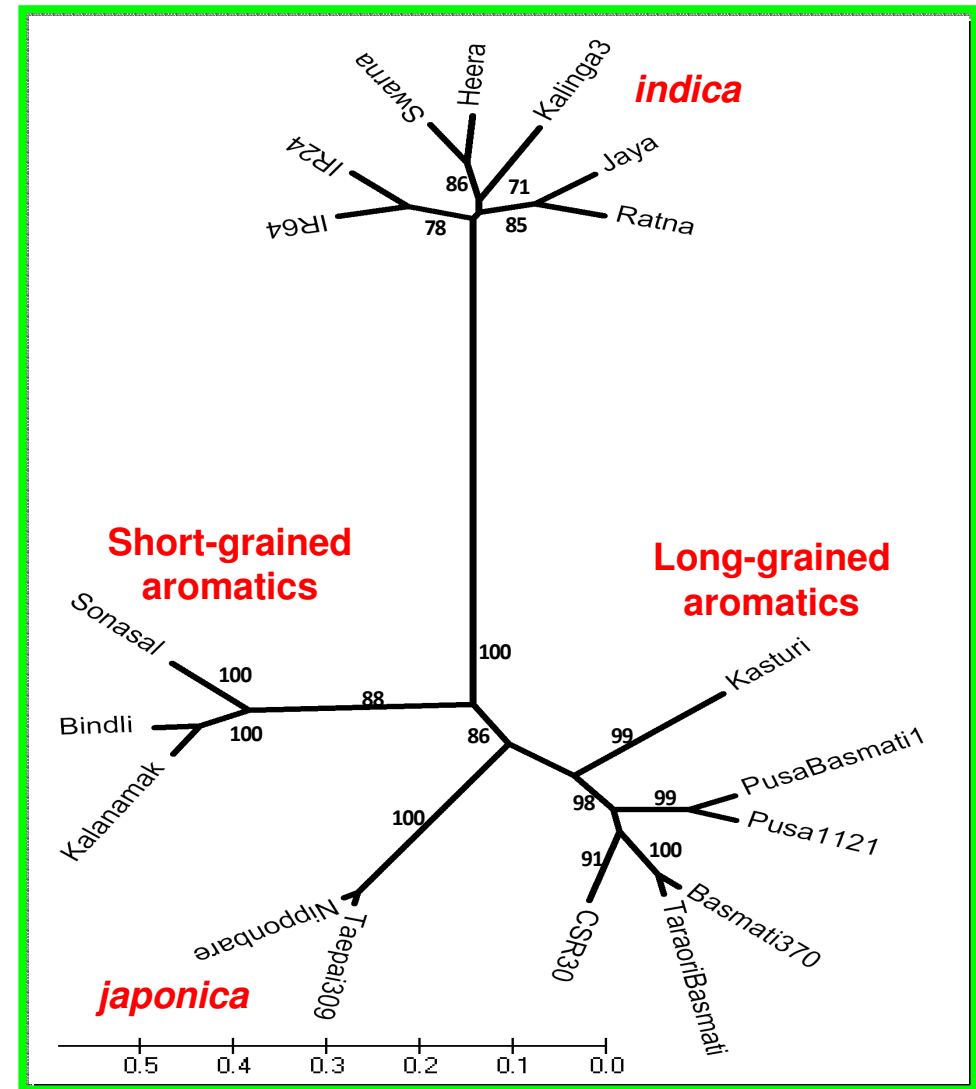
Molecular Diversity & Genetic Relationships Among Rice Genotypes Using Genic Non-coding Microsatellite (GNMS) Markers

BMC Genomics 2009, 10:140
doi:10.1186/1471-2164-10-140

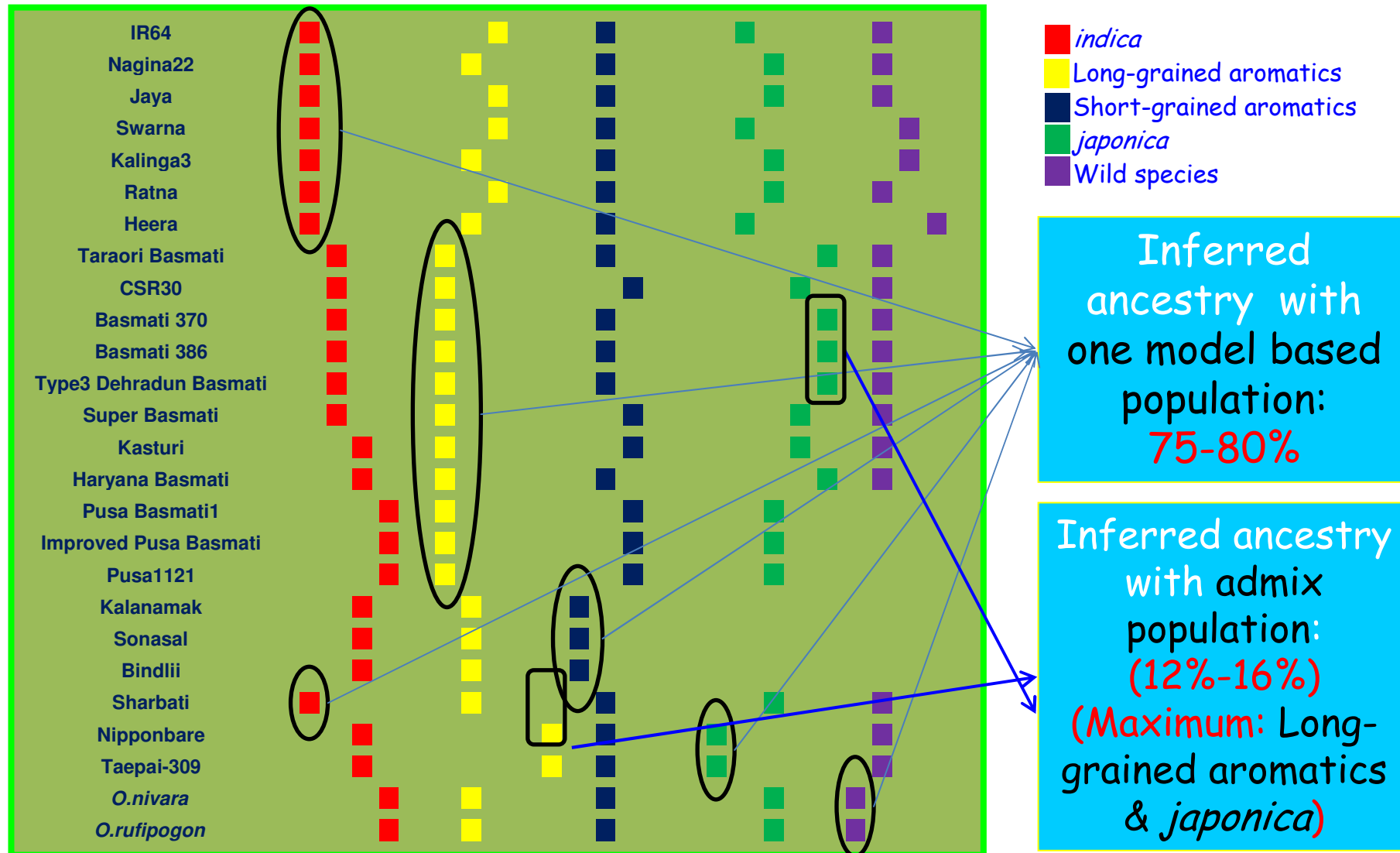
- Wider level of genetic diversity: 0.26 to 0.85 with an average of 0.67 using 75 GNMS markers
- Established Known phenotypic classification & molecular phylogenetic relationships among *indica*, aromatics & *japonica* domesticated rice cultivar groups

Long Grained Aromatics: Wider level of diversity (0.29 to 0.58, avg. 0.42)

Aromatics: Closer to *japonica*
indica: Diverse group



Inferred Ancestry & Phylogenetic Relationships Among Domesticated & Wild Rice Cultivars



Automated Fragment Analysis Using A GNMS Marker in β -galactosidase Gene: Amplified 8 Alleles

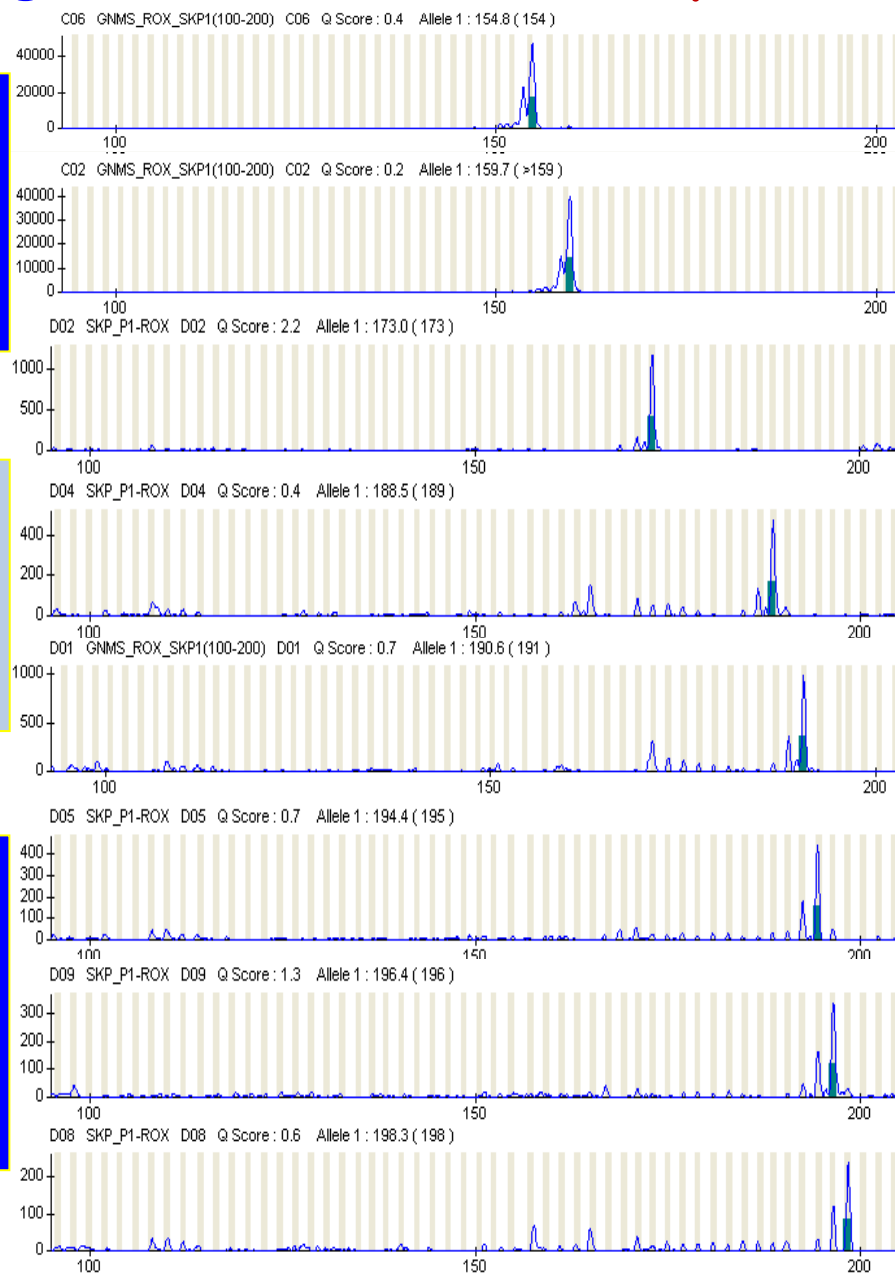
No. of alleles
amplified/locus:
5 to 12 Average:
7.5



30 GNMS
markers
assayed in 26
rice genotypes



Polymorphic
Information
Content:
0.56 to 0.92
Mean: 0.87



Nipponbare: 154 bp

IR64: 159 bp

Sonasal: 173 bp

Pusa1121: 189 bp

Kasturi: 191 bp

Taraori Basmati: 195 bp

Basmati 370: 196 bp

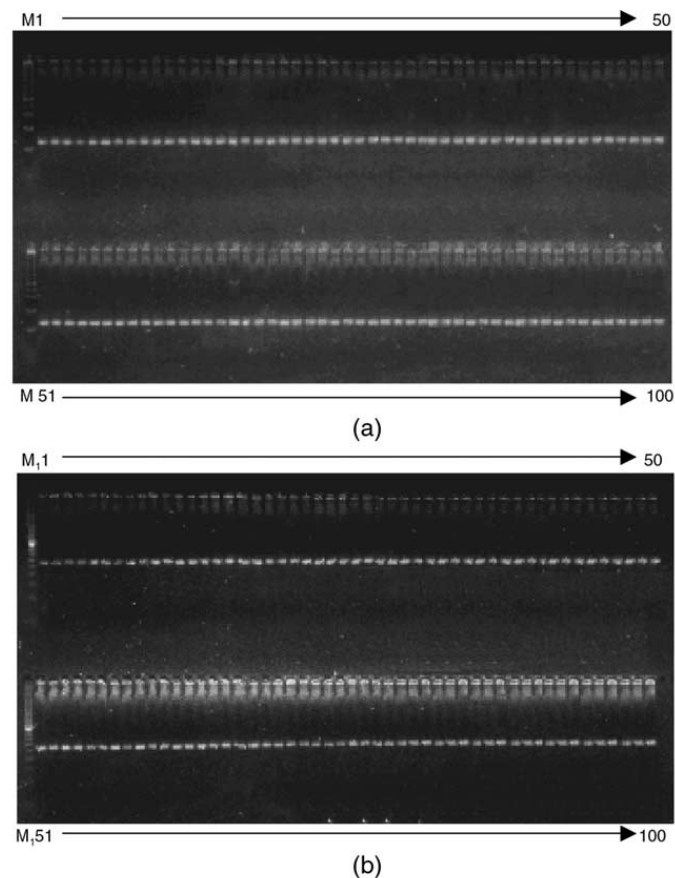
CSR30: 198 bp

DNA Barcoding of Indian Basmati Rice Varieties Using GNMS Markers



Distribution frequency of 118 alleles amplified from 31 polymorphic GNMS markers in a set of six long-grain Basmati rice varieties. Higher (29) number of alleles shared between PB1 and Pusa1121 followed by Basmati370 and Taraori Basmati (24).

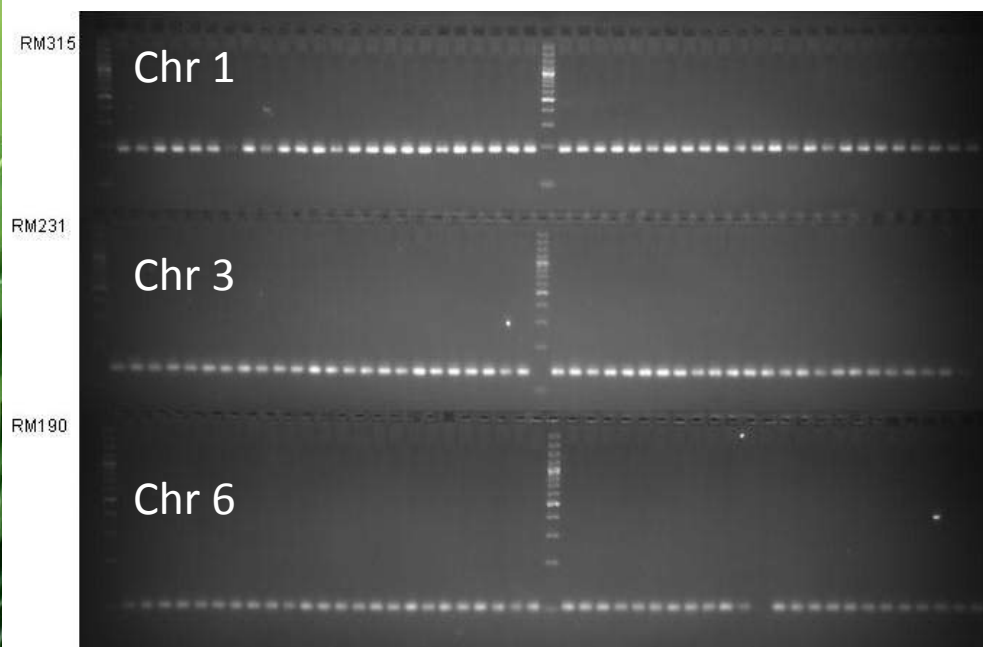
Within Variety Diversity: Case of Pusa Basmati1, the First Semi-dwarf Basmati Variety



Single plant analysis of nucleus (lanes 1–20), breeder (lanes 21–40), foundation (lanes 41–60), certified (lanes 61–80) and farmer's saved seed (lanes 81–100) using STMS markers RM 26 (a) and RM 220 (b). M – 50 bp DNA ladder; M1 – 20 bp DNA ladder.



Within Variety Diversity: Case of Nagina22, an Upland Drought-Tolerant Rice Variety



- 24 STMS markers used to assess intra-varietal polymorphism using 48 individual plants
- None of the markers detected polymorphism

Within Variety Diversity: Case of Galeiganthi, a Landrace from Farmer's Field

Frequency of different STMS alleles and genotypes				
Marker	Allele size (in bp)	Allele frequency	Genotypic class	Genotype frequency
RM 204	120	0.83	Homo (120)	0.780
	130	0.17	Homo (130)	0.110
			Hetero (120+130)	0.110
RM 248	90	0.86	Homo (90)	0.780
	100	0.06	Homo (100)	0.055
	70	0.08	Hetero (90+100)	0.055
			Hetero (70+90)	0.110
RM 231	226	0.81	Homo (226)	0.610
	220	0.19	Hetero (220+226)	0.390
RM 233B	143	0.78	Homo (143)	0.722
	157	0.22	Homo 157	0.167
			Hetero (143+157)	0.111
RM 235	110	0.83	Homo (140)	0.110
	140	0.17	Homo (110)	0.780
			Hetero (140+110)	0.110
RM 205	120	0.94	Homo (120)	0.945
	130	0.06	Homo (130)	0.055

- About 66% plants showed variation for at least one marker
- 50% plants were heterozygous for 1-4 loci
- Within variety diversity was much higher than other landraces studied and varieties in seed production chain.

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MARCH 2004

Summary

- Genetic diversity of rice in India has been assessed using RAPD, ISSR, AFLP, STMS and recently SNP markers
- Most studies have focused on specific groups of genotypes such as aromatic, landraces, regions etc. while efforts are limited for assessment of overall diversity.
- Rice genetic diversity assessed so far suggests a broad genetic base in India
- Genotype specific pattern have been developed particularly for the elite Basmati types for use in trade and commerce
- The landraces available today preserve the allelic richness
- Commercial cultivars are genetically homogenous while the landraces studied revealed composite genetic structure
- There is a need to constitute core and mini core collections based ~80,000 accessions preserved in gene bank, validate them and characterize them for genetic and phenotypic diversity.