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Original Article

Role of Artificial Selection Based on the Farmer's Choice in Diversification of Rice (*Oryza sativa* L.) Cultivars: Assessment of Character Weight of Aromatic Group

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Abstract

Recent years have seen a boom in the study of rice genetics and evolution, as was to be expected given the repeated sequencing of the entire rice genome. The most significant domestication-related genes have received the most attention in the cloning of rice genes. Two recent studies disclose the cloning of numerous genes linked to rice breaking. Two further articles on the spread of shattering in rice have since been published. Fresh insights from other areas of plant science, such archaeobotany, are also helping to shed light on how rice evolved in addition to DNA study. Although it may be believed that recent research on rice will provide answers to certain fundamental questions regarding the growth of the grain, seemingly incongruous results and their interpretations have left numerous crucial questions unresolved. A plant has many different characteristics, but when those characteristics are chosen for domestication, the process of selection becomes somewhat "artificial". The development and consideration of "Dendogram" is typically based on either "Morphological Characters" or "Genetic Materials." The purpose of this experiment was to show that the "Evolution of Domestic Characters" or "Farmers Factor," rather than the development of the species of *Oryza,* was responsible for the local level evolution of rice cultivars. We discovered that certain characteristics, such as elongation after cooking or spikelet quantity, were prioritized by our ancestors when choosing local cultivars.

Keywords:- Cluster analysis, Farmer Factor, *Oryza,* Rice Variety, Selection

Introduction

The Research on rice genetics and evolution has blossomed recent times, as was to be expected following the sequencing of the whole rice genome. The cloning of rice genes concentrated on the most significant domestication-related genes. The cloning of several genes associated to rice shattering was described early this century (Konishi *et al.* 2006; Li, *et al,* 2006). There have been two other articles on the growth of shattering in rice (Ji, *et al,* 2006; Lin, *et al.,* 2007). In addition to DNA research, fresh findings from other fields of plant science, such archaeobotanical, are shedding light on how rice evolved. Although it may be assumed that contemporary study on rice will answer some fundamental problems about the development of the grain that feeds half of humanity, seemingly contradictory findings and their interpretations have left several important issues unanswered.

A biological species made up of germplasm that can be crossed to create fertile hybrids is likened to the core gene pool of a crop (Harlan and deWet, 1971). Hybridization does occur when the species cohabit and flower at the same time, despite the fact that there are a number of barriers to it in the A-genome *Oryza sp.*(Oka, 1988). In Asia, introgression between the several A-genome *Oryza sp.* is

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common (Chen *et al.,* 2004; Kuroda *et al.,* 2005). There have been reports of hybridization between native and cultivated African species and *Oryza sativa*, an introduced species also carrying the A-genome, in Africa (Chu and Oka, 1970; Semon *et al,* 2005).

The japonica (keng) and the indica (hsien) subspecies or varietal classifications of Asian *O. sativa* L. have historically been identified in Chinese (Bray and Needham, 1984). Through investigations of germplasm collections, the primary components of Asian rice diversity towards the end of the 20th century have been found. Six different rice varieties: indica, aus (early summer), ashwina (early deep water), rayada (long duration deep water), fragrant, and japonica—were identified using isozymes (Glaszmann, 1987). The importance of the aus (indica aligned) and aromatic (japonica aligned) kinds has since been confirmed using SSR markers. It was also discovered that the Japonica varieties from the temperate and tropical zones showed differences (Garris *et al,* 2005). A morphologically separate group of Indonesian plants known as bulu or javanica, which has few tillers, lengthy panicles, and seeds with awns, is included in the tropical japonica variants. The habitats of some communities in the Ganges river delta were chosen for the ashwina and rayada varietal groups, the other two recognised varietal groupings by isozyme analysis. While rayada are long-lasting, deepwater kinds without secondary dormancy, ashwina are early maturing deepwater cultivars lacking considerable photoperiod sensitivity. The unusual characteristics of these two small varietal groupings may provide insight into the domestication of rice in the complex deepwater habitats. Germplasm collected during the last 40 years has been used in studies on rice diversification. The traditional lowland varieties in some regions, such as those of Myanmar, were either not harvested at all or just insufficiently before the introduction of improved varieties from breeding efforts. Studies on the genetic diversity of rice reveal an imbalanced sampling of germplasm from a brief period in the history of rice. Undoubtedly loss of some key germplasm hindered the understanding of rice evolution.

In recent rice research there is a lot of emphasis on the production of new rice plant types and several mega projects on rice that promise to increase the rice yield to feed the teeming human population on this planet (Ng'endo, *et al.,* 2022, Salem *et al,* 2022; Bin Rahman and Zhang, 2023). Several different approaches have been envisioned for this initiative. At present there are about 40,000 rice varieties worldwide and the International Rice Research Institute (IRRI) has rice grains of about 10,000 varieties, including rice cultivars and their wild relatives (Awan*et al,* 2017). There are now several research work going on that throws light on the evolution of rice and development of cultivars (Vaughan*et al.* 2008, Roy *et al,* 2022).
The purpose of this paper is to review some recent advances in the evolutionary history of rice. Prior to discussing the studies on the domestication of rice in Asia and Africa, it is important to consider the importance our ancestors gave to character traits of rice during the artificial selection of traditional rice also called rice land races.

Understanding the gene pools from which Asian and African rice originated is crucial to comprehend the domestication of these two types of rice. To do that, it is necessary to comprehend both the current state of these gene pools and their potential historical evolution. It's also important to realize that not all of the characters (traits) were given equal consideration by our ancient farmers. A naturally selected, undomesticated plant should never have evolved into a domesticated crop. Therefore, in addition to selection pressure from the environment, there was always a **"Farmers Selection" pressure.**

The Farmers Way: African and Asian cultures have chosen rice and modified their environments to grow it. The Diola of Senegal, for instance, cultivate rice in tidal marshes, which is remarkably similar to the 'kaipal' farming recorded in Kerala, India, early in the 20th century (Linares, 1981; Ramiah, 1937). To deal with seasonal seawater incursion, people in these regions separately created sophisticated diking, desalination, ridging, and transplanting methods.

The International Rice Research Institute's collection of cultivated rice accessions ranges in length from up to 30% longer to 30% shorter than wild rice. The longest and shortest seeds are found in African rice accessions of *Oryza barthii*. They differ by 15, and 20%, respectively, from the longest and shortest seeds of the cultivar *O. glaberrima*. As a result, based just on the size of the seed, it is impossible to differentiate between wild and farmed rice. Other characteristics, such the quantity of seeds per panicle and synchronous maturity, have proved more crucial throughout domestication. The number of panicles per plant varies greatly between rice cultivars. One or a very small number of productive tillers are seen in several varietal groups, particularly tropical japonica from Indonesia (bulu kinds). Domesticated deepwater rice culms can reach lengths of 5 or 6 m, while culm (stem) length is very variable (Catling, 1988). Only three traits, culm length, panicle length and spikelet shattering, were consistently recorded in six studies that investigated QTLs for domestication related traits (Bres-

Patry,2001). Secondary branching of panicles, spikelets per panicle and heading date were recorded in five of these studies (Lee, 2005).

In the current experiment, we used a total of 30 rice lines. Some of the rice lines were commercial Aromatic rice, some Non Aromatic ommercial kinds as well as some "breeding lines" that are being selected. 10 (Ten) agro-morphological traits that appear to be crucial for "Ecological selection" and "Yield" have been taken into account. Additional 10 (Ten) high-caliber characters that are "Economically Important" have been selected. A plant has a variety of traits, but when those traits are selected for domestication, the selection process is artificial selection. Typically, "Dendogram" preparation and consideration are based on either "Morphological Characters" or "Genetic Materials." The goal of this experiment was to investigate whether the evolution of rice cultivars was similar to the evolution of the different species of *Oryza*or were they due to the "Evolution of Domestic Characters" based on the **"**Farmers Selection Criteria/Factor instead at different localities

Material and Methods

Plant Material: Three replicates of 40 plants/variety each were used in the randomized block design (RBD) to grow the different rice genotypes. On the last week of June, seeds were sowed in the seed bed, and after 30 days, one robust seedling or hill was transplanted at a row x plant spacing of 25cm x 15cm. The usual agronomic procedures were used. For semi-dwarf genotypes, fertilizer was applied to the soil at a rate of 80:50:50 kg of N, P, and K per hectare (as urea, single super phosphate, and muriate of potash), and at a rate of 25:50:50 kg of N, P, and K per hectare for conventionally tall genotypes. Three divided dosages of fertilizer were used*viz.* 50% during land preparationand the remaining 20% in two equal portions during the maximum tillering and boot stages. Sprays of insecticide were used to manage pests and insects as and when necessary. At 85% of the seeds' maturity, harvesting was completed. For characterization, a total of five plants per replication per rice line were chosen at random, avoiding the boundary rows.

Table I: The name, accession number and source of the rice genotypes.

SL No	GENOTYPE	ACCESSION NO.	SOURCE
1.	PUSA BASMATI (EB)	IRGC-78422	IARI, India
2.	KASTURI (EB)	IRGC-60303	DRR, India
3.	IET 13544 (EB)	BI-20	DRR, India
4.	BASMATI-385 (EB)	IRGC-76317	Pakistan
5.	TRAVADI BASMATI (TB)	BI-58	DRR, India
6.	BASMATI 370 (TB)	IRGC-9026	Pakistan
7.	PAKISTANI BASMATI (TB)	IRGC-67746	Pakistan
8.	BASMATI 1 (TB)	IRGC-27798	Pakistan
9.	BASMATI 122 (TB)	IRGC-27805	Pakistan
10.	BASAMATI 123 (TB)	IRGC-27806	Pakistan
11.	BASMATI 107 (TB)	IRGC-27803	Pakistan
12.	BASMATI 433 (TB)	IRGC-27836	Pakistan
13	KARNAL LOCAL 1 (TB)	IRGC-78484	India
14.	AGULHA (EA)	IRGC-81660	Mozambique
15	KHAO DAWK MALI (EA)	IRGC-48220	Thailand
16.	KHAO DAWK MALI 105 (EA)	IRGC-27748	Thailand
17.	IR 878B4-220-3-1 (EA)	IRGC-32592	Philippines
18.	DELLA (EA)	IRGC-14529	U.S.A.
19.	LANGKAYAN (EA)	IRGC-71551	Malaysia

20.	UDARA (EA)	IRGC-71642	Malaysia
21.	PADI BAWANG (EA)	IRGC-25475	Indonesia
22.	RADHUNIPAGAL (IA)	BI-RP	CRRS, WB, India
23.	KATARIBHOG (IA)	BI-KB	CRRS, WB, India
24.	BADSHAHBHOG (IA)	BI-BB	CRRS, WB, India
25.	GOBINDOBHOG (IA)	BI-GB	CRRS, WB, India
26.	PSBRC-2 (NA)	IRGC-81704	IRRI, Philippines
27.	PSBRC-18 (NA)	IR-51672-62-2-1-1-2-3	IRRI, Philippines
28.	PSBRC-20 (NA)	IR-57301-195-3-3	IRRI, Philippines
29.	IR 64 (NA)	IRGC-66970	IRRI, Philippines
30.	IR 72 (NA)	IRGC-76330	IRRI, Philippines

TB = traditional Basmati, EB = evolved Basmati, EA = exotic aromatic, IA = indigenous aromatic, NA = non-aromatic, CRRS= Chinsura Rice Research Station,

Measurements of Agro-morphology, Quality Character and Character Weight of Rice Genotypes.

Agro-Morphology

The following characters were used for this investigation.

Days to Flowering (DTF): Expressed in number of days from sowing to 50% flowering, determines early or late varieties.

Plant Height (PLHT): At the time of harvest, the main culm was measured from the soil surface to the tip of the panicle (excluding awn, if any) in centimeters and the average denoted the mean plant height of each genotype. This character is important against water logging.

Number of Tillers per Plant (TN): At maturity, the total number of tillers, including those not bearing panicles, of each plant was counted and the average denoted the mean number of tillers per plant, directly proportional with yield.

Number of Panicles per Plant (PN): The total number of panicles of each plant was counted and the average value denoted the mean number of panicles per plant, directly proportional with yield.

Best Panicle Length (BPL): The length of the longest panicle was measured from the panicle collar to the tip for each plant and the average value calculated, directly proportional with yield.

Number of Spikelets per Panicle (SPLN): The total number of spikelets, fertile and sterile, of the best panicle was counted and the average value denoted the total number of spikelets per panicle, directly proportional with yield.

Percentage of Fertile Spikelets per Panicle (%FS): The total number of spikelets containing filled grains on the best panicle was counted and expressed as percentage of the total number of grains, directly proportional with yield.

Panicle Density (PD): The total number of spikelets, fertile and sterile, divided by the length of the best panicle and averaged denoted the panicle density, directly proportional with yield.

100 Seed Weight (SW): A hundred well developed, filled grains at approximately 14% moisture content was weighed in grams and the average of five plants denoted the 100 grain weight for each replication, directly proportional with yield**.**

Single Plant Yield (YLD): The panicles of a single plant were manually threshed; the seeds cleaned of chaff and other vegetative parts, weighed and averaged to obtain the plant yield in grams. The ultimate productivity of a plant which was considered for selection.

Quality Characters

Grain Length (GL): A total of 10 well-developed grains per plant were attached to a 5.5cm X 2.5cm double-sided tape on a 7cm X 4cm black chart paper. The length of the grains was measured with the help of a stage-micrometer and an eyepiece graticule under a dissecting microscope (Olympus). Standardization of the eyepiece graticule was done using a stage-micrometer. The average of the values expressed in millimeter for three replications was the grain length. This is considered as important commercial character from ancient time.

Grain Breadth (GB): Grain breadth was also measured as given for grain length. This is considered as important commercial character from ancient time.

Grain Length/Breadth (G-L/B) Ratio: The length of each grain was divided by the breadth of the same grain and the average calculated for the three replications.

Kernel Length (LBC): Filled grains of each rice lines were de-husked carefully, and the pericarp removed by polishing with sand–paper (Million flint paper, Grade-0, Million abrasives Pvt. Ltd., India). Ten clean, whole rice kernels were measured microscopically and the average of three replicates was the kernel length. The rice genotypes were assessed and designated on the basis of kernel length following the SES (IRRI, 1996; Table 2). This is considered as important commercial character from ancient time.

Table 2. The classification of rice kernel length.

Designation	Length (mm)
Extra long	7.5+
Long	6.61-7.5
Medium	5.51-6.60
Short	< 5.50

Kernel Breadth (BBC): The breadths of the kernels were measured, after polishing This is considered as important commercial character from ancient time.

Kernel Length/Breadth (L/B-BC) Ratio: The length of each kernel was divided by the breadth of the same kernel and the average calculated for three replicates of 10 kernels each. Based on the length/breadth ratio, or shape of the kernel, the rice genotypes were assessed and designated according to SES (1996) as given in Table 3.

Table 3. The classification of rice genotypes by kernel length/breadth ratio or shape.

Shape	Length/Breadth Ratio
Slender	> 3.0
Medium	2.1- 3.0
Bold	1.1- 2.0
Round	< 1.0

Length and Breadth of Cooked Kernels: From each rice genotype's 20 well-filled kernels were dehusked and had the bran layer polished off with sandpaper. The kernels were prepared in an LG Intellogrill microwave oven using the next procedure:

i) Single-distilled water was pre-heated in a microwave for five minutes at 1000 C.

ii) In little muslin bags, the polished kernels of the various rice genotypes were placed in water and cooked for 15 minutes.

iii) Ten intact kernels were removed from the cooked grain and measured microscopically for length (kernel length after cooking, LAC) and breadth (kernel breadth after cooking, BAC) in cold water. Three replications' average values were computed. The kernel length/breadth ratio after cooking (L/B-AC) was calculated by dividing LAC by BAC.

Cooked Kernel Elongation Ratio (CKE-R): Cooked kernel elongation was expressed as a ratio (CKE-R). The average length of the cooked kernels (LAC) was divided by the average length of the kernel before cooking (LBC) and expressed as the cooked kernel elongation ratio.

Evaluation of Aroma (ARO): A rapid, microscale method for evaluation of aroma from grain and leaf material was measured in the laboratory.

Evaluation of Grain Aroma: 10 kernels were pulverized into a coarse powder for each genotype and then placed in a 1.5ml Eppendorf tube with 500ml of 1.7% KOH solution. A total of 16 Eppendorf tubes, including a positive and a negative control, were placed in an Eppendorf rack and heated in an LG Intellogrill microwave oven at setting 4 (medium) for 30 seconds. Each panel had five qualified evaluators, and they instantly made sensory assessments of the scent. Each genotype was examined in at least 3 replicates.

Evaluation of Leaf Aroma: At the peak tillering stage, a 4 cm portion of the second leaf from the top of each genotype was taken from the field. The leaf was divided into small pieces, placed in 1.5 ml Eppendorf tubes, and treated according to the instructions provided for determining grain aroma.For each genotype, aroma was rated on a scale of 0 (no aroma), 1 (weak aromatic), 2 (aromatic), and 3 (strongly aromatic). The average aroma score was calculated from the individual ratings provided by the panelists. A genotype was categorized as aromatic if its average score was 1 or higher, and non-aromatic if it had a score below 1.

Alkali Spreading Value (ASV): An indication of the rice starch's gelatinization temperature is used to calculate the alkali spreading value. The 10ml of 1.7% KOH solution was added to a 90mm diameter plastic Petri dish containing six complete, hand-polished, and crack-free kernels of rice. The kernels were separated from one another by a sufficient amount of space. For 23 hours, the Petri dish was covered and incubated at 300C. After incubation, endosperm disintegration and kernel appearance were assessed visually in accordance with Table 2.4 (SES, IRRI, 1996).

Table 4: Numerical scale for scoring alkali spreading value.

SCORE	SPREADING	CLEARING
1	Kernels not affected.	Kernel chalky.
2	Kernel swollen.	Kernel chalky, collar powdery.
3	Kernel swollen, collar complete or narrow.	Kernel chalky, collar cottony or cloudy.
4	Kernel swollen, collar complete and wide.	Center cottony, collar cloudy.
5	Kernel split or segregated, collar complete and wide.	Center cottony, collar clearing.
6	Kernel dispersed merging with collar.	Center cloudy, collar clear.
7	Kernel completely dispersed and intermingled.	Center and collar clear.

All statistical analysis has been done using SPSS 10.0 software.

All dendogram has been prepared by using https://genomes.urv.cat/UPGMA
All Cluster analysis has been done by using https://genomes.urv.cat

Results

Table 5: The mean of the agro-morphological characters of the 30 rice genotypes.

GENOTYPE NAME	DTF	PLHT (cm)	TN	PN	BPL (cm)	SPLN	PD	%FS	SW (g)	YLD (g)
PUSA BASMATI 1	98.50	106.13	10.33	10.20	28.40	129.53	4.57	**60.6**	2.14	9.22
KASTURI	86.33	108.73	8.03	8.00	27.88	119.57	4.31	64.2	2.04	7.40
IET 13544	**75.83**	**63.90**	10.63	10.27	22.80	84.87	3.73	62.8	2.32	7.72
BASMATI-385	90.83	122.10	8.60	8.47	28.20	111.65	3.97	66.3	2.12	7.88
TRAVADI BASMATI	96.00	130.83	9.37	9.17	29.27	91.08	**3.14**	79.1	2.45	7.83
BASMATI 370	94.33	129.40	9.17	9.00	26.93	105.10	3.97	65.7	1.97	7.75
PAKISTANI BASMATI	95.83	138.05	11.15	11.15	28.67	107.67	3.76	80.9	2.21	11.74
BASMATI 1	97.17	152.83	9.23	9.17	31.43	125.13	4.01	82.6	1.96	8.16
BASMATI 122	96.17	142.27	8.63	8.43	28.37	124.33	4.39	89.7	2.16	8.78
BASAMATI 123	98.17	144.43	9.83	9.67	29.70	121.63	4.11	73.7	2.39	9.98
BASMATI 107	97.67	144.33	7.03	6.93	**32.33**	149.07	4.62	75.3	1.99	7.36
BASMATI 433	94.50	147.10	10.73	10.67	27.87	116.63	4.19	83.0	2.08	11.75
KARNAL LOCAL 1	90.83	136.10	**13.85**	**13.23**	27.60	91.80	3.33	73.2	2.25	9.24
AGULHA	125.17	150.73	**5.43**	**5.35**	24.63	200.10	8.13	66.1	**2.97**	16.37
KHAO DAWK MALI	121.83	150.83	8.47	8.47	24.10	169.53	7.09	75.4	2.58	14.39
KHAO DAWK MALI 105	120.67	148.20	8.70	8.67	23.60	147.23	6.25	82.6	2.46	17.48
IR878B4-220-3-1	93.67	89.23	7.75	7.72	22.60	200.93	8.93	64.2	2.30	12.13
DELLA	88.67	105.43	7.67	7.67	25.03	145.80	5.90	67.6	2.38	14.10
LANGKAYAN	98.00	120.65	6.40	6.27	**19.87**	130.34	6.54	75.7	1.80	**5.63**
UDARA	**128.33**	145.10	8.13	8.12	24.17	212.03	8.80	89.6	2.17	12.33
PADI BAWANG	101.00	125.00	6.00	5.93	21.97	155.37	7.07	83.4	1.48	6.54
RADHUNIPAGAL	123.17	**164.47**	8.23	8.23	24.60	226.10	**9.21**	**92.3**	**1.03**	11.05
KATARIBHOG	107.33	150.10	10.17	9.75	29.17	140.87	4.85	87.5	1.58	13.14
BADSHAHBHOG	111.67	153.23	11.37	11.27	27.23	239.40	8.82	90.1	1.15	16.57
GOBINDOBHOG	124.17	153.97	10.23	10.23	26.17	**239.73**	9.19	89.8	1.04	13.93
PSBRC 2	100.17	78.93	6.03	5.95	20.35	97.97	4.82	67.1	2.33	7.75
PSBRC 18	108.83	95.40	10.45	10.45	23.07	134.20	5.82	74.0	2.54	**18.67**
PSBRC 20	92.33	85.10	6.53	6.48	30.93	133.83	4.34	82.4	2.31	12.68
IR 64	87.50	64.60	10.03	9.87	20.40	**76.80**	3.80	85.2	2.26	9.38
IR 72	84.50	82.70	7.77	7.50	21.57	125.80	5.89	76.7	2.30	11.84
CD at $t_{5\%}$	**2.21**	**5.63**	**1.21**	**1.21**	**2.27**	**13.07**	**0.66**	**2.58**	**0.06**	**1.82**

DTH - days to 50% flowering; PLHT - plant height; TN - tiller number; PN - panicle number; BPL - best panicle length; SPLN – No. of spikelet/panicle; PD - panicle density, %FS - percent fertile seeds; SW - 100 seed weight; YLD - total plant yield. The highest and lowest values for each trait are given in bold.

Table 6: The mean of the quality characters of the 30 rice genotypes

GENOTYPE NAMES	GL (mm)	GB (mm)	G-L/B	LBC (mm)	BBC (mm)	L/B-BC	LAC (mm)	CKE-R	ARO	ASV
PUSA BASMATI 1	11.02	1.84	**5.99**	8.06	1.55	**5.19**	**16.23**	2.01	3.0	5.63
KASTURI	9.30	2.29	4.07	7.12	1.60	4.45	12.17	1.71	3.0	7.00
IET 13544	**11.14**	2.01	5.54	7.98	1.60	4.98	14.36	1.80	3.0	2.41
BASMATI-385	10.05	**1.81**	5.54	7.07	1.60	4.42	12.80	1.81	3.0	3.00
TRAVADI BASMATI	10.40	1.97	5.28	7.97	**1.54**	5.17	12.93	1.62	3.0	2.00
BASMATI 370	9.26	1.94	4.79	7.08	1.63	4.36	12.23	1.73	3.0	2.33
PAKISTANI BASMATI	10.75	1.86	5.80	**8.09**	1.61	5.05	14.02	1.73	3.0	3.10
BASMATI 1	9.06	2.05	4.42	6.84	1.64	4.21	10.10	1.48	3.0	2.00
BASMATI 122	8.65	2.31	3.75	6.64	2.08	3.20	11.47	1.73	3.0	3.97
BASAMATI 123	9.18	2.21	4.16	6.97	1.93	3.62	15.46	**2.22**	3.0	2.00
BASMATI 107	8.52	2.19	3.89	6.70	1.83	3.67	11.12	1.66	3.0	2.00
BASMATI 433	9.05	2.12	4.27	6.28	1.62	3.90	10.36	1.65	3.0	6.00
KARNAL LOCAL 1	10.99	2.08	5.27	8.07	1.76	4.60	13.73	1.70	3.0	2.00
AGULHA	9.86	2.70	3.65	7.85	2.22	3.53	11.65	1.48	3.0	4.66
KHAO DAWK MALI	9.36	2.42	3.88	7.55	2.23	3.39	9.98	**1.32**	3.0	2.75
KHAO DAWK MALI 105	9.63	2.32	4.15	7.12	1.86	3.83	10.34	1.45	3.0	2.50
IR878B4-220-3-1	8.41	2.41	3.50	5.96	2.13	2.80	8.33	1.40	3.0	3.10
DELLA	9.18	2.38	3.86	7.23	1.85	3.91	12.40	1.72	3.0	7.00
LANGKAYAN	8.50	2.17	3.91	6.76	1.78	3.81	8.91	1.32	3.0	2.00
UDARA	7.17	**2.76**	2.60	5.37	**2.45**	2.19	8.31	1.55	3.0	2.00
PADI BAWANG	6.97	2.18	3.19	5.06	1.77	2.87	7.95	1.57	3.0	2.03
RADHUNIPAGAL	**5.38**	2.11	**2.55**	3.98	1.82	2.18	7.79	1.96	3.0	2.02
KATARIBHOG	8.05	2.09	3.85	5.94	1.72	3.45	11.65	1.96	3.0	2.03
BADSHAHBHOG	5.90	2.28	2.59	4.16	1.97	**2.11**	8.47	2.04	3.0	7.00
GOBINDOBHOG	5.48	1.97	2.79	**3.88**	1.62	2.40	**7.37**	1.90	3.0	2.33
PSBRC-2	8.87	2.21	4.02	7.02	2.20	3.19	10.13	1.44	0.0	2.99
PSBRC-18	8.55	2.39	3.58	6.94	2.18	3.18	10.57	1.52	0.0	6.33
PSBRC-20	9.08	2.25	4.04	6.99	2.04	3.43	9.31	1.33	0.0	2.00
IR 64	8.87	2.24	3.95	7.05	2.05	3.43	9.83	1.39	0.0	2.00
IR 72	8.81	2.31	4.05	6.36	2.12	2.99	9.58	1.51	0.0	2.16
CD at $t_{5\%}$	**0.84**	**0.17**	**0.47**	**0.60**	**0.10**	**0.36**	**0.88**	**0.10**	**0.09**	**0.26**

GL- Grain length; GB - Grain breadth; GL/B - Grain length/breadth ratio; LBC - Kernel length; BBC - Kernel breadth; L/B-BC - Kernel length/breadth ratio; LAC - Kernel length after cooking; CKE-R - Cooked kernel elongation ratio; ARO – presence or absence of aroma. ASV - Alkali spreading value. The highest and lowest values for each trait are given in bold.

Table 7: The average intra- and inter-cluster distances (D^2 values) of the 30 rice genotypes given (The values in bold are intra-cluster distances and the rest are inter-cluster distances)

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
Cluster-I	**504.26**	867.07	805.30	1211.61	1613.16	2885.45
Cluster-II		**349.09**	660.64	687.97	1447.48	2048.95
Cluster-III			**0**	1420.14	2852.48	1985.92
Cluster-IV				**347.25**	1557.42	2187.69
Cluster-V					**438.42**	3929.22
Cluster-VI						**218.26**

Table 8: Genetic Distance Matrix Analysis Considering Morphological Characters only

DTF	PLHT	TN	PN	BPL	SPLN	PD	FS	
DTF	0	106.130	10.330	10.200	28.400	**129.530**	4.570	60.600
PLHT		0	8.030	8.000	27.880	**119.570**	4.310	64.200
TN			0	10.270	22.800	**84.870**	3.730	62.800
PN				0	28.200	**111.650**	3.970	66.300
BPL					0	**91.080**	3.140	79.100
SPLN						0	3.970	65.700
PD							0	0.000
FS								0

Table: 9 Principal components (8 data points in rows, 8 components in columns)

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DTF	-3.91	0.24	-0.90	-0.51	0.01	-0.00	-0.00	0.00
PLHT	-6.00	1.58	0.94	0.03	0.03	-0.00	-0.00	0.00
TN	5.05	-0.09	0.15	-0.02	0.04	0.08	-0.01	-0.00
PN	5.07	-0.10	0.15	-0.02	0.04	0.08	0.01	0.00
BPL	3.36	0.10	0.05	0.02	-0.30	-0.04	-0.00	-0.00
SPLN	-7.37	-1.83	0.39	0.08	-0.01	0.01	0.00	-0.00
PD	5.42	-0.33	0.29	-0.05	0.14	-0.12	-0.00	0.00
%FS	-1.64	0.42	-1.06	0.47	0.04	-0.01	0.00	0.00

Table 10: Distance Matrix (30 dimensions in rows, 8 components in columns)

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
PUSA BASMATI 1	-0.19	-0.07	0.02	-0.32	-0.30	0.22	0.08	0.67
KASTURI	-0.19	0.00	0.05	-0.03	-0.29	-0.06	0.14	-0.29
IET 13544	-0.18	-0.05	-0.36	-0.02	-0.24	0.39	-0.29	-0.20
BASMATI-385	-0.19	0.13	0.07	-0.09	-0.20	-0.05	0.01	-0.28
TRAVADI BASMATI	-0.18	0.32	-0.05	-0.00	-0.07	-0.13	-0.01	0.10
BASMATI 370	-0.18	0.20	0.08	-0.18	-0.07	-0.01	-0.02	-0.27
PAKISTANIBASMATI	-0.18	0.24	0.03	0.09	0.02	0.12	0.40	-0.13
BASMATI 1	-0.18	0.20	0.12	0.15	-0.09	-0.09	0.15	0.20
BASMATI 122	-0.18	0.17	0.03	0.28	0.06	-0.14	-0.07	0.20
BASAMATI 123	-0.18	0.17	0.13	-0.03	-0.09	0.02	0.03	0.02
BASMATI 107	-0.19	0.03	0.16	0.08	-0.25	-0.20	-0.05	0.14
BASMATI 433	-0.18	0.22	0.09	0.18	0.09	0.09	0.25	0.02
KARNAL LOCAL 1	-0.18	0.33	0.07	-0.01	0.05	0.43	-0.46	0.01
AGULHA	-0.18	-0.15	0.18	-0.31	0.05	-0.15	-0.18	-0.25
KHAO DAWK MALI	-0.19	-0.03	0.11	-0.24	0.18	-0.01	0.07	-0.14

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
KHAO DAWK MALI 105	-0.19	0.07	0.03	-0.19	0.27	-0.05	0.09	0.07
IR878B4-220-3-1	-0.17	-0.43	0.07	0.04	-0.10	0.10	-0.03	-0.00
DELLA	-0.18	-0.15	0.06	0.07	-0.13	-0.02	0.11	-0.01
LANGKAYAN	-0.19	0.02	0.00	-0.00	0.29	-0.23	-0.16	0.00
UDARA	-0.18	-0.19	0.06	-0.04	0.19	-0.01	0.02	0.11
PADI BAWANG	-0.19	-0.08	0.02	0.14	0.20	-0.24	-0.09	0.01
RADHUNIPAGAL	-0.18	-0.17	0.15	0.10	0.21	0.00	0.03	0.03
KATARIBHOG	-0.19	0.11	0.06	0.09	0.05	0.02	-0.31	0.02
BADSHAHBHOG	-0.18	-0.26	0.18	0.23	0.08	0.26	0.06	-0.05
GOBINDOBHOG	-0.18	-0.25	0.14	0.07	0.12	0.17	0.10	-0.08
PSBRC 2	-0.18	-0.01	-0.34	-0.43	0.07	-0.32	-0.07	0.08
PSBRC 18	-0.18	-0.12	-0.18	-0.27	0.08	0.21	0.29	0.04
PSBRC 20	-0.18	-0.17	-0.22	0.22	-0.44	-0.30	0.04	-0.09
IR 64	-0.17	0.08	-0.64	0.20	0.24	0.10	0.21	-0.06
IR 72	-0.18	-0.17	-0.18	0.25	0.05	-0.07	-0.30	0.15

Table 11: Genetic Distance Matrix Analysis Considering Quality Characters only

	SW	YLD	GL	GB	GLB	LBC	BBC	LBBC	LAC	CKER	ARO	ASV
SW	0	9.220	11.020	1.840	5.990	8.060	1.550	5.190	**16.230**	2.010	3.000	5.630
YLD		0	9.300	2.290	4.070	7.120	1.600	4.450	**12.170**	1.710	3.000	7.000
GL			0	2.010	5.540	7.980	1.600	4.980	**14.360**	1.800	3.000	2.410
GB				0	5.540	7.070	1.600	4.420	**12.800**	1.810	3.000	3.000
GLB					0	7.970	1.540	5.170	**12.930**	1.620	3.000	2.000
LBC						0	1.630	4.360	**12.230**	1.730	3.000	2.330
BBC							0	14.020	**1.730**	3.000	3.100	0.000
LBBC								0	**10.100**	1.480	3.000	2.000
LAC									0	1.730	3.000	3.970
CKER										0	3.000	2.000
ARO											0	2.000
ASV												

Table 12: Principal components (12 data points in rows, 12 components in columns)

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC1 0	PC1 1	PC1 2
SW	-4.13	-0.10	-0.33	0.39	0.16	-0.08	0.29	0.18	0.03	-0.00	0.00	0.00
YLD	8.55	-4.07	-0.27	-0.07	0.03	0.09	0.02	-0.01	-0.00	0.00	-0.00	-0.00
GL	5.9	1.4	-	0.4	-	-	-	0.1	0.0	-0.01	-0.00	-0.00

	PC 1	**PC 2**	**PC 3**	**PC 4**	**PC 5**	**PC 6**	**PC 7**	**PC 8**	**PC 9**	**PC10**	**PC11**	**PC12**
	2	2	0.32	3	0.53	0.07	0.17	1	6			
GB	-3.93	-0.39	-0.32	0.09	0.08	-0.27	-0.11	-0.07	0.06	0.02	0.02	0.00
G-L/B	-1.14	0.77	-0.26	0.13	0.10	0.47	-0.11	0.10	-0.08	0.01	0.01	0.00
LBC	2.68	1.02	-0.35	0.51	-0.31	-0.17	0.13	-0.16	-0.09	-0.01	0.00	-0.00
BBC	-4.43	-0.42	-0.40	0.18	0.21	-0.25	-0.10	0.00	-0.05	0.02	-0.02	0.00
L/B-BC	-1.80	0.76	-0.10	0.05	-0.06	0.43	0.10	-0.16	0.08	0.01	-0.01	0.00
LAC	8.98	2.08	0.52	-0.55	0.60	-0.13	0.04	0.00	0.00	0.01	-0.00	-0.00
CKE-R	-4.76	-0.28	-0.15	-0.18	0.41	0.05	-0.13	-0.05	0.02	-0.05	-0.00	0.00
ARO	-3.44	-0.04	0.03	-1.43	-0.52	-0.06	0.05	0.03	-0.02	-0.00	0.00	0.00
ASV	-2.52	-0.76	1.95	0.44	-0.16	-0.02	-0.02	0.01	-0.01	-0.00	0.00	0.00

Table 13: Distance Matrix (30 dimensions in rows, 12 components in columns)

	PC 1	**PC 2**	**PC 3**	**PC 4**	**PC 5**	**PC 6**	**PC 7**	**PC 8**	**PC 9**	**PC 10**	**PC 11**	**PC 12**
PUSA BASMATI 1	0.18	0.19	0.29	-0.04	0.19	0.18	-0.03	0.11	-0.20	0.36	-0.00	0.69
KASTURI	0.17	0.16	0.53	0.09	-0.15	-0.13	-0.00	-0.25	0.35	0.02	-0.04	0.03
IET 13544	0.18	0.24	-0.02	-0.06	0.06	0.10	-0.01	0.15	0.24	-0.10	-0.26	-0.02
BASMATI-385	0.18	0.20	0.04	-0.06	0.03	0.23	-0.16	0.38	-0.22	-0.05	0.32	-0.13
TRAVADI BASMATI	0.18	0.22	-0.09	-0.04	-0.03	0.20	0.25	-0.09	0.18	0.08	-0.16	-0.09
BASMATI 370	0.18	0.19	-0.0	-0.1	0.05	0.11	0.05	-0.0	-0.1	0.10	0.06	-0.1

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10	PC 11	PC 12
			3	0				9	3			5
PAKISTANIBASMATI	0.19	0.08	-0.02	-0.05	0.05	0.32	0.11	0.01	-0.27	0.29	0.04	-0.34
BASMATI 1	0.19	0.13	-0.13	-0.04	-0.23	0.17	0.01	-0.13	0.08	0.02	-0.14	-0.10
BASMATI 122	0.19	0.08	0.15	-0.06	0.03	-0.35	-0.01	0.15	-0.26	-0.18	-0.10	-0.20
BASAMATI 123	0.19	0.12	-0.01	-0.24	0.49	-0.27	0.24	0.12	0.16	-0.19	0.05	-0.04
BASMATI 107	0.19	0.17	-0.07	-0.12	0.03	-0.20	0.09	-0.16	-0.03	-0.06	0.16	0.13
BASMATI 433	0.19	-0.08	0.30	0.06	-0.23	0.20	-0.12	0.24	0.23	-0.17	-0.06	-0.07
KARNAL LOCAL 1	0.19	0.17	-0.10	-0.06	0.02	0.05	0.00	0.10	0.01	-0.19	-0.26	0.05
AGULHA	0.19	-0.18	0.03	0.05	-0.11	-0.15	0.39	0.06	0.03	-0.17	0.35	0.12
KHAO DAWK MALI	0.19	-0.15	-0.15	0.03	-0.22	-0.06	0.28	0.03	-0.40	-0.13	-0.05	0.15
KHAO DAWK MALI 105	0.18	-0.21	-0.17	-0.02	-0.14	0.20	0.23	0.05	0.16	-0.10	-0.03	0.36
IR878B4-220-3-1	0.19	-0.16	-0.09	0.02	-0.30	-0.09	-0.07	0.44	0.02	-0.08	-0.18	-0.02
DELLA	0.19	-0.12	0.33	0.04	-0.03	-0.05	0.25	-0.09	0.00	0.01	0.23	-0.18
LANGKAYAN	0.18	0.24	-0.12	0.01	-0.42	-0.11	-0.09	-0.34	-0.22	0.03	0.10	0.01
UDARA	0.18	-0.21	-0.18	-0.12	-0.05	-0.40	0.03	0.17	0.15	0.67	-0.18	-0.03
PADI BAWANG	0.19	0.10	-0.08	-0.17	-0.22	-0.20	-0.41	-0.03	0.18	0.08	0.30	0.01
RADHUNIPAGAL	0.18	-0.22	-0.07	-0.32	0.16	-0.05	-0.28	-0.26	-0.07	-0.15	-0.06	0.08
KATARIBHOG	0.1	-	-	-	0.2	0.0	0.0	-	0.0	0.0	-	-

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10	PC 11	PC 12
	9	0.10	0.09	0.21	1	9	1	0.14	9	1	0.11	0.16
BADSHAHBHOG	0.15	-0.36	0.34	-0.09	0.02	0.03	-0.25	-0.05	-0.19	-0.01	-0.23	-0.03
GOBINDOBHOG	0.17	-0.31	-0.08	-0.25	0.07	0.23	-0.16	-0.18	0.01	-0.14	0.13	0.07
PSBRC 2	0.18	0.12	-0.02	0.43	0.17	-0.21	-0.20	-0.01	-0.25	-0.13	-0.24	0.04
PSBRC 18	0.17	-0.27	0.14	0.29	0.14	0.08	0.15	-0.13	-0.06	0.19	-0.00	-0.19
PSBRC 20	0.19	-0.10	-0.21	0.34	0.07	0.12	-0.05	-0.11	0.13	-0.03	-0.09	-0.01
IR 64	0.19	0.04	-0.16	0.37	0.15	-0.06	-0.08	-0.21	0.06	-0.05	0.00	0.08
IR 72	0.19	-0.08	-0.17	0.31	0.19	0.04	-0.24	0.19	0.19	0.07	0.42	-0.02

Discussion

Cluster Analysis of the 30 Rice Genotypes using D^2 data.

There are five primary clusters made up of thirty different rice genotypes. **Table 7** provides the typical intra-cluster and inter-cluster distances. Cluster I had the largest average intra-cluster distance with a D2 value of 504.26, while Cluster VI received the shortest with a value of 218,26. The average distance between Clusters II and III was the smallest (D2 value: 660.64), while Clusters V and VI had the greatest average inter-cluster distance (D2 value: 3929.22). The two genotypes in Cluster I were identified after additional data analysis as Pusa Basmati 1, an EB, and Basmati 123, a TB. Cluster II consisted of 14 genotypes that were split up into four smaller groups. Sub-cluster IIA was composed of the EB, TB, and EA genotypes. The D2 value was 172.66 between Kasturi and Della and 338.38 between Basmati 433 and Della. In sub-cluster IIB, there were four TB genotypes and one EB genotype. The D2 value in this sub-cluster ranged from 37.19 to 161.28 between Basmati 385 and Basmati 370, whereas it was 161.28 between Travadi Basmati and Basmati 370. For the three TB genotypes that comprised Sub-cluster IIC, the D2 value ranged from 61.36 (between Basmati 1 and Basmati 107) to 143.05 (between Basmati 1 and Basmati 122). The two EA genotypes that made up sub-cluster IID had a D2 score of 158.68. Separately, the EA genotypes IR878B4-220-3-1 and IIC joined sub-cluster IIB.

Cluster III, an EB, included only one genotype, IET 13544. Cluster IV consisted of four EA genotypes with D2 values ranging from 74.48 to 762.78 between the Agulha and Udara and Khao-Dawk-Mali and Khao-Dawk-Mali 105 genotypes.

Sub-cluster IIC consisted entirely of three TB genotypes, and the D2 values between Basmati 1 and Basmati 107 and 122 varied from 61.36 to 143.05. Sub-cluster IID was composed of two EA genotypes with a D2 score of 158.68. Separately, the sub-clusters IIB and IIC welcomed the EA genotype IR878B4-220-3-1.

Cluster III included only a single genotype, an EB known as IET 13544. Cluster IV contained four EA genotypes with D2 values ranging from 74.48 (between Khao-Dawk-Mali and Khao-Dawk-Mali 105) to 762.78 (between Agulha and Udara).

The description above makes it unclear whether cultivar types were selected with more thought devoted to certain qualities.

Table 8 to 13 provide the genetic distance and distance of Principal Components among the Varieties considering Morphological Characters (Table 8 – Table 10) and Quality Characters (Table 11 – Table 13).

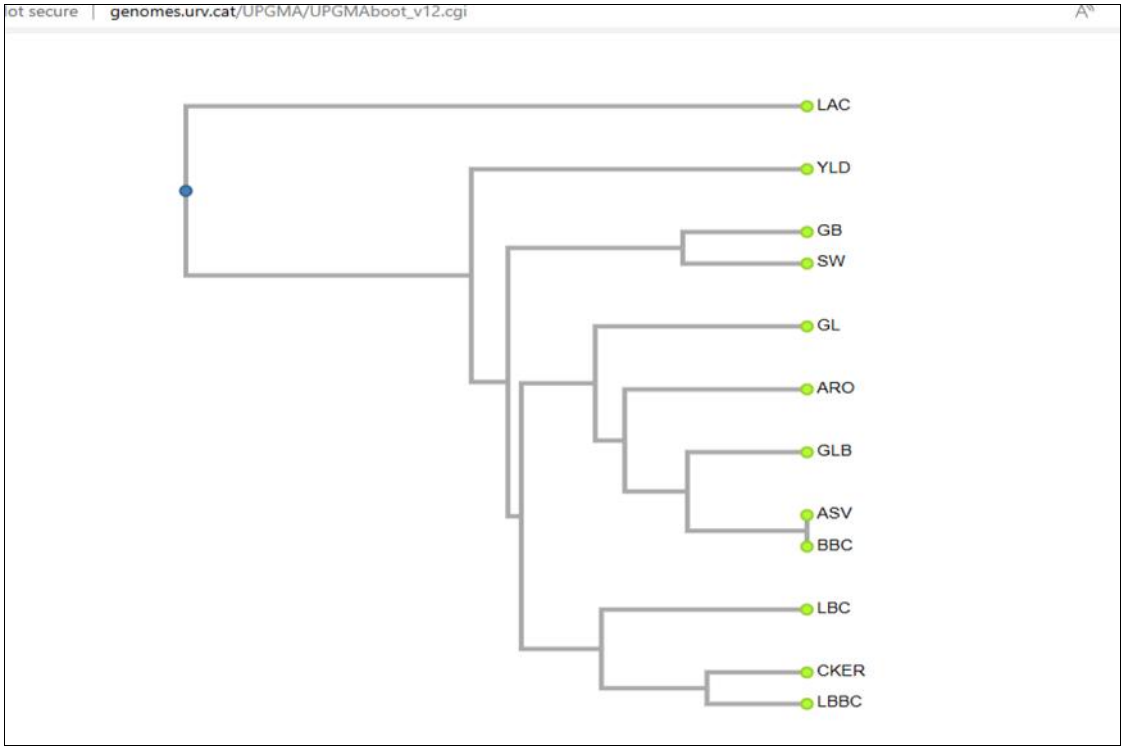
The Hypothesis: Farmers Factor

The status of real selection and the origin of alleles are revealed through multivariate analysis of morphological features. Four groupings are formed by the Heat Map of Character Expression **(Annexure I):** Plant Height/BPL, DTF/%FS, SPLN/PD, and TN/PN. In Karnal Local 1, the highest plant allele expression was observed, while the highest SPLN was found in IR8784B, Badshabhog, and Gobindobhog. For many characters, the PCA **(Annexure II)** also displays a single cluster and sparse data for others.

Grain quality and scent, as well as other quality characters, were clearly separated into two sub-selection groups by a multivariate analysis using a heat map **(Annexure III).** Additionally shown are the allele expressions. The maximum expression is found in Badshabhog, PSBRC 18, Radhunipagol, and Gobindobhog in terms of yield. Basmati 123 and Pusa Basmati 1 had the highest expression of the LAC allele. Kasturi, Basmati 433, and Pusa Basmati did not express the BBC allele.

A single cluster of four characters from the PCA of the quality characters appeared to be the Non Aromatic group, which is genetically 88.9% different from the Aromatic. The evolution and connectivity of the characters were revealed by the UPGMA analysis of morphological and Quality characters **(Figures 1 and 2).**

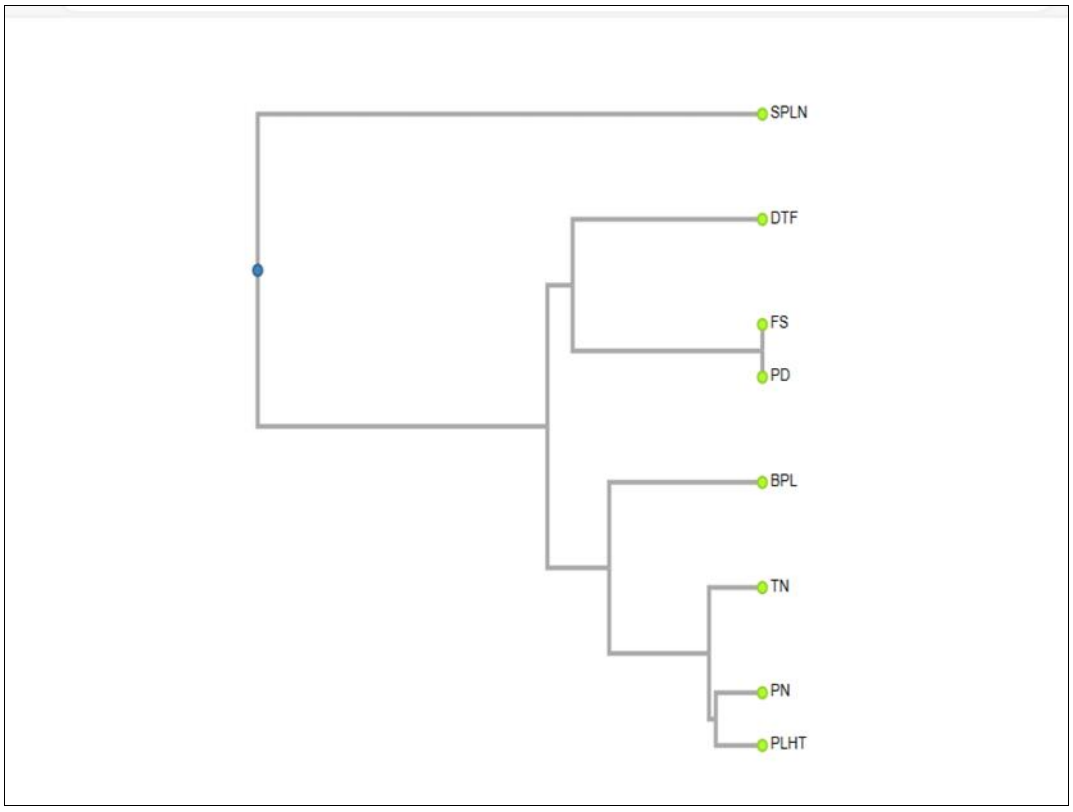
Figure 1: Dendogram of Probable evolution of selected Quality Characters and linkage



GL- Grain length; GB - Grain breadth; GL/B - Grain length/breadth ratio; LBC - Kernel length; BBC - Kernel breadth; L/B-BC - Kernel length/breadth ratio; LAC - Kernel length after cooking; CKE-R - Cooked kernel elongation ratio; ARO – presence or absence of aroma

The Heatmap also shows some signs of how an allele is expressed or how an allele is chosen. Remembering that these plants evolved through natural selection to have the most adapted morphology for that specific area is important while looking at their morphology. The traits TN, PN, PD, and BP L have little to no weight, whereas DTF and %FS were thought to be ecological types connected to plant photoperiod. On SPLN, a significant variation or selection pressure was applied. This is also evident from UPGMA analysis of morphological characters (Figure 1) where SPLN is showing divergence from all other characters.

Figure 2: Dendogram of Probable evolution of selected Morphological Characters and linkage



DTH - days to 50% flowering; PLHT - plant height; TN - tiller number; PN - panicle number; BPL - best panicle length; SPLN – No. of spikelet/panicle; PD - panicle density, %FS - percent fertile seeds; SW - 100 seed weight; YLD - total plant yield. The highest and lowest values for each trait are given in bold.

According to the Heatmap of qualitative attributes, **(Annexure IV).**there is no discernible difference in aroma among the various aromatic groups. GL, LBC, G-L/B, L/B-BC, ASV, SW, CKE-R, GB, and BBC were not given any weight. These were all fragrant rice ecotypes that had varying degrees of regional expression. LAC was under pressure during the selecting process because she is a very valuable quality character. A UPGMA study (Figure 2) revealed that the LAC allele has developed differently. The YLD belongs to the group of grain morphology alleles because it has a direct relationship to grain characteristics.

Conclusion

Cultivar evolution is entirely distinct from the evolution of the *Oryza sp*. Complex. While domestication is an artificial process, speciation is a natural one. Early farmers specifically chose some traits during domestication while discarding others. Most of these characters were either for high-quality or commercial varieties. *Oryza sp*. ecotypes have evolved in response to environmental demands. Cultivar evolution is unrelated to the evolution of *Oryza* species. More investigations are needed with other varieties from different rice growing nations to understand the cutivar evolution process.

Abbreviations used:

DTH - days to 50% flowering; PLHT - plant height; TN - tiller number; PN - panicle number; BPL - best panicle length; SPLN – No. of spikelet/panicle; PD - panicle density, %FS - percent fertile seeds; SW - 100 seed weight; YLD - total plant yield, GL- Grain length; GB - Grain breadth; GL/B - Grain length/breadth ratio; LBC - Kernel length; BBC - Kernel breadth; L/B-BC - Kernel length/breadth ratio; LAC - Kernel length after cooking; CKE-R - Cooked kernel elongation ratio; ARO – presence or absence of aroma.

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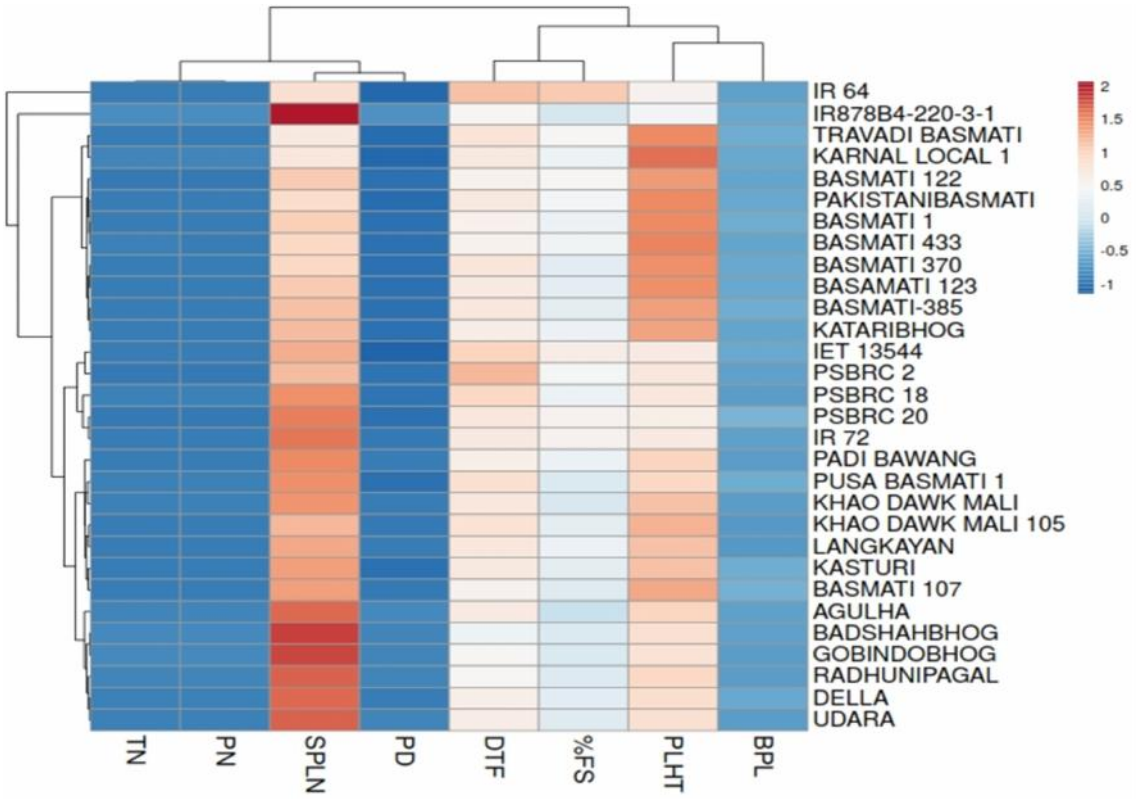
Conflict of Interest:

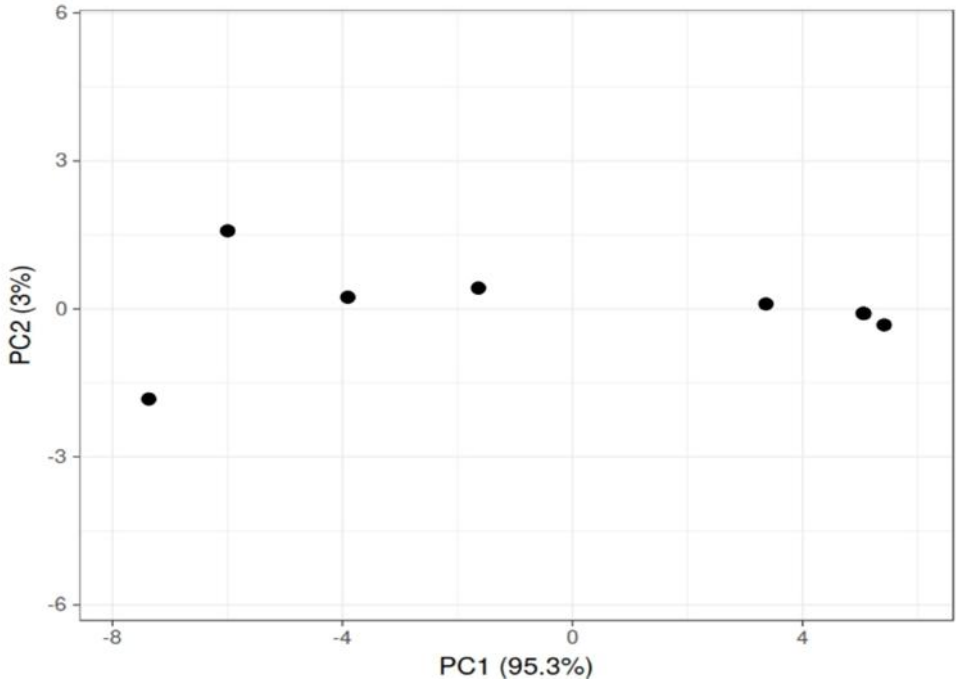
The First author has maintained all the rice lines, as Research Associate, PMCG Section, Bose Institute. There is no conflict of interest with anybody or organization.

Annexures:

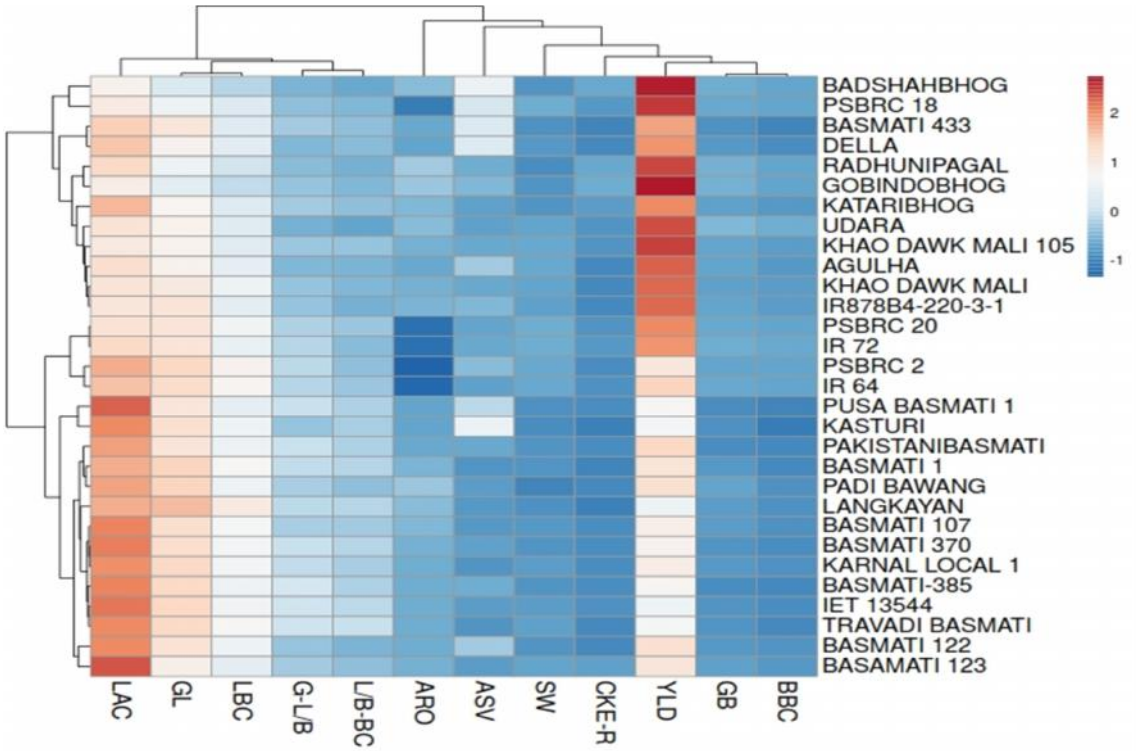
I: Heatmap of Morphological Characters



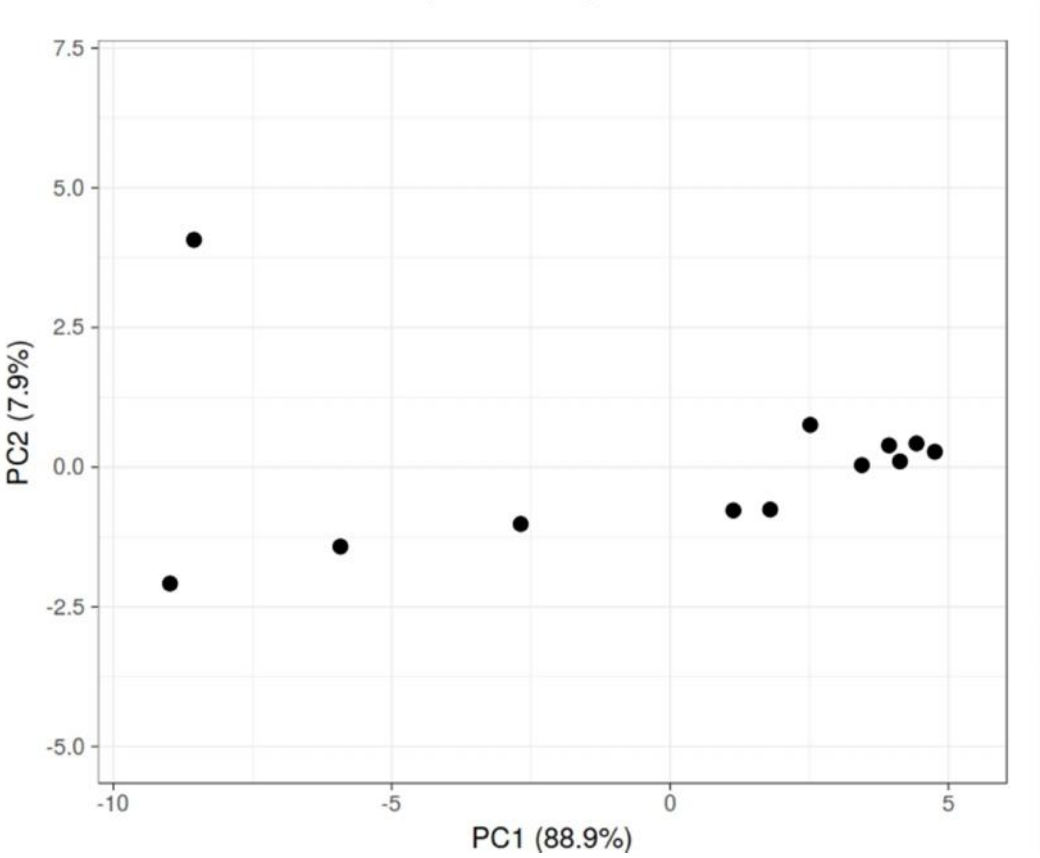
II. PCA analysis of Morphological Characters



III. Heatmap of Quality Characters



IV. PCA Analysis of Quality Characters



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