



## Comprehensive Multivariate Analysis Of Rice (*Oryza Sativa* L.) Genotypes Of Tamil Nadu For Yield And Yield Attributed Traits

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### ABSTRACT

An experiment was performed to assess the variability parameters for biometrical traits in 104 rice genotypes. Higher estimates of GCV and PCV were found for single plant yield and filled grains per panicle along with high heritability and genetic advance. Single plant yield exhibited significant positive genotypic correlation for most of the yield contributing characters like number of productive tillers, number of filled grains per panicle, number of tillers, panicle length and thousand grain weight. The highest positive direct effects on yield were exhibited by number of filled grains per panicle followed by number of productive tillers at genotypic level for the improvement of rice yield. Estimates of genetic variability analysis exhibited, single plant yield and number of filled grains per panicle are positive for practically all variability factors tested. The study revealed high genetic variability, indicating that the genotypes could be utilized for further rice breeding.

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**Keywords:** Genetic variability, correlation and path analysis, principal component analysis.

### Introduction

Rice (*Oryza sativa* L.), nearly half of the world's population consumes this "Global Grain"(Srinivas 2018), which is a staple and crucial security food crop. Almost every state in the nation is cultivating rice, but West Bengal, Uttar Pradesh, Andhra Pradesh, Punjab, and Tamil Nadu are the top producers of the grain. According to various estimates, approximately fifty thousand rice varieties are still grown throughout the nation (Patra 2000).

Genetic study determines rice genotype's intrinsic potential, the heritability of traits together with the potential for genetic advancement (Demeke *et al.*, 2023). With a focus on the impacts these parameters have on yield and yield-related variables, the current study investigates research on heritability, genetic advance, phenotypic

coefficient of variation (PCV), and genotypic coefficient of variation (GCV) in rice genotypes. The development of new breeding lines should increase rice's production potential with a view to feed the world's rapidly growing population. The main characteristic that is being pursued for improvement in rice under both favourable and unfavourable conditions is grain yield (Tiwari 2011). To generate high yielding varieties in the future, it is necessary to have knowledge regarding the genetic variability of the population and the correlation amidst yield and associated features.

The essential element of breeding programs for expanding the rice gene pool is the assessment of genetic variability in polygenic traits (Palaniyappan *et al.*, 2020). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are statistical terms used to quantify the variability of qualities within and between different genotypes of rice. PCV evaluates the amount of variation observed in a trait, whereas GCV measures the genetic variability underlying that trait (Yumkhaibam RS 2023).

Any breeding program's potential to succeed depends on its capacity to comprehend the genetic makeup of the selected character, forecast and create genetic variability in next generations, and analyse how the target character interacts with other characters. Since yield is a complicated trait that depends on many other traits, it's important to comprehend how other traits relate to yield in addition to knowing about genetic variability (Reddy *et al.*, 2013). Furthermore, since grain yield is dependent on a various number of component characters, understanding the relationships between yield, yield components, and quality traits as well as the direct and indirect effects of quality traits and yield on grain yield will be helpful in effectively improving yield (Singh *et al.*, 2020). A standardized regression coefficient called a path coefficient analysis is used to quantify the direct impact of one variable on another. The correlation coefficient is statistically divided into its direct and indirect effects, to measure each character's contribution to yield (Syed Sajid Ali 2021). A non-parametric multivariate technique called Principal component analysis is used to extract the most significant information from a data table including multiple intercorrelated quantitative dependent variables that describe observations (Nachimuthu *et al.*, 2014).

## Materials and methods

The study utilized 104 rice genotypes combining landraces and released varieties that were gathered from different regions of Tamil Nadu, as experimental material. The experiment was conducted at the V.O.C. Agricultural College and Research Institute, Killikulam, geographically located in 8°46' N latitude and 77°42' E longitude and at an altitude of 40 m above mean sea level (MSL) during Rabi, 2022. In a Randomized Block design, three replications of 25-days-old rice seedlings representing 104 genotypes were planted with the spacing between rows and plants was maintained at 20 cm and 15 cm, respectively. The recommended agronomic practice of was followed during the entire crop growth period for the better performance of the crop. Table.1 contains the list of experimental material.

For each of the 104 rice genotypes, the following characteristics *viz.*, were noted: days to 50% flowering, plant height, number of tillers, number of productive tillers, panicle length, number of filled grains, thousand grain weight, grain length, grain width, grain l/b ratio, and single plant yield. Five plants were tagged in each replication randomly and observations were recorded in the selected plants. The data were exposed to standard statistical analysis.

The coefficient of variation (GCV and PCV) was given by (Burton 1952) and the method proposed by (Panse and Sukhatme 1961) was used to estimate the analysis of variance (ANOVA). The pattern of variation in the ranges were grouped as low (<10%), moderate (10 - 20%) and high (> 20%) by (Madhavamenon 1973). The Burton and Devane, 1953 formula were used to assess the broad sense heritability of rice grain yield and yield components. Values falling within the heritability range of 0–30%, 30–60%, and >60% were classified as low, medium, and high, respectively. Genetic advance was measured using the Johnson *et al.*, 1955 approach, which distinguished between low (< 10%), moderate (10–20%), and high (> 20%) levels of significance. The correlation and path coefficient were calculated using the approach recommended by (Dewey and Lu 1959, Al-Jibouri *et al.* 1958). Diversity analysis like Principal component analysis was carried out using the software "pb perfect".

## Result and discussion

### *Genetic variability parameters*

The analysis of variability parameters and heritability provided insights into the extent of genetic variation and influence of genotype versus environment for the 11 rice traits (Table 2). A high magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was recorded for Plant height, Available online at: <https://jazindia.com>

number of tillers, number of productive tillers, number of filled grains/panicle, thousand grain weight, grain L/B ratio and single plant yield, out of which number of filled grains (34.98% for PCV and 34.56% for GCV) and single plant yield (49.81% for PCV and 49.44% for GCV) recorded the maximum. High GCV and heritability was observed for single plant yield (98.53%), number of tillers and productive tillers (97.43%), filled grains per panicle (97.60%), thousand grain weight (95.27%), grain breadth (92.44%) and other yield attributes. The high heritability estimates indicate these traits are less influenced by environment and largely under genetic control. Similar findings were reported in rice by (Madhavamenon 1973), reflecting the predominant genotypic effects on yield components. In contrast, moderate heritability was observed for phenology, days to 50% flowering (73.44%) and grain quality traits like grain length (88.30), suggesting greater environmental effects.

### **Genetic advance**

The genetic advance, representing the expected genetic gain from selection, was highest for filled grains per panicle (70.34%), number of tillers (69.28%), number of productive tillers (67.96%) and thousand grain weight (52.50%). High heritability coupled with high genetic advance implies robust scope for genetic improvement of these yield enhancing traits through breeding (Sharma 1998).

Overall, the results reveal abundant natural variation under strong genetic control for key rice yield components like tillering capacity, grain number and size. This offers broad opportunities for augmenting productivity through genotypic selection and hybridization. As (Verma 2017) elaborated, quantitative variability parameters provide critical insights into available genetic diversity, heritability and response to selection in rice. Knowledge of these factors will help guide an efficient breeding strategy.

**Table.2 Estimation of variability parameters for eleven biometric traits in rice genotypes**

Traits	Coefficient of variation		Heritability in broad sense $h^2$ (%)	Genetic advance	Genetic Advance as percent of Mean (%)
	Phenotypic	Genotypic			
<b>DFE</b>	9.96	8.53	73.44	13.12	15.06
<b>PH</b>	23.67	23.02	94.57	<b>53.09</b>	46.11
<b>NT</b>	34.52	34.07	97.43	16.40	69.28
<b>NPT</b>	33.86	33.42	97.43	13.09	67.96
<b>PL</b>	16.27	15.43	90.00	6.62	30.16
<b>NFG</b>	<b>34.98</b>	<b>34.56</b>	<b>97.60</b>	<b>89.87</b>	<b>70.34</b>
<b>TGW</b>	26.75	26.11	95.27	11.32	52.50
<b>GL</b>	16.16	15.18	88.30	2.14	29.39
<b>GB</b>	19.50	18.75	92.44	1.05	37.13
<b>L/B ratio</b>	24.12	23.48	94.71	1.24	47.07
<b>SPY</b>	<b>49.81</b>	<b>49.44</b>	<b>98.53</b>	49.69	<b>101.10</b>

DFE - Days to 50% flowering; PH - Plant Height (cm); NT - Number of Tillers; NPT - Number of Productive Tillers; PL - Panicle Length (cm); NFG - Number of Filled Grains; TGW - Thousand Grain Weight; GL - Grain Length (mm); GB - Grain Breadth (mm); L/B ratio - Grain Length/Breadth Ratio (mm); SPY - Single Plant Yield (g)

### **Genotypic Correlation Analysis**

The genotypic correlation analysis provided insights into the associations between different rice traits (Table 3, Fig.1). Grain yield exhibited significant positive correlation with number of productive tillers (0.44), number of filled grains per panicle (0.53), number of tillers (0.36), panicle length (0.33) and thousand grain weight (0.29). This agrees with earlier findings in rice on the strong contribution of yield components like tillering and grain number to productivity (Gravois and Helms 1992, Yoshida 1981). In contrast, non-significant and negative correlations were observed between grain yield and phenology traits like days to flowering (-0.17), grain breadth (-0.13), L/B ratio (-0.03) and the non-significant and negative correlations were observed between grain yield and plant height (0.04). This suggests yield improvement can be achieved without adverse effects on crop duration or plant height. Interestingly, grain breadth and grain length showed significant and non-significant negative associations with plant height with the values of -0.23 and -0.20, respectively. This implies that long slender grains are associated with shorter plants, while slender grains tend to occur in taller types. Breeding for long slender grains would therefore require selection for greater height. Overall, the correlation analysis indicates effective simultaneous selection for higher yield, optimum plant type and desired

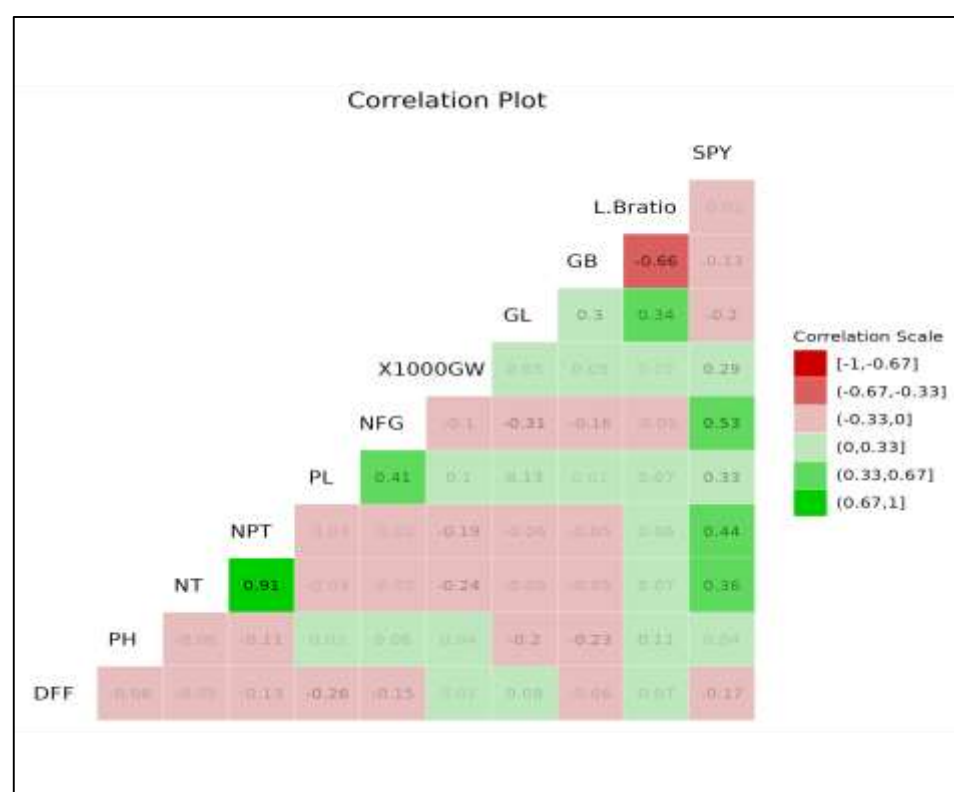
grain quality is feasible in rice. Favourable correlations were observed between yield attributes while associations with other traits were largely non-significant. These results agree with earlier findings by (Surek and Beser 2003, Sabesan *et al.*, 2009) on the lack of major correlations between yield and morphological traits in rice.

**Table.3 Genotypic correlation coefficient matrix for eleven biometric traits**

Traits	DFF	PH	NT	NPT	PL	NFG	TGW	GL	GB	L/B ratio	SPY
DFF	1	-0.08	-0.05	-0.12	-0.26**	-0.15	0.01	0.08	-0.06	0.06	-0.17
PH		1	-0.06	-0.11	0.03	0.06	0.04	-0.20*	-0.23*	0.11	0.04
NT			1	0.91****	-0.03	-0.02	-0.24*	-0.05	-0.05	0.07	0.36****
NPT				1	-0.03	-0.02	-0.19	-0.06	-0.05	0.06	0.44****
PL					1	0.41****	0.10	0.13	0.01	0.07	0.33****
NFG						1	-0.10	-0.31**	-0.16	-0.05	0.53****
TGW							1	0.05	0.05	0.02	0.29**
GL								1	0.30**	0.34****	-0.20*
GB									1	0.66****	-0.13
L/B ratio										1	-0.03
SPY											1

Significance levels:  $p < .0001$  '\*\*\*\*';  $p < .001$  '\*\*\*';  $p < .01$  '\*\*';  $p < .05$  '\*'

DFF - Days to 50% flowering; PH - Plant Height (cm); NT - Number of Tillers; NPT - Number of Productive Tillers; PL - Panicle Length (cm); NFG - Number of Filled Grains; TGW - Thousand Grain Weight; GL - Grain Length (mm); GB - Grain Breadth (mm); L/B ratio - Grain Length/Breadth Ratio (mm); SPY - Single Plant Yield (g)



**Fig.1. Correlogram of biometrical traits for Single Plant Yield (SPY)**

### Genotypic Path Analysis

The genotypic path analysis delineated the direct and indirect effects of different traits on grain yield (Table 4, Fig.2). The highest positive direct effects on yield were exhibited by number of filled grains per panicle (0.54) followed by number of productive tillers (0.44). The residual effect recorded was 0.28 this shows that 80% of

the contribution was accounted from the traits used in the study. This reveals the preeminent role of these components in determining rice productivity, consistent with earlier path analyses (Gravois and Helms 1992, Fujita *et al.*, 2013). Moderate positive direct effects were contributed by number of tillers (0.37), panicle length (0.34) and 1000 grain weight (0.29). In contrast, phenology (days to flower) and plant height showed negligible direct effects on yield, implying they are not useful selection criteria. Grain breadth had high negative direct effect (-0.30) on yield, while grain length showed negative effects via plant height and 1000 grain weight. Overall, the path analysis clearly elucidates the most important yield contributing traits in rice. Selecting genotypes with more productive tillers, higher grain number and moderately long panicles will be most effective for enhancing productivity. Furthermore, slender long grains can be combined with short stature to avoid negative indirect effects on yield. These findings will guide trait prioritization during phenotypic selection as well as development of selection indices for yield improvement in rice.

**Table.4 Genotypic Path analysis for eleven biometric traits in rice genotypes**

Traits	DFE	PH	NT	NPT	PL	NFG	TGW	GL	GB	L/B ratio	Correlations SPY
<b>DFE</b>	- <b>0.0125</b>	- 0.0051	0.0028	- 0.0803	- 0.0195	- 0.0895	0.0052	0.0182	0.0200	-0.0223	-0.1830
<b>PH</b>	0.0010	<b>0.0665</b>	0.0026	- 0.0703	0.0023	0.0346	0.0164	- 0.0418	0.0702	-0.0365	0.0449
<b>NT</b>	0.0007	- 0.0037	<b>0.0474</b>	0.5557	- 0.0018	- 0.0115	- 0.1084	- 0.0106	0.0171	-0.0232	0.3670
<b>NPT</b>	0.0017	- 0.0078	- 0.0437	<b>0.6031</b>	- 0.0022	- 0.0089	- 0.0854	- 0.0124	0.0164	-0.0207	0.4402
<b>PL</b>	0.0035	0.0022	0.0012	- 0.0191	<b>0.0689</b>	0.2295	0.0496	0.0271	- 0.0022	-0.0230	0.3378
<b>NFG</b>	0.0020	0.0042	0.0010	- 0.0097	0.0286	<b>0.5525</b>	- 0.0445	- 0.0622	0.0500	0.0165	0.5384
<b>TGW</b>	- 0.0001	0.0024	0.0114	- 0.1140	0.0076	- 0.0545	<b>0.4517</b>	0.0106	- 0.0155	-0.0053	0.2943
<b>GL</b>	- 0.0012	- 0.0141	0.0025	- 0.0378	0.0094	- 0.1735	0.0243	<b>0.1980</b>	-0.095	-0.1174	-0.2049
<b>GB</b>	0.0008	- 0.0154	0.0027	- 0.0327	0.0005	- 0.0913	0.0231	0.0623	- <b>0.3027</b>	0.2198	-0.1328
<b>L/B ratio</b>	- 0.0009	0.0075	- 0.0033	0.0383	0.0049	- 0.0280	0.0073	0.0714	0.2044	<b>-0.3255</b>	-0.0240

#### Residual effect: 0.2856

DFE - Days to 50% flowering; PH - Plant Height (cm); NT - Number of Tillers; NPT - Number of Productive Tillers; PL - Panicle Length (cm); NFG - Number of Filled Grains; TGW - Thousand Grain Weight; GL - Grain Length (mm); GB - Grain Breadth (mm); L/B ratio - Grain Length/Breadth Ratio (mm); SPY - Single Plant Yield (g)

#### Conclusion

For single plant yield (98.53%), number of tillers and productive tillers (97.43%), filled grains per panicle (97.60%), thousand grain weight (95.27%), grain breadth (92.44%), and other yield parameters, a high magnitude of genotypic coefficient of variation (GCV) and heritability was detected. The high heritability estimates suggest that these qualities are mostly controlled by genetics and are little affected by the environment. The highest percentages of filled grains per panicle (70.34%), tiller count (69.28%), productive tiller count (67.96%), and thousand grain weight (52.50%) were associated with the highest genetic progress, which indicates the projected genetic gain from selection. Breeding these yield-enhancing characteristics with high heritability and high genetic progress suggests a strong potential for genetic improvement. The number of productive tillers (0.44), filled grains per panicle (0.53), number of tillers (0.36), panicle length (0.33), and thousand grain weight (0.29) all showed a strong positive connection with grain yield. Number of filled grains per panicle (0.54) and number of productive tillers (0.44) showed the strongest beneficial direct influence on yield. This indicates how important these factors are in deciding rice productivity. To summarize, yield



components are important sources of genetic variation that can be used to increase rice production, as shown by both genotypic correlation and multivariate analysis. In varied genetic backgrounds, there is flexibility to improve grain output and quality due to the lack of significant connections with plant type. In order to adequately sample this variety, parents with complementing yield traits must be crossed.

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### References

1. Al-Jibouri, H. A. R., Saxena, M. C., & Singh, K. B. (1958). Genotypic and phenotypic correlation coefficients and path analysis in chickpea (*Cicer arietinum* L.). *Indian Journal of Genetics and Plant Breeding*, 18(2), 260-272.
2. Burton, GW. 1952. "Quantitative inheritance in grasses." *Pro VI Int Grassl Cong*:277-283.
3. Demeke, Birtucan, Tiegist Dejene, and Desta Abebe. 2023. "Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza Sativa* L.) genotypes at pawe, northwestern Ethiopia." *Cogent Food & Agriculture* 9 (1):2157099.
4. Fujita, Daisuke, Kurniawan Rudi Trijatmiko, Analiza Grubanzo Tagle, Maria Veronica Sapasap, Yohei Koide, Kazuhiro Sasaki, Nikolaos Tsakirpaloglou, Ritchel Bueno Gannaban, Takeshi Nishimura, and Seiji Yanagihara. 2013. "NAL1 allele from a rice landrace greatly increases yield in modern indica cultivars." *Proceedings of the National Academy of Sciences* 110 (51):20431-20436.
5. Gravois, KA, and RS Helms. 1992. "Path analysis of rice yield and yield components as affected by seeding rate." *Agronomy Journal* 84 (1):1-4.
6. Madhavamenon, Sivasubramanian and. 1973. "Genotypic and phenotypic variability in rice." *Madras Agricultural Journal* 60:1093-1096.
7. Nachimuthu, Vishnu Varthini, S Robin, D Sudhakar, M Raveendran, S Rajeswari, and S Manonmani. 2014. "Evaluation of rice genetic diversity and variability in a population panel by principal component analysis." *Indian journal of science and technology* 7 (10):1555-1562.
8. Palaniyappan, S, P Arunachalam, S Banumathy, ML Mini, and S Muthuramu. 2020. "Genetic parameters and character association studies in rice (*Oryza sativa* L.)." *Journal of Pharmacognosy and Phytochemistry* 9 (3):1652-1657.
9. Patra, BC. 2000. "Collection and characterisation of rice genetic resources from Keonjhar district of Orissa." *Oryza* 37 (4):324-325.
10. Reddy, G Eswara, BG Suresh, T Sravan, and P Ashok Reddy. 2013. "Interrelationship and cause-effect analysis of rice genotypes in north east plain zone." *The Bioscan* 8 (4):1141-1144.
11. Sabesan, T, R Suresh, and K Saravanan. 2009. "Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu." *Electronic Journal of Plant Breeding* 1 (1):56-59.
12. Sharma. 1998. "Optimization of selection indices and the use of information from unselected sources." *Theoretical and Applied genetics* 96:304-310.
13. Singh, Kumar Saurabh, Y Suneetha, G Vinay Kumar, V Srinivasa Rao, D Sandeep Raja, and T Srinivas. 2020. "Variability, correlation and path studies in coloured rice." *Int J Chem Stud* 8 (4):2138-2144.
14. Srinivas, T. 2018. "Genetic diversity studies in rice (*Oryza sativa* L.)." *Electronic Journal of Plant Breeding* 9 (4):1335-1341.
15. Surek, Halil, and Necmi Beser. 2003. "Correlation and path coefficient analysis for some yield-related traits in rice (*Oryza sativa* L.) under thrace conditions." *Turkish Journal of Agriculture and Forestry* 27 (2):77-83.
16. Syed Sajid Ali, Suresh BG, and G. Lavanya. 2021. "Genetic diversity and correlation studies in rice (*Oryza sativa* L.)." *International Journal of Chemical Studies* 9:2768-2772.
17. Tiwari, G. K., Singh, M. K., Singh, P., Singh, R. K., & Tiwari, S. 2011. "Genetic diversity and correlation studies in rice (*Oryza sativa* L.)." *International Journal of Chemical Studies* 9 (1).

18. Verma, S. K., & Srivastav, A. K. 2017. "Genetic variability, heritability, genetic advance and correlation studies in proximate traits, yield and yield contributing traits of rice (*Oryza sativa* L.). ." *Journal of Pharmacognosy and Phytochemistry* 6:1743-1747.
19. Yoshida, Shouichi. 1981. *Fundamentals of rice crop science*: Int. Rice Res. Inst.
20. Yumkhaibam RS, Ram M, Mehandi S, Prakash S. 2023. "Assessment of genetic variability for yield and yield contributing traits in rice (*Oryza sativa* L.). ." *The Pharma Innovation Journal* 12 (6):1816-1823.

**Table. 1 List of 104 rice genotypes under study**

S.No	Genotypes	S.No	Genotypes	S.No	Genotypes
01	Purpleputtu	46	Orisamani Samba	91	Harathi
02	Abiya	47	Sengalpattu Sirumani	92	Karthanavara
03	Chennakayamma	48	Aathurkicheli Samba	93	Chiruchitteni - 882
04	Shabhagidhan	49	Karuppu kavuni	94	Chomala – 2206
05	Vattan	50	Oriza Kuttai Sivappu Arisi	95	Aryan - 1204
06	Jaya	51	Ariyan	96	NL 24
07	Thamarai	52	Oheruchitteni	97	ASD 16
08	Sivappumalli	53	Chennellu 6806	98	RpBioPatho 1
09	Pisni	54	J – 13 100 days	99	TPS 5
10	Kalanamak	55	Mappillai Samba	100	RpBioPatho 2
11	Kalakuruvai	56	Kunju Kunju	101	TRY 3
12	Rajalakshmi	57	Navara Black	102	IRBB60
13	Navara	58	Aryan – 1102	103	ADT 37
14	Noothipathu	59	Shadabhar	104	Tetep
15	Kullakar	60	Keralakandasala		
16	Veethiruppu	61	Chembavu		
17	Swarnamasuri	62	Pusa Basumathi		
18	Aryan 6333	63	Kaivara Samba		
19	Chiruchitteni	64	kavuni		
20	Aryan 1203	65	Kuliyadichan		
21	Chitteni 520	66	Kallundaikar		
22	Navara 957	67	Orkaima		
23	Chembavu Chitteni	68	Meikuruvai		
24	Chenna	69	SriLanka		
25	Arupatham Kavuni	70	Adukan		
26	Karunkuruvai	71	Dhalaheera		
27	Keerai Samba	72	Anna 4		
28	Raja Guruvai	73	Chembavu 4331		
29	Sivan Samba	74	Kodivilaiyan		
30	Panangkaattu Vaazhai	75	Aryan - 5532		
31	Komban Samba	76	Mulampunchan		
32	Katti Samba	77	Channa Ponni		
33	Palkudavazai	78	Kalyani		
34	Oriza nettai	79	Geethanjali Basumathi		
35	Thanga Samba	80	Mozhikarumpu		
36	Kottara Samba	81	White Shannam		
37	Basumathi	82	Pant Sugandhi		
38	Vaikarai Samba	83	Pusa Sugandhi		
39	Rathali	84	Parithban		
40	Kothamalli Samba	85	Mahi Sugandhi		
41	Chithiraikar	86	Amman		
42	Sivappu Gowni	87	Jaisriram		
43	Arupatham Kuruvai	88	Virendra		
44	Milagu Samba	89	Mallikar		
45	Karuthakar	90	Seeraga Samba		