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Divergence studies in fine scented genotypes of rice for yield and quality characters

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Abstract

Rice is a cleistogamous cereal crop in the Gramineae family of the Cyperales order. It is a main food all over the world and a big source of calories. The yield and quality are the two most important characters for consumption and in international markets. The current study was aimed to evaluate diversity among the 21 quality and agronomic characters and to discovery elite parents for further hybridization programmes. With a 7.68m² net plot scale, the study used a Randomized Complete Block Design with three replications and 20 cm×15 cm spacing between row to plant. On a plot basis, factors such as grains yield per plot, panicles per metre square, tillers/square metre, test weight, harvest index, and days to 50% flowering were measured. Effective tiller count, panicle length, plant height, and total number of filled grains/panicle were all determined by randomly selecting five plants from each plot. Clusters were divided using the Unweighted variable Pair Group Method of the Average Linkage Cluster Analysis (UPGMA) and Euclidean distance as the dissimilarity index by using XLSTAT 2021 statistical software. Coefficient of variation revealed that quality characters showed huge amount of variation among the genotypes. The largest cluster, Cluster I, had 14 genotypes followed by clusters II, III, IV, and V. The intra cluster distance varied between 33.45 (cluster III) and 50.15 (cluster IV). Cluster V and II had the greatest inter cluster gap (100.40), while cluster II and I had the smallest (19.29).

Keywords: RCBD, coefficient of variation, cluster analysis, inter and intra cluster distance

1. Introduction

Rice is the second most grown crop in the world after maize, and it is an essential food for almost 3.5 billion people. Majority of the calories comes from rice crop for almost 21% of the world's population. For this huge population around the world, it is their main source of carbohydrates (Babu *et al.*, 2012) [2]. As a result, rice is the only crop capable of combating hunger and poverty in developing and densely populated areas. As a result, it is recognised as the "Grain of Life," as it unites nations and cultures. When contrasted to global rice production and consumption, Asia is the major producer and consumer among other continents. Globally, the number of people who consume rice is rising every day, resulting in a rise in rice demand. "By 2050, the world's population will have risen from 7.6 billion to 9.8 billion people" (Anonymous, 2017) [1]. As a result, with a growing population and limited natural resources, we must produce more high-quality goods. As a result, yield has become a major goal in many genetic improvement. Quality, however, is just as critical as quantity. Quality is the second most significant breeding target in 11 of the world's major rice-growing countries, according to a survey by (Juliano and Villared, 1993) [8]. Plant breeders are now concentrating their efforts on improving quality characteristics such as superior grains, fine cooking quality, lengthwise elongation, and good fragrance, which command high prices in both domestic and foreign markets (Bhattacharjee *et al.*, 2002) [5]. Aromatic forms, on the other hand, have certain disadvantages (Berner and Hoff, 1986) [4]. Among different varieties of rice, there is a lot of difference in quality and total diversity. However, only a few studies were available on the quality traits of rice (Rani *et al.*, 2008) [12]. Long-term breeding programme success and genetic resource exploitation require data of genetic diversity between present cultivars of any crop. (Belaj *et al.*, 2002) [3]. Researchers from all over the world were astounded by the variety of quality traits and decided to learn more about them in order to grow new elite varieties with higher yields and higher quality. The purpose of this experiment is to evaluate coefficient of variation and diversity among 41 genotypes.

2. Material and Methods

During *Kharif* 2020, the genetics of 21 yield and quality traits in 41 fine scented genotypes of rice with four checks were evaluated under the Section of Genetics and Plant Breeding, S.G.C.A.R.S, Kumhrawand, Jagdalpur, Bastar (C.G.). The present experiment was carried out in RBD with three replications and with 20 cm × 15 cm spacing between row to plants with 7.68m² net plot size. On a plot basis, factors such as grains yield per plot, panicles per metre square, test weight, days to 50% flowering, harvest index, and tillers per square metre were measured. Panicle length, plant height, effective tiller count and total number of filled grains/panicle were all determined by randomly selecting five plants from each plot. Kernel length, kernel width, grain length and grain width was calculated using vernier callipers by taking 10 fully developed grains from each replication and mean is obtained and “grain L:B ratio and kernel L:B ratio were based on DUS descriptive” (Shoba *et al.*, 2006) [13]. Elongation ratio was based on method described by Pokhrel *et al.* (1983) [11]. Head rice recovery was measured by taking 10 fully developed grains and subjecting to milling in hand held dehuller and counting the number of whole kernels obtained after milling. Cagampang's *et al.* (1973) [7] process for determining gel consistency (GC) was used. Alkali Spreading Value performed based on method given by Little *et al.* (1958) [10]. Spectrophotometrical technique was used to determine the amylose content in each rice sample using Juliano's modified process (1971) [9]. The CV for different observations were based on method given by Burton and De Vane (1953) [6]. Classification of coefficient of variation was done based on Sivasubramanian and Madhavamenon (1973) [14]. The statistical analysis coefficient of variation and cluster analysis was performed using XLSTAT 2021.

3. Results and Discussion

Coefficient of variation revealed the presence of huge variability among different genotypes for all the characters under investigation and is presented in (Table 1). Characters like amylose content (38.88%), alkali spreading value (37.26%), gel consistency (33.76%), test weight (24.90%), total number of filled grains/panicle (23.19%), kernel L:B (21.36%) and grain L:B (20.28%) showed high CV% values. Moderate CV% values were shown by characters like head rice recovery (18.18%), kernel length (17.30%), plant height (17.07%), grain length (15.42%), number of panicles/square meter (14.26%), grain yield per plot (14.14%), number of tillers/square meter (13.46%), number of effective tillers/plant (13.37%), grain breadth (12.57%), harvest index (12.37%) and kernel breadth (11.52%). Low CV% values were seen in characters like panicle length (8.73%), days to 50% flowering (6.67%) and kernel elongation ratio (6.18%). Cluster analysis divided the 41 fine scented rice genotypes into five clusters and were presented in (Table 2 and Figure 1). The genotypes were not distributed homogeneously in the clusters. Cluster I

had the most genotypes, with 14, followed by Clusters II (9 genotypes), III (8 genotypes), IV (7 genotypes), and V (3 genotypes). The pattern of community constellation demonstrated that there is a lot of variation. The inter and intra cluster distances between 5 clusters was presented in (Table 3 and Figure 2). The intra cluster distance range between 33.45 (cluster III) to 50.15 (cluster IV). Cluster V and II had the greatest inter cluster gap (100.40) depicting that these two clusters are highly diverse, while cluster II and I had the smallest (19.29) depicting these two clusters are less diverse. So to achieve a good heterotic effect and a lot of heterogeneity, parentages should be chosen from the clusters with a higher inter cluster difference. For all of the traits under investigation, the cluster mean values showed a wide range of variations, as shown in (Table 4 and Figure 3). Cluster I contained genotypes with the highest mean value for kernel breadth (2.23), while the genotypes in cluster II had the maximum mean value for amylose content (21.24), effective tillers/plant (8.37), number of tillers/square meter (268.88), number of panicles/square meter (261.22), test weight (27.104), grain breadth (2.53), alkali spreading value (4.47), panicle length (23.18), and grain yield (3.20), while maximum mean value for grain length (9.26), grain L:B (4.17), kernel length (6.64) and kernel L:B (3.36) were seen in cluster IV. Cluster V had maximum mean value for kernel elongation ratio (1.23), plant height (139.2), total days to 50 % flowering (112), head rice recovery (66.66), harvest index (56.01), gel consistency (83.66) and number of filled grains/panicle (131.60). Character contribution to divergence is a significant consideration in the selection and selection of parents. Hybridization between diverse parents produce more heterotic effects than the parents who are less diversified. The current research concluded that parental lines selected from cluster I (R 1656-2151-1-412-1, R 1919-537-1-160-1, CG Sugandhit Bhog (c), CG Devbhog (c), Indira Sugandhit Dhan-1 (c), Jeeraphool Mutant 5, Vishnubhog Mutant V-74-6, R2369-481-1-258-1, R2369-475-2-252-1, R2369-483-1-259-1, R2369-478-1-255-1, R2369-475-1-251-1, R2369-479-1-256-1, R2369-480-1-257-1) for kernel breadth while cluster II (R 2054-685-1-205-1, R1624-61-1-59-1, R1624-61-2-60-1, R1624-61-3-61-1, R1896-82-1-60-1, R2281-308-1-185-1, R2282-552-1-309-1, Dubraj (c), Kasturi) for amylose content, number of effective tillers/plant, grain breadth, panicle length, number of tillers/square meter, number of panicles/square meter, test weight, alkali spreading value, and grain yield, while cluster IV (R2054-147-1-103-1, R2054-147-2-104-1, R2054-147-3-105-1, R2032-87-1-23-1, Maharaji, RL 910 (LAYCHA), RM 504 (Mahraji) for kernel length, grain length, kernel L:B and grain L:B. Cluster V (Samundrachini 5-50, Ker ghul, Banspatri) for plant height, head rice recovery, days to 50 % flowering, harvest index, total number of filled grains/panicle, gel consistency and kernel elongation ratio could be used to obtain desired segregants in crossing programmes.

Table 1: Mean, Standard error, Standard deviation and Coefficient of Variation of 21 characters under study

| Characters | Minimum X_{Min} | Maximum X_{Max} | Mean (\bar{X}) | Std. Error (SE) | Std. Deviation (σ) | Coefficient of variation CV% |
|------------|-------------------|-------------------|--------------------|-----------------|-----------------------------|------------------------------|
| PH | 81.80 | 154.47 | 112.12 | 2.99 | 19.14 | 17.07 |
| PL | 18.87 | 28.00 | 22.79 | 0.31 | 1.99 | 8.73 |
| NETP | 6.27 | 10.43 | 8.13 | 0.17 | 1.09 | 13.37 |
| TNFGP | 50.20 | 171.47 | 115.24 | 4.17 | 26.72 | 23.19 |
| NTSM | 177.33 | 322.33 | 246.41 | 5.18 | 33.18 | 13.46 |
| NPSM | 170.67 | 314.67 | 236.41 | 5.26 | 33.71 | 14.26 |
| DTF | 90.00 | 118.00 | 107.00 | 1.11 | 7.14 | 6.67 |

| | | | | | | |
|-----|-------|--------|-------|------|-------|-------|
| HI | 40.17 | 59.74 | 48.62 | 0.94 | 6.01 | 12.37 |
| TW | 13.15 | 33.03 | 20.18 | 0.78 | 5.03 | 24.90 |
| HR | 43.33 | 93.33 | 60.41 | 1.72 | 10.98 | 18.18 |
| GL | 5.65 | 10.13 | 8.01 | 0.19 | 1.23 | 15.42 |
| GB | 1.72 | 2.92 | 2.32 | 0.05 | 0.29 | 12.57 |
| GLB | 2.05 | 4.66 | 3.51 | 0.11 | 0.71 | 20.28 |
| KL | 4.05 | 6.97 | 5.66 | 0.15 | 0.98 | 17.30 |
| KB | 1.57 | 2.72 | 2.08 | 0.04 | 0.24 | 11.52 |
| KLB | 1.54 | 3.59 | 2.77 | 0.09 | 0.59 | 21.36 |
| ASV | 1.25 | 6.75 | 3.60 | 0.21 | 1.34 | 37.26 |
| GC | 21.50 | 102.50 | 48.63 | 2.56 | 16.42 | 33.76 |
| AC | 2.59 | 25.23 | 17.95 | 1.09 | 6.98 | 38.88 |
| KER | 0.99 | 1.27 | 1.17 | 0.01 | 0.07 | 6.18 |
| GY | 2.15 | 3.80 | 2.84 | 0.06 | 0.40 | 14.14 |

Keywords: PH=Plant height; PL=Panicle length; NETP=Number of effective tillers per plant; TNFGP=Total number of filled grains per panicles; NTSM=Number of tillers per square meter; NPSM=Number of panicles per square meter; DTF=Days to 50% flowering; HI=Harvest index; TW=Test weight; HR=Head rice recovery; GL=Grain length; GB=Grain breadth; GLB=Grain length breadth ratio; KL=kernel length; KB=kernel breadth; KLB=Kernel length breadth ratio; ASV=Alkali spreading value; GC=Gel consistency; AC=Amylose content; KER=Kernel elongation ratio; GY=Grain yield per plot

Table 2: Distribution of 41 genotypes into 5 clusters

| Clusters | 1 | 2 | 3 | 4 | 5 |
|---------------------|-----------------------------|--------------------|-----------------------|-------------------|--------------------|
| Genotypes | R 1656-2151-1-412-1 | R 2054-685-1-205-1 | R1915-115-1-88-1 | R2054-147-1-103-1 | Samundrachini 5-50 |
| | R 1919-537-1-160-1 | R1624-61-1-59-1 | Nagri Dubraj Mutant-1 | R2054-147-2-104-1 | Ker ghul |
| | CG Sugandhit Bhog (c) | R1624-61-2-60-1 | Jhilli Mutant 13-5 | R2054-147-3-105-1 | Banspatri |
| | CG Devbhog (c) | R1624-61-3-61-1 | R2400-562-1-339-1 | R2032-87-1-23-1 | |
| | Indira Sugandhit Dhan-1 (c) | R1896-82-1-60-1 | R 2400-562-2-340-1 | Maharaji | |
| | Jeeraphool Mutant 5 | R2281-308-1-185-1 | JDP-2520-2-4-1 | RL 910 (LAYCHA) | |
| | Vishnubhog Mutant V-74-6 | R2282-552-1-309-1 | R-FS-2019-1 | RM 504 (Maharaji) | |
| | R2369-481-1-258-1 | Dubraj (c) | R-FS-2019-2 | | |
| | R2369-475-2-252-1 | Kasturi | | | |
| | R2369-483-1-259-1 | | | | |
| | R2369-478-1-255-1 | | | | |
| | R2369-475-1-251-1 | | | | |
| R2369-479-1-256-1 | | | | | |
| R2369-480-1-257-1 | | | | | |
| Number of genotypes | 14 | 9 | 8 | 7 | 3 |

Table 3: Estimates of intra (bold and diagonal) and inter cluster distances with in 5 clusters

| Class | 1 | 2 | 3 | 4 | 5 |
|-------|-----------------|-----------------|-----------------|-----------------|-----------------|
| 1 | 41.79744 | 19.29384 | 54.43416 | 93.2576 | 91.1692 |
| 2 | | 37.07202 | 55.44654 | 95.30557 | 100.4004 |
| 3 | | | 33.45556 | 46.90714 | 75.53664 |
| 4 | | | | 50.15322 | 68.45642 |
| 5 | | | | | 48.64644 |

Table 4: Cluster mean values of 21 different characters of 41 rice genotypes and bold one are highest value for respective characters

| Class | 1 | 2 | 3 | 4 | 5 |
|-------|---------|---------|---------|---------|---------|
| PH | 119.376 | 110.837 | 95.800 | 106.305 | 139.200 |
| PL | 23.000 | 23.185 | 22.492 | 22.324 | 22.556 |
| NETP | 8.133 | 8.374 | 7.933 | 8.367 | 7.400 |
| TNFGP | 128.262 | 119.800 | 107.667 | 84.981 | 131.600 |
| NTSM | 265.310 | 268.889 | 233.208 | 211.095 | 208.444 |
| NPSM | 253.095 | 261.222 | 226.000 | 197.857 | 201.778 |
| DTF | 111.143 | 109.778 | 104.375 | 96.000 | 112.000 |
| HI | 47.078 | 50.026 | 49.466 | 45.761 | 56.019 |
| TW | 17.098 | 27.104 | 17.851 | 21.943 | 15.901 |
| HR | 65.714 | 61.481 | 53.333 | 53.810 | 66.667 |
| GL | 6.734 | 8.998 | 8.270 | 9.263 | 7.325 |
| GB | 2.477 | 2.539 | 1.996 | 2.229 | 2.039 |
| GLB | 2.754 | 3.557 | 4.163 | 4.177 | 3.606 |
| KL | 4.619 | 6.554 | 5.792 | 6.640 | 5.233 |
| KB | 2.236 | 2.226 | 1.806 | 1.974 | 1.878 |
| KLB | 2.092 | 2.960 | 3.212 | 3.368 | 2.797 |
| ASV | 3.768 | 4.472 | 3.313 | 2.643 | 3.250 |
| GC | 42.250 | 45.167 | 44.500 | 55.571 | 83.667 |
| AC | 20.399 | 21.248 | 20.131 | 11.879 | 4.941 |

| | | | | | |
|-----|-------|-------|-------|-------|-------|
| KER | 1.200 | 1.165 | 1.182 | 1.093 | 1.232 |
| GY | 2.756 | 3.204 | 2.971 | 2.435 | 2.783 |

Keywords: PH=Plant height; PL=Panicle length; NETP=Number of effective tillers per plant; TNFGP=Total number of filled grains per panicles; NTSM=Number of tillers per square meter; NPSM=Number of panicles per square meter; DTF=Days to 50% flowering; HI=Harvest index; TW=Test weight; HR=Head rice recovery; GL=Grain length; GB=Grain breadth; GLB=Grain length breadth ratio; KL=kernel length; KB=kernel breadth; KLB=Kernel length breadth ratio; ASV=Alkali spreading value; GC=Gel consistency; AC=Amylose content; KER=Kernel elongation ratio; GY=Grain yield per plot

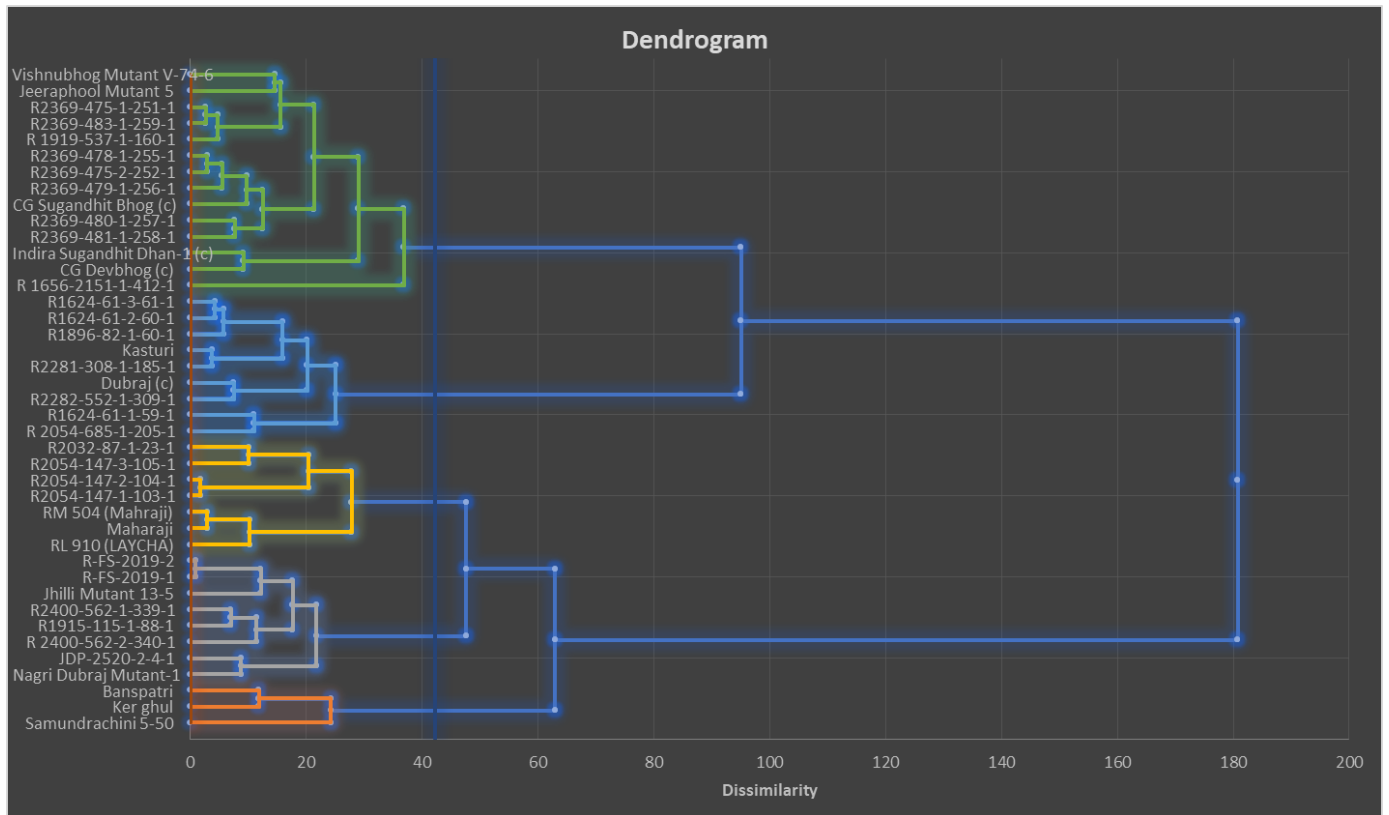


Fig 1: Dendrogram depicting the distribution of genotypes

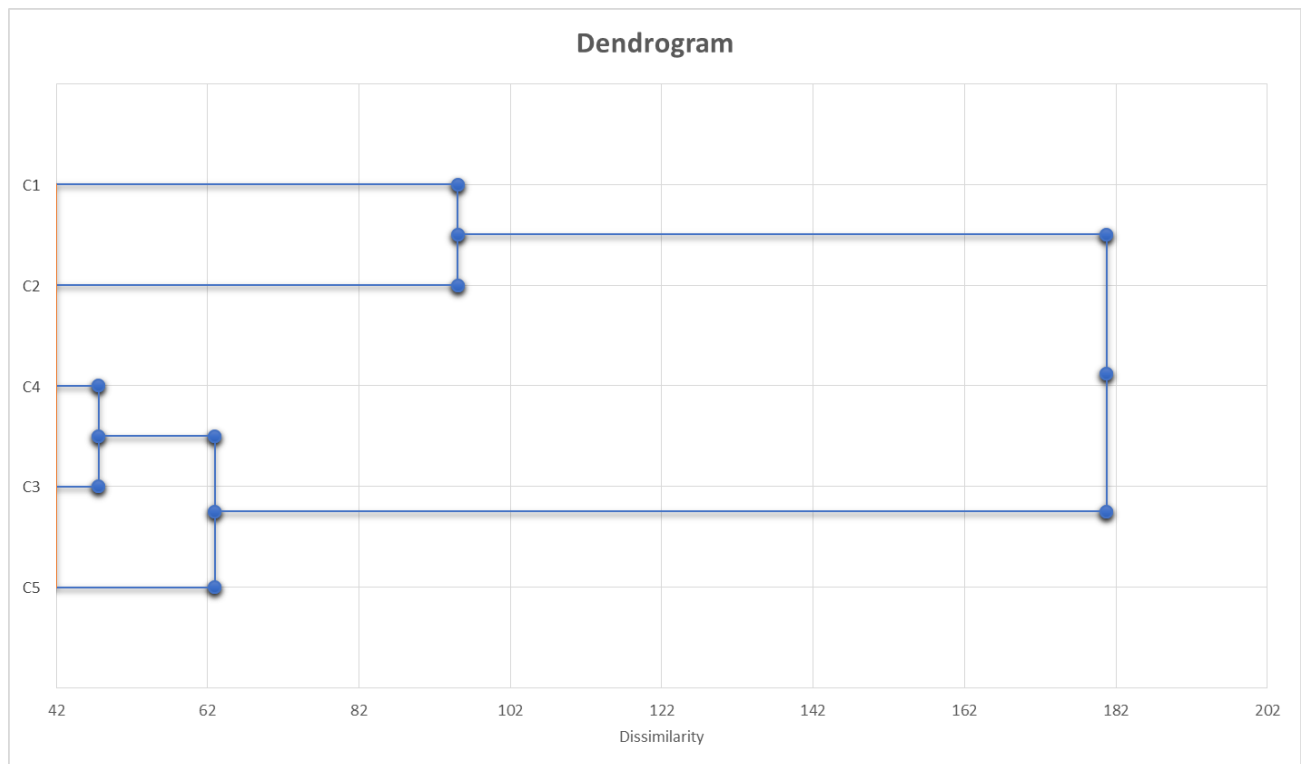


Fig 2: Dendrogram showing the distribution of inter and intra clusters

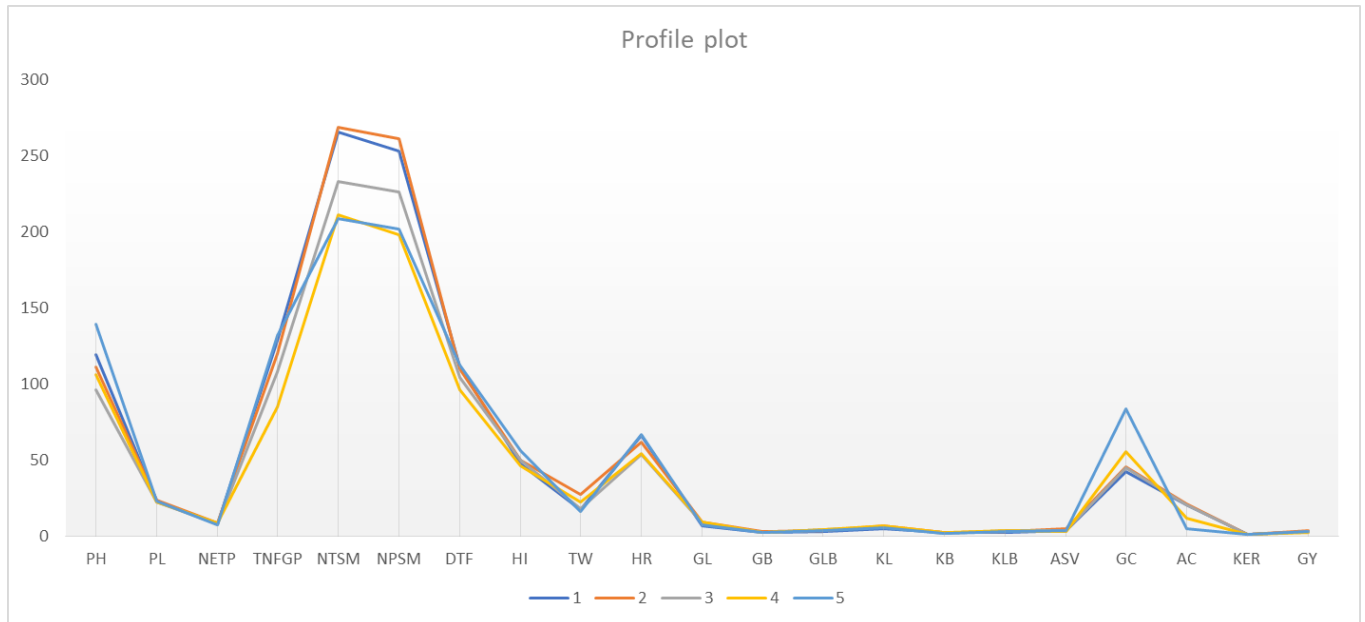


Fig 3: Profile plot showing the distribution of characters in 5 clusters

4. References

- Anonymous. The world population prospects: The 2017 Revision, published by UN Department of Economics and Social Affairs 2017.
- Babu VR, Shreya K, Dangi KS, Usharani G, Nagesh P. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. Int. J Sci. Res 2012;2(6):1-5.
- Belaj A, Satovic Z, Rallo L, Trujillo I. Genetic diversity and relationship in olive germplasm collection as determined by RAPD. Theor. Appl. Genet 2002;105(4):638-644.
- Berner DK, Hoff BJ. Inheritance of Scent in American Long Grain Rice 1. Crop Sci 1986;26(5):876-878.
- Bhattacharjee P, Singhal RS, Kulkarni PR. Basmati rice: a review. Inter. J. of Food Sci. and Tech 2002;37(1):1-12.
- Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agron. J 1953;45:478-481.
- Cagampang GC, Perez CM, Juliano BO. A gel consistency test for eating quality of rice. J Sci. Food Agric 1973;24(1):1589-1594.
- Juliano BO, Villareal CP. Grain quality evaluation of world rices. IRR1, Philippines 1993, 205p.
- Juliano BO. A simplified assay for milled rice amylose. Cereal Sci. Today 1971;16(1):334-338.
- Little RR, Hilder GB, Dawson EH. Differential effect of dilute alkali on 25 varieties of milled white rice. Cereal Chem 1958;35:111-126.
- Pokhrel A, Dhakal A, Sharma S, Poudel A. Evaluation of Physicochemical and Cooking Characteristics of Rice (*Oryza sativa* L.) Landraces of Lamjung and Tanahun Districts, Nepal. International journal of food science 2020;2020:1-11.
- Rani NS, Madliav MS, Pandey MK, Sundaram RM, Prasad GSV, Sudarshan I *et al.* Genetics and molecular approaches for improvement of grain quality traits in rice. Indian J Crop Sci 2008;3(1):1-14.
- Shobha Rani N, Shobha Rao LV, Viraktamath BC, Mishra B. National guidelines for the conduct of tests for distinctiveness, uniformity and stability. Directorate of Rice Research 2006,6-13.
- Sivasubramanian V, Madhavamenon P. Path analysis for yield and yield components of rice. Madras Agric. J 1973;60:1217-1227.