Electronic Journal of Plant Breeding, 9(4): 1450-1460 (Dec 2018) DOI: 10.5958/0975-928X.2018.00180.1
ISSN 0975-928X

**Research Article**

# Genetic variability studies in ADT 43/Seeraga samba cross derivatives of rice (*Oryza sativa* L.)

**M. S. Bharath*, M. Madhan Mohan[1], C. Vanniarajan[2], V. Veranan Arun Gridhari[2] and N. Senthil**
[*]Agricultural College & Research institute, Madurai-625-104
[1]Agriculural Research Station, Vaigai Dam, Theni District - 625 562
[2] Community Science College & Research institute, Madurai-625-104
[3] Agricultural College & Research institute, Coimbatore. 641-001, Tamil Nadu Agricultural University
[*]**E-Mail:** bharathms283@gmail.com

(Received: 11 Sep 2018; Revised: 28 Nov 2018; Accepted: 13 Dec 2018)

## Abstract

In the present investigation 11 quantitative characters *viz.*, days to 50% flowering, plant height, flag leaf length, flag leaf width, leaf length, leaf width, number productive tillers, panicle length, number of filled grain, thousand grain weight, single plant yield and 16 qualitative characters *viz.*, Hulling percentage, milling percentage, kernel Length, kernel breadth, Length /breadth ratio, kernel length after cooking, kernel breadth after cooking, linear elongation ratio, breadth elongation ratio, cooking time, water up-take, volume expansion ratio, alkali spreading value, gel consistency, amylose content and head rice recovery were studied for ADT43/Seeragasamba cross derivatives in $F_8$ generations. The quantitative characters had shown less difference between PCV and GCV. Out of eleven quantitative characters studied, five characters *viz.*, Flag leaf length, Leaf length, number of productive tillers, thousand grain weight and single plant yield had shown high phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV) along with high heritability($h^2$) and genetic advance (GAM). The quality characters *viz.*, Alkali spreading value and gel consistency had shown high phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV) along with high heritability ($h^2$) and genetic advance (GAM). These characters are less influenced by environment. The additive gene action governed the above-mentioned characters and additive gene actions are responsible for selection and is beneficial crop improvement programme.

**Key words**

Seeragasamba, ADT43, rice, paddy, land race, variability, quantitative characters, qualitative characters, PCV, GCV, heritability and genetic advance.

## Introduction

Rice, *Oryza sativa* (2n=24) finds its place in Indian culture from birth to death, which shows the richness of rice diversity for all seasons and all reasons. Rice is first referred in the Yajur Veda (Thiyagarajan and Biksham Gujja, 2012) and is an integral part of Indian culture. ‘Rice is Life’ since it is the main source of energy in the diet. India had produced 158.7 million tonnes of paddy from 43.5 million hectares during 2016.

The significant criteria in any crop improvement programme are the selection of genotypes with all possible desirable grain quality and yield contributing traits. Variability in genotypes for yield and its component traits forms the basic factor to be considered during selection. Any successful hybridization programme for varietal improvement mainly depends on the selection of parents having high variability, so that, the desired character combination may be selected to improve grain quality and higher grain yield. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the transmissibility of a character into further generations (Devi *et al.*, 2017).

Rice is consumed principally as a whole grain and the texture of the grain is a matter of primary importance. Rice quality is importance for all the people involved in producing, processing and consuming rice, because it affects the nutritional and commercial value of grains. Grain quality is based upon objective and subjective criteria, the relative importance of which depends on the particular end-use. The most important quality components, common to all users, include cooking, milling, appearance, processing and nutritional quality. Further grain quality has become an important issue affecting domestic consumption and international trade of rice.

The ADT 43(Female parent) is a medium slender grain type with good milling percentage and head rice recovery, and it is mostly consumed rice variety in thanjavur delta, the male parent (Seeragasamaba) is traditional aromatic rice, it is fine grain type, these rice mostly use to making a variety rice like biryani, fried rice etc.

As climate change has made frequent floods and prolonged droughts, the modern high yielding rice varieties and hybrids suffer most due to the erosion of its biodiversity and increase of mono cropping in agriculture. The significant characteristics of some of the traditional varieties are their medicinal, nutritional traits and their consumer preferences (Madhan Mohan *et al*., 2013).

## Material and Methods

The field investigation was carried out in Agricultural Research Station, Vaigai dam, Theni district, Tamil Nadu. Investigation was taken up primarily to study the genetic variability, quality attributes, and yield in ADT43/Seeragasamba in $F_8$ generations. The investigation related to cooking qualities of rice and physio-chemical analysis was carried out at Community College and Research Institute Madurai. Twenty-seven Homogenous lines developed from ADT43/ Seeragasamba cross derivatives were selected along with their parents.

| **Parents** | **Characters** |
|---|---|
| ADT 43 (Female parent) | ADT 43(IR 50 / White Ponni) is preferred for kuruvai season sowing. Medium slender grain with 110 days duration with medium height. The potential yield is 5.75t/ha. |
| Seeragasamba (Male parent) | Seeragasamba (landrace) is preferred for samba season sowing. Short slender grain with 140 days duration with plant height of 135 to 140 cm. The potential yield is 3.0t/ha. |

## Results and Discussion

The PCV and GCV were found to be high for the biometrical traits *viz.*, flag leaf length, leaf length, number of productive tillers per plant, thousand grain weight and single plant yield. The high magnitude of PCV and GCV for the above-mentioned traits suggested the presence of high degree of variability(Table & Fig. 1- 4). This indicates the existence of wide genetic base among the homogenous lines. Hence, these traits could give better scope for the improvement through simple or direct selection. These results were in conformity with the findings of Sravan *et al.* (2012) for flag leaf length; Balat *et al.* (2018) for leaf length; Umadevi *et al.* (2009) for number of productive tillers per plant; Srujana *et al.* (2017) for thousand grain weight and Dhurai *et al.* (2014) for single plant yield.

The quality traits *viz.*, alkali spreading value and gel consistency was found to be having high PCV and GCV. Similar findings were reported by Dhanwani *et al.* (2013)

Moderate PCV and GCV was found for the following biometrical traits *viz.*, days to 50% flowering, plant height, leaf width, panicle length and number of filled grains per panicle indicating the fair level of scope for phenotypic selection. The results were in accordance with the findings of Sravan *et al.* (2012) and Jaiswal *et al.* (2015) for days to 50% flowering; Sravan *et al.* (2012), Dhurai *et al.* (2014), Srujana *et al.* (2017), Dhanwani *et al.* (2013) and Yadav *et al.* (2010) for plant height; Chouhan *et al.* (2014) for leaf width; Dhurai *et al.* (2014) and Kahani & Hittalmani (2015) for panicle length and Sala & Shanthi .(2016) for number of filled grains per panicle.

Moderate PCV and GCV were found for the following quality traits *viz.*, milling percentage, kernel length, kernel breadth, kernel length/ breadth ratio, linear elongation ratio, amylose content and head rice recovery and were in line with the earlier results obtained by Manonmani *et al.* (2010) for milling percentage and linear elongation ratio; Sahu *et al.* (2017) for kernel length, kernel breadth, kernel length/breadth ratio and head rice recovery and Savitha and Kumari (2016) for amylose content.

Low estimates of phenotypic and genotypic coefficient of variations were observed for the quantitative and qualitative characters *viz.*, flag leaf width, hulling percentage, kernel length after cooking, kernel breadth after cooking, breadth elongation ratio, water uptake ratio and volume expansion ratio. Hence, it can be concluded that direct phenotypic selection for this trait may not be rewarding and larger sized population with wide genetic base may be required for further improvement The results were in accordance with the findings of Abarshahr *et al*. (2011) for flag leaf width; Manonmani *et al.* (2010) for hulling percentage, kernel length after cooking, kernel breadth after cooking and volume expansion ratio; Nandan *et al.* (2010) for water uptake and Ramchandra *et al.* (2015) breadth elongation ratio.

Cooking time showed a moderate PCV and a low GCV. So this trait cannot be considered for crop improvement programme, Dhurai *et al.* (2014) reported that the selection for this character may be misleading. Estimates of phenotypic and genotypic coefficients of variation alone are not sufficient to enough assess the heritable variation. For more reliable conclusion, estimates of high heritability and high genetic gain should be considered together (Johnson *et al.* 1955). The heritable fraction of the variation provides the base to the plant breeder for selection based on phenotypic performance. Heritability of a trait is an index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes, hence prior knowledge about the heritability of the traits is a prerequisite for the selection programme (Singh *et al.*, 2018). Therefore, the estimates of heritability and genetic advance would help to formulate a sound breeding programme. High heritability may not always associate with large genetic advance. Since high heritability does not always indicate a high genetic gain, heritability is recommended to be considered in association with genetic advance to predict the effect of selecting superior crops varieties.

Out of 11 characters studied, ten characters (DFF, PH, FLL, LL, LW, NFGP, TGW, NPT, PL, SPY) had shown high heritability and high genetic advance favoring additive gene action. The results were in accordance with the findings o f Saini *et al.* (2013) for days to 50% flowering; Srujana *et al.* (2017) and Devi *et al*. (2017) for plant height; Devi *et al.* (2017) for flag leaf length; Chouhan *et al.* (2014) and Shamim *et al.* (2017) for leaf length, leaf width; Srujana *et al.* (2017), Sravan *et al.* (2012) and Lingaiah *et al.*, (2015) for number of filled grains per panicle; Dhurai *et al.* (2014) and Sala & Shanthi (2016) for thousand grain weight, number of productive tillers per plant, panicle length and single plant yield.

Flag leaf width had shown high heritability and moderate genetic advance as percentage of mean. The results were in accordance with the findings of Revathi *et al.* (2016). It indicates the presences of additive and non-additive gene action for this trait. In such cases, recurrent selection method may be used to improve the population, Dhurai *et al.* (2014).

All the sixteen quality characters had shown a high heritability except cooking time had shown moderate heritability. Heritability was ranged from 47 to 99 per cent and genetic advance high for nine traits and the remaining had showed moderate. Johnson *et al.* (1955) have suggested that characters with high heritability coupled with high genetic advance would respond better to selection than those with high heritability and low genetic advance.

The high heritability and genetic advance were observed for milling percentage, kernel length, kernel breadth, L/B ratio, linear elongation ratio, alkali spreading value, gel-consistency, amylose content, and head rice recovery. Indicating the role of additive gene action and direct selections for these characters will help in crop improvement. Similar results were reported by Vanaja *et al.* (2006) for milling percentage and kernel breadth; Manonmani *et al.* (2010) for linear elongation ratio and alkali spreading value; parikh *et al.* (2012) for L/B ratio; Shamim *et al.* (2017) for kernel length; Ramacandra *et al*. (2015) for gel-consistency; Nirmaladevi *et al.*, (2015), for amylose content; Devi *et al.* (2017) for Head rice recovery.

Hulling percentage, kernel length after cooking, kernel breadth after cooking, water uptake, breadth elongation ratio and volume expansion ratio had shown high heritability with moderate genetic advance, indicating the presence of both additive and non-additive gene action and the recurrent selection method may be advocated to improve these characters. These findings were in conformity with earlier findings of Manonmani *et al.* (2010) for hulling percentage; Devi *et al.* (2017) for kernel length after cooking and kernel breadth after cooking; Babu *et al.* (2012) for water up taking; Ramachandra *et al.*,(2015) for breadth elongation ratio; Manonmani *et al.* (2010) for volume expansion ratio.

## References

Babu, V. R., Shreya, K., Dangi, K. S., Usharani, G., & Nagesh, P. 2012. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. *International Journal of Scientific and Research Publications,* **2**(6):1-5.

Balat, J. R., Patel, V. P., Visat, M. L., & Bhagora, R. N. 2018. Variability Analysis in $F_2$ Population of Rice (*Oryza sativa* L.) for Yield and Related Traits. *Int. J. Pure App. Biosci*, **6**(1): 1021-1027.

Chouhan, S. K., Singh, A. K., Aparajita, S., Ram, M., Singh, P. K., & Singh, N. K. 2014. Characterization and evaluation of *Oryza nivara* and *Oryza rufipogon*. *The Bioscan*, ***9***(2), 853–858.

Devi, K. R., Chandra, B. S., Lingaiah, N., Hari, Y., & Venkanna, V. 2017. Analysis of correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). *Agricultural Science Digest-A Research Journal,* **37**(1): 1-9.

Dhanwani, R. K., Sarawgi, A. K., Solanki, A., & Tiwari, J. K. 2013. Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza sativa* L.). *The Bioscan*, **8**(4): 1403-1407.

Dhurai, S. Y., Bhati, P. K., & Saroj, S. K. 2014. Studies on genetic variability for yield and quality characters in rice (*Oryza sativa* L.) under integrated fertilizer management. *The Bioscan*, **9**(2): 745-748.

Hanson WD, Robinson HF, Comstock RE 1956. Biometrical studies of yield in segregating population. Agron. J. **48**: 268-272.

Jaiswal, H. K., Srivastava, A. K., & Dey, A. 2007. Variability and association studies in indigenous aromatic rice (*Oryza sativa* L.) **44**(4): 351.

Johnson, H.W., Robinson, H.F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.,* **47**: 314 – 318.

Kahani, F., & Hittalmani, S. 2015. Genetic analysis and traits association in $F_2$ intervarietal populations in rice under aerobic condition. *Rice Research: Open Access*.

Lingaiah, N. 2015. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Asian Journal of Environmental Science*, **10**(1): 110-112.

Madhan Mohan, M., Balakrishnan, A., & Renganayaki, P. R. 2013. Research Note A high yielding seeragasamba rice culture VG 09006 and its medicinal properties. *Electronic Journal of Plant Breeding*, **4**(2): 1148–1154.

Manonmani, S., Malarvizhi, D., Robin, S., Umadevi, M., Ameenal, M., Pushpam, R., Manonmani, S., Malarvizhi, D., Robin, S., Umadevi, M., Ameenal, M., Pushpam, R., Sundaram, K.M & Thiyagarajan, K. 2010. Breeding three line rice hybrids with good grain quality. *Electronic Journal of Plant Breeding*, **1**(4): 1265-1269.

Nandan, R., Swetha and Singh, S.K. 2010. Character association and path analysis in rice (Oryza sativa L) genotypes. World Journal of Agricultural Sciences **6**: 201-206.

Nirmaladevi, G., Padmavathi, G., Kota, S., & Babu, V. 2015. genetic variability , heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L .). *sabrao Journal of Breeding and Genetics*, **47**(4), 424–433.

Parikh, M., Rastogi, N. K., & Sarawgi, A. K. 2012. Variability in grain quality traits of aromatic rice (*Oryza sativa* L.). *Bangladesh Journal of Agricultural Research*, **37**(4): 551-558.

Ramchander S. 2015. Quality Characteristics of Rice Mutants Generated Through Gamma Radiation in White Ponni, International Journal of Agriculture Sciences, ISSN: 0975-9107 & E-ISSN: 0975-9107, **7**(10):714-718.

Revathi, S., Sakthivel, K., Manonmani, S., Umadevi, M., Ushakumari, R., & Robin, S. 2016. Genetics of wide compatible gene and variability studies in rice (Oryza sativa L.). *Journal of Genetics*, ***95*(**2), 463–467.

Saini, P., Mary Francies, R., Joseph, J., Bastian, D., & Vigneshwaran, V. 2013. Genetic assessment of core set developed from short duration rice accessions held by Kerala Agricultural University. *Journal of Tropical Agriculture*, **51**(1–2): 126–131.

Sala, M., & Shanthi, P. 2016. Variability, heritability and genetic advance studies in F2 population of rice (*Oryza sativa* L.). *International Journal of Forestry and Crop Improvement*, **7**(1): 57-60.

Sahu, K. Parmeshwar, Deepak Sharma, Suvendu Mondal, Vikash Kumar, Satyapal Singh, Samarth Baghel, Ashish Tiwari, Gautam Vishwakarma and B. K. Das. 2017. Genetic variability for grain quality traits in indigenous landraces of Chhatisgarh, India. *Journal of Experimental Biology and Agricultural Sciences.* **5**(4): 439 - 455.

Savitha, P., and Kumari, R. U. 2016. Genetic variability studies in segregating generation for grain and nutritional quality traits in rice (*Oryza sativa* L.). *Journal of Applied and Natural Science,* **8**(1): 63-68.

Shamim, M. Z., Sharma, V. K., Manzar, H., & Bhushan, S. 2017. Grain Yield Components Analysis in Locally Adapted Rice Varieties Grain Yield Components Analysis in Locally Adapted Rice Varieties. *International Journal of Agriculture, Environment and Biotechnology*, **10**(October), 435–442.

Singh, A. K., Nandan, R., & Singh, P. K. 2018. Genetic variability and association analysis in rice germplasm under rainfed conditions. *Crop Res*, **47**(1): 2.

Sravan, T., Rangare, N. R., Suresh, B. G., & Kumar, S. R. 2012. Genetic variability and character association in rainfed upland rice (*Oryza sativa*. L). *Journal of Rice Research*, **5**(1): 24-29.

Umadevi, M., Veerabadhiran, P., & Manonmani, S. 2009. Genetic variability, heritability, genetic advance and correlation for morphological traits in rice genotypes. *Madras Agric. J*, **96**(7-12): 316-318.

Srujana, G., Suresh, B. G., Lavanya, G. R., Ram, B. J., & Sumanth, V. 2017. Studies on Genetic Variability, Heritability and Genetic advance for yield and quality components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, **6**(4): 564-566.

Thiyagarajan, T.M. and Biksham Gujja . 2012. Transforming Rice Production with SRI *sativa* L.). *Journal of bio-science*, **18**: 1-8.

(System of Rice Intensification) Knowledge and Practice. National Consortium of SRI (NCS). Hyderabad, India. pp.216

Yadav, S. K., Suresh, B. G., Pandey, P., & Kumar, B. (2010). Assessment of genetic variability, correlation and path association in rice (*Oryz*

### Table 1. Analysis variance of RBD for various quantitative traits

| Sources | *Df* | *Mean sum of square* | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | **DFF** | **PH** | **FLL** | **FLW** | **LL** | **LW** | **NPT** | **PL** | **NFG** | **TGW** | **SPY** |
| Replication | 1 | 14.507 | 331.202 | 58.424 | 0.033 | 46.511 | 0.236 | 3.879 | 63.007 | 0.590 | 0.309 | 15.657 |
| Genotypes | 28 | 465.414** | 539.526** | 158.464** | 0.017** | 166.696** | 0.039** | 19.753** | 19.916** | 364.879** | 26.280** | 81.385** |
| Error | 28 | 0.7140 | 7.3834 | 0.105 | 0.002 | 0.173 | 0.004 | 0.950 | 0.108 | 12.086 | 0.023 | 1.011 |

**Indicating Significances at 0.05% Level.

**DFF**- Days to 50%flowering, **PH**- Plant height, **FLL**-Flag leaf length ,**FLW**-Flag width, **LL**-Leaf length, **LW**-Leaf width, **PL**- Panicle length,**NPT**- Number of productive tillers per plant, **NGP** – Number of grains/panicle, **TGW**- 1000 grain weigh, SPY-Singleplant yield

### Table 2. Analysis variance of RBD for various qualitative traits:

| Sources | *Df* | *Mean sum of square* | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | **H** | **M** | **KL** | **KB** | **L/B** | **KLAC** | **KBAC** | **LER** | **BER** | **CT** | **WUP** | **VER** | **ASV** | **GC** | **AC** | **HRR** |
| Replication | 1 | 68.928 | 62.837 | 0.262 | 0.083 | 0.797 | 0.165 | 0.107 | 0.502 | 303.837 | 96.983 | 0.155 | 0.099 | 1.022 | 583.7306 | 1.9463 | 57.2613 |
| Genotypes | 28 | 41.486** | 89.632** | 1.445** | 0.129** | 0.574** | 0.856** | 0.095** | 0.111** | 308.051** | 4.057** | 0.457** | 0.126** | 3.064** | 1654.74** | 16.761** | 105.924** |
| Error | 28 | 0.393 | 0.407 | 0.001 | 0.008 | 0.023 | 0.008 | 0.006 | 0.003 | 308.120 | 1.447 | 0.018 | 0.015 | 0.014 | 115.188 | 3.7051 | 1.3646 |

**Indicating Significances at 0.05% Level.

**H%**-Hulling percentage **,M%**-Milling percentage **,KL**-kernel Length**, KB**-Kernel Breadth **,L/B**- Length /breadth ratio, **KLAC**- Kernel length after cooking, **KBAC**- Kernel breadth after cooking**, LER**- Length elongation ratio, **BER**- Breadth elongation ratio, **CT**- Cooking time, **WUP**- Water up-take, **VER**- Volume expansion ratio, **ASV**- Alkali spreading value, **GC**- Gel consistency, **AC**- Amylose content, **HRR%**- Head rice recovery

**Table 3. Estimation of variability for quantitative traits**

| Character | Mean | Range | PCV | GCV | Heritability ($h^2$) | GAM% |
|---|---|---|---|---|---|---|
| Days to 50 % flowering | 82.2 | 60-107 | 18.44 | 18.41 | 99 | 37.87 |
| Plant height(cm) | 114.6 | 80.5-136 | 14.42 | 14.22 | 97 | 28.91 |
| Flag leaf length(cm) | 35.6 | 24.6-68.7 | 24.98 | 24.96 | 99 | 51.39 |
| Flag leaf width(cm) | 1.20 | 1-1.4 | 8.20 | 7.13 | 75 | 12.79 |
| Leaf length(cm) | 37.4 | 24.0 -64.4 | 24.38 | 24.36 | 99 | 50.13 |
| Leaf width(cm) | 1.05 | 0.85-1.45 | 14.10 | 12.66 | 80 | 23.43 |
| No. of productive tillers | 12.8 | 7.5-19.5 | 25.04 | 23.87 | 90 | 46.86 |
| Panicle length(cm) | 20.4 | 15.0-28.3 | 15.44 | 15.35 | 98 | 31.46 |
| No .of filled grains per panicle | 99.6 | 67.5-127.5 | 13.78 | 13.33 | 93 | 26.56 |
| Thousand grain weight (grams) | 15.2 | 8-21.2 | 23.77 | 23.75 | 99 | 48.89 |
| Single plant yield(grams) | 19.45 | 11.0-32.6 | 32.98 | 32.58 | 97 | 66.28 |

**Table 4. Estimation of variability for quality traits**

| Characters | Mean | Range | PCV | GCV | Heritability ($h^2$) | GAM (%) |
|---|---|---|---|---|---|---|
| Hulling percentage (%) | 71.65 | 57.3-79.55 | 6.38 | 6.32 | 98 | 12.90 |
| Milling percentage (%) | 62.26 | 45.8-72.85 | 10.77 | 10.72 | 99 | 21.99 |
| Kernel Length (mm) | 5.35 | 3.95-6.5 | 15.88 | 15.86 | 99 | 32.64 |
| Kernel Breadth (mm) | 1.94 | 1.55 – 2.25 | 13.49 | 12.68 | 88 | 24.54 |
| Length /breadth ratio(mm) | 2.8 | 2.05 – 4.1 | 19.51 | 18.75 | 92 | 37.11 |
| Kernel length after cooking(mm) | 8.56 | 6.5 – 9.75 | 7.67 | 7.60 | 98 | 15.50 |
| Kernel breadth after cooking(mm) | 2.57 | 2.15 – 2.85 | 8.78 | 8.19 | 86 | 15.74 |
| Linear elongation ratio(mm) | 1.64 | 1.3 – 2.2 | 14.58 | 14.08 | 93 | 28.03 |
| Breadth elongation ratio(mm) | 1.34 | 1.14 – 1.50 | 6.78 | 6.16 | 82 | 11.54 |
| Cooking time(min) | 14.25 | 12 – 17 | 11.63 | 8.01 | 47 | 11.36 |
| Water up-take(ml) | 5.53 | 4.65 –.6.3 | 8.80 | 8.45 | 92 | 16.75 |
| Volume expansion ratio(ml) | 2.64 | 2.20 – 3.20 | 10.04 | 8.91 | 78 | 16.30 |
| Alkali spreading value(ASV) | 2.62 | 1.0 – 6.0 | 47.19 | 46.97 | 99 | 96.30 |
| Gel consistency (mm) | 83.96 | 31 – 121.0 | 35.42 | 33.04 | 86 | 63.48 |
| Amylose content (%) | 20.43 | 13.75 – 25.1 | 15.65 | 15.65 | 63 | 20.57 |
| Head rice recovery (%) | 54.01 | 42.15 – 68.4 | 13.38 | 13.55 | 97 | 27.22 |

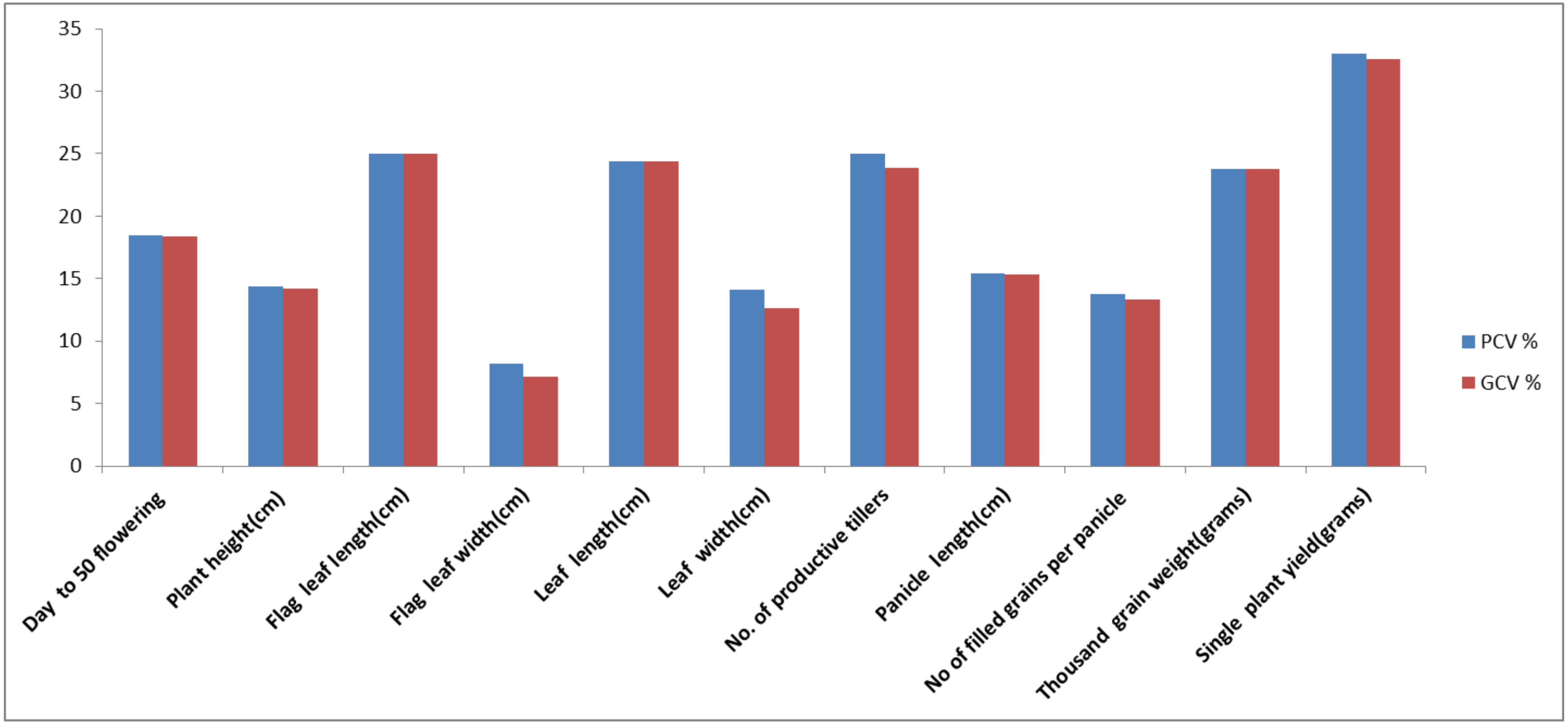

**Fig. 1. PCV and GCV for quantitative traits**

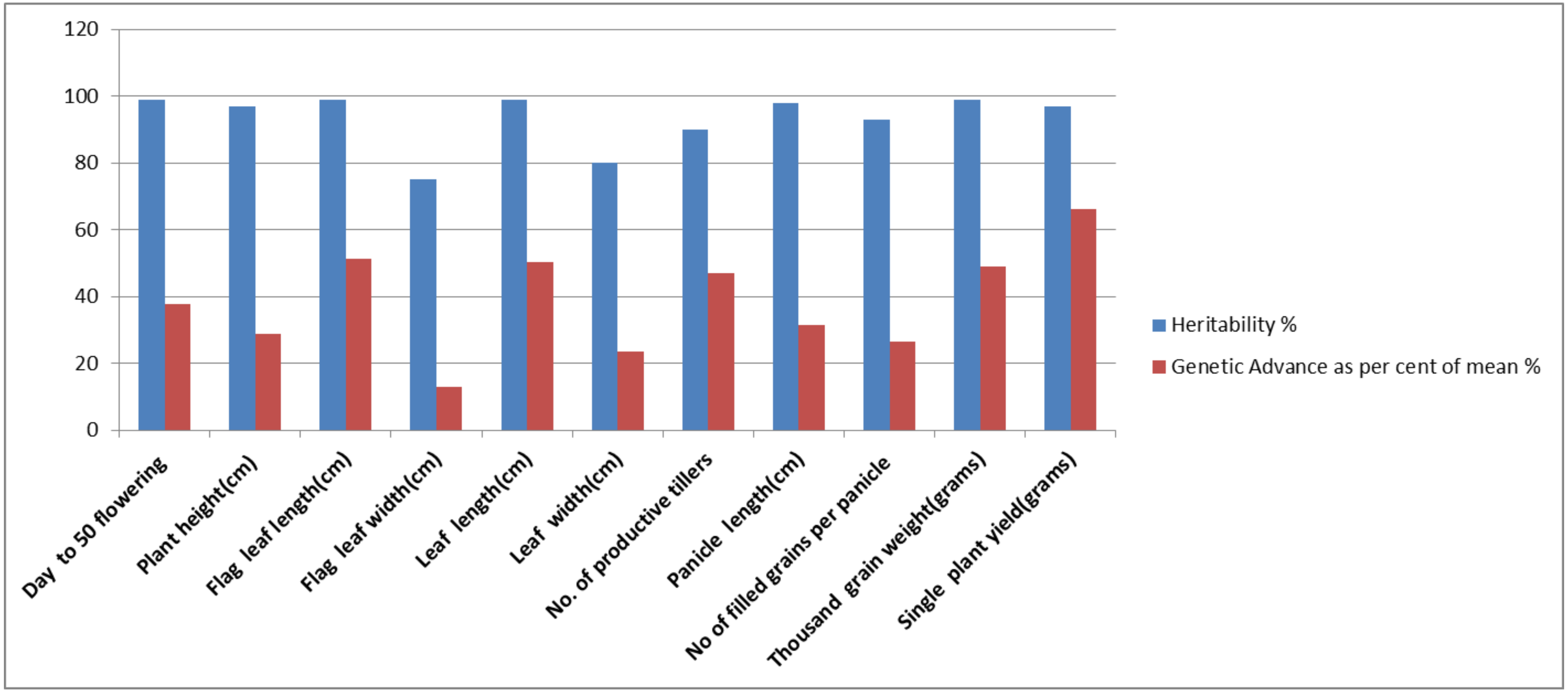

**Fig. 2. Heritability and Genetic Advance for quantitative characters**

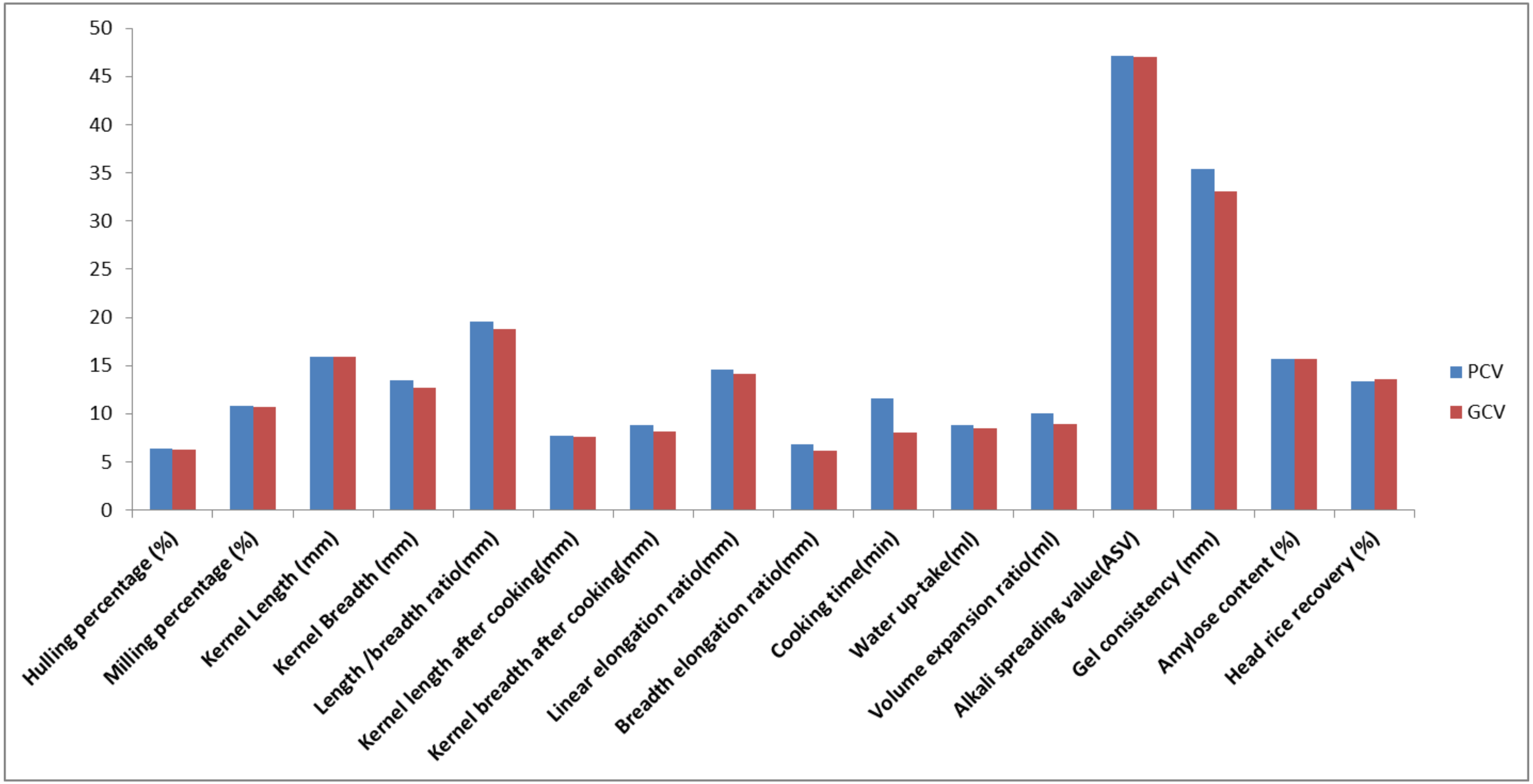

**Fig.3. PCV and GCV for qualitative traits:**

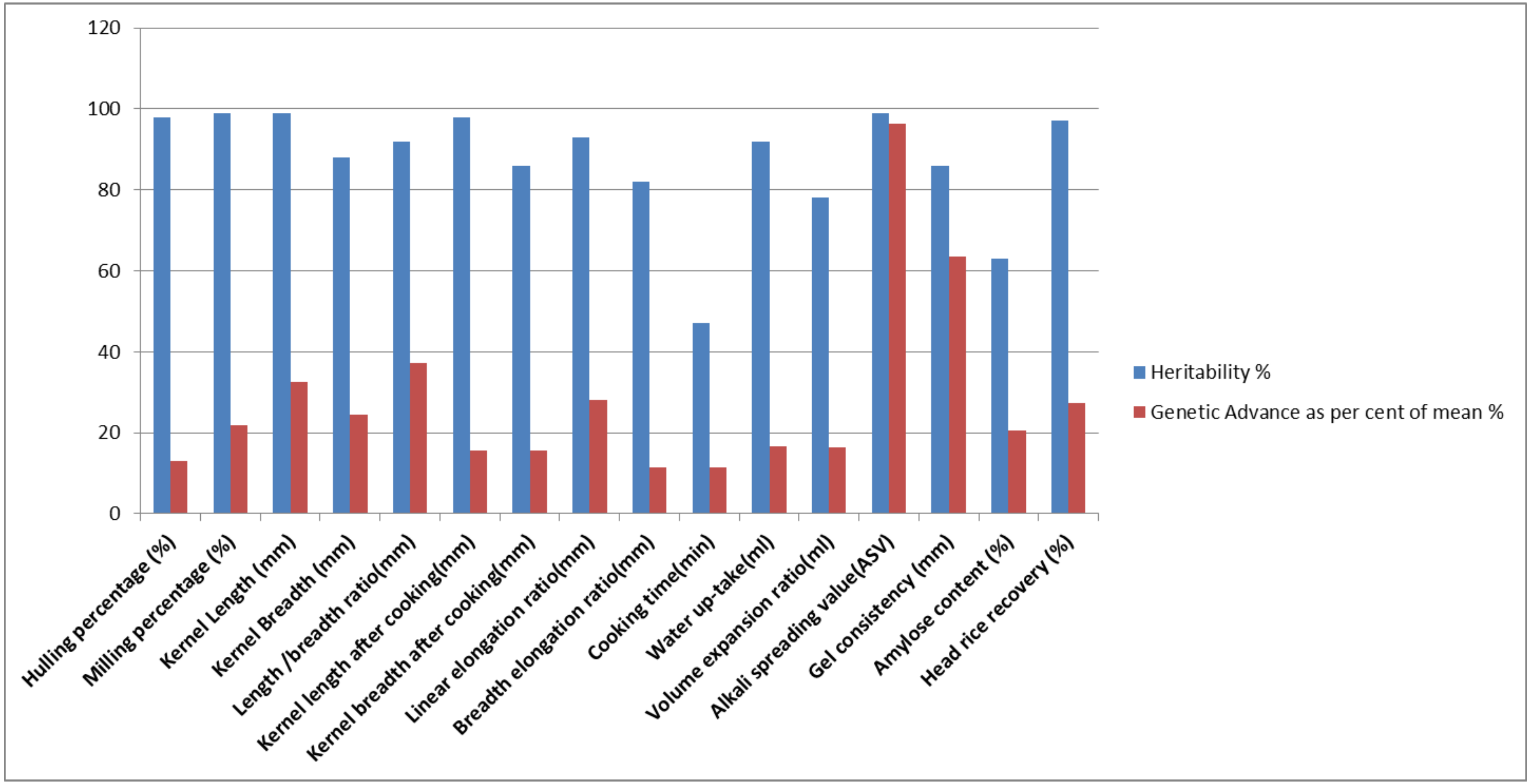

**Fig. 4. Heritability and Genetic Advance for qualitative traits**