Electronic Journal of Plant Breeding, 6(2): 506-511 (June 2015)
ISSN 0975-928X

Research Note

Variability, heritability and genetic advance studies in some indigenous genotypes of basmati rice (*Oryza sativa* L.)

C. R. Allam[1]*, H.K. Jaiswal[1] , A. Qamar[2] , Challa Venkateshwarlu[3] and Y.S. Reddy[3]
[1]Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005, Uttar Pradesh, India.
[2]Department of Plant Physiology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005, Uttar Pradesh, India.
[3]IRRI-South Asia Hub, ICRISAT, Patancheru-502324, Telangana, India.
Email: chinna.allam@gmail.com

(Received: 25 Oct 2014; Accepted: 14 Nov 2014)

Abstract
The investigation conducted with 25 rice genotypes comprising both Basmati and non-basmati types revealed significant differences among the genotypes for the yield, its components and some grain quality characteristics. The magnitude of differences between PCV and GCV was relatively low for all the traits, indicating less environmental influence. The GCV was higher for the characters alkali spread value, yield per plant and effective panicles. High heritability coupled with high genetic advance as per cent of mean was recorded for days to 50% flowering, plant height, panicle length, effective panicles per plant, spikelets per panicle, filled grains per panicle, test weight, yield per plant, brown rice length, brown rice L/B ratio, kernel length, kernel L/B ratio, kernel length after cooking, elongation ratio and alkali spread value indicating the additive gene effects in the genetic control of these traits and can be improved by simple selection in the present breeding material.

Keywords
Basmati rice, variability, heritability, genetic advance, grain quality.

Genetic variability is the pre requisite for any crop improvement programme. Improvement in any trait is solely depends on the amount of variability present in the base material of that trait. Heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of the characters from parents to offspring (Falconer, 1981). Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.,* 1992). Traditional basmati rice varieties are very low yielding due to their poor harvest index, tendency to lodging and increasing susceptibility to foliar diseases; hence there is a need to develop new varieties combining the grain quality attributes of basmati with high yield potential (Amarawathi *et al.*, 2008). The knowledge of variability, heritability and genetic advance are immense help to plant breeders to plan an effective breeding programme. Also these estimates help in estimation of environment influence on the expression of traits. This is especially important as the special quality of basmati rice is attributed to unique combination of soil, water, climate and cultural practices under which it is grown, besides its inherent genetics governing the features (Siddiq *et al.,* 2012). Hence the present investigation was undertaken to study the genetic variability, heritability and genetic advance in some indigenous basmati rice genotypes.

The experiental material used in the study comprised of 23 basmati rice genotypes grown in different agro-ecological zones of India. Two non-basmati genotypes were also included in study. The details of the genotypes are presented in Table-1. All genotypes were evaluated for grain yield and its attributing characters following randomized complete block design (RBD) with three replications during *kharif* season of two consecutive years of 2010 and 2011 at Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India. Transplanting was done 25 days after sowing of seeds in nursery bed in a $4m^2$ plot. Plant to plant distance was 15cm, row to row distance was 20cm and the crop was raised as per recommended package of practices to ensure normal crop. Observations were recorded on ten yield attributes viz., days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), effective panicles per plant (no.), spikelets per panicle (no.), filled grains per panicle (no.), spikelet fertility (%), test weight (gm) and yield per plant (gm) of ten randomly selected plants in each entry in a replication. Observations were also recorded to study grain quality characters viz., brown rice length (mm), brown rice breadth (mm), brown rice L/B ratio, kernel length (mm), kernel breadth (mm), kernel L/B ratio, kernel length after cooking (mm), elongation ratio, alkali spread value (Little *et al.*, 1958) and amylose content (*Juliano 1971*). INDOSTAT software was used for statistical analysis. The mean of the 25 genotypes were analyzed statistically by the method outlined by Ostle (1966). The analysis of variance for different characters was carried out in order to assess the genetic variability among genotypes as given by Cochran and Cox (1950). The level of significance was tested at 5% and 1% using F table values given by Fisher and Yates (1963). Both phenotypic and genotypic coefficient of variability for all characters as estimated using the formula of Burton and De Vane (1953). The broad sense heritability (h^2) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by Lush (1949) and Hanson (1956). Genetic advance for each character was estimated by using the formula of Johnson et al (1955). Genetic advance as per cent mean was categorized as suggested by Johnson et al (1955).

The mean sum of squares for 20 characters in 25 genotypes under study is presented in Table 2. Analysis of variance revealed highly significant differences among genotypes for all yield traits and some quality traits indicating the presence of adequate variability among the genotypes. However, other quality traits exhibited little variation as the genotypes under study are basmati and there should not be any deviation from basmati quality. The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficients of variation (GCV), heritability in broad sense (h^2) and expected genetic advance (GA) and genetic advance as per cent of mean (GAM) presented in Table 3. Variability is essential for wide adaptability and resistance to biotic and abiotic factors and hence, an insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. The phenotypic and genotypic variances measure the magnitude of variation arising out of differences in phenotypic and genotypic values. The absolute values of phenotypic and genotypic variances cannot be used for comparing the magnitude of variability for different characters, since the mean and units of measurement of the characters may be different. Hence, the coefficients of variation expressed at phenotypic and genotypic levels have been used. The relative values of these two types of coefficients give an idea about the magnitude of variability present in the germplasm (Lokesh *et al*., 2013).

In general, the values of PCV were higher than the values of GCV indicating that the apparent variation is not only due to genotypes but also due to influence of environment. The estimates revealed that PCV for all characters are slightly more than that of GCV indicating the less influence of environment. Similar results are found by Patel *et al.*, (2014), Subbaiah *et al.* (2011), and Shobha Rani *et al*. (2001). The GCV was higher for the characters alkali spread value (32.14), yield per plant (23.8) and effective panicles (20.48). Hence, these characters are relied upon and simple selection can be practiced for further improvement. The results are in consonance with Vanisree et al. (2013), Subbaiah et al. (2011), Panwar (2005), Hasib (2005) and in contrast with Yumnam et al. (2011).

High heritability (broad sense) estimates (>60%) were recorded for all the yield and quality traits viz. days to 50% flowering (99), days to maturity(99), plant height (99.8), panicle length (95.7), effective panicles (98), spikelets per panicle (99.3), filled grains per panicle (98.1), spikelet fertility (69.7), test weight (88.2) and yield per plant (93.2), brown rice length (99.5), brown rice L/B ratio (99.8), kernel length (99.9), kernel breadth (79.5), kernel L/B ratio (92.4), kernel length after cooking (98.7), elongation ratio (97.7), alkali spread value (99) and amylose content (94.4) indicating characters are least influenced by environment and selection for improvement is rewarding. However the quality trait brown rice breadth (28.9) had low heritability indicating the character is highly influenced by environmental effects and selection for improving is misleading. Similar findings are suggested by Mani *et al.* (1997), Chand *et al*.(2005), Panwar (2005), Hasib (2005) and Yumnam *et al*. (2011). However, Sawarker and Senapati (2014), and Dhanwani *et al*. (2013) obtained high heritability for brown rice breadth; Hasan *et al.* (2013), found low heritability for spikelet fertility, are in contrast with present findings. Since the estimates of heritability are in broad sense selection based on heritability alone is misleading hence another estimate called genetic advance is used for better prediction of characters under study.

The high genetic advance revealed by characters spikelets per panicle (74.7), filled grains (62.64), plant height (50.89), days to 50% flowering (21.62) and days to maturity (21.54), while other yield traits and all quality traits exhibited moderate to very low GA values (Table 3). The values of genetic advance as per cent of mean (GAM) were high (>20%) for characters alkali spread value (84.43), yield per plant

(60.69), effective panicles (53.55), plant height (43.91), spikelets per panicle (43.89), filled grains (42.29), test weight (35.69), brown rice L/B ratio (30.35), brown rice length (29.83), kernel length (29.72), KLAC (26.56), kernel L/B (26.32), panicle length (25.81), elongation ratio (22.6), days to 50% flowering (21.78), while moderate GAM (10-20%) for characters days to maturity (16.66), kernel breadth (13.73) and amylose content (12.88). However low GAM (<10%) were revealed by spikelet fertility (6.61) and brown rice breadth (2.16).

Heritability should be considered along with genetic advance as per cent of mean, however it is not necessary that character showing high heritability will also exhibit high genetic advance (Johnson et al., 1955). High heritability coupled with high GAM was observed with 15 characters indicating that characters viz., days to 50% flowering, plant height, panicle length, effective panicles per plant, spikelets per panicle, filled grains per panicle, test weight, yield per plant, brown rice length, brown rice L/B ratio, kernel length, kernel L/B ratio, kernel length after cooking, elongation ratio and alkali spread value are governed by additive genes and improvement is rewarding. Similar kind of results were obtained by Tirumala rao *et al.* (2014) Dhanwani *et al.* (2013), Vanisree *et al*. (2013), Babu *et al* . (2012). However, low GAM for days to 50% flowering was reported by Sawarker and Senapati (2014), Tirumala rao *et al.* 2014, Seyoum *et al*.(2012) and Kole *et al.* (2008); low GAM for grain yield per plant was reported by Venkanna *et al.* (2014) and Kole *et al*. (2008); low GAM for panicle length was reported by Paikhomba *et al*. (2013), Babu *et al.* (2012), Seyoum *et al.* (2012), Subbaiah *et al*.(2011) and Kole *et al.* (2008); moderate GAM for days to 50% flowering, plant height and low GAM for panicle length, spikelet fertility, days to maturity, test weight, grain yield per plant are reported by Hasan *et al.* (2013). High heritability coupled with moderate GAM was observed for characters days to maturity, kernel breadth and amylose content indicating characters governed by additive genes though influenced by environment. Similar findings are reported by Patel *et al.* (2014), Dhanwani *et al.* (2013), Vanisree *et al.* (2013), Subbaiah *et al.* (2011). However Babu *et al.* (2012) and Subbaiah *et al.* (2011) reported low GAM for kernel breadth; Sawarker and Senapati (2014) reported low GAM for days to maturity. High heritability coupled with low GAM is observed for the character spikelet fertility indicating non-additive gene action, high heritability is exhibited due to favorable influence of environment rather than genotype and selection of such traits may not be rewarding. Similar result obtained by Kole et al. (2008), contrast results reported by Sawarker and Senapati (2014) obtained high GAM for spikelet fertility. Low heritability coupled with low GAM is observed for the character brown rice breadth indicating the character is highly influenced by environmental effects and selection would be ineffective. However, Sawarker and Senapati (2014), reported high heritability and moderate GAM which is in contrast with the present finding.

From the present study, it is evident that genotypes studied may provide good source of material for further breeding programme. Therefore, the information on the genetic parameters such as coefficient of variation, heritability, genetic advance can help the breeder to evolve suitable basmati quality cultivars. On the basis of results summarized above, it is concluded that the great deal of variability for the important characters studied even in highly selected lines under the present investigation. High heritability coupled with high genetic advance was observed for the characters days to 50% flowering, plant height, panicle length, effective panicles per plant, spikelets per panicle, filled grains per panicle, test weight, yield per plant, brown rice length, brown rice L/B ratio, kernel length, kernel L/B ratio, kernel length after cooking, elongation ratio and alkali spread value indicated their due importance as the indicator characters and selection for these traits may be effective.

References

Amarawathi Y, Singh R, Singh A.K, Singh V.P, Mohapatra T, Sharma T.R, Singh N. 2008. Mapping of quantitative trait loci for basmati quality traits in rice (Oryza sativa L.). *Molecular Breed.*, **21**:49-65

Babu V.R, Shreya K, Dangi K.S, Usharani G and Nagesh P. 2012. Genetic variability studies for qualitative and quantitative traits in popular rice hybrids of india. *Internat. J. Scientific and Res. Public.*, **2**(6) ISSN: 2250-3153

Burton , G.W. and Devane, E.M. 1953. Estimating heritability in fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron. J.*, **45**: 478-481

Cochran, G. W. and Cox, M.G. 1950. Experimental designs. John wiley and sons, Newyork.

Chand, U., Katoch, P.C. and Vijay Kumar. 2005. Variability studies in some macromutations induced by EMS and gamma rays in Basmati rice T-23. *Annals of Biol.*, **21**(2): 137-141.

Dhanwani, R.K, Sarawgi, A.K, Solanki, A, and 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.

Fisher, R.A. and Yates, F. 1963. Statistical tables for biological, agricultural and medical research. Oliver and Boyd, London.

Falconer, D.S. 1981. Introduction to quantitative genetics. 2ad edition. Oliver and Boyd, Edinburg, London.

Hamdi, A. 1992. Heritability and combining ability of root characters in lentil (*Lens culinaris* Medik), *Egyptian J. Agric. Res.,* **70**(1): 247-255.

Hanson, C.H, Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating populations of Korean lespedza. *Agron. J.,* **48**(6): 268-272.

Hasan, M.J, Kulsum, M.U, Akter, A, Masuduzzaman, A.S.M and Ramesha, M.S. 2013. Genetic variability and character association for agronomic traits in hybrid rice (*Oryza sativa* L.) *Bangladesh J. Plant Breed. and Genet.,* **24**(1): 45-51.

Hasib, K. M. 2005. Genetic variability, interrelations and path analysis for panicle characters in scented rice. *Crop Res.,* (Hisar) **30**(1): 37-39.

Juliano, B.O. 1971. A simplified assay for milled rice amylose. *Cereal Sci., Today* **16**:334-338, 340, 360.

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

Kole, P.C, Chakraborty, N.R. and Bhat, J.S. 2008. Analasis of variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice. *Tropical Agric. Res. and Extension,* **11**: 60-64.

Little, R.R., G.B. Hilder and E.H. Dawson 1958. Differential effect of dilute alkali on 25 varieties of milled white rice. *Cereal Chemistry,* **35**:111-126.

Lokesh, B, Reddy, P.S, Reddy, R.V.S.K. and Sivaraj, N. 2013. Variability, heritability and genetic advance studies in Brinjal (*Solanum melongena* L.) *Electron. J. Plant Breed.,* **4**(1): 1097-1100.

Lush, J.L. 1949. Heritability of quantitative characters in farm animals. Proceedings of 8th congress of genetics, *Heriditas.,* **3**(1): 356-375.

Mani, S.C, Verma, S.K. and Sharma, R.K. 1997. Genetic variability and character association for panicle traits in Basmati rice. *Agric. Sci. Digest,* **17**(3): 155-157.

Ostle, B. 1966. Statistics in research 1st edition, Oxford and Indian Book House Private Limited, New Delhi.

Paikhomba, N, Kumar, A, Chaurasia, A.K. and Rai, P.K. 2013. Assessement of genetic parameters for yield and yield components in hybrid rice and parents. *J. Rice Res.,* **2**(1): 117.

Panwar, L.L. 2005. Genetic variability, heritability and genetic advance for panicle characters in transplanted rice. *Res. on Crops,* **6**(3): 505-508.

Patel, J.R, Saiyad, M.R, Prajapati, K.N, Patel, R.A. and Bhavani, R.T. 2014. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.) *Electron. J. Plant Breed.,* 5(3): 531-537.

Sawarkar, A. and Senapati, B.K. 2014. Polygenic variations and cause effect relationship in some photo-insensitive recombinant inbred lines (RIL's) of Basmati derivative. *African J. Biotechnol.,* **13**(1): 112-118.

Seyoum, M, Alamerew, S and Bantte, K. 2012. Genetic variability, heritability,correlation and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.) *J. Plant Sci.,* **10**: 3923/jps.2012.

Shobha Rani, N., Rama Prasad, A. S., Prasad, G. S. V., Bhaskara Reddy P. and Krishna Veni, B. 2001. Genetic variability for yield component in aromatic and quality rice germplasm. *Indian J. Plant Genet. Resource ,* **14**: 206-209.

Siddiq, E.A, Vemireddy L.R, and Nagaraju J. 2012. Basmati Rices: Genetics, Breeding and Trade. *Agric. Res.,* **1**(1):25-36.

Subbaiah, P.V, Sekhar, M.R, Reddy, K.H.P. and Reddy, N.P.E. 2011. Variability and genetic parameters for grain yield and its components and kernel quality attributes in CMS based rice hybrids (*Oryza sativa* L.) *Internat. J. Appl. Biol. and Pharmaceutical Technol.,* **2**(3): 603-609.

Tirumala rao, V, Mohan, Y.C, Bhadru, D, Bharithi, D. and Venkanna,V. 2014. Genetic variability and association analysis in Rice. *Internat. J. Appl. Biol. and Pharmaceutical Technol.,* **5**(2): 63-65.

Vanisree, S, Anjali, K, Damodar Raju, CH, Surender Raju, CH, and Sreedhar, M. 2013. Variability, heritability and association analysis in scented rice. *J. Biological Sci. Opinion,* **1**(4): 347-352.

Venkanna, V, Lingaiah, N, Raju, CH.S, and Rao, V.T. 2014. Genetic studies foe quality traits of F_2 population in rice (*Oryza sativa* L.). *Internat. J. Appl. Biol. and Pharmaceutical Technol.,* **5**(2): 125-127.

Yumnam, S, Nandeshwar, B.C, Bijan Adhikari, Senapati, B.K. 2011. Variability and Character association in recombinant lines F_6 of basmati derivative. *Curr. Advan. in Agric. Sci.,* **3**(1): 24-28.

Table 1. List of basmati varieties under study:

Sl.no	Variety	Parentage	Origin
1	TBD-1	Mutant of Taroari Basmati	BHU
2	TBD-2	Mutant of Taroari Basmati	BHU
3	TAROARI BASMATI	Pureline selection from local Basmati	Haryana
4	BASMATI 370	Pureline selection from local agro commercial group	Punjab
5	KASTURI BASMATI	Basmati 370/CR 88-17-1-5	DRR, Hyderabad
6	SONASAL BASMATI	-	Jammu & Kashmir
7	RANBIR BASMATI	Selection from Bas 370-90-95	Jammu & Kashmir
8	PUSA 2517-2-51-1	-	IARI, New Delhi
9	PUSA BASMATI-1	Pusa 167/Kernal local	IARI, New Delhi
10	PUSA BASMATI-1S-97	Selection from Pusa Basmati-1	BHU
11	PUSA 44	IARI 5901-2/IR-8	IARI, New Delhi
12	PUSA SUGANDH-3	-	IARI, New Delhi
13	PUSA SUGANDH-5	Pusa 3A/Haryana Basmati	IARI, New Delhi
14	HUBR-2-1	HBR 92/Pusa Basmati-1/Kasturi	BHU
15	BASMATI-24-1	Local land race	Maharaj ganj, U.P
16	BASMATI-24-5	Local land race	Partawal, U.P
17	BASMATI-24-7	Local land race	Siddardh nagar, U.P
18	VASUMATI	-	
19	PUSA SUGANDH-2	-	IARI, New Delhi
20	CSR-30(YAMINI)	Selection from Taroari Basmati	
21	JP-2	Collection from Basti	Uttar Pradesh
22	PUSA 1460	Improved Pusa Basmati-1	IARI, New Delhi
23	PUSA 1121(Pusa Sugandh-4)	Pusa 614-1-2/Pusa 614-2-4-3	IARI, New Delhi
24	MAHI SUGANDHA	BK 79/Basmati 370	Rajasthan
25	TYPE-3	Selection from Dehradoon Basmati	Uttar Pradesh

Table 2. Mean sum of squares of the twenty characters in basmati rice

Source of variation	Replication	Treatment	Error	C.V(%)	C.D. 5%
Degrees of Freedom	2	24	48		
Days to 50% Flowering	0.413	204.120**	0.705	0.84	1.378
Days to maturity	0.093	202.396**	0.675	0.63	1.35
Plant Height (cm)	0.982	1117.06**	0.573	0.65	1.242
Panicle Length (cm)	1.279	24.205**	0.353	2.1	0.975
Effective Panicles (no.)	0.213	11.264**	0.074	2.89	0.447
Spikelets/Panicle (no.)	0.373	2425.97**	5.901	1.42	3.988
Filled Grains (no.)	25.120	1734.05**	11.38	2.27	5.539
Spikelet Fertility (%)	0.492	23.470**	2.969	1.97	2.829
Test Weight (gms)	0.010	0.315	0.013	5.26	0.19
Yield per plant (gms)	0.538	18.988**	0.447	6.4	1.098
Brown Rice Length (mm)	0.005	2.330**	0.004	0.83	0.106
Brown Rice Breadth (mm)	0.000	0.005	0.002	2.38	0.078
Brown Rice L/B Ratio	0.000	0.596	0.000	0.56	0.036
Kernel Length(mm)	0.000	2.187*	0.001	0.43	0.054
Kernel Breadth (mm)	0.003	0.034	0.002	2.96	0.086
Kernel L/B Ratio	0.042	0.060	0.016	2.98	0.209
KLAC(mm)	0.036	6.048**	0.025	1.14	0.263
Elongation Ratio	0.000	0.075	0.000	1.32	0.039
Alkali Spread Value	0.053	7.692**	0.025	3.21	0.262
Amylose Content(%)	0.108	4.296**	0.083	1.22	0.474

**Significance at p=0.01

*Significance at p=0.05

Table 3. Variability and genetic parameters for twenty characters in basmati rice

Character	Mean	Range		Variance		PCV(%)	GCV(%)	h^2(%)	GA	GAM(%)
		Lowest	Highest	σ^2_p	σ^2_g					
Days to 50% Flowering	99.29	86	113	68.51	67.805	8.33	8.29	99	21.62	21.78
Days to maturity	129.25	116	143	67.917	67.24	6.37	6.34	99	21.54	16.66
Plant Height (cm)	115.89	82.96	159.7	372.736	372.162	16.65	16.64	99.8	50.89	43.91
Panicle Length (cm)	28.22	21.2	32.86	8.304	7.951	10.21	9.92	95.7	7.28	25.81
Effective Panicles (no.)	9.42	6	13	3.804	3.73	20.69	20.48	98	5.04	53.55
Spikelets/Panicle (no.)	170.18	120.66	238.33	812.592	806.691	16.75	16.68	99.3	74.7	43.89
Filled Grains (no.)	148.12	107.33	210.33	585.607	574.223	16.33	16.17	98.1	62.64	42.29
Spikelet Fertility (%)	87.1	79.73	91.86	9.803	6.833	3.59	3	69.7	5.76	6.61
Test Weight (gms)	2.2	1.59	2.74	0.114	0.101	15.32	14.38	88.2	0.78	35.67
Yield per plant (gms)	10.44	5.32	15.54	6.628	6.18	24.65	23.8	93.2	6.33	60.69
Brown Rice Length (mm)	7.77	6	9	0.78	0.776	11.36	11.33	99.5	2.31	29.83
Brown Rice Breadth (mm)	2.01	2	2.2	0.003	0.001	2.83	1.52	28.9	0.043	2.16
Brown Rice L/B Ratio	3.87	3	4.5	0.199	0.199	11.52	11.51	99.8	1.17	30.35
Kernel Length(mm)	7.57	6	9	0.73	0.729	11.27	11.26	99.9	2.25	29.72
Kernel Breadth (mm)	1.77	1.6	2	0.013	0.011	6.54	2.83	79.5	0.24	13.73
Kernel L/B Ratio	4.27	3.38	4.92	0.213	0.197	10.79	10.37	92.4	1.12	26.32
KLAC(mm)	13.99	11.26	16.9	2.033	2.008	10.19	10.12	98.7	3.71	26.56
Elongation Ratio	1.82	1.41	2.07	0.025	0.025	8.76	8.66	97.7	0.41	22.6
Alkali Spread Value	4.97	2	7	2.581	2.556	32.3	32.14	99	4.19	84.43
Amylose Content(%)	23.58	20.56	26.08	1.488	1.404	5.17	5.02	94.4	3.03	12.88