Genetic Parameters of Drought Related Traits in Rice

[*]Dr. Pallabi Dutta[1] Prof. P.K. Borua[2]

Assistant Professor, Dept of Botany, Silapathar Science College.
Professor, Dept of Lifesciences, Dibrugarh University
Corresponding Author: Dr. Pallabi Dutta

Abstract: *Early drought is the main environmental problem of rice production in Assam during Aahu season. Eight Aahu rice genotypes were examined to evaluate the nature and magnitude of variability, heritability and genetic advance of six drought related traits. The mean sums of square for all the six characters were significant indicating the presence of substantial amount of variability. All traits had showed high phenotypic coefficient of variation (PCV) than their corresponding genotypic coefficients of variation (GCV) indicating influence of environment on these traits. High estimates of heritability coupled with high genetic advance as per cent of mean were observed for traits viz. Tillers per plant (89.00 and 62.15), length of root (21.37 and 19.48), number of xylem vessels in root (82.12 and 44.88), number of stomata on upper surface (91.44 and 39.13), number of stomata on lower surface (98.28 and 58.08) and flag leaf length (78.00 and 36.29) indicating role of additive genes on the expression of these traits and possibility of fruitful phenotypic selection on the basis of these traits for drought tolerant segregants.*

Keywords: *upland rice, drought, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance.*

I.   Introduction

Yield is more or less affected by several biotic and abiotic stresses such as drought, pre-harvest sprouting, diseases, pests etc. Among these, drought and pre-harvest sprouting are major abiotic stresses causing grain loss. Drought affects 20% of the total rice-growing area in Asia [1]. More than 80% of the Asian regions are drought prone and the worldwide water shortage and uneven distribution of rainfall makes the improvement of drought resistance especially important [2]. Breeding for drought tolerance is usually performed by selecting genotypes for high yield under water limited conditions [3]. Drought may delay the phenological development of the rice plant [4] and affect physiological processes like transpiration, photosynthesis, respiration and translocation of assimilates to the grain [5] etc, ultimately affecting yield. Thus it is very important to select parents having resistance to drought is of utmost importance.

Genetic improvement mainly depends on the amount of genetic variability present in the population which is a ubiquitous property of all species in nature. The importance of genetic diversity in the selection of suitable genotypes for hybridization has been stressed by several scientists in different crops [6],[7],[8]. It results due to differences either in the genetic constitutions of the individuals of the population or due to the differences in the environment in which they grown. Estimation of genetic variability present in the germplasm of a crop is pre-requisite for making any effective breeding programme. These genetic variations might be either heritable or non-heritable. It could be of interest to know the magnitude of variation due to heritable component, which in turn would be a guide for selection for crop improvement programmes of the population. Thus genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice and other crops. For any trait of interest, observed phenotypic differences among individuals may be due to differences in the genetic codes for that trait or may be the result of variation in environmental condition. Most agronomically significant characters are known to be affected by environmental factors. Selection based on the phenotype might not be fruitful in such traits. In breeding programs, it is often difficult to manipulate such traits, since several inter-componental characters indirectly control these traits [9]. The measurement of genetic variation and understanding of mode of inheritance of quantitative traits, therefore, are essential steps in any crop improvement programme. Heritability estimates provide authentic information about a particular genetic attribute which will be transmitted to the successive generations. A broad-sense heritability estimate provides information on the relative magnitude of genetic and environmental variation in the population [10],[11],[12] and help breeders to determine the possible extent for improvement through selection. Again the heritable portion of the total variation might not be always due to additive gene action. Thus estimates of heritability alone give no clear indication of the associating genetic progress that would result from selecting the best plants. It is also essential to find out the relative magnitude of additive and non additive genetic variances with regard

to the characters of concern. The heritability along with phenotypic variance and the selection intensity, however, promise the estimation of genetic advance or response to selection which is more useful in the selection of promising lines [13],[14],[15].

II.   Materials And Methods

The details of the materials used and techniques adopted during the course of investigation are described below.

2.1. Experimental site and Climate:

The present investigation was conducted during the seasons 2013-2014, 2014-201 and 2015-2016 at a paddy growing field of Dhemaji district, Assam (North Latitude 27° 15' to 28° 00' and East Longitude 94° 05' to 95° 30'). The soil of the experimental field was alluvial sandy loamy with pH 5.5.

2.2. Experimental materials:

The experimental material of the study comprised of 8 ahu rice cultivars namely *Bejilahi, Betguti, Borguni, Kala-aahu, Kopouguni, Maiguni, Ranga-aahu* and *Rangadoria* collected from different pockets of Dhemaji district.

2.3. Experimental methods:

2.3.1. Layout plan:

The experiment was laid in Randomized Block Design replicated thrice. 45 days old seedlings were transplanted into the experimental site with 20 X 15 cm spacing. Row to row and hill (plant) to hill distance was 20 cm and 15 cm respectively.

2.3.2. Observations recorded:

The data were recorded five randomly selected plants from each replication leaving the first two border rows from all the four sides, in order to avoid the sampling error. The observations were recorded as per the following procedure. Readings from five plants were averaged replication wise and the mean data was used for statistical analysis for the characters as follow:

2.3.2.1. Number of tillers/plant:

The total numbers of tillers were counted as per plant basis.

2.3.2.2. Flag-leaf length:

Flag leaf length was measured from its base of attachment to the sheath to the tip of leaf blade and expressed in centimetre at 40 days after transplanting.

2.3.2.3. Length of root:

Length of root was measured in centimetre from the ground level to the top of the healthy root (excluding fibrous roots) at the time of maturity.

2.3.2.4. Number of xylem vessels:

Permanent slides of finely sectioned root by double stained method were prepared and counted the number of xylem vessels under light microscope.

2.3.2.5. Number of stomata (both upper and lower surface) (1.417 mm^2):

Slides were prepared by impression method (suggested by Bruce and Itzick, 2004) for counting number of stomata. Numbers of stomata were counted for each microscopic field with five replications under 10X x 40X magnification and the area of microscopic field was calculated using stage and ocular scale.

2.4. Statistical analysis:

The mean data recorded on the above observations were subjected to following statistical analyses:

2.4.1. Standard Error:

The standard error of the mean difference (SEM±) was calculated according to the expression suggested by Snedecor and Cochran, 1976 [16].

$$SEM = \sqrt{\frac{2EMS}{r}}$$

Where,

EMS = Error mean square

r = Number of replication

2.4.2. Coefficient of variation (C.V):

It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

$$CV\ (\%) = \frac{\text{Standard Deviation}}{\text{Mean}}$$

In the present investigation three types of coefficient of variations were estimated viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV). The formulae used to calculate PCV, GCV and ECV were given by Burton and Devane[17].

2.4.3. Phenotypic coefficient of variation (PCV):

$$PCV\% = \frac{\sigma 2p}{\bar{X}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic standard deviation

$\bar{X}$ = Mean

2.4.4.. Genotypic coefficient of variation (GCV):

$$GCV\% = \frac{\sigma 2g}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic standard deviation

$\bar{X}$ = Mean

GCV and PCV values were categorized as low, moderate and high values as indicated by Sivasubramanian and Menon [18]. It is as follow:

1-10%   : Low

11-20%   : Moderate

21% and above   : High

2.4.5. Heritability in broad sense (h2):

Heritability in broad sense is the ratio of genotypic variance to the total variance. It is that portion of total variability or phenotypic variability which is heritable and due to the genotype. Broad sense heritability was estimated as the ratio of genotypic variance to the phenotypic variance and was expressed in percentage [19].

$$h^2 = \frac{\sigma 2g}{\sigma 2p} \times 100$$

Where,

$\sigma^2 g$ = genotypic variance

$\sigma^2 e$ = phenotypic variance

The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al.*,[20].

0-30%   : Low

31-60%   : Moderate

61% and above   : High

2.4.6. Expected Genetic advance

Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. The extent of genetic advance to be expected from selecting five per cent of the superior progeny was calculated by using the following formula given by Johnson et al.[13].

GA = K. σp. h2

Where,

K = Constant selection differential at 5% level intensity (= 2.06)

σp = Phenotypic standard deviation

h2 = Heritability in broad sense

2.4.7. Genetic advance as percent of mean (GAM):

The formula of Genetic advance as percent of mean was as follow:

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = genetic advance

$\bar{X}$ = Grand mean

Genetic advance as per cent of mean was categorized as low, moderate and high by following Johnson *et al.*[13]. It is as follows.

0-10%   : Low

11-20%   : Moderate

Above 20%   : High

III.   Results And Discussions

Drought is one of the major abiotic stresses limiting plant production. It adversely affects rice production in the upland areas where rainfall distribution is uncertain. Early drought is the main environmental problem of rice production in Assam during *ahu* season. On average, the estimated yield loss to drought is 144kg/ha. annually in eastern India [21]. The only way to overcome this problem is the development of new technology and drought resistant varieties which posses certain desirable characteristics such as high root length, more xylem number, less number of stomata etc. Characters contributing to drought tolerance viz. root length, number of xylem vessels, number of stomata (both upper and lower surface), flag-leaf length and number of tillers per plant were considered together and scored as the character with the higher magnitude in the desired direction were given the first rank against each cultivar. Hence the cultivar with least overall score across six characters secured the first rank and the cultivar with the highest score secured the last rank (Table 1). Cultivar *Betguti* with overall score 9 across the six characters gets the first rank followed by cultivar *Rangadoria* (total score 20), *Maiguni* (23), *kapouguni* (25), *Borguni* (26) and Ranga-*ahu* (27).

Allah *et al.,*[22] reported that the highest xylem vessel number was observed in drought tolerant genotypes. Haque *et al.,* [23] also reported that xylem vessel number is positively correlated to drought resistance, hence could be directly involved in increasing drought resistance. They also confirmed that xylem vessel number can be used as selection indices in breeding drought resistance in rice. In the present study it was observed that this trait showed high heritability with high genetic advance indicating additive gene effect. Thus inclusion of this character as selection index in breeding programmes for drought tolerant rice will be rewarding. Total root length is strongly related to drought tolerance in rice under drought condition [24]. According to Allah *et al.,* [22] also drought tolerant rice genotypes had fewer numbers of roots, but a higher proportion of the roots were distributed in the lower soil layers below 20 cm. Haque *et al.,*[23] and Kanbar *et al.,*[25] also reported that root length correlated positively with drought resistance. According to Kamoshita, [26] root size, morphology and root depth and length are important in maintaining leaf water potential against evapotranspirational demand under water stress. Loresto *et al.,* [27] evaluated 27 rice varieties grown in aeroponic culture and found a positive but insignificant correlation between root length and field drought resistance at the vegetative phase. Fukai and Cooper, [28] and Kondo *et al.,* [29] also thought that a deeper root system in rice is a promising way of increasing water uptake, and ultimately grain yield under drought stress conditions. In present study this character had showed high heritability with high genetic advance as percentage of mean. Thus this trait might be included in breeding programmes for drought resistance crop production.

According to Allah *et al.,* [22], low tillering capacity appears to be one desirable characteristic when rice plant has to depend on soil moisture retained in the deep soil layers during drought stress. Flag leaf with short length is also one of the key weapons against drought [30]. These two traits also showed high heritability with high genetic advance and hence can be included in breeding programmes.

Table1: Traits contributing drought resistance in different rice cultivars and their ranks

| Sl no.	cultivars name	Length of root (cm)		No. of Xylem vessels		No. of Stomata (US)		No. of Stomata (LS)		Flag-leaf length (cm)		No. of tiller/plant		Total rank	Position
		Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank		
1	Bejilahi	32.7	2	3.6	6	45.4	6	61.6	8	46.78	7	11	4	33	8
2	Betguti	30.9	3	6.6	2	24.6	1	17.6	1	27.04	1	8.6	1	9	1
3	Borguni	26.7	5	6.6	2	45.4	6	55.6	6	39.84	4	9.8	3	26	5
4	Kala-aahu	19.2	8	5.2	4	39.6	5	59	7	43.8	5	9.2	2	31	7
5	Kapouguni	21.2	7	7.6	1	46	7	45.6	3	29.06	2	12.4	5	25	4
6	Maiguni	27.9	4	4	5	32.4	2	52.8	5	38.82	3	11	4	23	3
7	Ranga-aahu	22.8	6	5.4	3	37.2	4	52	4	50.02	8	9.2	2	27	6
8	Rangadoria	33.1	1	5.2	4	33.6	3	44.8	2	44.82	6	11	4	20	2

Table 2: Genetic parameters of important draught related traits of 8 aahu rice cultivars

According to Muhammad Shahid *et al.,* [30] number of stomata merits special attention in projects focused on development of drought resistant rice varieties. Thus effort may therefore, be made to incorporate this character in the upcoming commercial rice varieties. Liu, [31] also reported that number of stomata have relationship with moisture availability. Number of stomata on both surfaces showed high heritability along with genetic advance. Thus effective selection for this character might be possible.

Sl. No	Characters	GCV	PCV	h^2	GA %
1	Tiller/plant	31.94	33.81	89.00	62.15
2	Flag-leaf length	14.61	16.92	75.00	25.99
3	Length of the root	15.2	17.28	77.15	27.41
4	No. of xylem vessels	19.74	22.67	75.85	34.98
5	No. of stomata(U.S.)	15.8	16.71	89.58	30.64
6	No. of stomata(L.S.)	17.02	17.28	99.99	35.25

All six characters showed high heritability along with high genetic advance in present study (Table 2). Hence effective selection for these characters is possible in appropriate cross combinations and new drought resistance strains possessing these desirable characters may be synthesized.

Figure 1: Histogram showing Genetic parameters of important draught related traits of 8 aahu rice cultivars
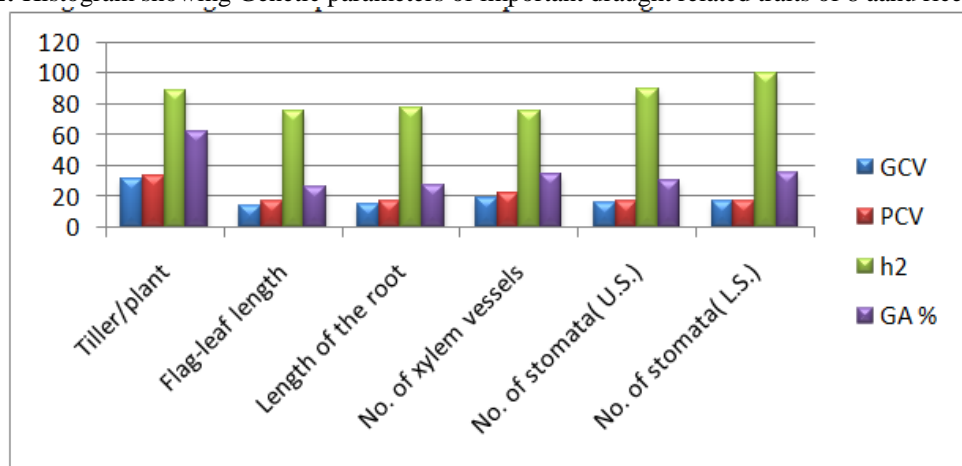
The *ahu* cultivar viz. *Betguti* had showed highest score regarding these six drought resistance contributing characters indicating its adorability in drought conditions. According to Garris *et al.,*[32] also aus rices are drought tolerant and early maturing. But Yue *et al.,* [33] concluded that *ahu* cultivars actually show drought escape by short life cycle.

IV.   Conclusion

Four cultivars viz. Betguti, Rangadoria, Maiguni and Kapouguni shows higher values for characters contributing to drought resistance along with high heritability and high genetic advance for those characters. So these cultivars might be used for future crop improvement programmes for flood prone areas.

Reference

[1]. Pandey, S., Bhandari, H. 2008. Drought Frontiers in Rice: Crop improvement for increased rainfed production. (Edited by Serraj, R., Bennett, J. and Hardy, B.), published by World Scientific Publishing and Los Banos (Philippines) IRRI, Singapore. pp.3-17.

[2]. Lue L. J. and Zhang Q. F. 2001. The status and strategy on drought resistance of rice (Oryza sativa L.). Chinese J. Rice Sci. **15:** 209-214.

[3]. Kumar A., Bernier Verulkar S, Lafitte H.R, Atlin G.N. 2008. Breeding for drought tolerance: Direct selection for yield, response to selection and use of drought-tolerant donors in upland and lowland-adapted populations. Field Crops Res. **107**: 221-231.

[4]. Inthanpan P. and Fukai S. (1988). Growth and yield of rice under sprinkler irrigation in south eastern Queensland, 2- Comparison with maize and grain sorghum under wet and dry conditions. Aust. J. Exp. Agric. **28**(2):243-248.

[5]. Turner N.C. 1986. Crop water deficits: decade of progress. Adv. Agron. **39**: 1-51.

[6]. Ivy N.A., Uddin M.S., Sultana R. and Masud M.M. 2007. Genetic divergence in maize (Zea mays L.). Bangladesh J. Breed. Genet. **20**(1): 53-56.

[7]. Mondal M.A.A., Hossain M.M., Rasul M.G. and Uddin M.S. 2007. Genetic diversity analysis in Potato (Solanum tuberosum L.). Bangladesh J. Bot. **36**(2): 121-125.

[8]. Haydar A, Ahmed M.B., Hannan M.M., Razvy M.A., Mandal M.A., Salahin M., Karim R. and Hossain M. 2007. Analysis of Genetic Diversity in Some Potato Varieties Grown in Bangladesh. Middle-East J. Scientific Res. **2**(3-4): 146-148.

[9]. Hittalmani S., Huang N., Courtois B., Venuprasad R., Shashidhar H.E., Zhuang J.Y., Zheng K.L., Liu G.F., Wang G.C., Sidhu J.S., Srivantaneeyakul S., Singh V.P., Bagali P.G., Prasanna H.C., McLaren G. And Khush G.S. 2003. Identification of QTL for growth and grain yield related traits in rice across nine locations of Asia. Theor. Appl. Genet. **107**: 679-690.

[10]. Dudley J.W. and Moll R.H. 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. Crop Sci. **9**(3):257-262.
[11]. Marwede V., Schierholt A., Moilers C. and Becker H.C. 2004. Genotype x environment interactions and heritability of Tocopherol contents in Canoloa. Crop Sci. **44**(3): 728-731.
[12]. Rafi S.A., and Nath U.K. 2004. Variability, Heritability, Genetic Advance and relationship of yield and yield contributing characters in dry Bean (Phaselous vulgaris L.). J. BioI. Sci. **4**(2): 157-159.
[13]. Johnson H.W., Robinson H.F. and Comstock R.E. 1955. Estimation of genetic and environmental variability in soybeans. Agron. J., **47**: 314-318.
[14]. [14] Iqbal S., Mahmood T., Tahira, Ali, M., Anwar M. and Sarwar M. 2003. Path coefficient analysis in different genotypes of soyabean (Glycine max L.). Pak. J. BioI. Sci. **6**(12):1085-1087.
[15]. Rohman M.M., Iqbal A.S.M., Arifin M.S., Akhtar Z. and Husanuzzaman M. 2003. Genetic variability, correlation and Path analysis in Mungbean. Asian J. Plant Sci. **2**(17-24): 1209-I211.
[16]. Snedecor G.W. and Cochran W.G. 1967. Statistical methods. VI Edition, published by Oxford and IBH Publishing Co. Culcutta, pp. 135-198.
[17]. Burton G. W. and Davane E. M. 1952. Estimating heritability in tall fescue (Festuca arundiancea L.) from replicated clonal material. Agron. J., **45**: 478-481.
[18]. Sivasubramanian S. and Menon M. 1973. Heterosis and inbreeding depression in rice. Madras Agril. J., **60**: 1139-1144.
[19]. Hanson C.H., Robinson H.F. and Comstock R.E. 1956. Biometrical studies of yield in segregating population of Korean lespedeza. Agron. J., **48**: 268-272.
[20]. Robinson H.F., Comstock R.E. and Harvery P.H. 1951. Genotypic and phenotypic correlations in corn and their implication in selection. Agron. J., **43**: 282-287.
[21]. Dey M.M. and Upadhyaya H.K. 1996. Rice Research in Asia: Progress and Priorities (Edited by Evenson, R.E., Herdt, R.W., Hossain, M.) published by Oxford University Press, Cary, NC, pp. 231–242.
[22]. Allah A.A., Badawy S. A., Zayed B.A. and El. Gohary A.A. 2010. The role of root system traits in the drought tolerance of rice (Oryza sativa L.) World Academy of Science, Engineering and Technology **68**:1378-1382.
[23]. Haque M.E., Chang T.T., Tepora N. and Loresto G.C. 1989. Root characteristics as selection indices for resistance in Rice. Philipp J. Crop Sci.**14** (1): 7-9.
[24]. Ingram K.T., Bueno F.D., Namuco O.S., Yambao E.B. and Beyrouty C.A. 1994. Rice Roots. Nutrient and Water Use. (Edited by G.J.D. Kirk) IRRI, Philippines. pp. 67-77
[25]. Kanbar A., Toorchi M. and Shashidhar H.E. 2009. Relationship between Root and Yield Morphological Characters in Rainfed Low Land Rice (Oryza sativa L.). Cereal Res.Communications **37**(2):261–268.
[26]. Kamoshita, A., Wade, L.J., Yamauchi, A., 2000. Genotypic variation in response of rainfed lowland rice to drought and rewatering. III. Water extraction during drought period. Plant Production Science **3**(2):189–196.
[27]. Loresto G.C., Zhang W.X., Chaudhary D. and Chang T.T. 1983. Aeroponic technique for screening the drought avoidance mechanism of rice genotypes by the root characters. Gareia de Orta Scr. Est. Agron. Lisbon **10**(1-2):77-82.
[28]. Fukai S. and Cooper M. 1995. Development of drought-resistant cultivars, using physio-morphological traits in rice. Field Crop Res. **40**(2): 67-86.
[29]. Kondo M., Pablico P.P., Aragones D.V., Agbisit R., Abe J., Morita S., Courtois B. 2003. Genotypic and environmental variations in root morphology in rice genotypes under upland field conditions. Plant and Soil **255**(1):189–200
[30]. Mohammad T., Deva W. and Ahmad Z. 2002. Genetic variability of different plant and yield characters in rice. Sarhad J. Agric., **18**: 207– 210.
[31]. Liu W.H. 1982. Preliminary studies on flag leaf characters. J. Shanxi Agric. Univ., **8**:11-12.
[32]. Garris A.J., Tai T.H., Coburn J., Kresovich S. and McCouch S. 2005. Genetic structure and diversity in Oryza sativa L. Genetics. **169**(3): 1631-1638.
[33]. Yue Bing., Xue W., Xiong L., Yu X., Luo L., Cui K., Jin D., Xing Y. and Zhang Q. 2006. Genetic basis of drought resistance at reproductive stage in rice: separation of drought tolerance from drought avoidance Genetics **172**(2): 1213–1228.