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Variability studies on banana (*Musa* spp.) genotypes of Nagaland

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Abstract

The north-eastern region of India including Nagaland is home to many indigenous *Musa* cultivars and wild/semi wild species. Many of the *Musa* species are extensively found in different agro-climatic condition and are widely distributed in northeast region of India, which has been primarily considered as the richest sources of natural banana diversity. The experiment was carried out in the Department of Horticulture, School of Agricultural Science and Rural Development, Nagaland University during the year 2019-2021. A total of twenty banana genotypes which include both wild and edible banana were considered for the study and the data was recorded *in situ* from different banana growing region covering fifteen villages spreading across five revenue districts of Nagaland. The genetic and phenotypic coefficient of variation, heritability and genetic advance were estimated for fourteen characters which included number of suckers, girth size, pseudo stem height, leaf blade length, leaf blade width, petiole length, bunch weight, number of hands/bunch, number of fingers/hand, fruit weight, pulp weight, weight of peel, fruit peel thickness and pulp: peel ratio. The analysis of variance indicated that the mean sum of square due to genotypes were highly significant for all the quantitative characters. Significant means sum of square due to fruit yield attributing characters revealed existence of considerable variability in material studied for improvement of various traits. Highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for bunch weight indicating selection for such characters would be more reliable to be used as selection for crop improvement. High degree of heritability estimates were obtained in case of fruit weight, pulp weight, girth size and weight of peel. High genetic advance were observed for leaf blade length and pulp weight indicating predominance of additive gene effect and possibilities of effective selection for the improvement of these characters.

Keywords: Banana, genetic variability, PCV, GCV, heritability, genetic advance

Introduction

The banana and plantain belong to the Musaceae family and have been available for human use for ages (Denham *et al.*, 2004 and Nayar, 2010) ^[5, 16]. In some of the African countries like Uganda, Bukaba and Tanzania it has established as a staple food and one of the most important traded tropical fruits in the world (Radha and Matthew, 2007) ^[17]. A large proportion of the bananas produced in countries such as India, Uganda, Brazil and China are consumed locally in many different forms with each country having its own traditional dishes and method of processing (Frison and Sharrock, 1998) ^[7]. As a diet, it is highly satisfying, easy to digest, nearly fat free, rich source of carbohydrate with calorific value of 67 g/100 g and is free from sodium making it a salt free diet suitable to all the age groups and people of all levels. It contains various vitamins and has therapeutic values for the treatment of many diseases (Singh, 2007) ^[28].

The north-eastern region of India including Nagaland is home to many indigenous *Musa* cultivars and wild/semi wild species. Many of the *Musa* species are extensively found in different agro-climatic condition and are widely distributed in northeast region of India, (Uma *et al.*, 2006) ^[34] which has been primarily considered as the richest sources of natural banana diversity (Hore *et al.*, 1992) ^[10]. Occurrence of *Eumusa* species such as *Musa nagalandiana*, *M balbisiana*, *M cheesmani*, *M flaviflora*, *M itinerans*, *M nagensium* and *M puspanjaliae* and species of the section *Rhodochlamys* commonly known as ornamental species were reported from Nagaland, Arunachal Pradesh, Tripura and other parts of Northeast India (Gurumayum *et al.* 2018; Sabu *et al.* 2013; Dey *et al.* 2014; Majumdar *et al.* 2013) ^[9, 25, 4, 15]. The primary objective of a crop improvement programmer is to assess genetic variability existing in that particular crop to the extent to which the character to be improved is heritable.

Critical estimation of variability existing in the base population is a prerequisite for successful crop improvement through various plant breeding methods. Burton (1952) [2] pointed out that calculating Genetic Coefficient of Variation (GCV) along with heritability could assess the best picture of amount of advancement to be expected by selection. Ramanujan and Thirumalachar (1967) [21] suggested that heritability estimate in the broad sense is reliable if accompanied by high genetic advance. Johnson *et al.* (1955) [11], Swarup, Chaugle (1967) [31] also considered that heritability estimates along with genetic gain were useful and more reliable than heritability estimates alone in predicting selection response. Effectiveness of selection based on phenotypic performance can be more useful and reliable only when selection is based on heritability estimates combined with genetic gain. Above all these, knowledge of the extent of variability in germplasm is an essential prerequisite in any breeding programmer. In banana, due to its high sterility and polyploidy of edible varieties (Stover and Simmonds, 1962) [30], classical breeding is difficult (Ganry, 1990) [8] and have resulted in increasing efforts to genetically improve the crop. Classical approaches for identification and analysis of genetic variability in fruit crops are based on morphological, physiological and agronomic traits. The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (Tiwari *et al.*, 2011) [32]. Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of a plant population or in environment they have grown. The existence of variability is essential for improvement of genetic material. Selection is also effective when there is significant amount of genetic variability among the individuals in breeding materials. Hence, the present investigation was laid out to assess the extent of genetic variation in banana genotypes of Nagaland.

Materials and Methods

The experiment was carried out in the Department of Horticulture, School of Agricultural Science and Rural Development, Nagaland University during the year 2019-2021. A total of twenty banana genotypes which include both wild and edible banana were considered for the study and the data was recorded *in situ* from different banana growing region covering fifteen villages spreading across five revenue districts of Nagaland. The genetic and phenotypic coefficient of variation, heritability and genetic advance were estimated for fourteen characters which included number of suckers, girth size, pseudo stem height, leaf blade length, leaf blade width, petiole length, bunch weight, number of hands/bunch, number of fingers/hand, fruit weight, pulp weight, weight of peel, fruit peel thickness and pulp: peel ratio. Biometric data were recorded and statistically analyzed following Fischer (1960) [6]. From the analysis of variance, genetic parameters like phenotypic and genotypic coefficient of variation (PCV and GCV), (Burton, 1952) [2], heritability estimates (Burton and de Vane, 1953) [3] and genetic advance (Allard, 1960) [1] were calculated.

Results and Discussion

Estimation of coefficients of variation

The estimates of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) have been presented in table 2. In the present study, PCV ranged from

0.72% to 53.05%. Highest PCV was observed in bunch weight (53.05%) followed by pulp weight (50.20%), weight of peel (48.83%) and fruit weight (46.45%). Lowest PCV value was seen in number of suckers (0.72%) followed by leaf blade width (17.55%) and leaf blade length (23.99%). On the other hand, the value of GCV ranged between 0.34% and 52.58%. Highest GCV was recorded for bunch weight (52.58%) followed by pulp weight (50.07%), weight of peel (48.67%) and fruit weight (46.42%). Lowest GCV was observed in number of suckers (0.34%) followed by leaf blade width (17.55%). These findings were in lines with the results of Rajamanickam and Rajmohan (2010) [19], Rajeevan and Geetha (1982) [20], Valsalakumari and Nair (1986) [35].

The phenotypic coefficient of variation was marginally higher than the corresponding genotypic coefficient of variation for all the characters which indicates the influence of environment in the phenotypic expression of the character under study. Overall not much difference was observed between PCV and GCV for the traits under study which indicates the maximum expression of genotype with less effect of environment on the traits. The traits which showed high phenotypic and genotypic coefficient of variations were of economic importance and there is scope for improvement of these traits through selection.

Heritability (h^2_{bs}) and genetic advance (GA)

Heritability estimates provides the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. Heritability estimates along with genetic advance are normally more useful in predicting the gain under selection than that of heritability alone. However it is not necessary that a character showing high heritability will also exhibit high genetic advance. The heritability are usually considered to be low if it is less than 30%, moderate between 30% and 60% and high heritability if it is more than 60% (Robinson *et al.*, 1949) [23] and as Johnson *et al.* (1955) [11] suggested genetic advance as per cent mean can be categorized as low (0-10%), moderate (10-20%) and high (20% and above). Heritability estimates provides the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection.

Heritability in broad sense gives the amount of heritable portion of a character. Characters with high heritability can be selected directly for improvement as they are less affected by the environment. In the present study, the result revealed high heritability (Table 2) which ranged from 47.57% (number of suckers) to 99.86% (fruit weight). The characters such as fruit weight (99.86%), pulp weight (99.45%), weight of peel (99.29%), girth size (99.28%), leaf blade length (98.63%), bunch weight (98.23%), petiole length (98.16%), pseudo stem height (97.09%), fruit peel thickness (95.63 %), leaf blade width (95.29%), pulp: peel ratio (94.86%), number of hands/bunch (91.74%) and number of fingers/hand (91.56%) recorded the higher heritability. Relatively higher values of heritability for these characters indicate that a large proportion of phenotypic coefficient of variance was attributable to the genotypic coefficient of variance. Sreerangaswamy *et al.* (1980) [29] has obtained high values of heritability for number of fingers/bunch, plant height and number of fingers/hand which was in line with the present findings. High heritability has also been described for pulp weight (Singh and Sharma, 1997) [27], pseudo stem girth size, bunch weight, number of fingers/bunch (Rajeevan and Geetha, 1982) [20], pseudo stem

height, bunch weight, girth size (Valsalakumari and Nair, 1986) [35] and bunch weight, plant height (Uma *et al.*, 2000) [33] and weight of finger, pulp weight, plant height and bunch weight (Rajamanickam, 2020) [18].

Heritability estimates along with genetic advance are more useful than the heritability value alone for selecting the best individual. Katiyar *et al.* (1974) [12] illustrated that heritability values alone are inadequate and cannot be taken as tool to calculate the amount of genetic progress achieved by selecting the best individual. In the present study a wide variation among characters for genetic advance was observed. Genetic advance as per cent of mean varied between 25.74% for number of suckers and 107.34% for bunch weight. High genetic advance as per cent of mean was recorded in almost all characters except for number of suckers. A relatively high genetic advance as per cent mean was observed in characters such as bunch weight (107.34%), pulp weight (102.86%) and weight of peel (99.88%), fruit weight (95.56 %) and pulp: peel ratio (66.29 %) and fruit peel thickness (61.87 %). As evident from the data, most of the traits exhibits high genetic advance where it can be assumed that these characters are governed by additive gene effects (Johnson *et al.*, 1955) [11]. Similar findings were reported by Rosamma and Namboodiri (1990) [24], Uma *et al.* (2000) [33]. These findings inferred that selection of bunch weight, pulp weight, weight of peel and fruit weight can bring about effective improvement and therefore maybe exploited in breeding programmers. High heritability does not necessary mean a high genetic advance for particular characters (Allard 1960) [1]. Heritability along with genetic advance is more advantageous than heritability alone in predicting the result and effectiveness in selecting the

best traits (Johnson *et al.*, 1955) [11].

Bunch weight and pulp weight recorded high estimates of PCV and GCV along with high heritability and genetic advance as per cent of mean revealing relatively low influence of environment on the traits proving themselves as primary selection criteria for improvement in banana. Similar findings were reported by Rekha and Prasad (1993) [22], Uma *et al.* (2000) [33], Kulkarni *et al.* (2002) [14] Kavitha *et al.* (2008) [13] and Rajamanickam and Rajmohan (2010) [19]. Similarly, fruit peel thickness recorded higher values of PCV, GCV and high estimates of heritability along with genetic advance as per cent of mean in the present study. The findings were in accordance with the observation of Sawant *et al.* (2016) [26].

Table 1: Mean, standard error mean and range for fourteen traits of banana genotypes

Characters	Grand mean	SEM ±	Range (Min-Max)
Number of suckers	3.23	0.36	2.30-4.67
Girth Size (cm)	64.10	0.89	24.27-100.17
Pseudo stem height (m)	5.53	0.15	2.03-8.07
Leaf blade length	217.47	3.5	71.00-309.00
Leaf blade width	66.68	1.47	49.00-91.00
Petiole length (cm)	58.30	1.22	24.33-84.67
Bunch weight (kg)	9.80	0.40	1.22-17.05
No. of hands/bunch	8.63	0.45	4.67-15.00
No. of fingers/hand	12.67	0.54	4.91-17.27
Fruit weight (g)	95.77	0.95	29.98-183.11
Pulp weight (g)	66.97	1.43	19.92-138.09
Weight of peel (g)	28.83	0.68	7.17-64.11
Fruit peel thickness	2.80	0.11	1.40-4.63
Pulp: peel ratio	2.41	0.11	1.18-4.45

Table 2: Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environment coefficient of variation (ECV), heritability (broad sense) and genetic advance (GA) as percentage of mean for fourteen traits of banana genotypes

Characters	GCV (%)	PCV (%)	ECV (%)	Heritability (%)	Genetic Advance as % of mean
Number of suckers	0.34	0.72	0.38	47.57	25.74
Girth Size (cm)	28.30	28.40	2.40	99.28	58.07
Pseudo stem height (m)	26.87	27.27	4.65	97.09	54.54
Leaf blade length	23.82	23.99	2.81	98.63	48.74
Leaf blade width	17.13	17.55	3.81	95.29	34.45
Petiole length (cm)	26.43	26.68	3.62	98.16	53.95
Bunch weight (kg)	52.58	53.05	7.05	98.23	107.34
No. of hands/bunch	30.05	31.38	9.02	91.74	59.30
No. of fingers/hand	24.31	25.41	7.38	91.56	47.93
Fruit weight (g)	46.42	46.45	1.72	99.86	95.56
Pulp weight (g)	50.07	50.20	3.71	99.45	102.86
Weight of peel (g)	48.66	48.83	4.11	99.29	99.88
Fruit peel thickness	30.71	31.41	6.57	95.63	61.87
Pulp: peel ratio	33.04	33.92	7.70	94.86	66.29

Conclusion

The analysis of variance indicated that the mean sum of square due to genotypes were highly significant for all the quantitative characters. Significant means sum of square due to fruit yield attributing characters revealed existence of considerable variability in material studied for improvement of various traits. Highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for bunch weight indicating selection for such characters would be more reliable to be used as selection for crop improvement. High degree of heritability estimates were obtained in case of fruit weight, pulp weight, girth size and weight of peel. High genetic advance were observed for leaf blade length and pulp weight indicating predominance of

additive gene effect and possibilities of effective selection for the improvement of these characters.

References

- Allard RW. Principles of plant breeding. John Wiley & Sons, Inc., New York, USA; c1960, p. 58-61.
- Burton CW. Quantitative inheritance in grasses. Process. 6th International Grassland Congress. 1952;1:277-283.
- Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal materials. Journal of Agronomy. 1953 Oct;45(10):478-81-481.
- Dey S, Jamir NS, Gogoi R, Chaturvedi SK, Hutoka YJ, Zubenthung PK. *Musa nagalandiana* sp. Nov.

- (Musaceae) from Nagaland, northeast India. *Nordic Journal of Botany*. 2014 Oct;32(5):584-8.
5. Denham SA, Salich M, Olthof T, Kochano A, Caverly S. Emotional and social development in childhood. In: *Childhood Social Development*; Smith PK, Hart CH, (Eds.). Blackwell Publishing Limited: Hoboken, NJ, USA; c2004, p. 307-328.
 6. Fischer RA. *The design of experiments*. Heffner, Publishing Co, Inc., New York, USA; c1960.
 7. Frison EA, Sharrock SI. Introduction: The economic, social, and nutritional importance of banana in the world. In: C Picq, E Foure, EA Frison (Eds.). *Bananas and Food security, International Symposium, Douala, Cameroon*. INIBAP, Montpellier, France. 1998 Nov 10;1014:2135.
 8. Ganry J. Les Recherché Sur les bananiers et plantains a l'Institut de Research surges Fruits et Agrumes. *Situation actually ET environment international*. *Fruits umero special*; c1990, p. 7-22.
 9. Gurumayum R, Sorokhaibam SS, Mohammed LK. Species diversity and distribution of *Musa* species (Musaceae) in Arunachal Pradesh, North Eastern India. *Annals of Plant Sciences*. 2018;7(6):2342-2346.
 10. Hore DK, Sharma BD, Pandey G. Status of banana in North-East India. *Journal of Economic and Taxonomic Botany*. 1992;16(2):447-55.
 11. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability of soybean. *Agronomy Journal*. 1955 Jul;47(7):314-8.
 12. Katiyar RP, Mishra B, Singh SN, Chauhan YS. Genetic variability, heritability and genetic advance of yield and its components in Indian mustard. *Indian Journal of Agricultural Science*. 1974;44:291-293.
 13. Kavitha PS, Balamohan TN, Kumar N, Veeraragavathatham D. Genetic variability studies in banana hybrids. *Asian Journal of Horticulture*. 2008;3(2):265-269.
 14. Kulkarni VM, Sriniva L, Satdive RK, Bapat VA, Rao PS. Dissection of the genetic variability in elite Indian banana genotypes. *Plant Genetic Resources Newsletter*. 2002;4(132):48-52.
 15. Majumdar K, Sarkar A, Deb D, Majumdar J, Datta BK. Distribution record of *Ensete glaucoma* (Roxb.) Cheesm. (Musaceae) in Tripura, Northeast India: A rare wild primitive banana. *Asian Journal of Conservation Biology*. 2013;2(2):164-167.
 16. Nayar NM. The Bananas: Botany, Origin, Dispersal. *Horticultural Reviews*. 2010 Jan 28;36(3):117-64.
 17. Radha T, Matthew L. *Fruits crop*. New India Publishing Agency, New Delhi; c2007, p. 33-58.
 18. Rajamanickam C. Genetic variability and correlation studies on endian (AAB) ecotypes of banana (*Musa* spp.). *International Journal Current Microbiology and Applied Science*. 2020;9(10):3223-3230.
 19. Rajamanickam C, Rajmohan M. Genetic diversity in banana (*Musa* spp.). *Madras Agricultural Journal*. 2010;97(4/6):106-109.
 20. Rajeevan PK, Geetha CK. Variability studies in banana. *South Indian Horticulture*. 1982;34:197-200.
 21. Ramanujam S, Thirumalachar DK. Genetic variability of certain characters in red pepper (*Capsicum annum* L.). *Mysore Journal of Agriculture*. 1967;1:30-36.
 22. Rekha A, Prasad MNV. Genetic variability and character association in banana. *Indian Journal of Horticulture*. 1993;50(1):36-40.
 23. Robinson HF, Comstock RE, Harvery VH. Estimates of heritability and degree of dominance in corn. *Agronomy Journal*. 1949;41:353-359.
 24. Rosamma CA, Namboodiri KMN. Genetic analysis of yield in banana. *Agricultural Research Journal of Kerala*. 1990;28(1/2):1-8.
 25. Sabu M, Joe A, Sreejith PE. *Musa velutina* subsp. *markkuana* (Musaceae): A new subspecies from northeastern India. *Phytotaxa*. 2013;92(2):49-54.
 26. Sawant GB, Dalvi VV, Bhavé SG, Haldankar PM, Mahadik SG. Genetic variability of banana (*Musa* spp.) in west coastal zone of India. *Electronic Journal of Plant Breeding*. 2016;7(4):1144-1150.
 27. Singh DB, Sharma TVRS. Genetic variability in banana. *Indian Journal of Horticulture*. 1997;54(2):124-127.
 28. Singh HP. National and international scenario of banana and plantain banana: Technological Advancement (eds. Singh HP and Uma S); c2007, p. 1-9.
 29. Sree Rangaswamy SR. Sambandamurthy S, Murugan M. Genetic analysis in banana. In: *National Seminar on Banana Production Technology*. Tamil Nadu Agricultural University, 1980, 50-56.
 30. Stover RH, Simmonds NW. *Bananas*. 3rd Edition. Longman, New York, USA; c1962.
 31. Swarup V, Chaugle DS. Studies on genetic variability in sorghum and phenotypic variations and its heritable components in some quantitative characters contributing towards yield. *Indian Journal of Genetics*. 1967;22:31-36.
 32. Tiwari R, Suresh BG, Mishra VK, Kumar A. Genetic variability and character association in direct seeded upland rice (*Oryza sativa* L.). *Environment and Ecology*. 2011;29(4A):2132-2135.
 33. Uma S, Dayarani M, Singh HP, Shyam B, Sathiamoorthy S. Studies on genetic variability in banana silk sub group (AAB). *Indian Journal of Horticulture*. 2000;57(2):106-109.
 34. Uma S, Siva SA, Saraswathi MS, Manickavasagam M, Durai P, Selvarajan R, *et al*. Variation and intraspecific relationships in Indian wild *Musa balbisiana* (BB) population as evidenced by random amplified polymorphic DNA. *Genetic Resources and Crop Evolution*. 2006 Mar;53(2):349-355.
 35. Valsalakumari PK, Nair PCS. Genetic variability in banana. *Agricultural Research Journal of Kerala*. 1986;24(1):66-72.