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**Ningombam Dianashwori Devi**  
Department of Genetics and  
Plant Breeding, Pandit Deen  
Dayal Upadhyay Institute of  
Agriculture Sciences, Utlou,  
Bishnupur, Manipur, India

**Rahanai Kh.**

Department of Genetics and  
Plant Breeding, Pandit Deen  
Dayal Upadhyay Institute of  
Agriculture Sciences, Utlou,  
Bishnupur, Manipur, India

**Ngashepam Paikhomba**

Department of Genetics and  
Plant Breeding, Pandit Deen  
Dayal Upadhyay Institute of  
Agriculture Sciences, Utlou,  
Bishnupur, Manipur, India

**Paonam Priyobrata Singh**

Department of Genetics and  
Plant Breeding, Pandit Deen  
Dayal Upadhyay Institute of  
Agriculture Sciences, Utlou,  
Bishnupur, Manipur, India

**Corresponding Author:**

**Ningombam Dianashwori Devi**  
Department of Genetics and  
Plant Breeding, Pandit Deen  
Dayal Upadhyay Institute of  
Agriculture Sciences, Utlou,  
Bishnupur, Manipur, India

## Evaluation of genetic parameters in different accession of U-morok (*Capsicum chinense* Jacq.)

**Ningombam Dianashwori Devi, Rahanai Kh., Ngashepam Paikhomba and  
Paonam Priyobrata Singh**

### Abstract

The present investigation was undertaken at the Department of Genetics and Plant Breeding Experimental field, Pandit Deen Dayal Upadhyay Institute of Agriculture Sciences, Utlou, Bishnupur District, Manipur to estimate the heritability, variability, and genetic advance in completely randomized block design with three replication in fifteen genotypes. High genotypic coefficients of variance (GCV%) were observed in several characters the highest being fruit dry weight (48.22) followed by fruit weight (34.17), plant height (29.02), fruit length (21.06). Moderate were observed in characters fruit diameter (17.6), fruit per plant (13.53), days to 50% flowering (12.05). Lowest were observed in primary branch (4.13), days to maturity (5.23). High Phenotypic coefficient of variance (PCV%) were observed in characters fruit dry weight (48.52) followed by fruit weight (33.40), plant height (29.48), primary branch (22.13), fruit diameter (21.30), fruit length (21.17). Moderate were observed fruit per plant (18.19), days to 50% flowering (12.11). Lowest was observed in days to maturity (5.64). The estimated heritability ranged from primary branch (3.49) to fruit weight (104). The estimate of GA per cent of mean were high for almost all the attributes. The estimated GA ranged from primary branch (1.27) to fruit dry weight (97.14). High heritability coupled with high genetic advance for several attributes like fruit length, fruit diameter, fruit weight, fruit dry weight, plant height, days to 50% flowering. Low heritability coupled with low genetic advance was observed in primary branch. High heritability coupled with low GA was observed in days to maturity. Moderate heritability with high GA was observed in fruit per plant.

**Keywords:** Genetic heritability, genetic variability, genetic advance

### 1. Introduction

The king chili also known as ghost chili paper, Naga King chili, ghost chili and Bhootjolokia is cultivated in the Northeastern states of India, the state includes Manipur, Arunachal Pradesh, Nagaland and Assam. It is also cultivated in the north eastern part of Bangladesh. It is a naturally occurring hybrid of *Capsicum chinense* and *Capsicum frutescens*. It belongs to the family solanaceae and chromosome number  $2n=2x=24$ . The plant is a self pollinated species but considered cross pollination (upto 10%). The cross pollination may be due to the presence of high insect population. The plant behaves as a semi-perennial plant if grown under optimal condition. The north eastern parts of India are recognized as the hot spot for chili diversity. The king chili is the best known among the many landraces of chili that are cultivated in the north eastern region of India. The king chili is considered as the world's hottest chili pepper certified by the Guinness book of world records in 2007. The king chili is rated at more than 1 million Scoville Heat Unit (SHUs). Investigation also revealed that chilli has higher anti-oxidative capacity than ginger, garlic, mint and onion (Shobana and Naidu, 2000) [1]. Capsaicinoids, the pungency principle of *Capsicum* used in different pharmaceutical application due to their analgesic, anti-arthritis, anticancer and antioxidant properties (Szolcsanyi, 2003, Prasad *et al.*, 2005, Mori *et al.*, 2006) [2, 3, 4]. The breeding efforts on king chilli have so far been neglected. Genetic variability is important for starting any improvement work in the population. Presence of high variability in this crop offers much scope for its improvement. Hence, an attempt was made to estimate genetic variability, heritability in the available germplasm of king chilli (*Capsicum chinense* Jacq.). Genetic variability is an essential component of any breeding programme, designed to improve the characteristics of crops. The available variability in a population can be partitioned into heritable and non-heritable with the aid of parameters such as phenotypic co-efficient of variance, heritability, and genetic advance which serve as a basis for selection of some outstanding genotype from existing ones.

## 2. Materials and Method

The present experiment was carried out at the Department of Genetics and Plant Breeding Experimental Field, Pandit Deen Dayal Upadhyay Institute of Agricultural Science, Utlou, Bishnupur District, Manipur. 15 genotypes of U-morok from different district of Manipur were collected and evaluated. The genotypes were raised in completely randomized design with 3 replication during the rabi season 2018-2019 with row to row spacing of 60cm and plant to plant spacing of 45cm. The genotypes were studied for 9 characters viz., fruit length (cm), fruit diameter (cm), fruit weight (g), fruit dry weight (g), plant height (cm), primary branch, days to 50% flowering, days to maturity, fruit per plant.

The method given by Panse and Sukhatme (1967) [5] were used to determined analysis of variance. The genotypic coefficient of variance and phenotypic co-efficient variance were determine by the method suggested by Burton (1952) [6]. Whereas, heritability (broad sense) and genetic advance as per cent mean were calculated as per Lush (1949) [7] and Burton and Devane (1953) [8] and Johnson et.al. (1995) [9] respectively.

## 3. Result and Discussion

The analysis of variance showed significant variation among the accessions for all the character studied. The difference among the replication was significant for all the character except for the character primary branch. Table 1 show the results of analysis of variance and significant difference of all the characters under study. Genetic variability in respect of range, mean, phenotypic and genotypic variance, PCV and GCV, heritability, genetic advance as percent mean for different characters is given in table 2.

Analysis of variance showed significant difference among the

genotypes for all characters except for the character primary branch. The present investigation showed variation of the character studied. High genotypic coefficients of variance (GCV%) were observed in several characters the highest being fruit dry weight (48.22) followed by fruit weight (34.17), plant height (29.02), fruit length (21.06). Moderate were observed in characters fruit diameter (17.6), fruit per plant (13.53), days to 50% flowering (12.05). Lowest were observed in primary branch (4.13), days to maturity (5.23). High Phenotypic coefficient of variance (PCV%) were observed in characters fruit dry weight (48.52) followed by fruit weight (33.40), plant height (29.48), primary branch (22.13), fruit diameter (21.30), fruit length (21.17). Moderate were observed in fruit per plant (18.19), days to 50% flowering (12.11). Lowest was observed in days to maturity (5.64). The high GCV and PCV observed were good scope for selection. The GCV were near to PCV for most of the characters, showing a highly significant effect of genotype and phenotypic expression with little effect of environment. Higher magnitude of heritability was observed in almost all the characters except for primary branch (3.49). The estimated heritability ranged from primary branch (3.49) to fruit weight (104). The estimate of GA per cent of mean were high for almost all the attributes. The estimated GA ranged from primary branch (1.27) to fruit dry weight (97.14). High heritability coupled with high genetic advance for several attributes like fruit length, fruit diameter, fruit weight, fruit dry weight, plant height, days to 50% flowering. Low heritability coupled with low genetic advance was observed in primary branch. High heritability coupled with low GA was observed in days to maturity. Moderate heritability with high GA was observed in fruit per plant.

**Table 1:** Analysis of variance for nine characters in king chilli accession

Sl. No.	Characters	Mean sum of square	Genotypes Error (d.f=14)	(d.f=30)	F value
1	Fruit length (x1)	2.73**	0.02		127.07
2	Fruit diameter (x2)	0.43**	0.008		55.96
3	Fruit weight (x3)	9.45**	0.20		46.26
4	Fruit dry weight (x4)	0.26**	0.003		78.81
5	Plant height (x5)	1694.04**	26.11		64.87
6	Primary branch (x6)	9.66	4.95		1.94
7	Days to 50% flowering (x7)	120.07**	8.33		14.40
8	Days to maturity (x8)	74.75**	6.04		12.36
9	Fruit per plant(x9)	44.66**	12.86		3.41

\*\*=Significant at 5% probability, d.f=degree of freedom.

**Table 2:** Estimate of genetic parameters for nine quantitative traits in king chilli.

Characters	Genotypic variance ( $\sigma^2_g$ )	Phenotypic variance ( $\sigma^2_p$ )	Genotypic coefficient of variance (GCV) (%)	Phenotypic coefficient of variance (PCV) (%)	Environmental coefficient of variance (ECV) (%)	Broad senses heritability ( $h_2$ ) (%)	Genetic advance as per cent mean
Fruit length(x1)	1.35	1.37	21.06	21.17	2.65	98.97	59.85
Fruit diameter(x2)	0.19	0.28	17.6	21.30	13.95	68.53	29.48
Fruit weight(x3)	4.62	2.1	34.17	33.40	7.10	104	49.37
Fruit dry weight (x4)	0.25	0.26	48.22	48.52	5.47	98.73	97.14
Plant height(x5)	812.04	838.15	29.02	29.48	5.20	96.88	58.21
Primary branch(x6)	0.17	5.12	4.13	22.13	21.76	3.49	1.27
Days to 50% flowering (x7)	55.87	64.2	12.05	12.11	4.65	87.02	90.05
Days to maturity (x8)	34.35	40.04	5.23	5.64	2.19	85	9.87
Fruit per plant(x9)	15.9	28.76	13.52	18.19	12.16	55.28	20.59

## 4. Conclusion

The analysis of variance revealed significant difference among the genotype for all the characters except for the

primary branch. The characters like fruit dry weight, fruit weight, fruit length, plant height contribute highest genotypic coefficient of variance (GCV). Highest phenotypic coefficient

of variance (PCV) were observed in fruit dry weight, fruit weight, fruit length, fruit diameter, primary branch, plant height. The magnitude of heritability was high in almost all the characters except for primary branch. Moderate magnitude heritability was observed in fruit per plant. High heritability coupled with high genetic advance were observed for several attributes like fruit length, fruit diameter, fruit weight, fruit dry weight, plant height, days to 50% flowering. Low heritability coupled with low genetic advance was observed in primary branch. High heritability coupled with low GA was observed in days to maturity. Moderate heritability with high GA was observed in fruit per plant. High heritability estimates indicate the presence of large number of fixable additive factors and therefore the attributes may be improved by selection. The characters with high heritability coupled with high genetic advance should be given top priority during selection for further utilisation in breeding programme.

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