

# Analysis of Yield and Yield Attributing Traits of Maize Genotypes in Chitwan, Nepal

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**Abstract** Fourteen maize genotypes were evaluated at National Maize Research Program (NMRP), Rampur, Chitwan, Nepal with objective was to explore genetic variability and investigate yield and yield attributing traits from 22<sup>nd</sup> October, 2014 to 12<sup>th</sup> April, 2015. The experiment was designed in randomized complete block with three replication. Phenotypic observation was taken for important quantitative traits viz. Soil Plant Analysis Development (SPAD) reading, days to 50% tasseling, days to 50% silking, ear height, plant height, days to physiological maturity, ear length, ear girth, ear weight, number of kernel row ear<sup>-1</sup>, number of kernel row<sup>-1</sup>, five hundred kernel weight. The result showed that traits plant height, ear height, ear length, ear girth, ear weight, no. of kernel row per ear, no. of kernel per row exhibited positive and highly significant correlation with grain yield per hectare while SPAD reading and five hundred kernel weight given significant correlation. The analysis also indicated that days to 50% tasseling and days to 50% silking explained negative and highly significant correlation with grain yield per hectare. Similarly, days to maturity showed negative and non significant correlation with grain yield per hectare. The result also reflected that genotype ARUN-1EV has been found comparatively superior to ARUN-2 for major yield components. The genetic study revealed that days to silking, days to tasseling and grain yield per hectare were highly heritable (>0.6). Higher GCV and high GAM indicated efficient indirect selection for higher grain yield per hectare based on these traits. Thus, high GAM and GCV was observed in ear weight, grain yield per hectare and ear height. Correlation analysis revealed that the traits plant height, ear length, ear girth, number of kernel per row, ear weight were most yield determinative traits and hence, simultaneous selection for these traits might bring an improvement in grain yield. The research gave the finding that use of ARUN-1EV can be reliable for further research and breeding programs.

**Keywords:** maize, GCV, GAM, genetic variance, correlation coefficient, genetic advance as percent of mean, genetic diversity

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## 1. Introduction

Maize (*Zea mays* L.), has, a remarkable productive potential among the cereals thus comes under world's three most important cereal crops. After Paddy, Maize is the second important cereal crop of Nepal in terms of area, production and productivity [20]. At present, the Maize sown area in Nepal is 9,28,761 ha with a total production of 22,83,222 metric tons and productivity of 2458 Kg ha<sup>-1</sup> [20]. In Chitwan, maize is cultivated on total area of 9750 ha with the total production of 29,250 metric tons and productivity of 3,000 Kg ha<sup>-1</sup> [20]. Out of total maize cultivated area in Terai region, 95.95 % area is under improved and 4.05 % area under local maize. Similarly, In Hills, 90.78 % area is under improved maize and 9.22 % area under local landraces and in High Hills, 88.93 % area is under improved maize and 11.07 % area with local landraces [20]. Maize display an orderly sequence of development of yield components namely number of ear

plant<sup>-1</sup>, number of kernel row<sup>-1</sup>, number of kernel row ear<sup>-1</sup> and hundred kernel weights [25]. Thus, indirect selection can be used through searching for improved yield components [27]. Grain yield is considered to have positive correlation with plant height, and hundred kernel weight [2], similarly days to silking showed positive correlation with grain yield plant<sup>-1</sup> [1]. Yield is a complex character, which is the product of multiplicative interactions of a number of its component characters [8], cannot be improved to a greater extent on its own. Hence, a clear picture of contribution of each component in final expression of complex character is essential [16]. Grzesiak [9] observed considerable genotypic variability among various maize genotypes for different traits. Ihsan *et al.*, [13] also reported significant genetic differences for morphological parameter for maize genotypes. This variability is a key to crop improvement [27]. Welsh [27] observed significant genetic variation in important agronomic traits especially earliness to sufficiently justify the initiation of selection program.

The potential of taking up infrared radiation and the ability of a leaf to stay green can be assessed indirectly by measuring the chlorophyll content [4]. The Soil Plant Analysis Development (SPAD) meter, SPAD-502 calculates the ratio of absorbance at 650 nm (chlorophyll absorbance peak) and at 940 nm (non-chlorophyll absorbance). SPAD reading shows a positive relation with yield in maize due to increased production and transport of energy from photosynthesis or negative due to remobilization of energy from chlorophyll. Genotypic and phenotypic variation accounts great importance during the process of any crop improvement. An insight into the degree of variability is of utmost importance as it provides the basis for effective selection. The phenotypic variation is simply expressed as the outcome of three major sources of variation: the genotype, the environment which includes all factors external to the plant that affect development and growth, and interactions of all kinds [18]. The total variance of a given character is its phenotypic variance ( $\sigma^2_p$ ) and environmental variance ( $\sigma^2_e$ ) which is the part of the phenotypic variance attributed to environmental conditions. Determination of genotypic and phenotypic correlation is very fundamental step in the formulation and implementation of various breeding programs and activities. Correlation measures the degree of association, genetic or non-genetic, between two or

more characters and is measured by a correlation coefficient [10]. Two types of correlations, phenotypic and genetic, are commonly discussed in plant breeding. Phenotypic correlation ( $r_p$ ) involves both genetic and environmental effects. Genetic correlation is the association of breeding values (i.e., additive genetic variance) of the two characters. Both measure the extent to which degree the same genes or closely linked genes cause co-variation in two different characters [10].

The study was conducted to determine the genetic variability among the different maize genotypes. The results from this investigation would serve as a guide to plant breeders to initiate a crop improvement program. Besides that, the correlations between the traits are also of great importance for to achieve the goals in breeding programs. A total of fourteen genotypes including one standard check variety were taken to conduct the research with following objectives:

- To estimate genetic components of yield and yield traits.
- To study the nature and magnitude of association among yield traits.
- To study the correlation between yield and yield attributing traits for grain yield improvement.

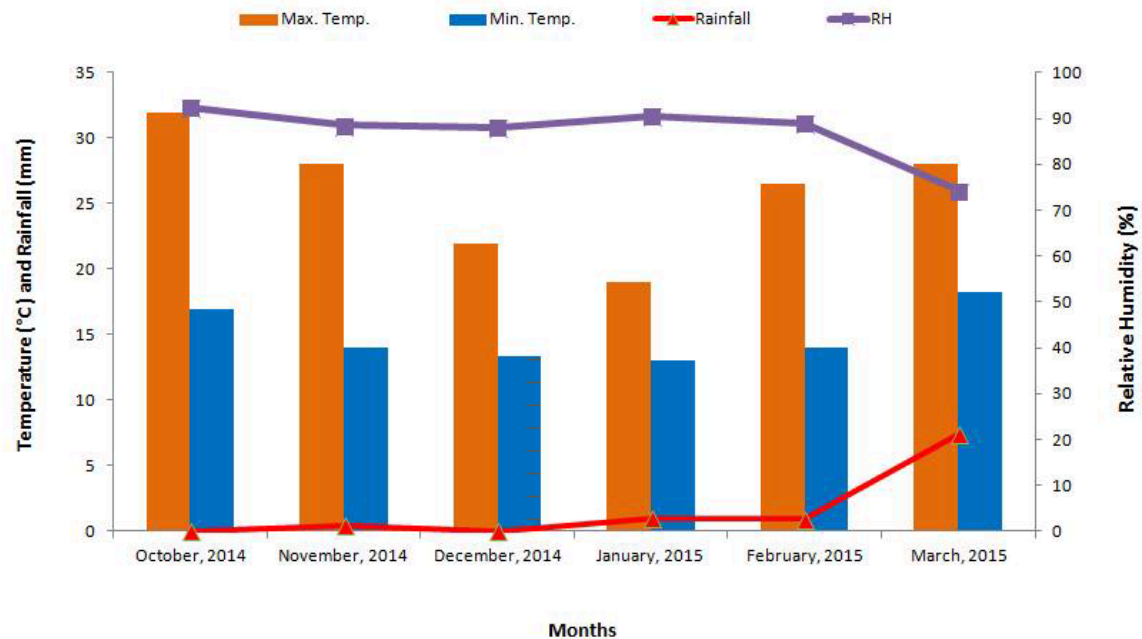


Figure 1. Meteorological data during the research period obtained from NMRP, Rampur

## 2. Materials and Methods

A field experiment was conducted in the study year 2014/15 under Institute of Agriculture and Animal Science (IAAS), Tribhuvan University at research field of National Maize Research Program (NMRP), Rampur, Chitwan, Nepal from 22<sup>nd</sup> October 2014 to 12th April, 2015. It is located at 27°37' N latitude and 84°25'E longitude with an elevation of 228 meters above mean sea level. The research site was climatically humid sub-tropical with average annual rainfall of 2000 mm. The meteorological data (Figure 1) were obtained from

meteorological station, National Maize Research Program, (NMRP), Rampur. The maximum rainfall was 20 mm during March, the maximum temperature was 32 degree Celsius during October, the maximum humidity was 94% during October while minimum rainfall was 0 mm, minimum temperature was 13 degree Celsius and minimum humidity was 75%.

### Experimental Details

The experiment was laid out in RCBD design with three replications with fourteen maize genotypes as treatments. These genotypes were allocated randomly to the fourteen plots of each replication. The plot size was 5.0 m × 3m with inter and intra row spacing of 75 and 25 cm, respectively. Each genotype was sown in each plot

with four rows each of 5 m length. All genotypes were obtained from NMRP, Rampur. Following is the list of genotypes used in research

**Table 1. List of Genotypes used in research**

Entry no.	Genotypes	Entry no.	Genotypes
1	ACROSS 2401	8	ARUN-2(std chk)
2	RAJAHAR LOCAL	9	FARMERS VARIETY
3	S97TEYGHAYB(3)	10	ZM-621/POOL-15
4	POP-445/POP-446	11	EEYC1
5	ARUN-1EV	12	KY/Pool-17
6	R.C/POOL-17	13	Pool-27
7	SO3TETAY/LN	14	Pool-15

Land preparation was performed by ploughing two times followed by land leveling. Farm yard manure (FYM) was applied at the rate of 10 tons ha<sup>-1</sup> and chemical fertilizers as per general recommendation for maize were applied at the rate of 120:60:40 NPK Kg ha<sup>-1</sup> of Nitrogen, Phosphorus and potassium respectively. Full dose of Phosphorus and Potassium and half dose of Nitrogen were applied at the time of sowing as basal application. Sowing was done on 22<sup>nd</sup> October, 2014 by manually operated sowing machine. Remaining half dose of Nitrogen was applied in two split doses during first and second weeding. Two hand weedings were carried out at 20-25 DAS. Thinning was done during first 15- 20 DAS. Earthing up was done as second weeding. The maize borer was controlled by placing granules of Phorate in top folding leaf. Phorate is an organophosphate used as an insecticide and acaricide. At normal conditions, it is a pale yellow mobile liquid poorly soluble in water but readily soluble in organic solvents. It is relatively stable and hydrolyses only at very acidic or basic conditions. It is very toxic both for target organisms and for mammals including human.

#### Data Collection

All the morphological data (quantitative) was recorded from five randomly selected plants of each plot except for 50% tasseling and silking. Observations were also taken for major yield attributing traits viz. 500 kernel weight (gm) with moisture adjustment at 14%, number of kernels per row, number of kernel rows per ear, ear length (cm), ear girth (cm), ear weight (gm). Similarly, observations for traits plant height (cm), ear height (cm), SPAD measures, days to 50% silking, days to 50% tasseling, days to physiological maturity and grain yield (t/ha) after moisture adjustment at 14% were taken.

#### Statistical Analysis

Statistical analysis was carried out by using softwares Excel, GENSTAT, MINITAB version 20 as well as correlation analysis was done using SPSS version 21.

#### Phenotypic and Genotypic Variance

These were calculated according to the formula given by Lush [19] and (Chaudhary & Prasad, [6]).

$$\text{Genotypic variance} = \sigma^2_g = (\text{TMSS} - \text{EMSS})/R$$

$$\text{Error variance} = \sigma^2_e$$

$$\text{Phenotypic variance} = \sigma^2_p = \sigma^2_g + \sigma^2_e$$

Where,

TMSS is treatment mean sum of square

EMSS is error mean sum of square

R is number of replication.

#### Genotypic and Phenotypic Coefficient of Variation

The genotypic and phenotypic coefficient of variation was computed according to [5] and expressed as percentage.

$$\text{Genotypic coefficient of variation (GCV)} = (\sigma_g / \bar{X}) \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = (\sigma_p / \bar{X}) \times 100$$

Where,

$\sigma_g$  = Genotypic standard deviation

$\sigma_p$  = Phenotypic standard deviation

$\bar{X}$  = General mean of the trait

In the above case, PCV and GCV values were categorized as low, moderate and high indicated by Sivasubramanjan & Menon [23] as follows:

0 – 10 % : Low

10 – 20 % : Moderate

>20 % : High

#### Broad sense heritability ( $h_{bs}^2$ )

The broad sense heritability estimated as the ratio of genotypic variance ( $V_g$ ) to the phenotypic variance ( $V_p$ ) and expressed in percentage [11].

$$\text{Broad sense heritability} (h_{bs}^2) = (V_g / V_p)$$

The heritability percentage categorized as low, moderate and high as followed by (Robinson, Comstock, & Harvey, Estimates of heritability and degree of dominance in corn, [22]) as follows:

0 – 0.30 : Low

0.30 – 0.60 : Moderate

> 0.60 : High

#### Genetic Advance (GA)

The extent of genetic advance to be expected by selecting about five percent of the genotypes was calculated by using the following formula given by [22].

$$GA = i \cdot \sigma_p \cdot h_{bs}^2$$

Where,

i = Efficacy of selection which is 2.06 at 5% selection intensity

$\sigma_p$  = Phenotypic standard deviation

$h_{bs}^2$  = Broad Sense Heritability

#### Genetic Advance as Percent of Means (GAM)

GA as per cent of mean (GAM) =  $(GA / \bar{X}) \times 100$

GA = Genetic advance

$\bar{X}$  = General mean of the trait

The GA as percent of mean was categorized as low, moderate and high as suggested by Johnson *et al.* [14].

0 - 10 % : Low

10 -20 % : Moderate

> 20 % : High

## 3. Results and Discussion

#### Mean Performance and Analysis of Variance

Mean values and significant levels of yield and yield attributing traits of fourteen maize genotypes are presented in Table 2 and Table 3. Significant results were observed for the traits grain yield kg ha<sup>-1</sup>, ear weight,

number of kernel row<sup>-1</sup>, number of row kernel per ear, ear length, ear girth, plant height, ear height, days to 50% silking, days to 50% tasseling and days to physiological maturity among the tested genotypes that indicated the presence of genotypic differences suggesting the importance of their genetic value in order to identify the best genetic makeup for a particular condition.

#### Days to 50 % Tasseling (DTT)

The result revealed that genotypes were highly significant for days to 50% tasseling (Table 2). The result indicated that the genotype S97TEYGHAYB (3) and POP-445/POP-446 tasseled earliest in 69 days while the genotype ACROSS-2401 tasseled in 91 days. It reflected that majority genotypes have DTT of 70-80 DAS (Table 2).

#### Days to 50% Silking (DTS)

The genotypes were highly significant ( $P \leq 0.05$ ) for DTS (Table 2). The result showed that S97TEYGHAYB(3) was early in days to 50% silking while ACROSS-2401 was found late in 50% silking in 92

days. Among the tested genotypes S97TEYGHAYB(3) and POP-445/POP-446 showed DTS between 70 to 75 DAS.10 genotypes showed DTS 75 to 85 DAS and 2 genotypes showed DTS 85 to 92 DAS.

#### Chlorophyll Nitrogen Implying SPAD Measures (SPAD Reading)

There was non-significant difference ( $P \leq 0.05$ ) in SPAD for the genotypes (Table 2). Maximum SPAD (51.74) had been showed by ARUN-2 (std chk) and minimum SPAD (44.59) had been showed by Pool-27.

#### Plant Height, cm (PH)

The result showed highly significant difference ( $P \leq 0.05$ ) in the PH for the genotypes (Table 2). Maximum PH (120.7) had been showed by FARMER VARIETY and minimum PH (80.7) had been showed by ACROSS-2401. RAJAHAR LOCAL, S97TEYGHAYB(3), POP-445/POP-446, ARUN-1EV, R.C/POOL-17, SO3TETEY/LN, FARMERS VARIETY, EEYC1, pool-15 were statistically similar to ARUN-2(std chk) (Table 2).

Table 2. Means for quantitative traits of fourteen maize genotypes in Chitwan, Nepal, 2014/15

Mean						
Treatment	SPAD	DTT	DTS	EH(cm)	PH(cm)	DTM
ACROSS- 2401	47.81	91.00 <sup>a</sup>	92.33 <sup>a</sup>	19.9 <sup>c</sup>	80.7 <sup>c</sup>	151.00 <sup>a</sup>
RAJAHAR LOCAL	47.17	86.33 <sup>b</sup>	89.00 <sup>a</sup>	34.3 <sup>cde</sup>	97.3 <sup>abc</sup>	147.67 <sup>abc</sup>
S97TEYGHAYB(3)	45.37	69.33 <sup>i</sup>	71.67 <sup>f</sup>	35.1 <sup>cde</sup>	99.6 <sup>abc</sup>	145.00 <sup>bc</sup>
POP-445/POP-446	48.01	69.33 <sup>i</sup>	72.33 <sup>f</sup>	32.2 <sup>de</sup>	97.1 <sup>abc</sup>	145.00 <sup>bc</sup>
ARUN-1EV	48.53	75.67 <sup>gh</sup>	80.00 <sup>cde</sup>	53.7 <sup>a</sup>	118.3 <sup>a</sup>	143.00 <sup>f</sup>
R.C/POOL-17	45.27	80.67 <sup>cd</sup>	83.67 <sup>bc</sup>	37.9 <sup>bcd</sup>	101.8 <sup>abc</sup>	148.67 <sup>ab</sup>
SO3TETEY/LN	50.00	79.00 <sup>cdefg</sup>	81.67 <sup>bcd</sup>	32.2 <sup>de</sup>	96.5 <sup>abc</sup>	148.67 <sup>ab</sup>
ARUN-2(std chk)	51.74	76.00 <sup>efgh</sup>	79.00 <sup>de</sup>	48.3 <sup>abc</sup>	120.3 <sup>a</sup>	143.67 <sup>bc</sup>
FARMERS VARIETY	49.59	77.00 <sup>efgh</sup>	80.33 <sup>cde</sup>	50.9 <sup>ab</sup>	120.7 <sup>a</sup>	145.00 <sup>bc</sup>
ZM-621/POOL-15	48.96	82.00 <sup>c</sup>	84.33 <sup>b</sup>	25.9 <sup>de</sup>	85.8 <sup>c</sup>	149.00 <sup>ab</sup>
EEYC1	46.96	79.33 <sup>cdef</sup>	82.33 <sup>bcd</sup>	30.5 <sup>de</sup>	95.1 <sup>abc</sup>	148.33 <sup>ab</sup>
KY/Pool-17	46.01	80.00 <sup>cde</sup>	83.33 <sup>bc</sup>	25.2 <sup>de</sup>	85.3 <sup>c</sup>	144.00 <sup>bc</sup>
Pool-27	44.59	74.33 <sup>h</sup>	78.00 <sup>c</sup>	31.4 <sup>de</sup>	91.1 <sup>bc</sup>	145.33 <sup>bc</sup>
Pool-15	51.58	77.67 <sup>defgh</sup>	81.00 <sup>bcd</sup>	49.5 <sup>abc</sup>	116.2 <sup>ab</sup>	148.67 <sup>ab</sup>
Grand mean	47.97	78.4	81.36	36.2	100.4	146.64
LSD (0.05)	Ns	3.065**	3.425**	13.88**	22.01**	4.565*
SEM (±)	1.907	1.054	1.178	4.78	7.57	1.570
CV %	6.9	2.3	2.5	22.8	13.1	1.9

\*(significant), \*\* (highly significant) & ns (non-significant) at  $p=0.05$ . Treatment means followed by same letter are not significant different at  $p=0.05$  by DMRT. SEM=Standard Error of Mean, LSD=Least Significant Difference & CV=Coefficient of Variance, SPAD=Spad Reading, DTT=Days to 50% Tasseling, DTS=Days to 50% Silking, EH=Ear Height, PH=Plant Height, DTM=Days to Maturity.

#### Ear Height, cm (Eht)

The result showed highly significant difference ( $P \leq 0.05$ ) in the EH for the genotypes (Table 2). Maximum EH(53.7cm) had been showed by ARUN-1EV and minimum EH(19.9cm) had been showed by ACROSS-2401. Pool-15, FARMERS VARIETY, ARUN-1EV was found statistically superior than ARUN-2(std chk) (Table 2).

#### Days to Physiological Maturity (DTM)

The result indicated that the days to physiological maturity was statistically significant ( $P \leq 0.05$ ) (Table 2). Maximum DTM(151 DAS) was observed in ACROSS-2401 which is late maturing genotype and minimum DTM (143DAS) was seen in ARUN-1EV which is early maturing genotype. RAJAHAR, LOCAL, S97TEYGHAYB(3), POP-445/POP-446, FARMERS VARIETY, KY/Pool-2,

Pool-27 were found statistically similar to ARUN-2 (standard check) (Table 2).

#### Number of Kernel Rows Ear<sup>-1</sup>(NKRE)

The result showed significant difference ( $P \leq 0.05$ ) in NKRE for genotypes (Table 3). Highest NKRE (13.07) has been observed in ZM-621/POOL-15 and lowest (9.60) has been shown by KY/Pool-17.

#### Number of kernel row<sup>-1</sup> (NKR)

The result showed significant difference ( $P \leq 0.05$ ) in NKR for the genotypes (Table 3). Maximum NKR (23.67) has been showed by FARMERS VARIETY and minimum (15.07) has been showed by KY/Pool-17. Variety S97TEYGHAYB(3), FARMERS VARIETY, ZM-621/POOL-15, RAJAHAR LOCAL, POP-445/POP-446, ARUN-1EV, R.C/POOL-17, SO3TETEY/LN, EEYC1,

Pool-27, Pool-15 were statistically similar to ARUN-2 (std chk) (Table 3).

Table 3. Means for yield and yield attributing traits of fourteen maize genotypes in Chitwan, Nepal, 2014/15

Treatment	EL(cm)	EG(cm)	NKRPE	NKPR	EW(gm)	FHKW(gm)	GYPH(kg)
ACROSS- 2401	13.54 <sup>a</sup>	12.26 <sup>abc</sup>	11.60 <sup>a</sup>	17.53 <sup>bc</sup>	64.7 <sup>bcd</sup>	150.7	493 <sup>ef</sup>
RAJAHAR LOCAL	13.93 <sup>a</sup>	11.95 <sup>bcd</sup>	12.40 <sup>a</sup>	19.80 <sup>ab</sup>	61.4 <sup>cd</sup>	112.0	728 <sup>def</sup>
S97TEYGHAYB(3)	13.95 <sup>a</sup>	12.51 <sup>abc</sup>	12.67 <sup>a</sup>	23.13 <sup>a</sup>	81.1 <sup>abc</sup>	120.7	2222 <sup>a</sup>
POP-445/POP-446	13.89 <sup>a</sup>	12.47 <sup>abc</sup>	12.67 <sup>a</sup>	20.73 <sup>ab</sup>	76.1 <sup>abc</sup>	122.0	1922 <sup>abc</sup>
ARUN-1EV	13.62 <sup>a</sup>	12.69 <sup>abc</sup>	12.13 <sup>a</sup>	21.67 <sup>ab</sup>	86.0 <sup>ab</sup>	134.0	2376 <sup>a</sup>
R.C/POOL-17	13.13 <sup>a</sup>	11.93 <sup>bcd</sup>	11.60 <sup>a</sup>	19.33 <sup>abc</sup>	61.1 <sup>cd</sup>	116.7	711 <sup>def</sup>
SO3TETEY/LN	13.71 <sup>a</sup>	13.30 <sup>ab</sup>	12.53 <sup>a</sup>	21.13 <sup>ab</sup>	87.2 <sup>ab</sup>	138.7	2175 <sup>ab</sup>
ARUN-2(std chk)	14.08 <sup>a</sup>	13.53 <sup>a</sup>	11.60 <sup>a</sup>	23.33 <sup>a</sup>	93.9 <sup>a</sup>	140.7	2232 <sup>a</sup>
FARMERS VARIETY	14.11 <sup>a</sup>	12.69 <sup>abc</sup>	11.33 <sup>a</sup>	23.67 <sup>a</sup>	88.7 <sup>ab</sup>	132.7	1982 <sup>ab</sup>
ZM-621/POOL-15	13.78 <sup>a</sup>	12.52 <sup>abc</sup>	13.07 <sup>a</sup>	20.53 <sup>ab</sup>	73.2 <sup>abc</sup>	117.3	820 <sup>def</sup>
EEYC1	13.39 <sup>a</sup>	12.51 <sup>abc</sup>	12.40 <sup>a</sup>	21.93 <sup>ab</sup>	81.3 <sup>abc</sup>	126.0	1073 <sup>cdef</sup>
KY/Pool-17	10.50 <sup>b</sup>	10.80 <sup>d</sup>	9.60 <sup>b</sup>	15.07 <sup>c</sup>	49.2 <sup>d</sup>	119.0	164 <sup>f</sup>
Pool-27	13.10 <sup>a</sup>	11.63 <sup>cd</sup>	11.33 <sup>a</sup>	20.93 <sup>ab</sup>	64.7 <sup>bcd</sup>	123.3	1278 <sup>bcde</sup>
Pool-15	13.31 <sup>a</sup>	13.18 <sup>a</sup>	12.67 <sup>a</sup>	20.67 <sup>ab</sup>	88.3 <sup>ab</sup>	130.0	1598 <sup>abcd</sup>
Grand mean	13.43	12.43	11.97	20.68	75.5	127.4	1412
SEM (±)	1.502	0.444	0.529	1.434	7.20	9.97	281.5
LSD (0.05)	0.517 <sup>**</sup>	1.289 <sup>*</sup>	1.537 <sup>*</sup>	4.169 <sup>*</sup>	20.92 <sup>**</sup>	ns	818.4 <sup>**</sup>
CV %	6.7	6.2	7.7	12.0	16.5	13.5	34.5

\*(significant), \*\*(highly significant) & ns(non significant) at p=0.05. Treatment means bearing same letter are not significant different at p=0.05 by DMRT. SEM=Standard Error of Mean, LSD=Least Significant Difference & CV=Coefficient of Variance, EL=Ear Length, EG=Ear Girth, NKRPE=Number of Kernel Row Per Ear, NKPR=Number of Kernel Per Row, EW=Ear Weight, FHKW=Five Hundred Kernel Weight, GYPP=Grain Yield Per Plant, GYPH=Grain Yield Per Hectare.

#### Ear Girth, cm (EG)

The result showed significant difference ( $P \leq 0.05$ ) in EG for genotypes (Table 3). Highest ear girth 13.53 cm was observed in ARUN -2(std chk) and lowest (10.80 cm) has been found KY/Pool-17. ACROSS- 2401, S97TEYGHAYB(3), POP-445/POP-446, ARUN-1EV, SO3TETEY/LN, FARMERS VARIETY, ZM-621/POOL-15, EEYC1, Pool-15 were statistically similar to ARUN -2(std chk) (Table 3).

#### Five Hundred Kernel Weights (FHKW)

The result demonstrated non significant difference ( $P \leq 0.05$ ) in FHKW for genotypes (Table 3). Maximum FHKW (150.7) has been showed by ACROSS-2401 and minimum (112.0) has been showed by RAJAHAR LOCAL.

#### Ear Length, cm (EL)

The genotypes were highly significant ( $P \leq 0.05$ ) for EL in which highest EL (14.11) has been shown by Farmer variety and minimum (10.50) has been showed by KY/Pool-17. ACROSS- 2401, RAJAHAR LOCAL, S97TEYGHAYB(3), POP-445/POP-446, ARUN-1EV, R.C/POOL-17, SO3TETEY/LN, FARMERS VARIETY, ZM-621/POOL-15, EEYC1, Pool-27 and Pool-15 were at par with ARUN-2(std chk) (Table 3).

#### Ear Weight, gm (EW)

Highly significant difference ( $P \leq 0.05$ ) obtained in EW for the genotypes (Table 3). Maximum EW (93.9) had been showed in ARUN-2 (std chk) and minimum EW (49.2) had been showed in KY/Pool-17. S97TEYGHAYB(3), POP-445/POP-446, ARUN-1EV, SO3TETEY/LN, FARMERS VARIETY, ZM-621/POOL-15, EEYC1, Pool-15 were statistically similar to ARUN-2 (std chk) (Table 3).

#### Grain yield (GYPH)- Kg Hectare<sup>-1</sup>

The result showed significant difference ( $P \leq 0.05$ ) in the grain yield kg ha<sup>-1</sup> for the genotypes. Among the tested genotypes ARUN-1EV has been found high yielder with grain yield of 2376 kg/ha and genotype KY/pool-17 with 164 kg/ha was low yielder genotype (Figure 2). The genotypes ARUN-1EV, S97TEYGHAYB (3), Farmers variety, SO3TETEY/LN, Pool-15, POP-445/POP-446 were found statistically at par with ARUN-2 (standard check) for grain yield kg/ha. The comparative yield of the genotypes are as shown in Figure 2.

#### Genetic parameters

##### Broad sense heritability (hbs<sup>2</sup>)

The considerable differences in heritability value for different characters were observed (Table 4). Among quantitative traits, high heritability (>0.60) has been observed for days to 50% tasseling (0.908), days to 50% silking (0.874), grain yield hectare<sup>-1</sup> (0.67), Moderate heritability (0.30 to 0.60) has been found for ear height (0.561), ear length (0.408), plant height (0.419), number of kernel row<sup>-1</sup> (0.344), days to physiological maturity (0.331), ear girth (0.339) and SPAD reading (0.118), ear weight (0.45), number of kernel row ear<sup>-1</sup> (0.376) (Table 4).

Grzesiak [9] reported high heritability for days to 50% Tasseling and days to 50% silking which is in agreement with our findings [25] reported high heritability for grain yield hectare<sup>-1</sup> which is very consistent with our finding. Simarliy, [2] reported moderately heritability for ear height which is in line with our finding. Grain yield ha<sup>-1</sup> and ear height had better genotypic variability, better broad sense heritability along with better GA which considered the good estimates for effective selection of a trait. This depicted that visual selection based on these traits among the genotypes would be used for improvement of grain yield.

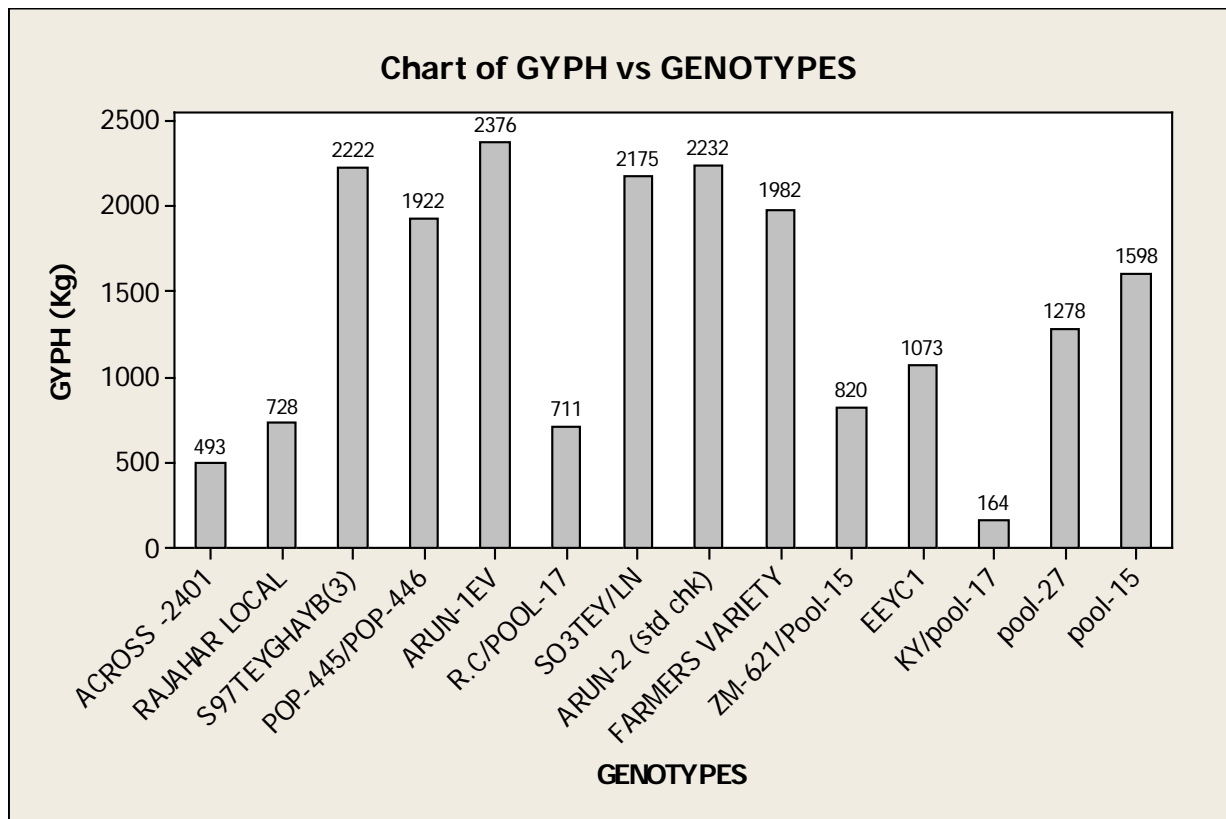


Figure 2. Grain Yield of fourteen genotypes of maize

**Genetic advance as percentage of mean (GAM)**

GAM at 5% selection intensity exhibited high differences for various quantitative characters (Table 4). High GAM having value more than 20% were estimated for ear weight, grain yield ha<sup>-1</sup> and ear height. GAM between 10 and 20 % has been observed for days to 50% tasseling, days to 50% silking, plant height, number of kernel per row. Lower values were estimated for five hundred kernel weights, number of kernel row ear<sup>-1</sup>, days to physiological maturity, ear girth, SPAD reading and ear length. GAM showed that ear weight, plant height and grain yield hectare<sup>-1</sup> were under control of additive genes. Similar findings were also reported by (Alvi *et al.*, 2003).

**Phenotypic and genotypic coefficient of variation (PCV and GCV)**

The considerable difference in PCV and GCV values for different traits has been observed (Table 4). Among the studied quantitative traits, high PCV and GCV values (>0.20) were estimated for grain yield kg ha<sup>-1</sup>, ear height, ear weight, whereas five hundred kernel weights, number of kernel per row, plant height, had moderate PCV (0.1 to 0.2) values and plant height, ear weight had moderate GCV (0.1 to 0.2) values. And ear length, days to physiological maturity, days to silking, days to tasseling, number of kernel row ear<sup>-1</sup>, ear girth, SPAD reading and days to physiological maturity had lower PCV and GCV value (0.0 to 0.1).

Table 4. Estimation of genetic parameters ( GAM, PCV AND GCV) for fourteen maize genotypes in Chitwan, Nepal, 2014/15

Variable	GCV	PCV	h <sub>bs</sub> <sup>2</sup>	GAM
Spad	2.519	7.332	0.118	1.783
DTT	7.3	7.663	0.908	14.326
DTS	6.603	7.063	0.874	12.715
DTM	1.305	2.268	0.331	1.547
PH	11.093	17.137	0.419	14.791
EH	25.856	34.507	0.561	39.911
EL	5.537	8.664	0.408	7.291
EG	4.431	7.605	0.339	5.318
NKRPE	5.941	9.688	0.376	7.506
NKPR	8.7	14.831	0.344	10.513
EW	14.922	22.255	0.45	20.612
FHKW	3.43	13.977	0.06	1.734
GYPH	49.193	60.106	0.67	82.939

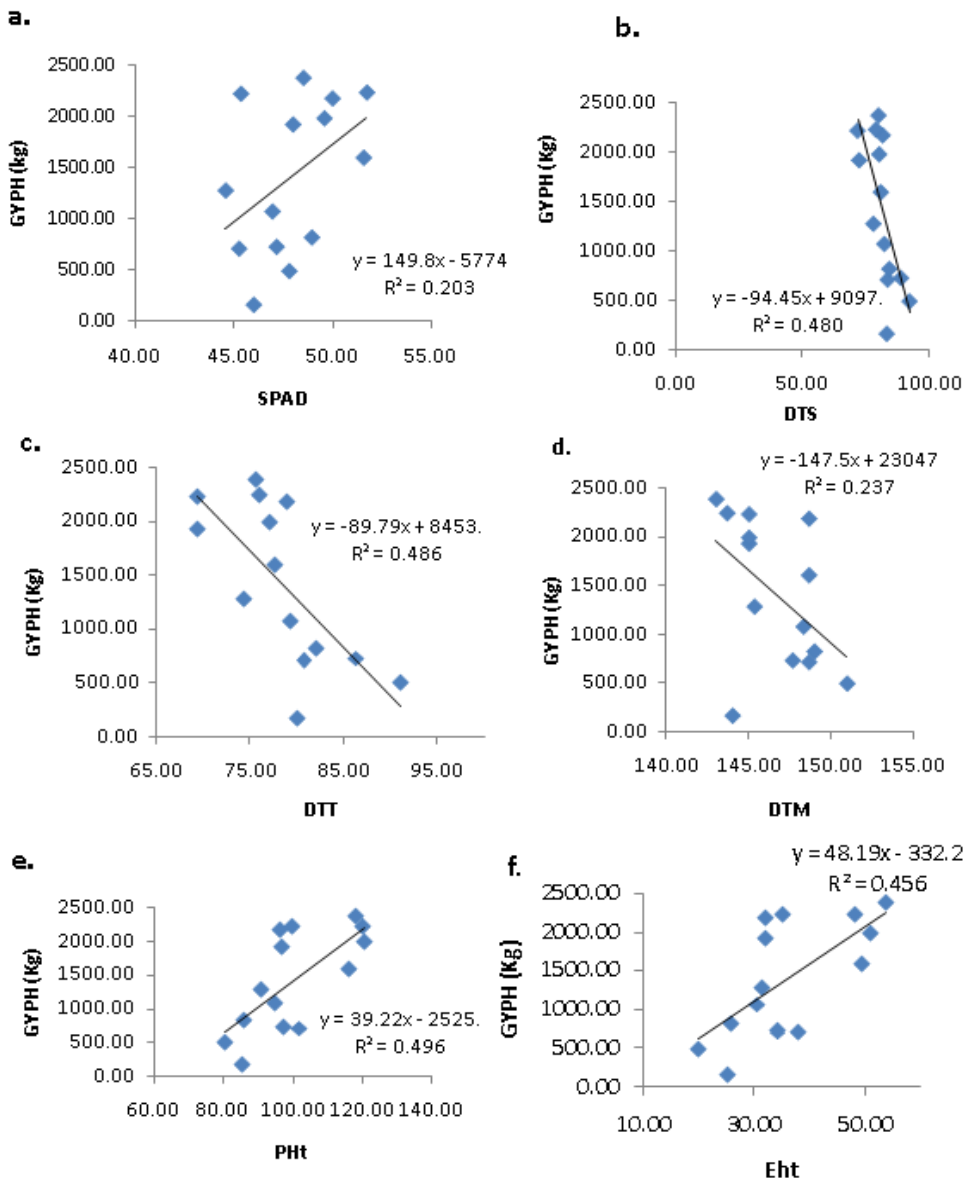
Vg=genotypic variance, Ve=environmental variance, Vp=phenotypic variance, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, GAM=genetic advance as percentage of mean, h<sub>bs</sub><sup>2</sup>=broad sense heritability, EL=ear length, EG=ear girth, NKRPE=number of kernel row ear<sup>-1</sup>, NKPR=number of kernel row<sup>-1</sup>, HKW= hundred kernel weights, PH=plant height, EH=ear height, DTM= days to physiological maturity, SPAD= soil and plant analyzer development, DTT= days to 50% Tasseling, DTS= days to 50% silking, and GYPH= grain yield ha<sup>-1</sup>.

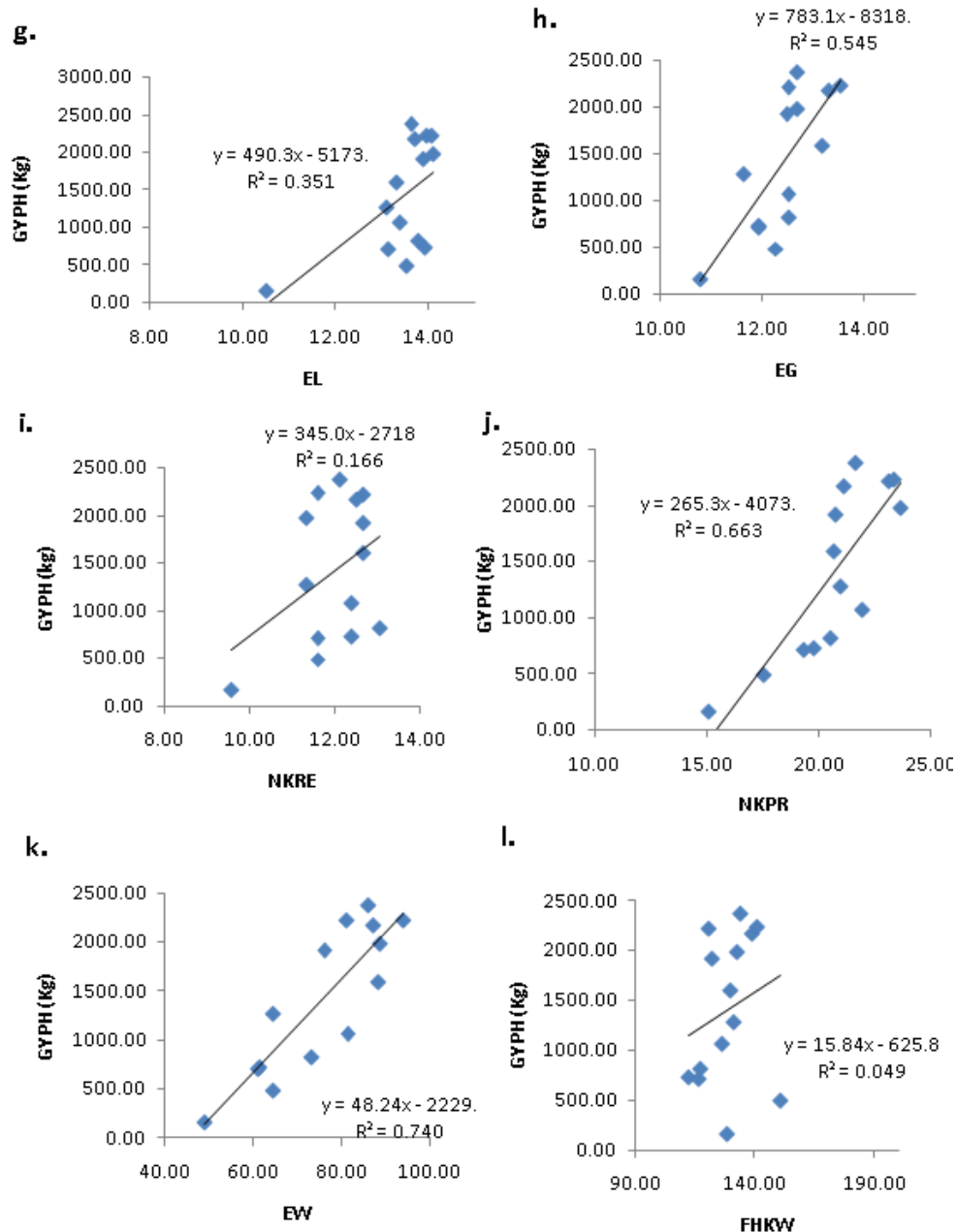
**Correlation coefficient**

Analysis of correlation coefficient of yield related traits revealed some fundamental basis. Regression equation shows the relationship between the grain yield ha<sup>-1</sup> with variables i.e. SPAD reading, days to 50% silking, days to 50% tasseling, days to physiological maturity, plant height, ear height, ear length, ear girth, number of kernel row ear<sup>-1</sup>, number of kernel row<sup>-1</sup>, ear weight and five hundred kernel weights. Among them SPAD reading, plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernel per row, ear weight and five hundred kernel weight showed positive correlation with grain yield ha<sup>-1</sup> (Figure 3). This means that grain yield per hectare increases with increase in value of SPAD reading, plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernel per row, ear weight and five hundred kernel weight. Ibitome [12] reported positive correlation of plant height, ear height, ear length with grain yield per hectare. Rafique et al. [21] reported positive correlations of ear length with grain yield ha<sup>-1</sup>. Similarly, days to 50% silking, days to 50% tasseling and days to maturity showed negative correlation with grain yield ha<sup>-1</sup> (Figure 3). Similar findings were reported by [15]. This means with more days to 50% tasseling and

silking there will be more vegetative growth and less time for reproductive growth which consequently results in less yield. On the other hand, farmers harvest the maize before the onset for other crops in their cropping pattern and as the crops takes more days to mature, farmers are compelled to harvest immature crop in limited harvesting date which results in less yield. So our findings suggest more the days to maturity lesser is the grain yield.

The high direct effect of plant height, ear height, ear length, ear girth, number of kernel row per ear, number of kernel per row and ear weight appeared to be the main factor for their strong association with grain yield per plant. Hence direct selection for these traits would be effective. Further, days to 50 per cent tasseling, days to 50 per cent silking and days to maturity recorded negative direct effect on grain yield in the present investigation and this is in agreement with the reports of Venugopal et al [24] and Kumar et al [17]. The traits grain yield hectare<sup>-1</sup>, ear height, ear length, plant height, number of kernel row<sup>-1</sup>, and ear girth have shown higher heritability and also expressed highly positive and significant correlation coefficient. Thus, these traits are to be considered in selecting genotypes for better crop improvement and breeding programs.





**Figure 3.** Estimated liner correlation. (a) between SPAD reading and grain yield  $\text{ha}^{-1}$  (GYPH), (b) between DTS (days to 50% silking) and grain yield  $\text{ha}^{-1}$  (GYPH), (c) between DTT (days to 50% tasseling) and grain yield  $\text{ha}^{-1}$  (GYPH), (d) between DTM (days to physiological maturity) and grain yield  $\text{ha}^{-1}$  (GYPH), (e) between PHt (plant height) and grain yield  $\text{ha}^{-1}$  (GYPH), (f) between EHt (ear height) and grain yield  $\text{ha}^{-1}$  (GYPH), (g) between EL (ear length) and grain yield  $\text{ha}^{-1}$  (GYPH), (h) between EG (ear girth) and grain yield  $\text{ha}^{-1}$  (GYPH), (i) between NKRE (number of kernel row ear<sup>-1</sup>) and grain yield  $\text{ha}^{-1}$  (GYPH), (j) between NKPR (number of kernel row<sup>-1</sup>) and grain yield  $\text{ha}^{-1}$  (GYPH), (k) between EW (ear weight) and grain yield  $\text{ha}^{-1}$  (GYPH), (l) between FHKW (five hundred kernel weight) and grain yield  $\text{ha}^{-1}$  (GYPH)

## 4. Summary and Conclusion

Genetic diversity among the different maize genotypes was observed from this study which is very useful for their improvement of agronomically important traits. Grain yield is the very complex parameter in Maize. Any minor change in any component leads to the yield loss. Grain yield and related traits are very sensitive to any crops. Association of different yield and yield attributing traits are very important to know their direct and indirect effects on grain yield. In this study we emphasized to determine the correlation coefficient of the traits in order to understand and identify the correlated traits that play a vital role in selection and breeding for simultaneous

improvement of genetic materials. Therefore these traits must be analyzed to know their relationship, their contribution, direct and indirect effects and their diversity among them for their grain yield.

For the trait grain yield  $\text{ha}^{-1}$  followed by number of kernel row ear<sup>-1</sup>, days to 50% tasseling, ear height and days to maturity genotype ARUN-1EV has been found comparatively superior to ARUN-2(std chk). For yield attributing traits like number of kernel row ear<sup>-1</sup>, number of kernel row<sup>-1</sup> and five hundred kernel weight genotype SO3TETEY/LN, FARMERS VARIETY and ACROSS-2401 showed highest value respectively.

Days to silking, Days to Tasseling and Grain Yield Per hectare were highly heritable. Similarly ear height, ear length, plant height, no of kernel per row, days to maturity,



ear girth, SPAD, ear weight, number of kernel row per ear were moderately heritable. Higher GCV and high GAM indicate efficient indirect selection for higher grain yield

ha<sup>-1</sup> based on these traits. Thus high GAM and GCV was observed in ear weight, grain yield per hectare and ear height.

**Table 5. Pearson's correlation coefficient among different yield and yield attributing traits of fourteen genotypes of maize in Chitwan, Nepal, 2014/15**

	SPAD	DTS	DTT	DTM	PHt	EHt	EL	EG	NKRE	NKPR	EW	FKW	GYPH
SPAD	1.00												
DTS	-0.04 <sup>ns</sup>	1.00											
DTT	-0.06 <sup>ns</sup>	0.98 <sup>**</sup>	1.00										
DTM	0.04 <sup>ns</sup>	0.45 <sup>**</sup>	0.48 <sup>**</sup>	1.00									
PHt	0.64 <sup>**</sup>	-0.26 <sup>ns</sup>	-0.34 <sup>*</sup>	-0.18 <sup>ns</sup>	1.00								
EHt	0.56 <sup>**</sup>	-0.24 <sup>ns</sup>	-0.34 <sup>*</sup>	-0.20 <sup>ns</sup>	0.96 <sup>**</sup>	1.00							
EL	0.33 <sup>*</sup>	-0.15 <sup>ns</sup>	-0.13 <sup>ns</sup>	0.20 <sup>ns</sup>	0.42 <sup>**</sup>	0.41 <sup>**</sup>	1.00						
EG	0.56 <sup>**</sup>	-0.21 <sup>ns</sup>	-0.21 <sup>ns</sup>	0.20 <sup>ns</sup>	0.60 <sup>**</sup>	0.56 <sup>**</sup>	0.62 <sup>**</sup>	1.00					
NKRE	0.45 <sup>**</sup>	-0.20 <sup>ns</sup>	-0.19 <sup>ns</sup>	0.32 <sup>*</sup>	0.34 <sup>*</sup>	0.33 <sup>*</sup>	0.69 <sup>**</sup>	0.70 <sup>**</sup>	1.00				
NKPR	0.31 <sup>*</sup>	-0.40 <sup>**</sup>	-0.40 <sup>**</sup>	-0.09 <sup>ns</sup>	0.50 <sup>**</sup>	0.52 <sup>**</sup>	0.68 <sup>**</sup>	0.52 <sup>**</sup>	0.53 <sup>**</sup>	1.00			
EW	0.51 <sup>**</sup>	-0.32 <sup>*</sup>	-0.32 <sup>*</sup>	0.02 <sup>ns</sup>	0.67 <sup>**</sup>	0.66 <sup>**</sup>	0.72 <sup>**</sup>	0.84 <sup>**</sup>	0.58 <sup>**</sup>	0.74 <sup>**</sup>	1.00		
FKW	0.04 <sup>ns</sup>	0.12 <sup>ns</sup>	0.11 <sup>ns</sup>	0.09 <sup>ns</sup>	0.19 <sup>ns</sup>	0.17 <sup>n</sup>	0.20 <sup>ns</sup>	0.36 <sup>*</sup>	-0.11 <sup>ns</sup>	-0.07 <sup>ns</sup>	0.40 <sup>**</sup>	1.00	
GYPH	0.31 <sup>*</sup>	-0.59 <sup>**</sup>	-0.60 <sup>**</sup>	-0.19 <sup>ns</sup>	0.60 <sup>**</sup>	0.60 <sup>**</sup>	0.62 <sup>**</sup>	0.67 <sup>**</sup>	0.39 <sup>**</sup>	0.59 <sup>**</sup>	0.78 <sup>**</sup>	0.35 <sup>*</sup>	1.00

\*\* . Correlation is significant at the 0.01 level (2-tailed).

\*. Correlation is significant at the 0.05 level (2-tailed).

ns= non significant

SPAD= SPAD chlorophyll reading, DTS=days to 50% silking, DTT=days to 50% tasseling, DTM=days to physiological maturity, PHt=plant height, EHt= ear height, EL=ear length, EG=ear girth, NKRE=number of kernel row ear<sup>-1</sup>, NKPR=number of kernel row<sup>-1</sup>, EW=ear weight, FKW=five hundred kernel weight, GYPH=grain yield ha<sup>-1</sup>.

DTT and DTS had negatively and highly correlation with GYPH. Correlation analysis revealed that the traits plant height, ear height, ear length, ear girth, number of kernel row ear<sup>-1</sup>, ear weight were the most yield governing traits and hence, simultaneous selection for these traits might bring an improvement in grain yield. Besides the correlation *inter se* associations also provide huge support on these six traits from all other yield related components.

The variability shown by different genotypes for different yield attributing quantitative traits can be used for the development of the high yielding and better performing variety. In this study, grain yield hectare<sup>-1</sup>, ear height, ear length, plant height, number of kernel row<sup>-1</sup>, and ear girth have shown higher heritability and also expressed highly positive and significant correlation coefficient. Hence, these traits can be considered for future breeding programs. Based on the heritability and correlation of these traits we found that genotype ARUN-1EV was highly important for using in the consequent breeding activities for achieving higher yield and stability. However, ARUN-2 was used in the research as Standard Check genotype as it was considered high yielding with better stability but from the research we found ARUN-1EV superior to ARUN-2 with higher yield and statistically similar with other yield governing traits.

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