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# Correlation analysis of maize (Zea mays L.) genotypes: A review

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Abstract— In many regions of world, maize is one of the most significant crops grown for staple foods. To increase the effectiveness of breeding programs using the right selection indices, it is very important to be aware of the correlations between grain yield and its numerous causal (contributory) components. This article presents the results of many studies that were carried out to ascertain the nature of relationships between grain yield and its contributing factors and to pinpoint those factors with significant effects on yield with the goal of using them as selection criteria by using path coefficient analysis (PCA). The direct and indirect impacts of cause factors on effect variables are displayed through path analysis. This approach divides the components of the correlation coefficient between two traits into those that assess the direct and indirect effects. Plant height, number of kernels per row, ear per pant, ear height, leaf width, days to 50% silking, tasseling, ear diameter, ear length, thousand kernel weight, days to physiological maturity, tassel length, and ear weight may have significant (or non-significant) influence on grain yield, either positively or negatively. The present review of different studies might be useful to the breeders to select the potential parental materials for maize improvement program in Nepal as well as region with similar geographical topography.

Keywords-Breeding, correlation coefficient, maize, yield

# I. INTRODUCTION

Maize is a popular grain crop farmed all over the world (Food, 2020). It has a very high yield potential than any other cereals and thus is popularly known as the 'queen of cereals' (Magar et al., 2018). After wheat and rice, it is the third most important cereal (Vinay Kumar, 2011). It is a key staple food crop that provides a significant amount of raw materials for livestock and a variety of agro-allied industries around the world (Kandel et al., 2018). In terms of acreage and production, maize ranked second next to rice in Nepal (Abziew, 2016). However, because of its high production potential and supportive environment for cultivation in the country, it demands special attention. For decades, improved cultivars from the International Institute of Tropical Agriculture (IITA) and the International Maize

and Wheat Improvement Center (CIMMYT) have been widely used in the country. However, producers and consumers do not appreciate or cultivate them, and they need be modified for critical agronomic qualities (Karki, 2013). A few features, particularly grain yield, need to be improved in promising populations established from some of the types (Yuan et al., 2019). The most efficient selection technique is determined by the correlations between attributes (Inamullah et al., 2011). Several researchers have undertaken correlation studies on maize (Karki, 2013). However, the outcome varies depending on the features, population, and location(Pariyar et al., 2018).

Maize is one of the most important staple food crops for mountain people in Nepal, and it may be used for both feed and fodder (Kandel and Shrestha, 2020). Knowledge of the link between yield and yield component is essential yield for developing improvement programs (Khodarahmpour, 2012). Studies on the correlation coefficients of various characters are a valuable criterion for identifying desirable qualities that boost grain production in breeding programs (Dewey & Lu, 1959). As a result, correlations between yield and various yield components are an important consideration when developing a yield improvement program (Dewey & Lu, 1959). Correlations, in combination with path coefficient analysis, are a useful technique for determining the relationship between yield contributing features and grain yield, as well as quantifying the direct and indirect effects of these characters on grain yield (ElLakany & Russell, 1971). As a result, an attempt was made to establish the correlation coefficient along with path value for the association between grain yield and yield component of early maize genotype, demonstrating the magnitude of direct and indirect effect of various yield components on grain yield of early maize (Verhulst et al., 2012). Despite its high yield potential, maize production in Nepal is modest (Rijal et al., 2016). With rising industrial demand, maize production must increase at a considerably higher rate than it is now(Genotypes & Baitadi, 2016). Grain yield per unit area is heavily influenced by cultivars with favorable features(Ndhlela et al., 2014). It is critical to understand the relationships between different features, particularly grain yield, which is the most important end goal in any breeding program, in order to generate successful genotypes(Health & Pool-, 2018).

### **OBJECTIVES OF THE STUDY**

i. To develop promising genotypes, for starters (Pariyar et al., 2018).

ii. To investigate the relationship between grain yield and yield attributing qualities, as well as to estimate the genetic components of grain yield and yield attributing traits(Open et al., 2019). The goal of this review was to see if there was a link between distinct quantitative features in maize and grain yield.

### II. MATERIAL AND METHODOLOGY

The materials and methods for this review paper were gathered from a variety of sources, including research papers, journals, websites, articles, and books. All of the information presented in this review was previously discovered by other scholars. We also gathered information from their publications and journals to use in our maize genotype correlation research in Nepal.

### III. DISCUSSIONS

#### Analysis of Variance and Mean performance

For all of the features tested, the analysis of variance revealed extremely significant differences between genotypes, showing that the experimental materials were genetically distinct. This demonstrates that there is enough room among the available genotypes to pick promising lines for improving maize genetic yield potential (Mustafa, H.SB. Ahsan, M. Aslam, M. Ali, Q. Hasan, E. Bibi, T. Mehmood, 2013). Significant results were observed among the tested genotypes for the traits grain yield ton ha-1, ear weight, number of kernel row-1, 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, indicating the presence of genotypic differences and the importance of their genetic value in order to identify the best genetic makeup for a particular condition (Bello et al., 2010).

### Correlation

The correlation value indicates the type and extent of the relationship that exists between two characters. Correlation is also a metric that identifies features that should be considered in order to boost yield. The genetic link between the features could be the cause of trait correlation. The sort of relationship between grain yield and its component qualities is critical from the standpoint of the breeder (B. T. Magar et al., 2021). Higher genotypic correlations than phenotypic correlations revealed a higher genetic relationship between traits and yield, as well as lesser disparities between GCV and PCV for most traits, owing to a lower modifying effect of environment on character association (Vaezi et al., 2000). In most cases, the genotypic correlation was larger than the phenotypic correlation in all of the trials, showing a stronger degree of linkage among the features. As a result, phenotypic trait selection would be effective in producing genetic gain (Beulah et al., 2018).

Grain yield ton ha-1, plant height, ear height, 1000-kernel weight, days to physiological maturity, days to 50% silking, and days to 50% tasselling all had high estimates of genotypic and phenotypic variance, indicating the presence of sufficient inherent genetic variance over which selection can be effective. The phenotypic correlation coefficients between yield and yield components revealed that grain yield and related factors varied significantly across genotypes (Of et al., 2010).

### Plant height, leaf breadth, and ear height

For all genotypes, the PH, EH, and leaf width indicated a highly significant difference (P0.05) (standard check). Plant height, ear height, and leaf breadth had no significant

link with grain yield ton ha-1, according to the phenotypic correlation of all genotypes (Ghimire et al., 2017).

# Number of kernel row per ear, number of kernels per row and ear per plant

The number of kernel rows per ear, the quantity of kernels per row, and the ear per plant are all factors to consider. The number of kernel rows per plant, the number of kernels per row, and the ear per plant all showed that genotypes were highly significant (Amgai, 2021). The number of kernel rows per ear, number of kernels per row, and ear per plant all exhibited a non-significant link with grain yield ton per hectare, according to the phenotypic correlation of all genotypes. The number of kernel rows per ear and grain yield have a non-significant negative relationship, according to phenotypic correlation (Ghimire et al., 2015). The number of ears per plant was also shown to be positively and non-significantly associated to grain yield ton ha-1, confirming our findings (Raut et al., 2017).

### Days to 50% silking, and Days to 50% tasseling

For days to 50% tasselling and days to 50% silking, the results demonstrated that genotypes were significantly significant. Days to 50% silking and days to 50% tasselling had no significant link with grain yield ton ha-1, according to the phenotypic correlation of all genotypes (Agbaje et al., 2000).

### Tassel length, ear diameter, and ear length

For all genotypes, ear diameter, ear length, and tassel length are highly significant (P0.05). Grain yield ton ha-1 has previously been associated in a positive and highly significant way to ear diameter, ear length, ear weight, and tassel length (Barros et al., 2010).

### Ear weight and thousand kernel weight

The results showed that there was no significant difference in TKW between genotypes (P0.05).

Ear diameter, ear length, thousand kernel weight, days to physiological maturity, tassel length, and ear weight had a substantial positive association with grain yield ton ha-1, according to phenotypic correlation of all genotypes (Pariyar et al., 2018). The strongest link to grain yield was ear diameter and thousand kernel weight, followed by number of kernels per row, ear length, days to physiological maturity, and ear height (Raut et al., 2017).

### Days to physiological maturity

The days to physiological maturity were found to be statistically significant (P0.05). The grain production per hectare is positively influenced by thousand kernel weight and days to physiological maturity (Barros et al., 2010).

Several maize researchers have previously published similar conclusions on a range of subjects, including the

ISSN: 2456-1878 (Int. J. Environ. Agric. Biotech.) https://dx.doi.org/10.22161/ijeab.76.17 relationship between grain yield and ear length, diameter, husk weight, 1000 grain weight, and days to physiological maturity (Dewey & Lu, 1959). Other studies have revealed no significant relationship between grain yield and ear height, number of kernels per row, or number of ears per plant, implying that selecting for higher levels of these traits may not result in a significant increase in grain yield (Abziew, 2016). Days to 50% silking and tasseling had a non-significant positive relationship with grain yield (Rajesh Singh & Kumar, 2017). High densities were often used to obtain correlations between yield components and yield components with yield that would be most valuable to maize breeders for prediction purposes (Figliuolo et al., 2007). Because the number of ears per plant was discovered to be the most important factor, the findings suggest that each plant should be stressed to the point of barrenness in order to establish the best relationship between yield components and yield (ElLakany & Russell, 1971). As the value of the ear aspect grew (i.e. the cob was more damaged), grain yields decreased (Tripathi et al., 2016). When looking at genetic correlations between different quantitative variables, it's critical to look at the material's genetic base as well as environmental impacts (Neupane et al., 2020).

## IV. CONCLUSION

In conclusion, different studies about correlation analyses revealed that grain yield is mostly positively correlated with all variables, with the exception of the inverse relationships between the number of kernel rows per ear and the ear aspect. The results of the correlation analysis show that some characteristics can be picked while also being improved. For instance, a higher thousand seed weight could result in a higher grain output. An increase in the number of leaves per plant may result in an increase in ear height. Similar to how days to silking and tasseling can be selected and improved simultaneously when breeding for early maturity, ear height and plant height can be selected concurrently when breeding for small stature. The genotypes' total mean performance implies that there is a lot of variances in the germplasm that might be utilized in quality protein maize breeding to create acceptable hybrids and varieties. Because of its positive relationship with production, the large genetic increase seen for thousand seed weight indicated that there is potential for improving this trait and, and consequently, the yield.

### REFERENCES

[1] Abziew, E. A. F. Ab (2016). Its antimicrobial effects, according to the International Journal of Advanced Research

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in Biological Sciences. 145–148 in Int. J. Adv. Res. Biol. Sci., 3(4). <u>www.ijarbs.com</u>

- [2] G. Agbaje, Y. Abayomi, and F. Awoleye (2000). In the Nigerian forest zone, grain yield potential and associated features in maize (Zea mays L.) cultivars. Ghana Journal of Agricultural Science (Ghana Journal of Agricultural Science) (Vol. 33, Issue 2). <u>https://doi.org/10.4314/gjas.v33i2.1870</u>
- [3] S. Amgai, S. Amgai, S. Amgai, S. (2021). Himalayan College of Agricultural Sciences and Technology, Local innovation documentation: a case study of Mustang district. November.
- [4] L. B. Barros, R. M. P. Moreira, and J. M. Ferreira (2010). In family farm systems, phenotypic, additive genetic, and environment linkages of maize landraces populations. https://doi.org/10.1590/s0103-90162010000600010 Scientia Agricola, 67(6), 685–691.
- [5] D. R. Dewey and K. H. Lu (1959). A Correlation and PathCoefficient Analysis of Crested Wheatgrass Seed Production Components 1, Agronomy Journal 51(9), 515– 518.
  <u>https://doi.org/10.2134/agronj1959.00021962005100090002</u>
- [6] M. A. ElLakany and W. A. Russell (1971). Characteristics of Maize and Yield in Inbred Testcrosses at Different Plant Densities Crop Science, vol. 11, no. 5, pp. 698–701. <u>https://doi.org/10.2135/cropsci1971.0011183x00110005002</u> <u>8x</u>
- [7] Figliuolo, G., Budak, H., Campus, T., Romana, C. M., Science, B., Program, B., & Author, C. Figliuolo, G., Budak, H., Campus, T., Romana, C. M., Science, B., Program, B., & Author, C. (2007). Using Multivariate Analysis to Estimate Genetic Variation among Dent Corn Inbred Lines and Topcrosses. 1(2), 63–70.
- [8] B. Ghimire, D. Timsina, and J. Nepal (2015). The link between chlorophyll content and yield contributing factors in early maize varieties was investigated (Zea mays L.). 134–145 in Journal of Maize Research and Development. <u>https://doi.org/10.3126/jmrd.v1i1.14251</u>
- [9] B. P. Kandel, N. R. Adhikari, B. B. Adhikari, and M. Tripathi (2018). In Chitwan, Nepal, hybrid maize performed well. 31(1), 43–51, Bangladesh J. Plant Breed Genet.
- Bishnu Prasad Kandel and K. Shrestha (2020). Maize hybrids' performance in Nepal's interior plains was assessed. Heliyon, vol. 6, no. 12, e05542, doi:10.1016/j.heliyon.2020.e05542.
- [11] T. Karki (2013). The normalized difference vegetation index was used to predict maize yield and make nitrogen recommendations. 82–88 in Nepal's Agronomy Journal. <u>https://doi.org/10.3126/ajn.v3i0.900</u>
- [12] Z. Khodarahmpour, Z. Khodarahmpour, Z. Khodarahm (2012). In a heat stress condition, morphological classification of maize (Zea mays L.) genotypes was performed. 4(5), 31–40, Journal of Agricultural Science. <u>https://doi.org/10.5539/jas.v4n5p31</u>
- [13] P. B. Magar, G. B. Khatri-Chhetri, S. M. Shrestha, and T. R. Rijal (2018). During the summer at Rampur, Chitwan, Nepal, maize genotypes were tested for resistance to

ISSN: 2456-1878 (Int. J. Environ. Agric. Biotech.) https://dx.doi.org/10.22161/ijeab.76.17 southern leaf blight (Bipolaris maydis). 115–122 in the Journal of the Institute of Agriculture and Animal Science. https://doi.org/10.3126/jiaas.v33i0.20693

- [14] B. Neupane, A. Poudel, and P. Wagle (2020). In the midhills of Nepal, a varietal evaluation of promising maize genotypes was conducted. 127–139 in Journal of Agriculture and Natural Resources, vol. 3, no. 2. https://doi.org/10.3126/janr.v3i2.32491
- [15] H. Of, Q. Protein, and M. Zea (2010). 10(2), 2166–2175. Genetic Variability and Correlation in Single Cross.
- [16] Open, A., Bartaula, S., Panthi, U., Timilsena, K., Sharma Acharya, S., & Shrestha, J. (2019). (2019). Maize genetic progress, heritability, and variability Genotypes of Zea Mays L. 163–169 in Res. Agric. Livest. Fish, 6(2). www.agroaid-bd.org/ralf,
- [17] Pariyar, K., Sapkota, P., Panta, S., Buda, P., and Karki, T. B. Pariyar, K., Sapkota, P., Panta, S., Buda, P., and Karki, T. B. (2018). In Nepal's Mid-Western Region, performance and variance in phenotypic features of maize genotypes were studied. 109–113 in the International Journal of Agriculture, Environment, and Food Sciences. https://doi.org/10.31015/jaefs.18018
- [18] D. S. J. Rajesh Singh and A. Kumar (2017). Path Coefficient Analysis for Grain Yield and Its Attributes in Maize (Zea mays L.) 6(4), 2851–2856, International Journal of Current Microbiology and Applied Sciences. <u>https://doi.org/10.20546/ijcmas.2017.604.327</u>
- [19] S. K. Raut, S. Kant Ghimire, R. Kharel, C. Bahadur Kuwar, M. Sapkota, U. Kumar, and S. Kushwaha (2017). Maize Yield and Yield Attributing Traits Research 3(6), 123–129, American Journal of Food Science and Health. http://www.aiscience.org/journal/ajfsh http://creativecommons.org/licenses/by/4.0/
- [20] M. P. Tripathi, J. Shrestha, and D. B. Gurung (2016). During the winter season in Nepal, commercial maize hybrids were evaluated in a variety of Terai habitats. 2(1), 1–12. Journal of Maize Research and Development. <a href="https://doi.org/10.3126/jmrd.v2i1.16210">https://doi.org/10.3126/jmrd.v2i1.16210</a>
- [21] T. R. Rijal, G. KC, K. B. Koirala, and J. Shrestha (2016). In Nepal's Terai and Inner Terai, maize genotypes were tested for Turcicum leaf blight (Exserohilum turcicum). Journal of Maize Research and Development (<u>https://doi.org/10.3126/jmrd.v2i1.16221</u>)
- [22] L. Genotypes and I. N. Baitadi, Genotypes and Baitadi, Genotypes and Baitadi, Genotypes and Baitadi, Genotypes (2016). MAIZE (Zea. August.) VARIABILITY, CORRELATION, AND PATH COEFFICIENT ANALYSIS <u>https://doi.org/10.13140/RG.2.2.32171.75046</u>
- [23] E. P. Health & K. Y. Pool (2018). ANALYSIS OF MAIZE GENOTYPE YIELD AND YIELD ATTRIBUTING TRAITS IN CHITWAN, NEPAL Co-funded by PlantHealth master's program and the European Union's Erasmus + program. June.
- [24] T. Ndhlela, L. Herselman, C. Magorokosho, P. Setimela, C. Mutimaamba, and M. Labuschagne. 22. Ndhlela, T., Herselman, L., Magorokosho, C., Setimela, P., Mutimaamba, C., & Labuschagne, M. (2014). AMMI biplots were used to investigate the genotype-environment

interaction in maize grain yield. 1992–1999. In Crop Science, 54(5), 1992–1999. https://doi.org/10.2135/cropsci2013.07.0448

- [25] L. Genotypes and I. N. Baitadi (2016). August. https://doi.org/10.13140/RG.2.2.32171.75046
  VARIABILITY, CORRELATION, AND PATH COEFFICIENT ANALYSIS IN MAIZE (Zea)
- [26] S. K. Ghimire, B. R. Ojha, and K. B. Koirala (2017). Genetic Parameter Estimation, Correlation, and Path Coefficient Analysis of Maize Genotypes (Zea Mays L .). July 2020.
- [27] B. P. Kandel, N. R. Adhikari, B. B. Adhikari, and M. Tripathi (2018). In Chitwan, Nepal, hybrid maize performed well. 31(1), 43–51, Bangladesh J. Plant Breed Genet.
- [28] Bishnu Prasad Kandel and K. Shrestha (2020). Maize hybrids' performance in Nepal's interior plains was evaluated. Heliyon, vol. 6, no. 12, e05542, doi:10.1016/j.heliyon.2020.e05542.
- [29] Karki, T. (2013). The normalized difference vegetation index was used to predict maize yield and make nitrogen recommendations. 82–88 in Nepal's Agronomy Journal. <u>https://doi.org/10.3126/ajn.v3i0.9009</u>