

(88.253±17.45), highest value for number of ears (1.322±0.23), highest value for number of rows per ear (14.11±1.98), maximum days to complete 50% tasseling (39±6.18), maximum days to complete 50% silking (51±7.38) and more days interval between anthesis and silking (12±4.19). Cluster C was found to have five genotypes having similar performance of having maximum ear length (14.45±2.44), maximum value for yield per plant (111±23.04), maximum value for 100 grain weight (30.71±5.94) and maximum number of grains per row (35.83±7.47).

Cluster analysis grouped 30 maize QPM hybrids into three groups A, B and C having similar performance in agro-morphological traits (Figure 8) [45-48]. Cluster A consisted of 13 genotypes that had characteristics features of having highest days to complete 50% tasseling (48±2.18), highest days to complete 50% silking (50±2.17), least value for plant height (198.59±16.66), least value for ear height (106.86±10.83), maximum grain moisture contents (33.46±2.81), maximum value for ear aspect (3.00±0.51) and maximum numbers of rotten ears (1±1.09). Cluster B comprised of 14 hybrids that had prominent features of similar performance like maximum ear height (122.93±10.83), minimum grain moisture contents (31.01±2.81). Cluster C was found to have three hybrids with similar agro-morphological traits like minimum days to complete 50% tasseling (46±2.18), minimum days to complete 50% silking (47±2.71), maximum plant height (241.87±16.66) and maximum numbers of lodged plants (4.33±2.96).

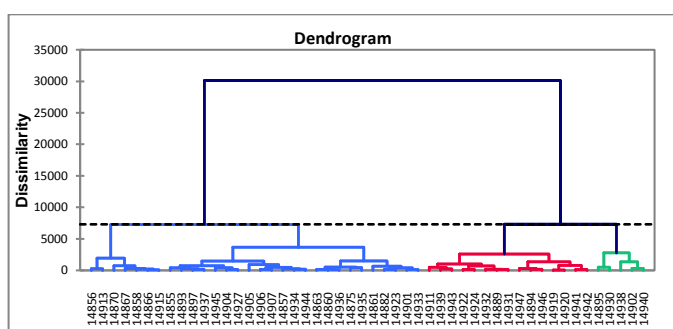


Figure 9: Cluster analysis of 50 maize inbred lines

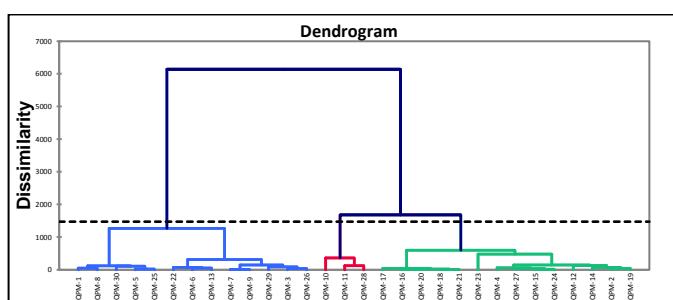


Figure 10: Cluster analysis of 30 QPM hybrids

4. CONCLUSIONS

As there was no opaque 2 gene in 50 genotypes therefore for the breeding of maize genotypes with high level of tryptophan, opaque 2, opaque 7 and flourey 2 genes should be incorporated by introducing QPM lines from CIMMYT for quality protein bio-fortification to alleviate protein malnutrition. Correlation plays pivotal role in the selection of right traits for breeding purposes. Different quantitative traits preferably plant height, ear height, field weight, grain moisture, plant lodging and grain moisture contents or the combination of few or more can be useful for breeding programs. The identification of high level of genetic diversity during the current study could be used for maize germplasm characterization, conservation and further improvement in maize breeding.

REFERENCE

[1] FAO, IFAD and WFP. 2015. The State of Food Insecurity in the World 2015. Meeting the 2015 international hunger targets: taking stock of uneven progress. Rome, FAO.

[2] Ranum, P., Peña-Rosas, J.P., Garcia-Casal, N.M. 2014. Global maize production, utilization, and consumption. *Annals of the New York Academy of Sciences*, 1312 (1), 105-112.

[3] Gibbon, B.C., Larkin, B.A. 2005. Molecular genetic approaches to developing quality protein maize. *Trends Genet*, 21, 227-233.

[4] Young, V.R., Scrimshaw, N.S., Pellet, P.L. 1998. Significance of dietary protein source in human nutrition: animal and/or plant proteins? pp 205—221. In: J. C. Waterlow, D. G. Armstrong, L. Fowden, and R. Riley (eds), *Feeding a World Population of more than Eight Billion People*. Oxford University Press in associate with Rank Prize Funds, New York.

[5] Vivek, B.S., Krivanek, A.F., Palacios-Rojas, N., Twumasi-Afriyie, S., Diallo, A.O. 2008. Breeding quality protein maize (QPM): Protocols for developing QPM cultivars. CIMMYT.

[6] Paroda, R., Prasanna, B.M., Mal, B., Dasgupta, S., Jat, M.L. 2015. Maize for food, feed, nutrition and environmental Security. Proc. 12th Int. Maize conf., 30Oct-1Nov, Bangkok, Thailand.

[7] Soave, C., Suman, N., Viotti, A., Salamini, F. 1978. Linkage relationships between regulatory and structural gene loci involved in zein synthesis in maize. *Theoretical and Applied Genetics*, 52 (6), 263-267.

[8] Kodrzycki, R., Boston, R.S., Larkins, B.A. 1989. The opaque-2 mutation of maize differentially reduces zein gene transcription. *The Plant Cell*, 1 (1), 105-114.

[9] Munck, L. 1992. The case of high-lysine barley breeding. pp 573—601. In: Shewry (ed), *Barley, Genetics, Biochemistry, Molecular Biology and Biotechnology*, CAB International, Wallingford.

[10] Olakojo, S.A., Omuetti, O., Ajomale, K., Ogunbodede, B.A. 2007. Development of quality protein maize: biochemical and agronomic evaluation [desarrollo de maíz qpm: evaluación bioquímica y agronómica]. *Tropical and Subtropical Agroecosystems*, 7, 97-104.

[11] Crow, J.F., Kermicle, J. 2002. Oliver Nelson and quality protein maize. *Genet*, 160 (3), 819-821.

[12] Gunaratna, N.S., Groote, H.D., Nestel, P., Pixley, K.V., McCabe, G.P. 2010. A meta-analysis of community-based studies on quality protein maize. *Food policy*, 35 (3), 202-210.

[13] Jacobs, D.R., Meyer, K.A., Kushi, L.H., Folsom, A.R. 1998. Whole-grain intake may reduce the risk of ischemic heart disease death in postmenopausal women: the Iowa Women's Health Study. *American Journal of Clinical Medicine Research*, 68, 218-219.

[14] Saiki, R.K., Gelfand, D.H., Stoffel, S., Scharf, S., Higuchi, R., Horn, G.T., Mullis, K.B., Erlich, H.A. 1988. Primer directed-enzymatic amplification of DNA with a thermostable DNA polymerase. *Science*, 239, 487-491.

[15] Beckmann, J.S., Soller, M. 1990. Toward a unified approach to genetic mapping of eukaryote based on sequence tagged microsatellite sites. *Biotechnol*, 8, 930-932.

[16] Sood, A., Thakur, K., Sharma, P.N., Gupta, D., Singode, A., Rana, M., Lata, S. 2017. A Comprehensive Study of Variation in Selected QPM and Non-QPM Maize Inbred Lines. *Agricultural Research*, 1-11.

[17] Steel, R.D.G., Torrie, J.H., Dickey, D.A. 1997. Principles and Procedures of Statistics: A Biometrical Approach, (3rd ed.) McGraw Hill Book Co., New York, USA.

[18] Rencher, A.C. 1995. Methods of multivariate analysis: Cluster analysis, (2nd ed.). John Wiley and Sons inc. USA.

[19] Weinstein, J. 2008. A post genomic visual icon. *Science*, 319, 1772-1773.

[20] Babu, R., Nair, S.K., Kumar, A., Vekantesh, S., Sekhar, J.C., Singh, N.N., Srinivasan, G., Gupta, H.S. 2005. Two-generation marker aided backcrossing for rapid conversion of normal maize lines to quality protein maize (QPM). *Theoretical and Applied Genetics*, 111, 888-897.

[21] Ghimire, B., Timsina, D. 2015. Analysis of yield and yield attributing traits of maize genotypes in Chitwan, Nepal. *World Journal of Agricultural Research*, 3 (5), 153-162.

[22] Dijak, M., Modarres, A.M., Hamilton, R.I., Dwyer, L.M., Stewart, D.W., Mather, D.E., Smith, D.L. 1999. Leafy reduced-stature maize hybrids for short-season environments. *Crop Science*, 39 (4), 1106-1110.

[23] Ihsan, H., Khalil, I.H., Rahman, H., Iqbal, M. 2005. Genotypic variability for morphological and reproductive traits among exotic maize hybrids. *Sarhad Journal of Agriculture*, 21, 599-602.

- [24] Shrestha, J. 2013. Agro-morphological characterization of maize inbred lines. *Sky Journal of Agricultural Research*, 2 (6), 85-87.
- [25] Yucel, C., Hizli, H., Firincioglu, H.K., Cil, A., Anlarsal, A.E. 2009. Forage yield stability of common vetch (*Vicia sativa* L.) genotypes in the Cukurova and GAP Regions of Turkey. *Turkish Journal of Agriculture*, 33 (2), 119-125.
- [26] Golam, F., Farhana, N., Zain, M.F., Majid, N.A., Rahman, M.M., Rahman, M.M., Kadir, M.A. 2011. Grain yield and associated traits of maize (*Zea mays* L.) genotypes in Malaysian tropical environment. *African Journal of Agricultural Research*, 6 (28), 6147-6154.
- [27] Singha, N., Prodhana, S.H. 2000. Character association in green maize. *Env. Eco.*, 18, 962-5.
- [28] Najeeb, S., Rather, A.G., Parray, G.A., Sheikh, F.A., Razvi, S.M. 2009. Studies on genetic variability, genotypic correlations and path coefficient analysis in maize under high altitude temperate ecology of Kashmir. *MNL*, 46.
- [29] Bocanski, J., Sreckov, Z., Nastasic, A. 2009. Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays* L.). *Genetika*, 41 (2), 145-154.
- [30] Iqbal, J., Shinwari, Z.K., Rabbani, M.A. 2015. Maize (*zea mays* L.) Germplasm agro-morphological characterization based on descriptive, cluster and principal component analysis. *Pakistan Journal of Botany*, 47, 255-264.
- [31] Malik, H.N., Malik, S.I., Hussain, M.O.Z.A.M.I.L., Chughtai, S.U.R., Javed, H.I. 2005. Genetic correlation among various quantitative characters in maize (*Zea mays* L.) hybrids. *Journal of Agriculture, Forestry and the Social Sciences*, 3, 262-265.
- [32] Chase, S.S., Nanda, D.K. 1967. Number of leaves and maturity classification in *Zea mays* L. *Crop Science*, 7, 431-3.
- [33] Edmeades, G.O. 1996. Developing Drought and Low N-tolerant Maize: Proceedings of a Symposium, March 25-29, CIMMYT, El Batan, Mexico. CIMMYT.
- [34] Tandzi, N.L., Ngonkeu, E.L.M., Youmbi, E., Nartey, E., Yeboah, M., Gracen, V., Mafouasson, H.A. 2015. Agronomic performance of maize hybrids under acid and control soil conditions. *IJAAR*, 6 (4), 275-291.
- [35] Akbar, M., Shakoor, M.S., Husein, A., Sarwar, M. 2008. Evolution of maize 3-way crosses through genetic variability, broad sense heritability, characters association and path analysis. *Journal of agricultural research*, 46 (1), 39-45.
- [36] Sabaghnia, N., Dehghani, H., Alizadeh, B., Moghaddam, M. 2011. Yield analysis of rapeseed (*Brassica napus* L.) under water-stress conditions using GGE biplot methodology. *Journal of Crop Improvement*, 25 (1), 26-45.
- [37] Alvi, M.B., Rafique, M., Tariq, M.S., Hussain, A., Mahmood, T., Sarwar, M. 2003. Character association and path coefficient analysis of grain yield and yield components maize (*Zea mays* L.). *Pakistan Journal of Biological Sciences*, 6 (2), 136-138.
- [38] Yan, W., Tinker, N.A. 2005. An integrated system of biplot analysis for displaying, interpreting and exploring genotype by-environment interactions. *Crop Science*, 45, 1004-1016. DOI:10.2135/cropsci2004.0076.
- [39] Aliyu, B., Ng, N.Q., Fawole, I. 2000. Inheritance of pubescences in crosses between Cowpea (*Vigna unguiculata* (L.) WAIP) and *V. Rhomboidea* Burt. *Davy*.
- [40] Bantte, K., Prasanna, B.M. 2003. Simple sequence repeat polymorphism in Quality Protein maize (QPM) lines. *Euphytica*, 129, 337-344.
- [41] Bender, D.A., Bender, A.E. 1999. *Benders' Dictionary of Nutrition and Food Technology* (7th ed.). Woodhead Publishing. Abington.
- [42] Danson, J.W., Mbogari, M., Kimani, M., Lagat, M., Kuria, A., Diallo, A. 2006. Marker assisted introgression of opaque-2 gene into herbicide resistant elite maize inbred lines. *African Journal of Biotechnology*, 5 (24), 2417-2422.
- [43] FAO. 2002. *World Agriculture: Towards 2015/2030. Summary Report*. FAO, Rome.
- [44] FAO. 2014. *The state of food insecurity in the world 2014*, FAO.
- [45] Gupta, P.K., Varshney, R.K., Sharma, P.C., Ramesh, B. 1999. Molecular markers and their applications in wheat breeding. *Plant Breed*, 118 (5), 369-390.
- [46] Lopez, M.A., Gloverson, L., Larkins, B. 2004. Genetic mapping of opaque2 modifier genes. *Maize Genetics Cooperation Newsletter*, 69, 165.
- [47] Prasanna, B.M., Vasal, S.K., Kassahun, B., Singh, N.N. 2001. Quality protein maize.
- [48] Shanker, A.K., Cervantes, C., Loza-Tavera, H., Ayudainayagam, S. 2005. Chromium toxicity in plants. *Environment International*, 31, 739-753.
- [49] Yan, W., Rajcan, I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Sci*, 42, 11-20. <http://crop.sci-journals.org/cgi/content/abstract/42/1/11>.

