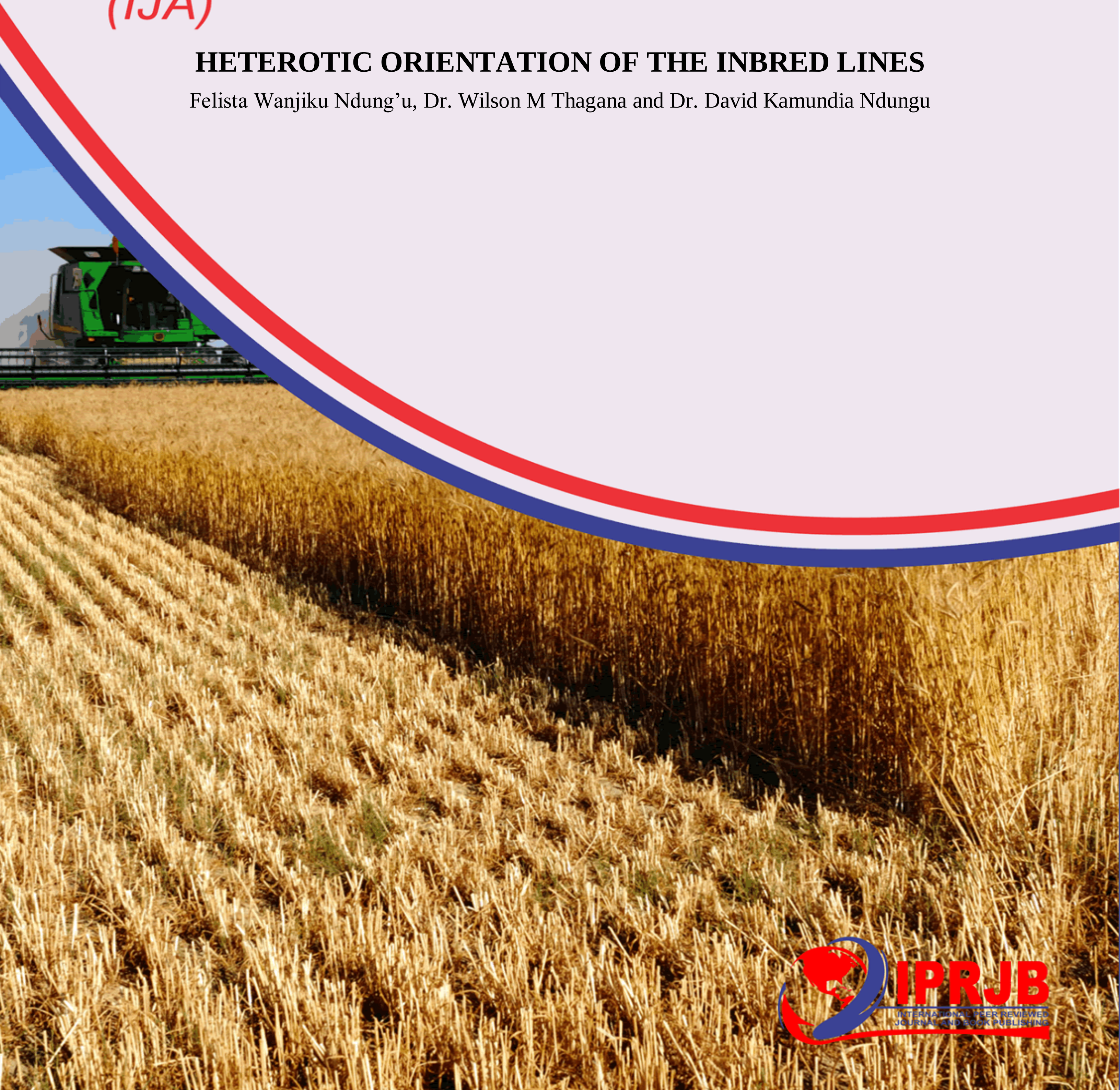
International Journal of
Agriculture
(IJA)

HETEROTIC ORIENTATION OF THE INBRED LINES

Felista Wanjiku Ndung'u, Dr. Wilson M Thagana and Dr. David Kamundia Ndungu



IPRJB
INTERNATIONAL PEER REVIEWED
JOURNAL AND BOOK PUBLISHING

International Journal of Agriculture
ISSN 2520-4629X (Online)
Vol.4, Issue 1, pp 1 - 14, 2019

www.iprjb.org

HETEROTIC ORIENTATION OF THE INBRED LINES

[1*]Felista Wanjiku Ndung'u
[1]Post Graduate Student: Kenyatta University
*Corresponding Author's Email: ndungu.nfelista@gmail.com

[2]Dr. Wilson M Thagana
Lecturer: Kenyatta University, Nairobi, Kenya

[3]Dr. David Kamundia Ndungu
Chief Officer-Agriculture: Kiambu County Government

Abstract

Purpose: The main purpose of the study was to determine the heterotic orientation of the inbred lines

Methods: The lines used in the study were derived from a segregating population in the F_4. They were crossed to two single cross testers CIMMYT Tester A (CML312/CML442) and Tester B (CML395/CML444) through the Line by tester mating design. The 98 crosses developed through line by tester cross of 49 lines in the F_4 and two testers Tester A and Tester B were studied for resistance to NLB and other yield related traits including : days to anthesis, days to silking, ear aspect, plant height, ear height, field weight and Grain moisture. The experiment was conducted in the 2017 main growing season in three mid-altitude maize growing regions of Kenya (Kakamega, Muranga, Embu). Data was analyzed using REML, META-R and AGD-R tools.

Results: The study found out that The heterotic orientation was determined for the lines and that differed across the 3 sites. The 3 sites were treated as independent environments due to genotype x environment interactions. The classification of the lines differed across the three locations having most of the lines in Muranga falling under the heterotic groups A and B. For Embu and Kakamega, fewer lines were classified into either heterotic group a and B having none of the lines in heterotic group a in Kakamega.

Unique Contribution to Theory, Practice and Policy: The study recommeded that Knowledge of heterotic groups of the lines is of importance in the introductions in order to exploit their use in the breeding programme. The lines may hence require some further testing with alternative testers in order to fully classify them into their various heterotic groups.

Key Words: *Heterotic Orientation, Inbred Lines*

1.0 INTRODUCTION

1.1 Heterotic Classification

Maize is grown all over the world with the United states as the maize leading producer accounting for 40% of the entire world's harvest (Martinez, 2011). While maize comprises a consumption of over 60% in developing countries, it is of less importance in the developed countries. Maize was introduced to Africa in the 16th-18th century. It has since become Africa's staple food. In Kenya, the counties that produce maize include: uasing Gishu, Trans Nzoia, Nakuru, Nyeri, Embu, Kakamega, Taita taveta, Kirinyaga and Kwale. The estimate area under maize is at 1.5million hectares. Maize production in Kenya has been on decline since 2006 having dropped from 34 million bags in 2006 to 25 million bags in 2008 from an estimated area of 1.6 million hectares (Kamau, 2013).

The decline in production has been attributed to factors like drought, high cost of inputs, low soil fertility, pest and diseases (Mearns, 2015). In Kenya, 80% of the land mass receive less than 250mm of rainfall in a season hence the need to breed maize varieties that can utilize the low water levels and varieties that can tolerate diseases and pests. In a maize breeding program, inbred lines classification into heterotic groups is the first step. This would provide the exploitation of maximum heterosis of lines. In the availability of large numbers of inbred lines and determined testers, performance of the lines through testcrosses would be used as a criterion to group the lines Melchinger 1999(Mearns, 2015).

In the recent past, molecular markers have been used in classification of lines and populations hence obtaining a clear picture on the heterotic patterns that are promising (Reif *et al*., 2003). Testcrosses are used to determine the potential of inbred lines in a breeding program. Choice of testers is hence crucial for selection of genotypes for their use in hybrid development.

Maize breeders have in the past used several techniques to study genetics of quantitative traits amongst them grain yield. Line by tester is an efficient method and allows the inclusion of a large number of lines hence provide combining ability estimates that are reliable. The SCA is described as performance of the crosses as better as or poorer than what was expected as per the average performance of the potential lines used in the cross (Sparague and tatun, 1942). SCA is an indication that the value of superior genotypic crosses in intra group crosses is represented in selection of inbred lines as it assists in identifying specific inbred lines for use in hybrid development and also determine heterotic grouping for different genotypes. According to Hallauer and Miranda (1981), lines that complement each other are obtained from heterotic groups that differ and that exhibit high and positive SCA estimates.

The SCA estimates for grain yield according to Menkir *et al*., (2004) have been used in classification of maize into different heterotic groups (Melani and Carena 2005, Fan *et al*., 2008). A line, depending on its performance could also be in more than one heterotic group in a particular combination since heterotic groups may be conceptual (Hallauer and Carena 2009). Melchinger and Gumber (1998) recorded that heterotic groups classify entries of related or unrelated genotypes from a similar or different population that shows combining abilities or the heterotic response that are similar once crossed with distinct genotypes.

Maize lines are classified into various heterotic groups through various ways. These are applied across the globe (Fan *et al.*, 2009). Use of SCA estimates is the traditional way used in the availability of line-pedigree data and cross yield data to allocate inbreds to various heterotic groups. The second way is through use of molecular markers in order to attain the genetic similarity (GS) or distance (GD) estimates in order to classify the inbred lines to given heterotic groups. The methods accuracy is not guaranteed. Fan *et al*., (2009) applied a different method through use of heterotic groups specific and general combining ability to assign inbreds to heterotic groups. This method was said to of efficience in comparison to SSR markers. Menkir *et al*., (2004) used both yield based SCA and molecular markers to categorize the lines into various heterotic groups.

Melchinger (1999) concluded that in the existence of a large number of germplasm and with availability of proven testers, the line by tester should be a better criterion to classify lines into heterotic groups. Barata and Carena (2006) recorded massive inconsistency in molecular marker classification and field trial based in diverse inbred entries. They were for the opinion that the groups with germplasm and heterotic properties that were similar could not be accurately identified using molecular markers. Extensive field tests were recommended across different environments to categorize the lines to different heterotic groups.

Hallauer *et al*., (2010) concluded that in testing large numbers of progeny, mating designs could be of importance as they are used broadly across locations in a number of years to categorize inbred lines into heterotic groups. However, stability of heterotic groups differs depending on the situation. Identification of heterotic groups that could be crosses of known genotypes is important and they express higher levels of heterosis (Carena and Hallauer 2001, Troyer 2006, Mandes *et al*., 2015). They are of importance in development of maize hybrids (Barata and carena 2006, Carena & Wicks III, 2006).

Maize breeding depends almost entirely on identifying heterotic patterns and heterotic groups for utilization (Melani and Carena, 2005). A groups of germplasm source that can be inter-crossed consistently to develop crosses that are better compared to when crosses are made from lines in a similar group represents heterotic groups 1(Hallauer and Carena, 2009)

Maize breeding in Kenya depends on four heterotic groups developed from collections from growers and introduction. The variations of the collections could be high due to interchange of germplasm across the borders. Existence of the groups indicates that there is heterosis within the groups from farmers and heritability of this and the heterotic patterns is not established. In any breeding programme, population improvement through selection is influenced mostly by heterotic groups. Understanding of heterotic patterns is hence crucial in exploitation of heterosis (Preciado-Ortiz and Johnson 2004).

Knowledge on heterotic groups of various collection or introductions is hence crucial in breeding to allow exploitation of heterosis in any breeding programme. This results in good heterotic pattern combinations to obtain disease resistant, early or late maturing and high yielder hybrids. Information on heterotic groups is of importance in developing high performing hybrid crosses and improving populations obtained from collections and introductions. Heterosis is attained when the progeny of crosses from inbreds perform above the average of the parents. Heterotic manifestation is dependent on genetic divergence of two parental varieties. Genotypes can be classified into heterotic groups which is dependent on the similarity in CA and the heterosis once crossed with genotypes from different genetic groups (Melchinger & guber,1998).

Different patterns have been in use in different countries for hybrid development which depends on their adapdability. For USA and Europe, Reid x Lancaster pattern is common and is exploited (Orda's 1991). Major pattern used in China is domestic x LSC in the North maize area while summer region exploit domestic x PN (Li *et al.*, 2004). Japan uses the US dent x Northern/European flint (Enoki *et al*,. 2002). In East Africa, the pattern used is KSII x EC573 for highlands in Kenya. Pool A and Pool B have been developed for the medium altitude areas of Kenya.

Breeders are therefore able to group genotypes into heterotic patterns in order to develop high performing hybrids by use of the knowledge on heterosis (Reif *et al.*, 2005).

2.0 METHODOLOGY

The lines used in the study were derived from a segregating population in the $F_{4.}$ They were crossed to two single cross testers CIMMYT Tester A (CML312/CML442) and Tester B (CML395/CML444) through the Line by tester mating design. The 98 crosses developed through line by tester cross of 49 lines in the F_4 and two testers Tester A and Tester B were studied for resistance to NLB and other yield related traits including : days to anthesis, days to silking, ear aspect, plant height, ear height, field weight and Grain moisture. The experiment was conducted in the 2017 main growing season in three mid-altitude maize growing regions of Kenya (Kakamega, Muranga, Embu). Data was analyzed using REML, META-R and AGD-R tools.

3.0 RESULTS

3.1 Specific Combining Ability for yield and heterotic orientation of the lines for individual sites

Table 1: Specific Combining Ability for yield and heterotic orientation of the lines for individual sites

Muranga				Embu			Kakamega		
Line	Heterotic Group	CML395/ CML444	CML312/ CML442	Heterotic Group	CML395/ CML444	CML312/ CML442	Heterotic Group	CML395/ CML444	CML312/ CML442
1	A	1.34**	0.89	A	-0.05	-0.04**		-0.14	0.21
12		-0.21	-0.79	B	0.02	0.17**	B	-0.06	0.24*
17	A	0.48	-1.82**	B	0.01**	0.02		-0.14	0.15
18	A	-0.84	-1.87**		-0.11	0.21		-0.26	0.09
19	A	1.30**	-1.14**		0.05	-0.18		0.03	0.11
2	B	-0.68	0.97**		0.09	0.16		-0.29	0.08
26	A	0.49	-2.21**	A	0.14	-0.22*		-0.10	-0.26
29	B	0.11	1.51**		0.34	0.10	B	-0.07**	0.01
31	B	-0.13	1.41**		0.17	0.01		0.05	-0.09
33	B	-0.14	1.41**		0.21	0.02		-0.06	0.14
34	B	0.02	1.16**		0.18	-0.05		0.19	-0.12
35	B	-0.23	1.37**		0.08	-0.13		0.15	-0.02
4	A	-0.28	-1.04**		-0.18	-0.19		-0.11	-0.17
41	B	0.15	1.16**		0.03	0.06		0.07	0.02
43	B	-0.24	0.72**		0.21	0.04		0.33	-0.08
45	B	-0.35	2.14**		-0.12	0.24		0.10	-0.04
47	A	0.44	-2.54**	A	0.30	-0.15**		0.48	-0.18
51	A	0.63	-2.61**		0.02	-0.01		-0.06	-0.25
61	B	0.77	1.15**		-0.09	-0.30		0.35	-0.19
63	A	0.22	-3.44**	A	0.05**	-0.25**		0.27	-0.21
67	A	-0.86	-4.14**		-0.30	-0.05		-0.14	-0.24
73	B	0.69	2.08**		-0.30	0.03		-0.29	-0.03
75	A	1.18**	0.12		-0.37	0.23		-0.32	0.15
78	B	-0.07	1.55**		-0.12	0.07		-0.38	0.27
79	B	-0.39	2.04**		0.14	0.05		-0.05	0.03
81	A	0.20	-1.25**		0.10	0.25		0.27	0.01
9	A	-0.20	1.83**	B	-0.19**	0.05	B	0.09	0.04**

CML395/CML444=Tester B, CML312/CML412=Tester A, *=Significant, **=highly significant

3.1.2 Discussion

Classification of the lines into heterotic group A (CML312/CML442) and B (CML395/CML444) were dependent on the SCA effects for grain weight such that lines exhibiting positive and significant SCA with (CML312/CML442) tester A were oriented into the opposite heterotic group which is B and lines exhibiting positive and significant SCA with (CML395/CML444) tester B were oriented into the opposite heterotic group which is A.

Lines exhibiting positive and significant SCA to the two testers were oriented to group AB. Lines exhibiting negative and significant SCA with tester A were oriented into heterotic group A while lines exhibiting negative and significant SCA with tester B were oriented into heterotic group B. Results for the SCA effects of top testcrosses and their corresponding testers for NLB resistance and other yield related traits were presented for all the three sites (Kakamega, Muranga and Embu).

Muranga

At Muranga, 3 lines (line 1, 19 and 75) expressed positive and significant SCA effects with CML395/CML444 hence were oriented into group A. A total of 14 lines (Line 2, 29,31,33,34,35,41,43,45,61,73,78,9,790 lines expressed positive and significant SCA effects with CML312/CML442 hence were oriented into group B. 11 lines exhibited negative and significant SCA with CML312/CML442 hence were oriented into group A.

A total of 13 lines were oriented to heterotic group A while 13 lines were oriented to heterotic group B. A total of 26 lines were classified under group A and B but the rest of the lines could not be classified with the two testers.

Embu

In Embu, 2 lines exhibited positive and significant SCA for yield with CML395/CML444 and were oriented into group A. 1 line exhibited positive and significant SCA with CML312/CML442 and were oriented into group B. 1 line had negative and significant SCA effects with CML312/CML442 and were oriented into group A.

A total of 4 lines were oriented to heterotic group A while 3 lines were oriented to heterotic group B. A total of 7 lines were classified under group A and B in Embu but the rest of the lines could not be classified with the two testers.

Kakamega

In Kakamega, 1 line exhibited negative and significant SCA effects with CML395/CML444 and was classified into group B. 2 lines exhibited positive and significant SCA with CML312/CML442 and was classified into group B.

A total of 3 lines were classified into heterotic group B in Kakamega. The rest of the lines could not be classified by the two testers.

4.0 CONCLUSIONS AND RECOMMENDATIONS

4.1 Conclusion

The classification of the lines differed across the three locations having most of the lines in Muranga falling under the heterotic groups A and B. For Embu and Kakamega, fewer lines were classified into either heterotic group a and B having none of the lines in heterotic group a in Kakamega. Lines classified into heterotic group A could be crossed with germplasm in heterotic group B in order to exploit higher levels of heterosis. Lines classified into heterotic group B could also be crossed with germplasm from heterotic A in order to exploit maximum levels of heterosis. Hallauer and carena (2009) reported that heterotic groups represent a group of genotypes that when crossed consistently give better crosses than when crosses are made within the same group.

According to Menkir *et al*., (2004), SCA estimates for grain yield have been used widely to classify maize lines into heterotic groups. Some of the lines were classified under different heterotic groups across the environments. Line 17 was classified into heterotic group A in Muranga and into heterotic group B in Embu. Line 9 was classified into heterotic group B in both Embu and Kakamega and into heterotic group A in Muranga. Hallauer and Carena (2009) reported that a line could be in more than one heterotic groups and this would depend on the performance in the particular combination as heterotic groups could be conceptual.

4.2 Recommendations

Knowledge of heterotic groups of the lines is of importance in the introductions in order to exploit their use in the breeding programme. The lines may hence require some further testing with alternative testers in order to fully classify them into their various heterotic groups. Significant interactions between the lines and the testers is evidence that the rank of the lines differs depending on testers used, a suitable tester may then be selected to classify new germplasm.

References

Adipala, E., P. E. Lipps. and L. V. Madden. (1993) Reaction of maize cultivars from Uganda to *Exserohilum turcicum.* Phytopathology 83:217-223.

Alake, C. O., Ojo, D. K., Oduwaye, O. A., & Adekoya, M. A. (2008) Genetic variability and correlation studies in yield and yield related characters of tropical maize (*Zea mays* L.). Asset Series A, *8*(1), 14-27.

Albrecht T., Wimmer V., Auinger H.-J., Erbe M., Knaak C., et al., (2011) Genome based prediction of testcross values in maize. Theor. *Appl. Genet*. 123: 339–350

Al-Tabbal, J. A., & Al-Fraihat, A. H. (2012) Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. Journal of Agricultural Science, 4(3), 193.

Asoro F. G., Newell M. A., Beavis W. D., Scott M. P., Jannink J.-L., (2011) Accuracy and training population design for genomic selection on quantitative traits in elite North American oats. Plant Gen 4: 132–144.

Barata, C. and Carena, M.J. (2006). Classification of North Dakota maize inbred lines into heterotic groups based on molecular and testcross data. Euphytica 151: 339-349.

Bernardo R., Yu J., (2007) Prospects for genome wide selection for quantitative traits in maize. Crop Sci. 47: 1082–1090.

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.

Browning B. L., Browning S. R., (2009) A unified approach to genotype imputation and haplotype-phase inference for large data sets of trios and unrelated individuals. J. Hum. Genet. 84: 210–223.

Carena MJ and Hallauer AR (2001) Response to inbred progeny recurrent selection in Leaming and Midland Yellow Dent populations. Maydica 46: 1-10.

Carena MJ and Wicks III ZW (2006) Maize early maturing hybrids: An exploitation of U.S. temperate public genetic diversity in reserve. Maydica 51: 201-208.

Carson M. L., (1995) Inheritance of latent period length in maize infected with *Exserohilum turcicum*. Plant Dis. 79: 581–585.

Chung CL, Jamann T, Longfellow J, Nelson R (2010) Characterization and fine-mapping of a resistance locus for northern leaf blight in maize bin 8.06. Theor Appl Genet121(2):205–227.

CIMMYT,(1985) Managing trials and reporting data for CIMMYT's International Maize Testing Programme.CIMMYT, El Batan, Mexico.

Collard B. C. Y., Mackill D. J., (2008) Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philos T Roy Soc B 363: 557–572.

Cukandor, O.B., J.F. Miller and J.J. Hammond, (1997) Combining ability of the stay green trait and seed moisture content in sun flower. *Crop Sci*. 37: 378-382.

Daetwyler H. D., Hickey J. M., Henshall J. M., Dominik S., Gredler B., et al. , (2010a) Accuracy of estimated genomic breeding values for wool and meat traits in a multi-breed sheep population. Anim. Prod. Sci. 50: 1004–1010.

Daetwyler H. D., Pong-Wong R., Villanueva B., Woolliams J. A., (2010b) The impact of genetic architecture on genome-wide evaluation methods. Genetics 185: 1021–1031

De Roos A. P. W., Hayes B. J., Goddard M. E., (2009) Reliability of genomic predictions across multiple populations. Genetics 183: 1545–1553.

Dingerdissen A., Geiger H., Lee M., Scheckert A., Welz H., (1996) Interval mapping of genes for quantitative resistance of maize to Setosphaeria turcica, cause of northern leaf blight, in a tropical environment. Mol. Breed. 2: 143–156.

Dodds PN, Rathjen JP (2010) Plant immunity: Towards an integrated view of plant-pathogen interactions. Nat Rev Genet 11(8):539–548.

Drechsler, C. (1923) Some graminicolous species of *Helminthosporium*. I. J. Agri. Res. 24:641-739.

Durrishahwar, H., Rehman, S.M.A., Shah,I.A.K and Ali, F. (2008) Recurrent selection for yield and yield associated traits under leaf blight (*Helminthosporium maydis*) stress in maize. *Sarhad Journal of Agriculture,* 24(4): 599-605.

Dunn, G. M. and T. Namm. (1970) Gene dosage effects on monogenic resistance to northern corn leaf blight. Crop Sci. 10:352-354.

Elshire R. J., Glaubitz J. C., Sun Q., Poland J. a., Kawamoto K., et al., (2011) A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. PLoS ONE 6: e19379].

Enoki, H., H. Sato, and K. Koinuma. (2002) SSR analysis of genetic diversity among maize inbred lines adapted to cold regions of Japan. Theoretical Applied Genetics 104:1270-1277.

Erbe M., Hayes B. J., Matukumalli L. K., Goswami S., Bowman P. J., et al., (2012) Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels. J. Dairy Sci. 95: 4114–4129.

Falconer, D. S. (1989) Introduction to Quantitative Genetics. 3rd ed. Longman, London, England, pp 125-132.

Falconer, D. S and Mackay, T. F. C. (1996) Introduction to quantitative genetics. 4th ed. Longman, Essex, England, pp 200-215.

Falconer D. S., Mackay T. F. C., (1996) Correlated response to selection, 320–322 Introduction to Quantitative Genetics, Ed. 4. Longmans Green, Harlow, Essex, UK

Fan XM, Chen HM, Tan J, Xu CX, Zhang YM, Huang YX and Kang MS (2008) A new maize heterotic pattern between temperate and tropical germplasms. Agronomy Journal 100: 917-923.

Ganal M. W., Durstewitz G., Polley A., Bérard A., Buckler E. S., et al. , (2011) A large maize (Zea mays L.) SNP genotyping array: development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome. PLoS ONE 6: e28334.

Gaunt, R. E. (1995) New technologies in disease measurement and yield loss appraisal. Can. J. Plant Pathol. 17:185-189.

Gebrekidan, B, Wafula, B., and Njoroge, K. (1992) Agroecological zoning in relation to maize research priorities in Kenya. In: *KARl: Review of the National Maize Research Program.* Proceedings of a Workshop Held between November 19 and 23, 1991, Kakamega, Kenya. Kenya Agricultural Research Institute (KARl) and the International Service for National Agricultural Research (ISNAR), Nairobi, Kenya.

Gevers HO (1975) A new major gene for resistance to Helminthosporium turcicum leaf blight of maize. Plant Dis Rep 59:296–299.

Gravois, K.A. and R.W. McNew, (1993) Combining ability and heterosis in U.S. southern long rice grain. *Crop Sci*. 33: 90-95.

Guzman P., Lamkey K., (2000) Effective population size and genetic variability in the BS11 maize population. Crop Sci. 40: 338–346

Hadfield J. D., (2010) MCMC Methods for multi-response generalized linear mixed models: The MCMCglmm R Package. J. Stat. Softw. 33: 1–22.

Hallauer AR and Carena MJ (2009) Maize Breeding. In Carena MJ (ed) Handbook of plant breeding: Cereals. Springer, New York, p. 3-98.

Hallauer AR, Carena MJ and Miranda FJB (2010) Quantitative genetics in maize breeding. 3rd edn, Springer, New York, 663p.

Hallauer, A. R. and Miranda Fo, J. B. (1981) Quantitative genetics in maize breeding. 2nd ed. Iowa State University press, Ames, Iowa. pp 26-40.

Hallauer, A.R. and J.B. Miranda, (1988) Quantitative genetics in maize breeding. 2nd ed. Iowa State Univ. Press. Ames. pp. 64-71.

Hayes B. J., Bowman P. J., Chamberlain A. C., Verbyla K., Goddard M. E., (2009a) Accuracy of genomic breeding values in multi-breed dairy cattle populations. Genet. Sel. Evol. 41: 51.

Hayes B. J., Bowman P. J., Chamberlain A. J., Goddard M. E., (2009b) Invited review: genomic selection in dairy cattle: progress and challenges. J. Dairy Sci. 92: 433–443

Heffner E. L., Lorenz A. J., Jannink J.-L., Sorrells M. E., and (2010) Plant breeding with genomic selection: gain per unit time and cost. Crop Sci. 50: 1681–1690.

Hilu H. M. and A. L.Hooker, (1963) Host-pathogen relationship of *Helminthosporium turcicum* in resistant and susceptible corn seedlings. Phytopathology. 54:570-575.

Hooker, A. L. (1961) A new type of resistance in corn infected with *Helminthosporium turcicum*. Plant Dis. Reptr. 45:780-781.

Joshi, V. N., R. B. Dubey and S. Marker, (2002) Combining ability for polygenic traits in early maturity hybrids of maize (*Zea mays* L.). *Indian J. Plant Breed. Genet.* 62: 312-315.

Kamau M. (2013) Journal of agricultural & food information 14 (2), 132- 150.

Kang'ethe, W.G. (2004) Agricultural development and food security in Kenya: A case for more support. A paper prepared for agriculture and food organisation (September).

Karkkainen H. P., Sillanpaa M. J., (2012) Back to basics for bayesian model building in genomic selection. Genetics 191: 969–987.

Kempthorne, O. (1957) An Introduction to Genetic Statistics. New York: John Wiley & Sons, Inc. London: Chapman & Hall Ltd. pp. 458-471.

Kumar, S., Singh, H. B., Sharma, J. K. (2007) Combining ability analysis for grain yield and other associated traits in rice. Oryza, 44(2): 108-114.

Legarra A., Robert-Granié C., Manfredi E., Elsen J.-M., (2008) Performance of genomic selection in mice. Genetics 180: 611–618

Levy, Y. and Cohen, Y. (1983) Biotic and environmental factors affecting infection of sweet corn with *Exserohilum turcicum*. *Phytopathology* 73:722-725.

Li, Y., Y. Shi, Y. Song, J. Du, R. Tuberosa, and T. Wang. (2004) Analysis of genetic diversity in maize inbred lines based on AFLP markers. Maydica 49:89-95.

Lorenz A. J., Smith K., Jannink J.-L., (2012) Potential and optimization of genomic selection for Fusarium head blight resistance in six-sow barley. Crop Sci. 52: 1609–1621

Madden LV, Hughes G, van den Bosch F (2007) The study of plant disease epidemics(APS Press, St. Paul, MN), p 432.

Melania, M. D. and Carena, M. J. (2005) Alternative maize heterotic patterns for Northern Corn Belt. Crop Science, 45: 2186-2194.

Manwiller, A., W.K.K. Mmatta & T. Ambeta (1985) Breeding Hybrid maize at Muguga. Record of Research. KARI Annual Report 61-62.

Martin M., Miedaner T., Dhillon B. S., Ufermann U., Kessel B., et al. , (2011) Colocalization of QTL for gibberella ear rot resistance and low mycotoxin contamination in early european maize. Crop Sci. 51: 1935–1945.

Mbithi, L.M. (2000), Agricultural policy and maize production in Kenya: Universiteit Gent,Unpublished Ph.D Thesis.

Melchinger, A.E., R.K. Gumber. (1998) Overview of heterosis and heterotic groups in agronomic crops. pp. 29-44. In K.R. Lamkey, J.E. Staub (ed.), Concepts and breeding of heterosis in crop plants. CSSA, Madison, WI.

Melchinger, A. E. (1999) Genetic diversity and heterosis. In: Coors, J. G. and Pandey, S. (Eds). The genetics and exploitation of heterosis in crops. American society of Agronomy/crop Science Society of America Inc., Madison, Winconsin, pp 99-118.

Menkir, A., Berhan, M., Ingelbrecht, C. L and Adepoju, A. (2004) Grouping of tropical midium altitude maize inbred lines on the basis of yield data and molecular analysis. Theoretical Applied Genetics, 108: 1582-1590.

Mendes UC, Miranda-Filho JB, Oliveira AS and Reis EF (2015) Heterosis and combining ability in crosses between two groups of open-pollinated maize populations. Crop Breeding and applied Biotechnology 15: 235-243.

Messmer M. M., Melchinger A. E., Boppenmaier J., Brunklaus-Jung E., Herrmann R. G., (1993) Relationship among early European maize inbreds: I. Genetic diversity among Flint and Dent lines revealed by RFLPs. Crop Sci. 32: 1301–1309.

Meuwissen T. H., Hayes B. J., Goddard M. E., (2001) Prediction of total genetic value using genome-wide dense marker maps. Genetics 157: 1819–1829 Nadeau C., Bengio Y., 2003. Inference for the generalization error. Mach. Learn. 52: 239–281.

Nicholoson, R. L. and H. L. Warren,(1975) Criteria for evaluation of resistance to Maize anthracnose. Phytopathology 66:86-66.

Nyoro, J., Kirimi, L and Jayne, T.S. (2004), “Competitiveness of Kenyan and Ugandan maize production: Challenges for the future”,Working Paper 10,Egerton University, Tegemeo Institute, Nairobi.

Parentoni, S. N., Magalhaes, J. V., Pacheco, C. A. P., Santos, M. X., Abadie, T., Gamap, E. E. G., Guimavaes, E. O., Meirelles, M. F., Lopes, M. A., Vasconcelos, M. J. V. and Paiva, E. (2001) Heterotic groupings based on yield- specific combining ability data and phylogenetic relationship determined by RAPD markers for 28 tropical maize open pollinated varieties. Euphytica, 121: 197-208.

Pataky, J. K. (1994) Effects of races 0 and 1 of *Exserohilum turcicum* on sweet corn hybrids differing for Ht-and partial resistance to northern leaf blight. Plant Dis.78:1189-1193.

Payak, M.M. and Sharma, R.C. (1985) Maize diseases and their approach to their management. *Tropical Pest Management*, 31: 302-310.

Pedersen, W. L. and M. G. Oldham. (1992) Effect of three tillage practices on development of northern corn leaf blight *Exserohilum turcicum* under continuous corn. Phytopathology 76:1161-1164.

Perkins J. M., Pedersen W. L., (1987) Disease development and yield losses associated with northern corn leaf blight on corn. Plant Dis. 71: 940–943.

Pixley, K. and Banziger, M. (2001) Open-pollinated maize varieties. A backward step or valuable option for farmers? Integrated Approaches to higher maize productivity in the new millennium. Proceedins of the seventh Eastern and Southern Africa Maize Regional Conference. 5-11 February, 2001. Nairobi, Kenya: CIMMYT and KARI, 2001: 22-28.

Poland J. a., Bradbury P. J., Buckler E. S., Nelson R. J., (2011) Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. Proc. Natl. Acad. Sci. USA 108: 6893–6898.

Pratt, R. C., E. Adipala, and P. E. Lipps, (1993) Characterization of race-specific resistance to *Exserohilum turcicum* races 0 and 1 in maize OhS0 S1 progenies.Plant Dis. 77:1227-1232.

Pratt RC, Gordon SG (2005) Breeding for resistance to maize foliar pathogens. Plant Breeding Reviews, ed Janick J (John Wiley & Sons, Oxford), pp 119–173.

Rawlings, J.O. and D.L. Thompson, (1962) Performance level as criterion for the choice of maize testers. *Crop Sci.* 2: 217-220.

Raymundo, A. D. (1978) Epidemiology of northern corn leaf blight as affected by host resistance and yield losses following simulated epidemics. Ph.D.Thesis, University of Illinois, Urbana -Champaign. 111pg.

Raymundo A. D., Hooker A. L., (1981) Measuring the relationship between northern corn leaf blight and yield losses. Plant Dis. 65: 325–327

Rebourg C., Chastanet M., Gouesnard B., Welcker C., Dubreuil P., et al., (2003) Maize introduction into Europe: the history reviewed in the light of molecular data. Theor. Appl. Genet. 106: 895–903.

Reif, J.C., A.R. Hallauer, A.E. Melchinger. (2005) Heterosis and heterotic patterns in maize. Maydica 50:215-223.

Riedelsheimer C., Czedik-Eysenberg A., Grieder C., Lisec J., Technow F., et al., (2012) Genomic and metabolic prediction of complex heterotic traits in hybrid maize. Nat. Genet. 44: 217–220.

Rutkoski J., Benson J., Jia Y., Brown-Guedira G., Jannink J.-L., et al., (2012) Evaluation of genomic prediction methods for fusarium head blight resistance in wheat. Plant Gen 5: 51–61.

Shakoor, M. S., Akbar,M., & Hussain, A. (2007) Correlation and path coefficients studies of some morphophysiological traits in maize double crosses. *Pak. J. Agri. Sci., 44*(2), 213-216.

Sharma D., and Aujla S.S. (1968). *J. Res. Punjab Agric.Univ. Ludhiana* 5: 501-504.

Sharma, S.M., S. Narwal, R. Kumar and S. Dass, (2004) Lin x tester analysis in maize (*Zea mays* L.). *Forage Res.* 30: 28-30.

Sharma, P., Khoyumthem, P., N. B. and Singh, N. K. (2005) Combining ability and gene action for quality studies in Basmati rice (Oryza sativa L.). Indian Journal of Genetics, 65(4): 290-292.

Shushay, W., Abrha, H. Z., Zeleke & Gissa, D. W. (2013) Line × tester analysis of maize inbred lines for grain yield and yield related traits. Asian Journa of Plant Science Research 3(5).

Singh, Rajesh; Mani, V.P.; Koranga, K.S.; Bisht, G.S.; Khandelwal, R.S.; Bhandari, P. and Pant, S.K. (2004) Identification of additional sources of resistance to *Exserohilum turcicum* in maize (Zea mays L.*). SABRAO Journal of Breeding and Genetics.* 36 (1) 45-47.

Singh, R.K. and B.D. Chaudhary. (1979) Biometrical methods in quantitative genetic analysis. Kalyani publs. Pp: 127-223.

Slopeck, S. W. (1989) An improved method of estimating percent leaf area diseased using a 1 to 5 disease scale. Can. J. Plant Pathol. 11:381-387.

Solomonovich, S. Levy Y., and J. K. Pataky (1992). Yield losses in sweet corn hybrids in response to defoliation and infection by *Exserohilum turcicum.* Phytoparasitica 20(2):113-121.

Sprague, G. F. and Tatum, L. A. (1942) General Vs Specific Combining ability in single crosses of corn. Journal of American Maize Society of Agronomy, 34: 923-932.

Technow F., Riedelsheimer C., Schrag T. A., Melchinger A. E., (2012) Genomic prediction of hybrid performance in maize with models incorporating dominance and population specific marker effects. Theor. Appl. Genet. 125: 1181–1194.

Troyer AF (2006) Adaptedness and heterosis in corn and mule hybrid. Crop Science 46: 528-543.

Uddin, M. S., F. Khatun, S. Ahmed, M. R. Ali and S. A. Bagum (2006) Heterosis and Combining Ability in Field Corn (*Zea mays* L.). *Bangladesh J. Bot.* **35** (2): 109-116.

Ullstrup, A. J. (1970) A comparison of monogenic and polygenic resistance to *H. turcicum* in corn. Phytopathology 60:1597-1599.

Vacaro, E., Barbosa-Neto, J, F., Pegoraro, D. G., Nuss, C. N. and Conceicano, L. D. H. (2002) Combining ability of twelve maize populations. Pesquisa-Brasileira, 37: 67-72.

Van Inghelandt D., Melchinger A. E., Martinant J.-P., Stich B., (2012) Genome-wide association mapping of flowering time and northern corn leaf blight (*Setosphaeria turcica*) resistance in a vast commercial maize germplasm set. BMC Plant Biol. 12: 56.

VanRaden P. M., 2008. Efficient methods to compute genomic predictions. J. Dairy Sci. 91: 4414–4423

Venkatesan, M., Anbuselvam, Y., Elangaimannan, R. and Karthikeyan, P. (2007) Combining ability for yield and physical characters in rice. Oryza, 44(4): 296-299.

Vivek, B. S., Kasango, J. S., Chisoro, S. and Magorokosho, C. (2007) Fieldbook: Software for managing maize breeding program: A Cookbook for handling field experiments, data, stocks and pedigree information. CIMMYT, pp 12-30.

Weber K. L., Thallman R. M., Keele J. W., Snelling W. M., Bennett G. L., et al., (2012) Accuracy of genomic breeding values in multi-breed beef cattle populations derived from deregressed breeding values and phenotypes. J. Anim. Sci. 10.2527/jas.2011–4586

Welz HG, Geiger HH (2000) Genes for resistance to northern corn leaf blight in diverse maize populations. Plant Breed 119(1):1–14.

Wisser R. J., Balint-Kurti P. J., Nelson R. J., (2006) The genetic architecture of disease resistance in maize: a synthesis of published studies. Phytopathology 96: 120–129