

International Journal of

# Agriculture

*(IJA)*

## **YIELD OF THE TESTCROSSES ACROSS THE DIFFERENT ENVIRONMENTS**

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



## YIELD OF THE TESTCROSSES ACROSS THE DIFFERENT ENVIRONMENTS

<sup>1</sup>\*Felista Wanjiku Ndung'u

<sup>1</sup>Post Graduate Student: Kenyatta University

\*Corresponding Author's Email: [ndungu.nfelista@gmail.com](mailto:ndungu.nfelista@gmail.com)

<sup>2</sup>Dr. Wilson M Thagana

Lecturer: Kenyatta University, Nairobi, Kenya

<sup>3</sup>Dr. David Kamundia Ndungu

Chief Officer-Agriculture: Kiambu County Government

### Abstract

**Purpose:** The main purpose of this paper was to determine the yield of the testcrosses across the different environments.

**Methods:** The lines used in the study were derived from a segregating population in the F<sub>4</sub>. 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<sub>4</sub> 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).The yield was evaluated by analyzing the grain weight of the crosses using CIMMYT IMIS field book. The data collected for NLB and other yield related traits was analyzed using the CIMMYT META R and AGD R (2015). In the analysis, lines, plots and site were used as fixed factors. Replications, incomplete blocks were used as random factors

**Results:** The study found out that the maize crosses exhibited different yield performance across the three locations even under similar agronomic management practices. Testcrosses developed with Tester A recorded higher yields in Kakamega and Embu while in Muranga the crosses developed from Tester B recorded higher average yields.

**Unique Contribution to Theory, Practice and Policy:** The study recommended that The top performing crosses could hence be subjected to further trials hence recommended for high yielding varieties in best suited regions in the country. The lines could further be developed to breed for high performing hybrids that would be best suited for different agro-ecological zones across the country in different combinations.

**Key Words:** *Yield, Testcrosses, Environments*

## 1.0 INTRODUCTION

### 1.1 Yield potential of the crosses in t/ha

Maize is a staple to over 85% of the Kenyan population. Individual consumption ranges at 98-100 kilograms that is an estimate of 2700 thousand metric tonnes annually (Nyoro *et al.*, 2004). Small scale growers account for 70% of the total production. The other 30% is from large scale growers (Export processing zone Authority, 2005).

Most of the crop is grown for subsistence by the small scale growers who then retain some 58% for household use from the total output (Mbithi, 2000). With the annual consumption requirement annually, deficits have to be acquired through importation. Unsuitable weather conditions are mostly said to be the cause for low yields in some years. However, average yields have been at a constant average of 2 tonnes per hectare which is below the 6 tonnes per hectare which should be the potential. This has been attributed to inadequate uptake of technology which includes planting of high yielding hybrid seed maize, lack of fertilizer use to avoid incurring high input costs and lack of credit (Republic of Kenya, 1997; 2004; Kangethe, 2004).

Lack of credit impacts inadequate capital hence farmers cannot afford to procure inputs which include certified seed, fertilizers and pesticides. Kenya incurs higher costs of production than other maize growing regions of other countries. This hence impacts negatively the maize surplus due to cheaper imports from other countries like Uganda (Nyoro *et al.*, 2004).

Maize yield is highly determined by growth and development of the plant, photosynthesis and the efficiency of the photosynthate partitioning into grain. Yield is also as a result of interaction between genotype, environment and management (Fageria *et al.*, 2006). The environmental factors of importance are water, temperature and solar radiation. The factors vary with the different growing seasons and cannot be controlled by the growers. Maize growth could be Subdivided into two growth stages, the vegetative growth and the reproductive growth stages. The vegetative stage growth occurs between seedling emergence and vegetative growth stage. After the maize crop reaches physiological maturity, environmental stress does not affect yield. Factors such as lodging, stalk breakage and ear dropping can damage the plant and decrease the harvestable yield.

Yield comprises of physical elements that correlate to the produced grain directly. These components are interrelated and have compensatory effects. The primary components which are the first order yield traits (number of ears, number of kernels, kernel weight) effects directly impact on the final yield and also the yield components whose effects are indirect that may develop later (Fageria *et al.*, 2006).

Genotype by Environment interactions in maize breeding are challenging as they are an indication of failure in genotypes consistent response across different environmental conditions. On the basis of diverse biotic and abiotic factors, Africa's maize production environments vary. Africa is variable. This hence results in GxE interactions that are complex for important traits disease resistance and yield (Vivek *et al.*, 2010; Sibiyi *et al.*, 2012). Identification of stable genotypes for wide range of environments is the best way in minimizing GxE interactions. Presence of the interactions could also be exploited by selection of superior genotypes to suit specific environments (Alwala *et al.*, 2010).

When variations caused by hybrid x environment are partitioned into GCA x E and SCA x E, both the components are mostly significant for yield and other agronomic components. It is an indication that the GCA of the parent lines and SCA of the hybrids change with environments. Apart from identifying crosses that are high yielding, it is important to identify parent lines that possess not only high grain yield means but also with high stability for GCA effects for adjustment of environmental changes (Fan *et al.*, 2013).

## **2.0 METHODOLOGY**

The lines used in the study were derived from a segregating population in the F<sub>4</sub>. 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<sub>4</sub> 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).The yield was evaluated by analyzing the grain weight of the crosses using CIMMYT IMIS field book. The data collected for NLB and other yield related traits was analyzed using the CIMMYT META R and AGD R (2015). In the analysis, lines, plots and site were used as fixed factors. Replications, incomplete blocks were used as random factors.

## **3.0 RESULTS**

### **3.1 Yield of the testcrosses across the environments in tonnes per hectare**

**Table 1: Yield of the testcrosses across the environments in tonnes per hectare**

Line	Kakamega		Embu		Muranga	
	Tester A	Tester B	Tester A	Tester B	Tester A	Tester B
1	4.94	3.29	4.47	3.94	8.16	10.25
2	5.38	2.08	6.08	3.64	8.18	7.42
4	3.89	2.26	5.16	2.75	5.98	8.37
5	5.43	3.87	5.49	3.66	7.68	7.95
9	5.71	3.84	5.55	2.73	9.21	8.50
12	5.13	3.55	6.93	4.36	6.27	8.40
17	5.19	3.18	5.69	4.19	4.72	8.82
18	5.34	2.17	6.14	2.69	5.02	8.23
19	5.23	3.48	4.33	4.28	6.02	10.32
24	5.42	2.94	5.08	4.42	8.02	8.89
26	3.27	2.83	3.78	5.06	4.30	8.53
27	4.79	2.58	6.89	5.32	7.45	7.98
29	4.98	3.00	5.52	5.51	8.69	8.67
31	4.46	3.88	5.59	4.51	8.50	8.47
32	5.37	3.99	4.65	3.58	6.19	8.24
33	4.47	3.64	5.18	4.51	8.42	8.43
34	5.05	4.63	4.66	5.45	8.42	8.54
35	4.65	4.38	4.66	4.00	8.59	8.18
38	4.99	4.07	7.20	4.43	6.56	8.96
40	3.37	4.26	5.29	3.46	6.87	8.30
41	4.39	3.46	5.39	3.57	8.18	8.64
43	4.72	4.63	5.63	5.17	7.67	7.84
44	5.38	4.12	3.38	5.18	5.88	8.53
45	4.90	4.02	6.66	3.41	9.31	7.68
46	6.17	3.74	4.06	2.09	6.83	8.58
47	4.04	4.97	4.81	5.82	4.09	8.95
48	4.52	2.99	5.44	3.10	6.56	9.03
50	5.47	3.63	6.37	3.13	7.26	8.46
51	3.52	3.05	5.12	4.38	3.99	8.99
52	4.61	3.44	3.18	1.93	7.03	7.21
53	4.32	3.99	4.27	3.53	7.25	8.57
54	4.48	3.01	4.86	2.85	6.34	8.20
58	5.32	4.78	3.03	4.45	6.50	8.59
61	3.65	4.64	3.94	3.74	8.52	9.02
62	6.10	4.39	6.11	4.60	6.22	7.17
63	3.65	4.65	3.88	3.95	3.12	9.00
66	4.29	3.03	4.75	4.21	8.02	7.96
67	3.65	2.67	4.95	2.21	2.17	7.58
69	4.85	2.73	4.57	5.39	7.55	8.90
71	4.28	3.70	5.94	2.42	7.56	8.19
72	3.43	2.36	4.21	2.42	7.62	8.00
73	4.37	2.31	5.29	2.44	9.73	10.13
74	3.09	2.49	7.34	3.37	7.68	9.47
75	4.99	2.23	6.60	1.61	7.37	9.50

76	4.41	3.32	5.39	3.88	6.37	9.07
78	5.33	3.21	5.29	2.77	8.97	7.93
79	5.53	3.25	5.88	5.04	9.33	7.99
81	5.33	5.51	6.29	4.06	5.68	8.88
87	3.38	1.86	5.82	3.52	7.71	8.00
Tester	2.07	2.68	2.62	5.31	6.29	6.18
<b>Mean</b>	<b>4.63</b>	<b>3.46</b>	<b>5.19</b>	<b>3.84</b>	<b>7.00</b>	<b>8.47</b>
<b>LSD (0.05)</b>	<b>1.72</b>	<b>1.75</b>	<b>2.33</b>	<b>2.45</b>	<b>0.98</b>	<b>1.53</b>
<b>Mse</b>	<b>1.19</b>	<b>1.42</b>	<b>1.53</b>	<b>1.65</b>	<b>0.24</b>	<b>0.69</b>
<b>CV</b>	<b>23.62</b>	<b>34.48</b>	<b>23.87</b>	<b>33.49</b>	<b>6.95</b>	<b>9.82</b>
<b>P</b>	<b>0.004</b>	<b>0.003</b>	<b>0.030</b>	<b>0.056</b>	<b>0.000</b>	<b>0.002</b>
<b>P</b>	**	**	*	+	***	**
<b>Min</b>	<b>2.07</b>	<b>1.86</b>	<b>2.62</b>	<b>1.61</b>	<b>2.17</b>	<b>6.18</b>
<b>Max</b>	<b>6.17</b>	<b>5.51</b>	<b>7.34</b>	<b>5.82</b>	<b>9.73</b>	<b>10.32</b>

### 3.2 Discussion

The testcrosses performed differently across the three locations due to G x E interactions.

#### Kakamega

The highest yielding cross in Kakamega was Tester A x L46 with a yield of 6.17t/ha. The second highest yielding was Tester A x L62 yielding 6.1t/ha. The highest yielding cross with Tester B was Tester B x L81. Overall performance of the crosses with tester A was higher than the crosses with tester B.

The highest yielding crosses with tester A yielded 6.17t/ha while the lowest with tester A yielded 2.07t/ha. The highest yielding cross with tester B yielded 5.51t/ha while the lowest yielded 1.86t/ha.

#### Embu

The highest yielding crosses with tester A in Embu yielded 7.34t/ha while the lowest had a yield of 2.62t/ha. The highest yielding cross with tester B had a yield of 5.82t/ha while the lowest had a yield of 1.61t/ha.

The top 10 highest yielding crosses in Embu were;

Tester A/Line 74- 7.34t/ha, Tester/line 12- 6.93t/ha, Tester/Line 27- 6.89t/ha, Tester/Line 45- 6.66t/ha, Tester/Line 75- 6.6t/ha, Tester A/Line 50- 6.37t/ha, Tester A/Line 81- 6.29t/ha, Tester A/Line 18- 6.14t/ha, Tester A/Line 62- 6.11t/ha and Tester A/Line 2- 6.08t/ha.

All the top best performing crosses were crosses with tester A.

#### Muranga

This region recorded the highest yield performance compared to Kakamega and Embu. The highest performing cross recorded a yield of 10.32t/ha. The lowest yielder for Muranga had a yield of 2.17t/ha. For the crosses with tester A, the highest yield was 9.73t/ha while the lowest was 2.17t/ha. For the tester B crosses, the highest yield recorded was 10.32t/ha while the lowest was 6.18t/ha.

While in the other regions tester A crosses were performing better, in Muranga the crosses with tester B were leading.

The top best performing crosses in Muranga were;

Tester B/Line 19- 10.32t/ha, Tester B/Line 1- 10.25t/ha, Tester B/Line 73- 10.13t/ha, Tester A/Line 73- 9.73t/ha, Tester B/Line 75- 9.5t/ha, Tester B/Line 74- 9.47t/ha, Tester A/Line 79- 9.33t/ha, Tester A/Line 45- 9.31t/ha, Tester A/Line 9- 9.21t/ha, Tester B/Line 76- 9.07t/ha, Tester B/Line 61- 9.02t/ha and Tester B/Line 63-9t/ha.

## **4.0 CONCLUSIONS AND RECOMMENDATIONS**

### **4.1 Conclusion**

The maize crosses exhibited different yield performance across the three locations even under similar agronomic management practices. Testcrosses developed with Tester A recorded higher yields in Kakamega and Embu while in Muranga the crosses developed from Tester B recorded higher average yields. According to Fageria *et al.* (2006), yield can be considered as a result of interaction between genotype, agronomic management and the environment.

### **4.2 Recommendations**

The top performing crosses could hence be subjected to further trials hence recommended for high yielding varieties in best suited regions in the country. The lines could further be developed to breed for high performing hybrids that would be best suited for different agro-ecological zones across the country in different combinations. Trethowan *et al.* (2001) recorded that plant breeders would need to understand the relationship between the yield testing environments in order to concentrate on germplasm that is well adapted to different production environments.

### **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 MJ (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 Genet*121(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: *KARI: Review of the National Maize Research Program*. Proceedings of a Workshop Held between November 19 and 23, 1991, Kakamega, Kenya. Kenya Agricultural Research Institute (KARI) 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. 2<sup>nd</sup> ed. Iowa State University press, Ames, Iowa. pp 26-40.
- Hallauer, A.R. and J.B. Miranda, (1988) Quantitative genetics in maize breeding. 2<sup>nd</sup> 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. Repr.* 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-row 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.
- Nicholason, 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., Lisek 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., Abhra, H. Z., Zeleke & Gissa, D. W. (2013) Line × tester analysis of maize inbred lines for grain yield and yield related traits. *Asian Journal 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
- Zeeshan, M., Ahsan, M., Arshad, W., Ali, S., Hussain, M., & Khan, M. I. (2013) Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays* L.) hybrids. *International Journal of Advanced Research*, 1(5), 24-29. Retrieved from <http://www.journalijar.com>
- Zhao Y., Gowda M., Liu W., Wurschum T., Maurer H. P., et al. , (2011) Accuracy of genomic selection in European maize elite breeding populations. *Theor. Appl. Genet.* 124: 769–776