

Review on Genetic Variability and Correlation of Yield and Yield Component Traits of Quality Protein Maize (*Zea mays L.*) Varieties

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ABSTRACT

Maize (*Zea mays L.*) belongs to the grass family *Poaceae* (*Gramineae*). It has a diploid number of twenty chromosomes ($2n = 20$). The present review objective was to review on genetic variability and correlation of yield and yield component traits of quality protein maize varieties. Maize is highly cross-pollinated plant. It is relatively easy to capture pollen from tassel and to prevent pollination by covering the extended pistils before they emerge. This aids in controlling pollination and making a planned crosses between quality protein maize plants. Generally, quality protein maize has high level of lysine and tryptophan amino acids that improve nutritional value of food to supplement the diet of human being. This review implies the importance of genetic variability in improvement of yield and yields components traits of quality protein maize through selection. Yield components were either negative or positive highly correlated with each other and grain yield for quality protein maize hybrids and open pollinated varieties. This review recommend that review potential quality protein maize varieties with high yielding and product quality could be used for quality protein maize breeding programs for grain yield component traits improvement.

Keywords: Amino acid, correlation, genotype, phenotype, protein, varieties

INTRODUCTION

Maize (*Zea mays L.*) belongs to the grass family *Poaceae* (*Gramineae*). Maize has a diploid number of twenty chromosomes ($2n = 20$) (Coulter *et al.*, 2010). It has a large genome with a total gene number of forty-two thousand to fifty-six thousand (Semagn, 2012). Maize is considered as the most important strategic cereal food crop in the world. Maize is cultivated on nearly one hundred fifty million hectares in in the world having wider diversity of soil fertility, soil ph value, climate condition, diversified varieties and management practices that contributes 36% in the world grain production (Coulter *et al.*, 2010).

The major maize producing countries were United States, China, Brazil, Ethiopia and Mexico account for 70% of world production (Pandey *et al.*, 2016). Maize is Ethiopia's leading cereal crop in terms of production with 3.1 tons produced by one hectare of land (CSA, 2013). In terms of cultivated area, it is the second most widely cultivated crop next to teff. Normal maize is different from quality protein

maize in terms of nutritional contents. Ethiopian farmers grow quality protein maize for subsistence with 75% of all quality protein maize output consumed by farming households and for economic development in the country (CSA, 2013). It is a primary source of energy supplement that contribute up to 60% of energy, 30% of protein and 90% of starch in human diet (Coulter *et al.*, 2010).

The o_2 mutation was found to be the most suitable for genetic manipulation in breeding programs aimed at developing maize high in lysine and tryptophan (Novacek *et al.*, 2013). Maize homozygous for the recessive (o_2) mutation was shown to have substantially higher lysine and tryptophan content than maize that was either homozygous dominant (O_2O_2) or heterozygous (O_2o_2) for the opaque-2 locus. The opaque-2 maize kernels were dull and chalky had 15-20% less grain weight and were more susceptible to several diseases and insects. These obstacles made most research programs to stop their work on opaque-2 (Novacek *et al.*, 2013).

Therefore, the present review objective was to review on genetic variability and association of yield and yield component traits of quality protein maize varieties.

LITERATURE REVIEW

Origin and Distribution of Quality Protein Maize

Quality protein maize originated from Mesoamerica by artificial selection converted from a low yielding progeny into high yielding forms, with a large cob of female inflorescence bearing up to thousand seeds (Gambin *et al.*, 2006). The center of origin for *Zea mays* has been established as Mesoamerican region, now Mexico and Central America (Gambin *et al.*, 2006). Quality protein maize spread around the world after European discovery in the fifteenth century (Pandey *et al.*, 2016). The early American civilizations were based on quality protein maize which made settled life possible (Pandey *et al.*, 2016).

Botanical Description of Quality Protein Maize

Quality protein maize is a thick-stemmed annual grass with a single stem, one to five meters tall with one or more tillers (Pandey *et al.*, 2016). Quality protein maize has a diameter between five and six centimeters (Gemechu *et al.*, 2016). Quality protein maize is woody and filled with sweet pith, internodes and nodes that around 20cm each length. Quality protein maize has shallow, fibrous roots that grow to a depth of 40cm (Gemechu *et al.*, 2016). Aerial, adventitious roots form at the nodes and the base of the stem. Quality protein maize leaves are large up to 10cm wide, 50cm long and sheath-like at their base and extended blade in the shape of a strip with parallel veins. Under these leaves and close to the stems, the ears grow (Jean du Plessis, 2003). Quality protein maize is monoecious and diclinous with male and female inflorescences born separately on the same maize plant (Gemechu *et al.*, 2016).

Human intervention in the development of quality protein maize as a crop is aided by the fact; quality protein maize is a monoecious crop with separate male and female flower structures borne on the same maize plant (Pandey *et al.*, 2016). Pollens are dispersed by wind, making maize highly cross-pollinated. At the same time, it is relatively easy to capture pollen from the tassel and to prevent pollination by covering the extended pistils before they emerge (Gemechu *et al.*, 2016). This aids in controlling pollination

and making a planned crosses between quality protein maize (Pandey *et al.*, 2016).

Taxonomy of Maize

Maize belongs to tribe Maydeae of the grass family Poaceae. The genus *Zea* consists of species including *Zea diploperennis*, *Zea perennis*, *Zea luxurians*, *Zea nicaraguensis* and *Zea mays* (Ali *et al.*, 2014). The species *Zea mays* is divided into subspecies like *huehuetenangensis*, *mexicana*, *parviglumis* and *mays* of which the subspecies *mays* are economically important. The other subspecies are teosintes which are wild grasses in Mexico and Central America. Hypothesis on origin of maize proposed that maize was produced by natural hybridization between two wild grasses of *Tripsacum* and a perennial subspecies of teosinte (Pandey *et al.*, 2016).

Production of Quality Protein Maize

Quality protein maize is a cereal crop which is cultivated widely throughout the world and highest production among all cereals (Pandey *et al.*, 2016). Quality protein maize is staple food in Ethiopia and used in animal feed. Quality protein maize has genetic variability, which enables it to thrive in tropical, subtropical and temperate climate condition. Quality protein maize is the most versatile crops having wider adaptability under varied agro-climatic conditions. Quality protein maize is known as queen of cereals, because it has the highest genetic potential of yield among cereal crops. United States of America is the largest producer of quality protein maize and contributing nearly 35 % of total production in the world (Ali *et al.*, 2014). Brazil and Argentina are quality protein maize producing countries after United States of America.

Quality protein maize is Ethiopia's major cereal crop in terms of total production and number of farm holdings (Ali *et al.*, 2014). Quality protein maize as a processed form, it is used as fuel like ethanol and starch. Starch in turn involves enzymatic conversion into products such as sorbitol, dextrine and lactic acid and appears in household items such as beer, ice cream, syrup, batteries, mustard, cosmetics, aspirin and paint (Jean du Plessis, 2003). Selection produced quality protein maize that can grow up to 5m height that contains 800-1000 kernels covered by modified leaves that protect the kernels from desiccation (Gemechu *et al.*, 2016).

Quality Protein Maize Production Constraints

Farmers expressed drought as major abiotic constraint to quality protein maize production in all regions (Rosegrant *et al.*, 2009). Drought was a concern even in primarily irrigated systems due to periodic uncertainty regarding water and time availability. Farmers in Ethiopia also identified floods, soil erosion and soil infertility as negative impacts on quality protein maize productivity. Traditional planting, lodging and weeding practices are labor intensive and have impact on productivity of quality protein maize (Gemechu *et al.*, 2016).

Farmers in Ethiopia identified wide range of biotic constraints to quality protein maize production like insect pests, including corn borer, cutworm and corn leaf aphid, which were common across all agro-ecological regions (Novacek *et al.*, 2014). White grubs, stem borers and termites were major maize field insects in all agro-ecologies. Aphid, locust, red ant and tassel beetle were also reported by farmers due to their substantial yield loss (Gemechu *et al.*, 2016). Grain weevils and rodents were the primary cause of post-harvest storage losses across quality protein maize agro-ecological regions. Quality protein maize production also faced a great obstacle due to reported disease causing viruses. Diseases identified by farmers included head smut, turicum blight, downy mildew and banded leaf and sheath blight (Novacek *et al.*, 2013).

Nutritional Evaluation and Utilization of Quality Protein Maize in Ethiopia

Quality protein maize is a major source of energy supplement that contributes to 30% of protein, 60% of energy and 90% of starch in human's diet (Novacek *et al.*, 2014). Therefore, utilization of quality protein maize can correct this deficiency. As researchers have compared the chemical composition of QPM with NM, the percentage lysine content of QPM varies between 0.33 and 0.54 with an average of 0.38 (Gemechu *et al.*, 2016). The amino acid profiles show that higher levels of arginine, cysteine, tryptophan and lysine than NM, while the level of methionine in QPM was less than in NM (Ali *et al.*, 2014). This review indicated that the energy available from quality protein maize is higher than from normal maize.

Availability of protein and amino acids were in quality protein maize higher than in normal maize (Novacek *et al.*, 2014). This review

shows that significant difference in apparent and true digestibility of amino acids between quality protein maize and normal maize. On the other hand, normal maize is low in protein in addition to its general deficiency in essential amino acids, particularly lysine and tryptophan. Nutritional review of quality protein maize in various countries has proved the superiority of quality protein maize over normal maize in the feeding of various animals (Ali *et al.*, 2014). This review show that animals and humans had high lysine and tryptophan maize gained weight twice the rate of animals and human food on normal maize without additional protein supplements. This review was shown that children fed with high lysine and tryptophan maize were healthier and reduced stunting and better growth enhancing capabilities, compared with children fed normal maize.

Genetic Variability of Quality Protein Maize

The development of high lysine and tryptophan maize involves manipulating three distinct genetic systems (Gambin *et al.*, 2006). These are recessive allele of the opaque-2 gene (*o2o2*), modifiers of *o2o2* that containing endosperm to confer higher lysine and tryptophan and genes that modify the opaque-2- induced soft endosperm to hard endosperm (Gambin *et al.*, 2006). The recessive allele of opaque-2 gene is central component of the genetic variability that confers high levels of lysine and tryptophan in maize endosperm protein. The *o2* allele is inherited in a simple recessive manner (Ali *et al.*, 2014).

The presence of *o2* in the homozygous recessive state (*o2o2*) is pre-requisite for entire process of obtaining high lysine and tryptophan maize. The presence of *o2* gene in different maize genotypes changes the relative share of protein fractions and change quality. The enhancers consist of minor modifying loci that effect lysine and tryptophan levels in the endosperm. The *o2* mutation and the enhancers are by themselves, not sufficient to develop agronomical acceptable quality protein maize with high lysine and tryptophan (Gambin *et al.*, 2006).

Phenotypic Variability of Quality Protein Maize

Variation is the occurrence of differences among individuals due to differences in their genetic composition and the environment in which they are raised (Gambin *et al.*, 2006). If

the character expression of two individuals measured in an environment different for both differences in expression would result from environment control, such variation called phenotypic variation (Gambin *et al.*, 2006). Phenotypic variation due to genotype was inherited for phenotypic traits of quality protein maize. Phenotypic variability in quality protein maize is representative of the phenotypic diversity that exists in the inbred lines that mature in growing environment (Egli, 2011). Quality protein maize phenological traits, both the upper and lower limit of variation were expanded for plant height, ear length, uppermost internode with a developed ear, number of internodes above the uppermost ear, leaves with epicuticle wax and percentage of leaves with no epicuticle wax (Egli, 2011). The lower limit of variation was expanded for days to flowering, kernel weight and leaf number.

Measurement of Genetic Diversity of Quality Protein Maize

The most central quality measurement of quality protein maize are protein, oil and starch (Egli, 2011). The chemical concentrations quality protein maize were assessed for various nutrients and amino acids including the physical quality parameters like softness of endosperm, density and kernels mashing of the grain (Milander *et al.*, 2015). The chemical quality maize parameters were focused on nitrogen, phosphorus, potassium, calcium and magnesium from macro nutrient while zinc, copper and manganese among micro elements with lysine and tryptophan as well as lipid (Egli, 2011). Increasing plant density would reduce the physical quality like biomass weight, kernel density and kernel weight. This review confirmed that quality protein maize homozygous recessive *o2* mutation has extensively higher lysine and tryptophan content than both heterozygous (*O2o2*) and homozygous dominant (*O2O2*) for the opaque-2 locus.

Heritability

Heritability is proportion of total variation caused by genotype. It is very difficult to determine the presence, amount and types of genetic variability if phenotypic expressions are influence by the environment (Egli, 2011). Heritability in broad sense is the proportion of the total genetic variability to the total phenotypic variance. Since broad sense, heritability does not give a clear sense of transmissibility of variation from generation to

generation (Mohammedi, *et al.*, 2003). Because, genetic variation includes the fixable and non-fixable variation, its utilization is limited in quality protein maize improvement. Heritability in narrow sense is the ratio of additive genetic variance to phenotypic variance (Mohammedi, *et al.*, 2003). Heritability values for quantitative characters are low due to their sensitivity to environment effect. The greater the proportion of total variability is due to the environment more difficult to select for inherited differences of quality protein maize (Egli, 2011). Heritability enables the plant breeder to recognize genetic difference among strains and variance indicates for improvement of population of quality protein maize (Hailu *et al.*, 2015). As reported by Hailu *et al.*, (2015) broad sense heritability estimate was ranged from 24.44 for anthesis-silking interval to 96.02 for 1000-kernel weight. Higher heritability estimates were scored for 1000-kernel weight (96.02), leaf length (74.79), plant height (69.47), days to 50% anthesis (69.46), days to 50% silking (68.75), leaf width (64.70), ear length (64.62) and leaf area (63.95) (Hailu *et al.*, 2015). Moderate heritability estimates were observed for grain yield per hectare (58.42), ear height (52.99) and days to maturity (50.07), number of kernels per row (47.38) and kernel per ears (32.26) (Oppong *et al.*, 2014). High heritability estimates suggest selection of such character could be fairly easy (Oppong *et al.* 2014). Therefore, 1000-kernel weight, leaf length, plant height, days to 50% anthesis, days to 50% silking, leaf width and leaf area could easily be passed from one generation to the next generation that enhancing the efficiency of selection in quality protein maize improvement program (Hailu *et al.*, 2015). This indicated that the traits are under genetic control and environmental factors did not greatly affect their phenotypic variation. Moderate heritability estimates were observed for grain yield per hectare, ear length and days to maturity, number of kernels per row and kernel per ear indicating these traits may respond positively to phenotypic selection (Hailu *et al.*, 2015).

Genetic Advance

Improvement in mean genetic value of selected quality protein maize over the base population is usually termed as genetic advance under selection. Muli *et al.* (2016) reported that genetic advance as percent of mean (GAM) at 5% selection intensity ranged from 2.76% for days to maturity to 50.69% for grain yield per

hectare. There was high genetic advance expressed as a percent of mean for traits like grain yield (50.69%), 1000-kernel weight (39.44%), ear length (25.13%) and plant height (22.64%) (Muli *et al.*, 2016). On the other hand, traits like number of kernels per row (20.00%), ear diameter (19.79%), leaf area (19.01%), anthesis-silking interval (16.72%), leaf width (15.67%) and leaf length (13.21%) had moderate genetic advance as percent of mean and the traits like days to 50% anthesis (7.47%), days to 50% silking (6.86%) and days to 90% maturity (2.76%) had low genetic advance as percent of mean (Hailu *et al.*, 2015).

Genetic advance as percentage of mean was higher for traits such as grain yield per hectare, 1000-kernel weight and ear length showing that these traits are under control of additive gene action. On the other hand, Muli *et al.* (2016) that reported high genetic advance for plant height, kernel per ears, 1000 kernel weight, ear height and grain yield per hectare. The traits like days to maturity and days to 50% silking indicated low values of genetic advance as percent of mean and which correspondingly indicated low value of genetic variation for traits as indicated by low GCV and PCV values (Muli *et al.*, 2016).

This review implies the importance of genetic variability in improvement of quality protein maize through selection. As reported Mbuya *et al.* (2011), the yield for inbred line CML359 was 5521 kg/ha.

Therefore, whenever the best 5% high yielding inbred lines is selected as a parent, mean grain yield could be improved by 2798.61 kg/ha. As a review, mean genotypic value of the new population of grain yield would be improved from 5521 to 8319.61 kg/ha per one selection cycle for the line CML359. The present review revealed high heritability consideration coupled with high expected genetic advance as percent of mean for kernel weight, ear length and plant height moderate heritability estimates with higher genetic advance. This indicated these traits could be improved more easily than the other traits through simple selection.

Therefore, even if heritability estimates provide the basis for selection on phenotypic performance, the heritability estimates and genetic advance should be always considered simultaneously, as high heritability is not always associated with high genetic advance (Semagn *et al.*, 2012).

Importance of Genetic Diversity for Quality Protein Maize improvement

Genetic enhancement strategy of quality protein maize has been started when it started to be domesticated and produced allelic diversity. Segregation nature of quality protein maize was improved by selection and introduce into recombination and mutation contributed to variability in maize germplasm. Landraces of quality protein maize is used in maize improvement as reported by Semagn *et al.* (2012). A landrace is dynamic populations of cultivated maize that has distinct identity, genetically diverse, locally adapted and associated with traditional farming systems (Semagn *et al.*, 2012).

Landraces have been characterized using various morphological characters. With the advent of DNA-based markers, characterization using molecular markers is preferred choice, mainly due to their abundance and environment-neutral behavior. However, landraces being heterogeneous in nature, large number of individuals in each of accessions are required to be genotyped (Sharma *et al.*, 2010). A minimum of fifteen individuals are required to be characterized allelic diversity present in a population of quality protein maize. The natural variability of landraces has been exploited for various biotic stress resistance, abiotic stress tolerance and quality protein improvement of quality protein maize (Sharma *et al.*, 2010). Sequencing of primitive' landrace would further provide insight into the genome architecture, the regulation of major genes responsible for its primitive nature and would in turn help in understanding its evolution and devising strategies for better utilization of the valuable landraces in the breeding programme (Sharma *et al.*, 2010).

Quality Protein Maize Breeding Program in Ethiopia

The major objective of quality protein maize breeding is to create new and improved genotypes with features that contribute to greater yield potential, increased yield stability and improved product quality. Quality protein maize landraces composed of maize varieties developed by farmers through natural and artificial selection is adapted to local environmental conditions and management (Semagn *et al.*, 2012). The major breeding approach for increasing productivity is production of hybrids using heterosis breeding.

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Success of this method depends on development and identification of suitable inbred lines using an appropriate mating design and selection of most promising heterotic normal maize hybrid (Sharma *et al.*, 2010). For the production of quality protein maize hybrid, the ultimate aim is to combine the advantage of heterosis with amino acid composition using quality protein maize donors. The quality protein maize donor inbred developed through intra-population selection for genetic modifiers in opaque-2 backgrounds and used for conversion of non-quality protein maize inbred to their quality protein maize version.

At CIMMYT, a conservative approach is adapted to develop modified opaque 2 genotypes to balance between protein level, grain quality and yield amount. Gupta *et al.* (2013) was reported to distinct polymorphism by primers can discriminate quality protein maize donors from respective non-quality protein maize parents between homozygous (o2o2) and heterozygous (o2o2) opaque-2 back crosses progeny.

This paves the way for rejection of non-target back cross progenies to eliminate the need to grow F2 that save labor and material resources for amino acid development (Gupta *et al.* 2013). Research programs on breeding for high quality protein maize were stimulated during the discovery of o2o2 mutants. Backcrossing was used for mass conversion of standard maize inbred lines into opaque-2 variants, with their combination abilities for yield and other important agronomical traits (Sharma *et al.*, 2010). In breeding method and approach used

two unique and essential steps in the development of quality protein maize germplasm (Sharma *et al.*, 2010).

The first is to simultaneously identify segregants in a family or population having the o2 allele in homozygous recessive (o2o2) condition with a hard endosperm. The second step is to identify and confirm quality protein maize percentage of tryptophan and protein in a sample, through laboratory analysis (Vivek *et al.*, 2008).

Correlation of Yield and Yield Component Traits of Quality Protein Maize

Yield components were highly correlated with grain yield for quality protein maize hybrids (Sharma *et al.*, 2010). Number of ears per plant was highly positive correlated with grain yield. Kernels per ear, kernels per row, ear circumference and ear length were highly positively correlated with grain yield of quality protein maize. Cox *et al.* (2006) was reported that the number of kernels per ear had highly positive correlated with ear length and ear circumference. Kernel weight had highly positively correlated with ear circumference for quality protein maize hybrids, while number of kernels per rows was negatively correlated with days to maturity of quality protein maize hybrids (Cox *et al.*, 2006). Harvesting index was highly positively correlated with grain yield and number of ears per plant (Abbas *et al.*, 2013). Weak positively correlated were found between kernel weight and grain yield than kernels per ear and related yield components, suggesting that the greatest relative stress was present during pollination and early grain fill (Sharma *et al.*, 2010).

Table1. Phenotypic correlation coefficients of yield related traits of quality protein maize

	DM	PTP	PH	EPP	EL	KPE	TKW	BM	GY	HI
DT	0.5**	0.2	0.01	0.6**	0.5**	0.3*	0.4*	0.2	0.6**	0.5**
DM		0.01	0.1	0.2	0.01	0.1	0.2	0.01	0.1	0.2
PTP			0.4*	0.3*	0.4*	0.2	0.2	0.6**	0.7**	0.3*
PH				0.4*	0.4*	0.3*	0.4*	0.6**	0.4*	0.3**
EPP					0.4*	0.8**	0.6**	0.4*	0.3*	0.2
EL						0.1	0.6**	0.3*	0.5**	0.4*
KPE							-0.4*	0.4*	0.3*	0.4*
TKW								0.2	0.5**	0.3*
BM									-0.1	0.4*
GY										0.6**

Source: Abbas *et al.*, 2013,

**,* indicates highly significant at 1% and significant at 5% probability levels, respectively. DT = Days to tassels, DM = Days to maturity, PTP = Productive tillers per plant, PH = Plant height, EPP = Ear per plant, EL= Ear length, KPE = Kernel per ear, TKW = 1000 kernel weight, BM = above ground biomass, GY = Grain yield and HI= Harvest index.

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Table.2. Genotypic correlation coefficients of yield related traits of quality protein maize

	DM	PTP	PH	EPP	EL	KPE	TKW	BM	GY	HI
DT	0.8**	0.2	0.5	0.8**	0.7*	0.6	0.5	0.4	0.6	0.9**
DM		0.6	0.7	0.8*	0.6	0.5	0.4	0.8*	0.6	0.7
PTP			0.8*	0.8*	0.8*	0.9**	0.7	0.8*	0.9**	0.8*
PH				0.8*	0.8*	0.8*	0.8*	0.9**	0.8*	0.7
EPP					0.8*	0.9**	0.8*	0.8*	0.9**	0.8*
EL						0.9**	0.8*	0.8*	0.9**	0.8*
KPE							-0.8*	0.8*	0.9**	0.9**
TKW								-0.4	0.8*	0.8*
BM									-0.6	0.6
GY										0.8*

Source: Abbas *et al.*, 2013

*, ** = Significant a 5% and 1% probability level, respectively. DT = Days to tassels, DM = Days to maturity, PTP = Productive tillers per plant, PH = Plant height, EPP = Ear per plant, EL= Ear length, KPE = Kernel per ear, TKW = 1000 kernel weight, BM = above ground biomass, GY = Grain yield and HI= Harvest index.

Yield Components Traits of Quality Protein Maize

Yield components traits of quality protein maize are used to measure yield productivity. These yield component traits include days to tassels, days to maturity, productive tillers per plant, plant height, ear per plant, ear length, kernels per ear, 1000 kernels weight, above ground biomass, grain yield, leaf length, leaf width, leaf area, ear diameter and harvest index (Gupta *et al.* 2013).

Diversity of Quality Protein Maize Varieties in Ethiopia

Table3. High yielding improved hybrid and OPV quality protein maize varieties

Varieties	Year of release	Hybrid/ OPV	Rain fall (mm)	Altitudes ((m)(a.s.l))	Yield (Qt/ha)	
					Farmers field	Research Station
H542	2018	Hybrid	800-1200	800-1000	40-46	43-46
BH543	2016	Hybrid	850-1200	600-1200	42-47	45-49
BH545	2018	Hybrid	900-1250	700-1000	45-50	50-54
Gibe-1	2017	OPV	850-1200	600-1000	35-40	40-44
Gutto	2014	OPV	1000-1300	600-950	32-37	36-41
Gibe-2	2014	OPV	860-1230	500-900	34-38	38-43
Abo-Bako	2016	OPV	800-1200	400-1000	32-37	37-42
Gibe-3	2017	OPV	900-1250	800-1000	30-36	34-38
Morka	2016	OPV	950-1260	700-1000	34-38	37-41
Kuleni	2015	OPV	850-1230	760-1000	32-36	35-39
Rare-1	2013	OPV	860-1200	450-950	31-37	34-39
Hora	2014	OPV	950-1200	360-890	34-38	38-42
MH140	2013	Hybrid	870-1230	800-1200	43-47	48-52
Melkasa-2	2005	OPV	800-1200	450-900	32-36	36-40
MH130	2016	Hybrid	850-1230	800-1200	42-46	47-51
AMH853	2016	Hybrid	900-1260	850-1200	43-46	48-53
Melkasa-5	2006	OPV	860-1250	600-900	36-39	38-42
MH140	2017	Hybrid	750-1200	500-850	46-50	49-55
Vimilia K1	2016	OPV	890-1260	750-900	30-35	34-38
Nata K6Q	2016	OPV	850-1230	650-850	34-39	37-42

Source: CIMMYT-Ethiopia, 2016, Muli *et al.*, 2016 and Milander *et al.*, 2015

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In Ethiopia, more than forty improved varieties of quality protein maize including hybrids and open pollinated varieties developed and released by the Ethiopian Institute of Agricultural Research (EIAR) in collaboration with the International Maize and Wheat Improvement Center (Sharma *et al.*, 2010).

SUMMARY AND CONCLUSION

Generally, quality protein maize has high level of lysine and tryptophan amino acids that improve nutritional value of food to supplement the diet of human being. The biological value of protein is reviewed on the average proportion of absorbed protein that is successfully retained by the body for maintenance and growth of human being. Nutritional value is closely related to protein quality, which in case of maize is limited due to low concentration of essential amino acids. The present review confirmed on quality protein maize homozygous recessive (*o2o2*) mutant gene has higher lysine and tryptophan content than both heterozygous (*O2o2*) and homozygous dominant (*O2O2*) for opaque-2 locus. The major objective of quality protein maize breeding programme is to create new and improved cultivars with features that contribute to high yield potential with stability and improved product quality. The quality measurements of quality protein maize are protein, carbohydrate, oil and starch in terms of genetic variability, heritability and genetic advance under selection. This review implies the importance of genetic variability in improvement of yield and yields components traits of quality protein maize through selection. Yield components were either negative or positive highly correlated with each other and grain yield for quality protein maize hybrids and open pollinated varieties.

PROSPECTIVE RECOMMENDATION

This review recommend that identified potential quality protein maize varieties with high yielding and product quality could be used for quality protein maize breeding programs for grain yield component traits improvement. The potential quality protein maize varieties should be review for the future in different agro-ecologies for yield and yield component traits improvement under different agro-ecologies.

REFERENCES

- [1] Abbas HG, Mahmood A, Ali Q, Khan MA, Nazeer W (2013). Genetic variability, heritability, genetic advance and correlation

- studies in cotton (*Gossypiumhirsutum L.*). Int Res Microbiol, 4: 156-161.
- [2] Ali Q, Ahsan M, Ali F, Ali A, Kanwal N (2014). Genetic correlation and hybrid vigor for physiological traits of *zea mays*. Nat Sci, 12: 50-59.
- [3] CSA (Central Statistical Agency) (2013). Agricultural Sample Survey, 2011/2012 (2004 E.C.), Vol. 1 Report on Area and Production of Major Crops (Private Peasant Holdings, Meher Season). Addis Ababa, Ethiopia.
- [4] Coulter, J.A., E.D. Nafziger, M.R. Janssen and P. Pedersen (2010). Response of *Bt* and near-isoline corn hybrids to plant density. Agron. J. 102:103-111.
- [5] Cox, W.J., R.R. Hahn and P.J. Stachowski (2006). Time of weed removal with glyphosate affects corn growth and yield components. Agron. J. 98:349-353
- [6] Dagne W, Maryke TL, Bindiganavile SV (2011). Protein quality and endosperm modification of quality protein maize (*Zea mays L.*) under two contrasting soil nitrogen environments. Field Crops Res, 121: 408-415.
- [7] Egli, D.B. (2011). Time and the productivity of agronomic crops and cropping systems. Agron. J. 103:743-750.
- [8] Gemechu N, Sentayehu A, Leta T (2016). Review on quality protein maize breeding for Ethiopia. Journal of Biology, Agriculture and Health Care.
- [9] Gambín, B.L., L. Borrás and M.E. Otegui (2006). Source-sink relations and kernel weight differences in maize temperate hybrids. Field Crops Res. 95:316-326.
- [10] Gupta HS, Babu R, Agrawal PK, Mahajan V, Hossain F and Thirunavukkarasu N (2013). Accelerated development of QPM hybrid through marker assisted introgression of opaque-2 allele. Plant Breeding 132(1): 77-82.
- [11] Hailu, A, Woldeab, G, Dawit, W and Hailu, E (2015). Evaluation of QPM varieties to dominant race stem rust (*Puccinia graminis sp. tritici*) pathogen. Science Innovation, 3: 121-126. j.si.20150306.20
- [12] Jean du Plessis (2003). Maize production department: Agriculture Republic of South Africa.
- [13] Mbuya K, Nkongolo KK, Kalonji-Mbuyi A, Kizungu R (2011). Participatory selection and characterization of QPM varieties in Savanna agro-ecological region of DR-Congo. J Plant Breed Crop Sci, 2: 325-332.
- [14] Milander J.J, Z Jukic, S.C Mason, T.D Galusha and Z. Kmail (2015). Maize yield components as influenced by plant population in Croatia and Nebraska. Agron. J. (Submitted).

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- [15] Mohammedi S.A, B.M. Prasanna and N.N. Singh (2003). Sequential path model for determining relationship among grain yield and related characters in maize. *Crop Sci.* 43:1690-1697.
- [16] Muli JK, Budambula NL, Mweu C, Imbo MC, Anami SE (2016). Genetic improvement of African maize towards drought tolerance: A Review.
- [17] Novacek M.J, S.C Mason, T.D Galusha and M. Yaseen (2013). Twin rows minimally impact irrigated maize yield, morphology and lodging. *Agron. J.* 105:268-276.
- [18] Novacek M.J, S.C Mason, T.D Galusha and M. Yaseen (2014). Bt transgenes minimally influence maize grain yields and lodging across plant populations. *Maydica* 59: 90-95.
- [19] Oppong A, Bedoya C.A, Ewool M.B (2014). Bulk genetic characterization of Ghanaian maize landraces using microsatellite markers. *Maydica* 59:1-8.
- [20] Pandey N, Hossain F, Kumar K, Vishwakarma AK, Muthusamy V (2016). Molecular characterization of endosperm and amino acids modifications among quality protein maize inbreds. *Plant Breeding*, 135: 47-54.
- [21] Rosegrant MR, Ringler C, Sulser TB, Ewing M, Palazzo A, Zhu T (2009). Agriculture and food security under global change: prospects for 2025/2050. IFPRI, Washington, DC.
- [22] Semagn K, Magorokosho C, Vivek BS, Makumbi D, Beyene Y, Mugo S, Prasanna BM and Warburton ML (2012). Molecular characterization of diverse maize inbred lines from southern Africa using single nucleotide polymorphic markers. *BMC Genomics* 13: 113.
- [23] Sharma L, Prasanna BM and Ramesh B (2010). Phenotypic and microsatellite-based diversity and population genetic structure of maize landraces in India from the north east Himalayan region. *Genetica* 138:619-631
- [24] Vivek BS, Krivanek AF, Palacios-Rojas N and Diallo AO (2008). Breeding quality protein maize Protocols for developing QPM cultivars. Mexico, D.F., CIMMYT, pp. 5.

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