



Breeding for Quality Protein Maize (QPM)

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improvement of protein quality mechanism of $\alpha 2$ mutant and problem associated with $\alpha 2$ mutant, breeding, genetics and molecular approach that could be used to get efficient QPM cultivars [5-7].

Introduction

To review the quality traits, measurements and possible breeding methods to improve protein quality of maize.

1.1. Background

1.1.1. Maize kernel structure

Maize kernel mainly consists of three parts: pericarp (6%), embryo (12%) and endosperm (82%). The pericarp is the outer covering of the kernel that protects and preserves the nutrient value inside of it. A thin, suberized nucellar membrane acquired from the outer epidermal wall of the nucellus persists as a continuous covering between the aleurone and the pericarp [8]. The embryo is located in one face of the basal part of the kernel. A mature embryo is comprised by the embryo axis and the scutellum. Both the embryo and endosperm contain proteins but the germ proteins are superior in quality as well as quantity. Most of the volume and weight of the kernel is accomplished by the endosperm. It can be divided into three parts: starchy endosperm, aleurone layer, and the basal transfer layer. The aleurone layer is the outer most layers secreted by specialized cells, rich in hydrolytic enzymes. Starch-rich endosperm is present within the aleurone layer having vitreous and starchy regions [9-12].

The zein proteins form insoluble accretions which are acquired in a vitreous region called protein bodies in the lumen of rough endoplasmic reticulum and it is densely packed between starch grains towards maturity (Gibbon, and Larkins, 2005). Zeins are the prolamins of maize grain which are soluble in an alcohol having one major class (α -zeins) and three minor classes (β , γ , and δ). These four types constitute about 50-70% of maize endosperm and are essentially rich in glutamine, leucine and proline and poor in lysine and tryptophan (Nelson, 1969) [13,14].

Higher proportion of leucine (18.7%), phenylalanine (5.2%) isoleucine (3.8%), valine (3.6%) and tyrosine (3.5%) are normally present in zein fraction, while other essential amino acids such as threonine (3%), histidine and cysteine (1%), methionine (0.9%), lysine (0.1%) are in smaller amounts and is significantly deficient in tryptophan as it is devoid from the major prolamin fraction (α -zeins) of maize kernel. Non-zeins include other proteins such as globulins (3%), glutelins (34%) and albumins (3%). The nonzein protein fraction is balanced and rich in lysine and tryptophan (Vasal, 2002) [15-17] (Figure 1).

Malnutrition is a persistent problem in Africa, especially in rural areas. It is caused by a lack of essential nutrients, particularly protein and energy. This is due to a combination of factors, including low agricultural productivity, limited access to markets, and poor dietary diversity. The consequences of malnutrition are widespread, affecting physical and mental health, and leading to stunted growth and reduced productivity in the long term. Addressing this issue requires a multi-faceted approach, including improving agricultural practices, enhancing market access, and promoting dietary diversification.

adverse pleiotropic effects. So, researchers use two genetic systems by exploiting double-mutant combinations and. Simultaneous use of

al. 2002), provided to Dr. Edwin Mertz seeds of opaque-2 maize to be included in his group's systematic effort to identify maize accessions with improved protein quality (Paes and Bicudo, 1994). Soon after the discovery of the nutritional benefits of the o2 mutation, it began to be incorporated into many breeding programs worldwide, with a major emphasis on conversion of normal endosperm populations and inbred lines to o2 versions through a direct backcross approach (Prasanna et al., 2001). However, enthusiasm over the direct use of the o2 mutation in breeding programs soon subsided after the discovery of serious negative secondary (pleiotropic) effects of this mutation [44]. The soft endosperm of o2 genotypes initially caused up to a 25% yield loss due to the lower density of the opaque grains, as well as increased susceptibility to fungal ear rots and storage pests (Vasal, 2000). The soft endosperm texture also is not acceptable to many in the developing world who are accustomed to harder grain types. Such negative secondary effects severely limited practical use of the mutation in the field. Fortunately, during the process of converting normal maize populations to o2 versions, partially hardened endosperm (i.e. vitreous) or modified grains had been observed by many researchers including breeders at CIMMYT in Mexico. Separation of such grains when encountered began as early as 1969 by Dr. John Lindquist (Vasal, 2000). Besides, the first published report highlighting the importance of such grain modification in reducing the negative pleiotropic effects of the o2 mutation was published in 1969 (Paetz et al., 1969). Selection for hard endosperm modification was rapidly incorporated into o2 breeding schemes. Occurring at the beginning of QPM breeding efforts at CIMMYT focused on conversion of a range of sub-tropical and tropical lowland adapted, normal endosperm populations to o2 versions through a backcross-recurrent selection procedures, with a focus of accumulating the hard endosperm phenotype, maintaining protein quality and increasing yield and resistance to ear rot (Villegas et al. 1992). The improved populations were released for direct use in the field as open pollinated varieties (OPV's), or individual plants were self-pollinated to form inbred lines used in hybrid formation. Similar programs with sustained breeding of QPM also continued at the University of KwaZulu-Natal (previously University of Natal), South Africa and the Crow's Hybrid Seed Company at Milford, Illinois USA (Prasanna et al., 2001) [45].

• Marker-assisted selection

There is a need of marker-assisted selection because of mainly three reasons:

1. In each backcross generation needs to be selected to identify the opaque-2 recessive gene and a minimum of six backcross generations are required to recover satisfactory levels of recurrent parent genome.

2. To maintain the homozygous opaque-2 gene, multiple modifiers must be selected.

3. Rigorous biochemical tests to ensure enhanced lysine and tryptophan levels in the selected materials in each breeding generation require. After the sequencing of the maize genome has been completed, a large number of the market system are now available that are associated with o2 and endosperm modification phenotype (Singh, et al. 2017). A convenient utilization of such markers will greatly enhance the efficiency of selection for improvement of grain protein in maize furthermore reduce the cost and time. Both foreground MAS and background MAS can be efficiently utilized for selecting o2 phenotype more over assuring maximum recovery of the recurrent parent. MAS used for development of QPM parental lines and developed QPM hybrid in less than half the time required through conventional breeding (Singh, et al. 2017).

Various markers are used to introgress o2 gene into elite maize inbred lines by rapid backcross conversion programme. They found that using a marker for QPM and endosperm modification can enormously improve the selection efficiency for isolating fully modified kernels in QPM background (Singh, et al. 2017) [46].

• Impact of QPM

QPM could have an impact in areas where maize constitutes a large proportion of the diet, especially as a source of protein, and where children and lactating mothers suffer protein deficiency. With the discovery of opaque-2 mutation, this natural recessive mutation causes alteration in amino acid composition and opaque phenotype of endosperm by regulation of specific zein genes and combined use of the o2 gene and genetic modifiers. Modified marker assisted back cross breeding used to develop QPM versions of normal maize inbreds with desirable endosperm characteristics and seed yield. These QPM introgression lines may be united to develop QPM hybrids. There may be increasing use of molecular genetic tools in QPM research in the future.

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