

Qualitative Characterization of Proteins in Common and Quality Protein Maize Corn by Mass Spectrometry

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Abstract : During the last decades, the world has experienced a rapid industrialization and an expanding economy favoring a demographic boom. As a consequence, countries around the world have focused on developing new strategies related to the production of different farm products in order to meet future demands. Consequently, different strategies have been developed seeking to improve the major food products for both humans and livestock. Corn, after wheat and rice, is the third most important crop globally and is the primary food source for both humans and livestock in many regions around the globe. In addition, maize (*Zea mays*) is an important source of protein accounting for up to 60% of the daily human protein supply. Generally, many of the cereal grains have proteins with relatively low nutritional value, when they are compared with proteins from meat. In the case of corn, much of the protein is found in the endosperm (75 to 85%) and is deficient in two essential amino acids, lysine, and tryptophan. This deficiency results in an imbalance of amino acids and low protein content; normal maize varieties have less than half of the recommended amino acids for human nutrition. In addition, studies have shown that this deficiency has been associated with symptoms of growth impairment, anemia, hypoproteinemia, and fatty liver. Due to the fact that most of the presently available maize varieties do not contain the quality and quantity of proteins necessary for a balanced diet, different countries have focused on the research of quality protein maize (QPM). Researchers have characterized QPM noting that these varieties may contain between 70 to 100% more residues of the amino acids essential for animal and human nutrition, lysine, and tryptophan, than common corn. Several countries in Africa, Latin America, as well as China, have incorporated QPM in their agricultural development plan. Large parts of these countries have chosen a specific QPM variety based on their local needs and climate. Reviews have described the breeding methods of maize and have revealed the lack of studies on genetic and proteomic diversity of proteins in QPM varieties, and their genetic relationships with normal maize varieties. Therefore, molecular marker identification using tools such as mass spectrometry may accelerate the selection of plants that carry the desired proteins with high lysine and tryptophan concentration. To date, QPM maize lines have played a very important role in alleviating the malnutrition, and better characterization of these lines would provide a valuable nutritional enhancement for use in the resource-poor regions of the world. Thus, the objectives of this study were to identify proteins in QPM maize in comparison with a common maize line as a control.

Keywords : corn, mass spectrometry, QPM, tryptophan

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