Chapter 1

Introductory Chapter: Introduction to Biotechnological Approaches for Maize Improvement

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Additional information is available at the end of the chapter

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1. Introduction

Maize (*Zea mays* L.) is an important staple food crop worldwide. It is the third most important cereal crop after wheat and rice [1]. Maize is economically used for both livestock feeds and human consumption. The agricultural production of maize will have to increase by 60% over the next 40 years due to the growing world's population [1]. Additionally, a quarter of agricultural lands worldwide have suffered degradation, and there is a deepening awareness of the long-term consequences of a loss of biodiversity in terms of climate change. Oilseed crops, including maize, also play an important role in the agricultural economy. Globally, the demand for vegetable oils is increasing due to the increasing per capita consumption of oil in our daily diets and its use as biofuels [2]. By 2050, the global demand for vegetable oils is expected to be more than twice the current production. Though the need for maize crop is expected to increase, the crop productivity is limited by many abiotic and biotic stresses. A range of new technologies have been developed to enhance the productivity of this crop. Here, the current work presents an overview and discusses recent progresses on maize research that could open up new opportunities for crop improvement.

2. Technologies developed to enhance maize productivity

Molecular breeding approach in maize starts with identifying and validating quantitative trait loci (QTLs) linked to abiotic stress tolerance. Following the identification and validation of the markers associated with QTLs for traits of interest, the candidate QTLs or genes can be introgressed in elite lines through marker-assisted backcrossing. Over the past years, linkage mapping was used to identify QTLs [3]. However, association genetics is currently used to enhance this work in numerous crops [4]. Nested association mapping is also being utilized for the genome-wide dissection of complex traits in maize crop [5]. Association mapping is highly recommended to be used for identifying traits associated with abiotic stresses [6]. Marker-assisted backcrossing has also been utilized for complex traits such as tolerance to drought, salinity, and heat, which are the key traits targeted for improving and developing crops that are adapted to low rainfall, salinity, and high temperature conditions. Marker-assisted backcrossing may not be an effective approach for introgressing QTLs in some cases. On the other hand, two other molecular breeding approaches, marker-assisted recurrent selection and genomic selection, can overcome this issue [7]. The genetic progress obtained using marker-assisted recurrent selection and genomic selection is greater than that can be obtained using marker-assisted backcrossing. Another technology for enhancing complex traits has been developed and is based on genome-wide selection. Although marker-assisted backcrossing and marker-assisted recurrent selection need provided QTL information for complex traits, information on marker trait associations is not necessarily needed for genome-wide selection [8]. Furthermore, genome-wide selection relies on the information associated with the prediction of the genomic-recorded breeding values of progeny.

Most areas planted with maize currently involve transgenic varieties, and the vast majority of hybrids are now resistant to insects and herbicides. Bt maize containing the protein cry-1fAb has been started to be grown in 2007 in order to control *Spodoptera frugiperda*. RR maize, which is resistant to glyphosate-based herbicides, was then used as an alternative for the management of weeds. Maize productivity relies on the genetic characteristics of the hybrid grown, environmental conditions, and the farming technology used [9]. The potential for the grain production may be affected by the interaction between the hybrid and the cultivation conditions. Cardoso et al. [10] recorded varying responses of cultivars being well-adapted to a wide range of conditions, in which they maintain their productivity. In conclusion, besides the potential use of biotechnological and genetic approaches in the improvement of different plant species [11–19], they could be used for improving maize yield and quality. The current work would shed light on the advancements made in those technologies.

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References

[1] FAO. World Agricultural Production [Internet]. 2011. Available from: http://faostat.fao.org/default.aspx [Accessed: 2013-June-14]

[2] Samarth NB, Mahanwar PA. Modified vegetable oil based additives as a future polymeric material-review. Open Journal of Organic Polymer Materials. 2015;**5**:1-2

[3] Varshney RK, Tuberosa R. editors. Genomics-Assisted Crop Improvement: Genomics Approaches and Platforms. Vol. 1. The Netherlands: Springer; 2007

[4] Hall D. Using association mapping to dissect the genetic basis of complex traits in plants. Briefings in Functional Genomics. 2010;**9**:157-165

[5] Yu J et al. Genetic design and statistical power of nested association mapping in maize. Genetics. 2008;**178**:539-551

[6] Gupta PK et al. Linkage disequilibrium and association studies in plants: Present status and future prospects. Plant Molecular Biology 2005;**57**:461-485

[7] Tester M, Langridge P. Breeding technologies to increase crop production in a changing world. Science. 2010;**327**:818-822

[8] Jannink JL et al. Genomic selection in plant breeding: From theory to practice. Briefings in Functional Genomics 2010;**9**:166-177

[9] Tollenaa M, Lee EA. Yield potential, yield stability and stress tolerance in maize. Field Crops Research, Amsterdam. 2002;**75**:161-169

[10] Cardoso MJ, Carvalho HWL, Rocha LMP, Pacheco CAP, Guimaraes LJM, PEO G, Parentony SN, Oliveira IR. Identificação de cultivares de milho com base na análise de estabilidade fenotípica no Meio-Norte brasileiro. Revista Ciência Agronômica, Fortaleza. 2012;**43**:346-356

[11] El-Esawi MA. SSR analysis of genetic diversity and structure of the germplasm of faba bean (*Vicia faba* L.). Comptes Rendus Biologies. 2017;**340**:474-480

[12] El-Esawi M, Arthaut L, Jourdan N, d'Harlingue A, Martino C, Ahmad M. Blue-light induced biosynthesis of ROS contributes to the signaling mechanism of Arabidopsis cryptochrome. Scientific Reports. 2017;**7**:13875

[13] El-Esawi MA, Elkelish A, Elansary HO, et al. Genetic Transformation and Hairy Root Induction Enhance the Antioxidant Potential of *Lactuca serriola* L. Oxidative Medicine and Cellular Longevity, vol. 2017, Article ID 5604746, 8 pages. DOI:10.1155/2017/5604746

[14] El-Esawi MA, Elansary HO, El-Shanhorey NA, Abdel-Hamid AME, Ali HM, Elshikh MS. Salicylic acid-regulated antioxidant mechanisms and gene expression enhance rosemary performance under saline conditions. Frontiers in Physiology. 2017;**8**:716. DOI: 10.3389/fphys.2017.00716

[15] Vwioko E, Adinkwu O, El-Esawi MA. Comparative physiological, biochemical and genetic responses to prolonged waterlogging stress in okra and maize given exogenous ethylene priming. Frontiers in Physiology. 2017;**8**:632. DOI: 10.3389/fphys.2017.00632

[16] El-Esawi MA. Micropropagation technology and its applications for crop improvement. In: Anis M, Ahmad N, editors. Plant Tissue Culture: Propagation, Conservation and Crop Improvement. Singapore: Springer; 2016b. pp. 523-545

[17] El-Esawi MA. Nonzygotic embryogenesis for plant development. In: Anis M, Ahmad N, editors. Plant Tissue Culture: Propagation, Conservation and Crop Improvement. Singapore: Springer; 2016c. pp. 583-598

[18] El-Esawi MA. Somatic hybridization and microspore culture in *Brassica* improvement. In: Anis M, Ahmad N, editors. Plant Tissue Culture: Propagation, Conservation and Crop Improvement. Singapore: Springer; 2016d. pp. 599-609

[19] El-Esawi MA, Germaine K, Bourke P, Malone R. AFLP analysis of genetic diversity and phylogenetic relationships of *Brassica oleracea* in Ireland. Comptes Rendus Biologies. 2016b; **339**:163-170