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Research review paper

Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics

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ABSTRACT

Advances in next-generation sequencing and genotyping technologies have enabled generation of large-scale genomic resources such as molecular markers, transcript reads and BAC-end sequences (BESs) in chickpea, pigeonpea and groundnut, three major legume crops of the semi-arid tropics. Comprehensive transcriptome assemblies and genome sequences have either been developed or underway in these crops. Based on these resources, dense genetic maps, QTL maps as well as physical maps for these legume species have also been developed. As a result, these crops have graduated from 'orphan' or 'less-studied' crops to 'genomic resources rich' crops. This article summarizes the above-mentioned advances in genomics and genomics-assisted breeding applications in the form of marker-assisted selection (MAS) for hybrid purity assessment in pigeonpea; marker-assisted backcrossing (MABC) for introgressing QTL region for drought-tolerance related traits, *Fusarium* wilt (FW) resistance and *Ascochyta* blight (AB) resistance in chickpea; late leaf spot (LLS), leaf rust and nematode resistance in groundnut. We critically present the case of use of other modern breeding approaches like marker-assisted recurrent selection (MARS) and genomic selection (GS) to utilize the full potential of genomics-assisted breeding for developing superior cultivars with enhanced tolerance to various environmental stresses. In addition, this article recommends the use of advanced-backcross (AB-backcross) breeding and development of specialized populations such as multi-parents advanced generation intercross (MAGIC) for creating new variations that will help in developing superior lines with broadened genetic base. In summary, we propose the use of integrated genomics and breeding approach in these legume crops to enhance crop productivity in marginal environments ensuring food security in developing countries.

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Contents

1. Introduction

Legumes form an important constituent of food crops consumed globally and complement cereal crops as a source of dietary protein. In addition to providing important micronutrients to human beings, they also fix atmospheric nitrogen, which consequently increase soil fertility and production of other cereal crops. Legumes are also important source of fodder in many agricultural systems and are grown increasingly on a large-scale in semi-arid tropics (SAT). SAT regions cover many developing countries from Africa, Asia to Latin America, and they are characterized by low and erratic rainfall, prolonged dry seasons, and soils with low fertility. This environment is home to the poor and one-sixth of the world's human population (http://oar.icrisat.org/5283/1/Impact-Flyer-%20Africa.pdf).

Agriculture in the SAT regions is generally undertaken by smallholder farmers and is the mainstay of their livelihood. Among several food crops, chickpea (*Cicer arietinum*), pigeonpea (*Cajanus cajan*) and groundnut or peanut (*Arachis hypogaea*) are the leading legume crops to feed underprivileged living in the SAT, which is also called "habitat of the hungry". As these legume crops are grown in harsh environments and exposed to various biotic and abiotic stresses, their productivity has not increased significantly for the last 50 years (Fig. 1) (FAO, 2012). It is, therefore, important to enhance productivity of these crops to cope up with increased demand by the expanding human population. Although some progress has been made in this direction through conventional breeding methods which may be

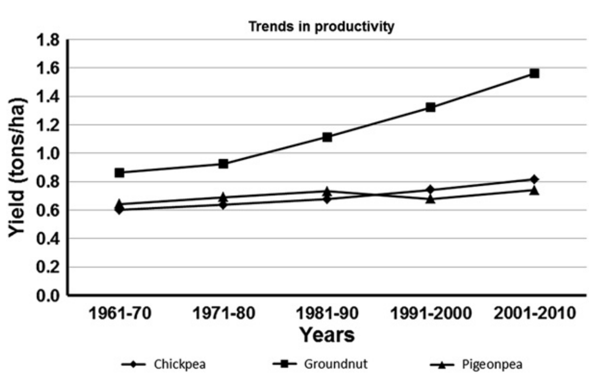

Fig. 1. Trends in crop productivity of three SAT legume crops. Trends in crop productivity during last five decades have been shown in chickpea, pigeonpea and groundnut. Except a small growth in the case of groundnut, in general, the crop productivity has been remained almost stagnant in the SAT legume crops.

attributed to insufficient understanding of the underlying genetical or molecular mechanisms conferring resistance/tolerance to biotic/abiotic stresses. Advances in genomics have improved our understanding towards genetic architecture and molecular mechanism for complex traits which led to identification of marker-trait associations for economically important traits in order to enhance selection efficiency in breeding. Tremendous progress made in recent years in genomics research of SAT legume crops namely chickpea, pigeonpea and groundnut has prompted us to review the achievements made so far along with initiatives and future prospects for further genetic enhancement.

2. SAT legume crops and production constraints

2.1. Chickpea (*Cicer arietinum L.*)

Chickpea, also known as garbanzo bean, is a self-pollinated diploid ($2n = 2\times = 16$) crop with genome size of 740 Mb (Arumuganathan and Earle, 1991). The seeds of chickpea are rich in protein (24.6%), carbohydrate (64.6%) and vitamins (Abu-Salem and Abou, 2011). During 2010, chickpea covered a total of 11.9 Mha worldwide with a global production of 10.9 million tons (Mt) and average yield of 913 kg/ha (FAO, 2012). Several abiotic and biotic stresses pose a big threat to high and stable yields of chickpea in the farmers' fields. Among abiotic stresses, terminal drought is a major problem for the crop grown under rainfed conditions as it delays flowering and affects seed yield. In addition to the above, this crop is also sensitive to lower temperature (<10 °C) mainly during reproductive period (Bakht et al., 2006) and to salinity (NaCl) during flowering and podding stages (Flowers et al., 2010). Salinity can affect the root nodules by decreasing their number, size and N_2-fixation capacity. Important biotic stresses affecting chickpea production are, *Fusarium* wilt (FW) caused by *Fusarium oxysporum* f.sp. *ciceri*, reduces yield up to 90% (Singh and Reddy, 1991) and *Ascochyta* blight (AB) caused by *Ascochyta rabiei* (Pass.) Labrousse, may cause total crop loss (Singh and Reddy, 1996). Other biotic stresses of chickpea are *Botrytis* gray mold (BGM) caused by *Botrytis cinerea* Pers. ex. Fr., leaf spot by *Alternaria* spp., black root rot by *Fusarium solani*, *Phytophthora* root rot by *Phytophthora megasperma* and *Pythium* damping-off by *Pythium ultimum*, rust by *Uromyces* and beet western yellow virus (BWYV) causing narrow leaf (Nene and Reddy, 1987). Pod borer or *Helicoverpa armigera* is the major insect pest of chickpea and it feeds on leaves and developing seeds (Sharma et al., 2005). Because of its complex nature and non-availability of good resistance sources in cultivated gene pool,

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