

Translational genomics for improving dryland crops

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Extended Summary

Although crop improvement programs have made excellent progress in enhancing crop productivity and production, there is still a huge scope to fill the yield gap for majority of crops in dryland areas. Genomics-assisted breeding can help enhancing crop productivity as well as nutrition in these crops. However, until recently, majority of the dryland crops have remained untouched with genomics revolution. Two key reasons for this situation include engagement of only few institutes and availability of limited resources at international level for research and development in these crops.

With an objective to address these issues, the Center of Excellence in Genomics and Systems Biology (CEGSB) at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) floated several multi-institutional consortia. As a result of collaborative efforts from such strong partnership, a large number of genomic resources including genome assemblies for 9 crops have been developed and several improved lines have been developed through molecular breeding. In summary, translational genomics approach has transformed the so-called ‘orphan crops’ to ‘genomic resources-rich crops’ and contributed to develop several improved lines in some dryland crops.

Genome sequencing

We have deployed next-generation sequencing (NGS) technologies in developing high quality reference genomes for the so-called orphan crops in dryland regions (Table 1). Pigeon pea was the first orphan legume crop, and probably the first non-industrial crop, for which NGS was adopted for developing its draft genome sequences (Varshney *et al.*, 2012; Saxena and Varshney, 2017). Subsequently genome sequence assemblies were developed for chickpea (Varshney *et al.*, 2013; Thudi and Varshney, 2017), diploid progenitor genomes of cultivated groundnut (Chen *et al.*, 2016; Bertoli *et al.*, 2016) and pearl millet (Varshney *et al.*, 2017a). Genome sequence for sorghum was made available by the US led team in collaboration with ICRISAT (Peterson *et al.*, 2009).

In addition to sequencing the genomes of ICRISAT mandate crops, the CEGSB scientists also collaborated with several partners to sequence genomes of other plant species such as adzuki bean (*Vigna angularis*) (Yang *et al.*, 2015; Kang *et al.*, 2015), mung bean (*Vigna radiata*) (Kang *et al.*, 2014), sesame (*Sesamum indicum*) (Wang *et al.*, 2014) and longan (*Dimocarpus longan*) (Lin *et al.*, 2017). In summary, we have led/contributed in sequencing of genomes of 9 dryland crops so far.

Germplasm characterization

In order to harness genetic diversity from germplasm collection in these important crops, various re-sequencing efforts were carried out. For instance, in the case of chickpea, ICRISAT-led team has undertaken the sequencing of thousands of chickpea genomes as part of ‘The 3,000 Chickpea Genome Sequencing Initiative’ - an international effort to sequence and phenotype the chickpea global composite collection. Similar efforts were carried out in pigeon pea (Varshney *et al.*, 2017b), groundnut (Pandey *et al.*, 2017; Clevenger *et al.*, 2017), sorghum and pearl millet (Varshney *et al.*, 2017a). Genome-wide association studies using re-sequencing and genotyping data together with multi-location phenotyping data have provided marker-trait association in several cases.

Table 1. Advances in the genomics, trait mapping and molecular breeding in the ICRISAT mandate crops during last 11 years

Features	Chickpea		Pigeon pea		Groundnut		Sorghum		Pearl millet	
	2007	2019	2007	2019	2007	2019	2007	2019	2007	2019
<i>Genomic resources</i>										
Genome assembly	No	***	No	***	No	**	No	**	No	***
Transcriptome assembly	No	***	No	***	No	***	No	**	No	**
Genetic maps	*	***	No	***	*	***	**	***	*	***
<i>Marker genotyping platforms</i>										
SSR markers	**	***	*	***	*	***	***	****	*	***
SNP markers	No	***	No	***	No	**	**	****	No	****
DArT markers	No	***	No	***	No	***	No	***	No	*
KASP assays	No	***	No	***	No	**	No	No	No	No
GoldenGate	No	**	No	**	No	**	No	No	No	No
SNP arrays	No	***	No	***	No	***	No	No	No	No
<i>Trait mapping</i>										
Biotic stress	*	***	No	***	*	**	**	***	*	**
Abiotic stress	*	***	No	**	No	*	*	***	*	**
Other traits	*	***	No	**	*	***	*	**	*	***
Diagnostic markers	No	***	No	***	No	***	No	**	No	**
<i>Molecular breeding products</i>										
Superior line	No	***	No	No	No	***	*	**	*	**

*limited, ** optimum, *** abundant, **** highly abundant, No- non availability

Trait mapping

By using genomic resources, genotyping platforms and working in collaboration with breeders, physiologists, pathologists, entomologists, microbiologists, and genetic resource and pre-breeding specialists from ICRISAT and other collaborating institutes, 20 to 50 traits have been mapped in the ICRISAT mandate crops. It is important to mention here that mapped traits do not essentially mean that diagnostic markers are available for all these traits. In fact, in terms of availability of diagnostic markers, they are available for limited number of traits so far. Efforts need to be accelerated to map desired traits in cost-effective and faster manner.

Product development

Molecular markers associated with different breeding traits were deployed in several breeding programs both in ICRISAT as well as collaborating national programs in India and Africa. As a result of extensive collaboration with breeders, several superior lines have been developed for a number of traits in different crops. CEGSB has now initiated some efforts in the area of deployment of genomic selection in crop improvement programs.

Summary and outlook

As evident from above, because of strong partnership coupled with technological advances, the CEGSB/ICRISAT has made significant efforts in the area of development of genomic resources and generation of molecular breeding products in several dryland crops (Table 1). Furthermore, 380 scientists from national/international institutes/universities have been trained by organizing 11 training courses. With the availability of ample genomic resources, trained national partners and reduction in the cost of genotyping, we anticipate accelerated use of translational genomics approach in crop improvement programs to develop climate resilient varieties in dryland regions.

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