

Genomic approaches for unravelling the potentials of crop wild relatives

Opinion

Crop wild relatives (CWR) are genetically related to the cultivated crops and thus can provide useful gene for the improved breeding of crops. Thus CWRs serve as potential genetic resources that can provide solution to the various challenges of the modern crops arising out of global climate change and diseases. The importance and utility of CWRs have been well documented with several recent studies focussing on its characterization and conservation.¹⁻⁵

Advances in the field of genomics and sequencing technologies have enable the integration of these technologies with conventional breeding knowledge for the characterization of wild crop populations and efficient utilization. Using genomic approaches it is possible to identify novel genetic resources from the CWRs⁶ and also to isolate the existing genetic diversity from the closely-related domesticated crops.⁷ Using available model genome sequences such as *Arabidopsis thaliana*, *Oryza sativa*, *Musa acuminata*, etc. as referral sequence several CWRs can be characterized for understanding the complex domesticated species. Using the recent technologies made in the field of DNA sequencing techniques better understanding of the crops and their wild relatives can be achieved at the genome level.⁸ By referring these already sequences genomes as referral models or by resequencing their wild relatives several other crops or species can be characterized using comparative and functional genomics.⁹

Whole chloroplast genome sequencing of the CWRs and their analysis also reveal the evolutionary and genetic relationship of the closely related species and also the domesticated crops. For such studies approaches for direct mapping of sequences to a reference chloroplast genome⁹ or *de novo* assembly the reads first and subsequent isolation of chloroplast contigs by homology search¹⁰ can be used.

Transcriptome analysis (TA) of the CWRs will also help in the interpretation of their functional elements of the genome.^{11,12} Using the next-generation deep sequencing of the CWR transcriptomes useful genetic information could be obtained for improvement of economically viable crops such as banana or potato.^{13,14}

Thus it can be concluded that CWRs are the one of the most potential resources to overcome the problems of global food security and sustainable crop production. However in order to realize their potential it is imperative to fully understand and characterize these CWRs using genomics and other modern biological tools. Rapid loss of habitats compounded with stresses and diseases and neglect of the CWRs is fast becoming an important issue to address before these hugely important genetic resources are lost forever.

Priority crops and their region of high diversity should be urgently identified and appropriate actions should be taken up at the local as well international level for their conservation and proper utilization.

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Robert Thangjam

Department of Biotechnology, Mizoram University, India

Correspondence: Robert Thangjam, Department of Biotechnology, Mizoram University, Aizawl - 796004, Mizoram, India, Tel +91 9436352386, Email robertthangjam@gmail.com

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Conflict of interest

The author declares no conflict of interest.

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