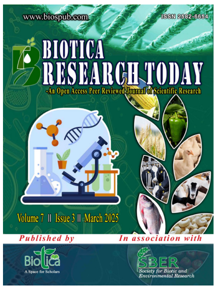

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Plant Gene Editing Approaches in Crop Wild Relatives for *De Novo* Domestication

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Abstract

The crop wild relatives (CWR) have been domesticated and were used for the conventional crop breeding programme as a source of genes tolerant to biotic and abiotic stress. With the advancement of modern biotechnological tools the genes of CWR were available in various public databases. This knowledge can be utilized for developing new cultivars from CWR by utilizing CRISPR/Cas9 technology. The CRISPR/Cas9 technology has been effectively applied in some of the CWR *viz. Solanum pimpinellifolium*, ground cherry (*Physalis pruinosa*), green millet *Setaria viridis*, *Oryza glaberrima* (Kabre), *Solanum peruvianum*, *O. alta*, Sea barleygrass (*Hordeum marinum*) for modifying various agronomically important traits. In this context here we discuss about the application of genome editing technologies in different CWRs and how it can be utilized for the de novo domestication of CWR.

Keywords: CRISPR-Cas9, Crop wild relatives, *de novo*, Wild

Introduction

The crop wild relative (CWR) is an important source of novel genes related to both biotic and abiotic stress. They are always important for crop improvement especially for the identification of novel alleles related to agronomically important traits. The crops plants were evolved from the wild plant species because of the mutations in the plant genome. The wild plants have always been domesticated and they can play an important role in improving crop yield in agriculture. The traditional methods may need thousands of years for domestication of wild plants. In order to develop new varieties with stress tolerance the genetic diversity of wild plants should be utilized. CWR will be available as wild species in natural habitat or close to their centre of origin. Numerous genes were present in these wild species which can be utilized to widen the genetic mechanism of cultivated crops by introducing novel genes for meeting the global food crisis. With the emergence of genome editing technologies the de novo domestication of wild plants will be achieved within few generations. This modern technology can bring wild as well as partially domesticated crop plants for developing agriculture for attaining sustainable goals for meeting the global food demand. With the latest biotechnological tools such as transcriptomics with *in-silico* analysis the identification of physiological pathways and functional genes associated with transcription factors related to various stress tolerance in wild plants can be studied which can be further utilized for future crop breeding programme. In this context we discuss about the CWR which is already being used for genome editing and the importance of these genetic resource for future crop improvement programme.

Application of Genome Editing in CWR

Genome editing is one of the latest emerging tools which can be used for the improvement of wild plants. The technology has already been used in many of the wild plants *viz. Solanum pimpinellifolium*, ground cherry (*Physalis pruinosa*), green millet *Setaria viridis*, *O. glaberrima* (Kabre), *Solanum peruvianum*, *O. alta*, Sea barley grass (*Hordeum marinum*). Some of the important traits and the target genes modified by gene editing tools were listed in (Table 1). *De novo* domestication of wild tomato using genome editing was reported by have reported (Zsögön *et al.*, 2018). The six genes in *Solanum pimpinellifolium* was edited by CRISPR-Cas9 and modifications of nutrient content, size, shape, fruit number and plant architecture in one generation. Recent studies reported genetic transformation protocols for African

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landraces rice (*O. glaberrima*) using CRISPR/Cas9-based vectors for improving plant height, seed size and yield. The fungal disease resistance related genes was obtained by CRISPR-Cas9 gene editing of SpPR-1, SpProSys, SpMlo1 in wild *Solanum peruvianum*. Gene editing using CRISPR/Cas9 was developed for Sea barley grass (*Hordeum marinum*). The wild green millet (*Setaria viridis*) the seed shattering gene *SvLes1* was modified by CRISPR-Cas9 tool.

Table 1: List of CWR utilized for plant genome editing for *de novo* domestication

Sl. No.	Name of CWR	Target genes	Trait	References
1	*Solanum pimpinellifolium*	Self-pruning (SP), Ovate (O), Fruit weight (FW2.2) and Lycopene beta cyclase (CycB)	Morphology, size, number nutritional value of fruit	Zsögön *et al*., 2018; Li *et al*., 2018
2	*Physalis pruinosa*	improvement-related gene CLV1 fruit abscission gene jointless-2	fruit abscission	Lemmon *et al*., 2018
3	*Oryza glaberrima*	HTD1 gene, GS3, GW2 and GN1A	Plant height, tillering	Lacchini *et al*., 2020
4	*Oryza alta*	Pentatricopeptide repeat (PPR1)	grain yield, stem diameter	Yu *et al*., 2021

Conclusion

The rise in global population and changing climatic factors are one of the main factors that affect agriculture production. Modern technologies like CRISPR-Cas promises a short term solutions through enhancement of crop yield for achieving sustainability in agriculture sector. There is lot of data available in public data base about the genes and their functions of CWR. This knowledge should be utilized for developing high yielding crop varieties with stress tolerance under normal conditions. Moreover genome edited plants can be developed from CWR without losing their specific traits.

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