

Biotica Research Today



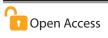
Article ID: RT1595

Application of Biotechnological Tools for Tropical Tuber Crop Improvement

B.G. Sangeetha^{1*}, E.R. Harish¹, R. Arutselvan¹ and C. Pradeepika²

¹Division of Crop protection, ICAR-Central Tuber Crops Research Institute, Sreekariyam, Thiruvananthapuram, Kerala (605 017), India

²Section of Crop Utilization, ICAR-Central Tuber Crops Research Institute, Sreekariyam, Thiruvananthapuram, Kerala (605 017), India



Corresponding Author

B.G. Sangeetha ⊠: Sangeetha.G@icar.gov.in

Conflict of interests: The author has declared that no conflict of interest exists.

How to cite this article?

Sangeetha *et al.*, 2024. Application Biotechnological Tools for Tropical Tuber Crop Improvement. *Biotica Research Today* 6(3), 117-119.

Copyright: © 2024 Sangeetha *et al.* This is an open access article that permits unrestricted use, distribution and reproduction in any medium after the author(s) and source are credited.

Abstract

Tropical root and tuber crops serve as second main food crop after cereals. They are wealthy source of dietary fibres and play key role in the food security of global population. Cassava, sweet potato, yams, taro, tannia and minor tuber crops are the tropical tuber crops mainly cultivated in India. Despite of its agricultural importance most of the tropical tuber crops are not as much of exploited like other food crops. By various modern biotechnological approaches such as next generation sequencing (NGS) with the aid of various omics technologies the various novel traits of tuber crops can be identified. Application of plant biotechnology have already proven as promising technology for developing economically important plant varieties with novel traits even with interspecies crosses. Here we describe the past developments and modern approaches of plant biotechnology for the improvement of tropical tuber crops.

Keywords: Biotechnology, Food, Sweet potato, Tuber

Introduction

The important tropical tuber crops grown in India are given in table 1. These crops are climate resilient with the ability to survive drought, low fertile soils and tolerant to pest and diseases. They play important role in sustainable food production and are also included in the indigenous tribal food system. Africa is the major producer of root and tuber crops followed by Asia, Europe and America (FAO, 2022). Similarly in case of global production of root and tuber crops (32.91%) contributed by cassava followed by (12.72%) by sweet potatoes, (8.23%) by yams and (2.4%) from aroids. They are used as stimulants, tonics, carminatives and expectorants with medicinal properties.

Application of Plant Tissue Culture Techniques in Tropical Tuber Crops

With the application of tissue culture and various biotechnological approaches there was significant increase in production of quality planting material of tuber crops. In case of tuber crops *in vitro* micropropagation of cassava,

sweet potato, taro, elephant foot yam, Xanthosoma, yams and chinese potato was already reported. The cross incompatibility and somatic hybrids of sweet potato and Ipomoea spp. was developed through somatic hybridization and it was first developed in China. Various tissue culture methods such as meristem stem culture, somatic embryogenesis, synthetic seed technology, callus culture and direct adventitious organogenesis were proved as one of the promising technology for sweetpotato production. In vitro mass propagation protocol was developed for A. paeoniifolius using petiole, leaf and corm bud explants. Further tissue-culture-based protocols were developed for generating virus-free plants of yams. Embryo culture and wide crosses was applied for the transfer of desirable traits such as disease insect resistance, yield from wild to cultivated yams.

Molecular Markers for Improvement of Tropical Tuber Crops

With the high-throughput genome sequencing and relatively

Article History

RECEIVED on 15th March 2024

RECEIVED in revised form 25th March 2024

ACCEPTED in final form 26th March 2024



Common Name	Scientific Name	Chromosome No.	Family
Cassava	Manihot esculenta Crantz	2n = 36	Euphorbiaceae
Sweet potato	<i>Ipomoea batatas</i> (L.) Lam.	2n = 90	Convolvulaceae
Greater yam	Dioscorea alata (L.)	2n = 40, 60, 80	Dioscoreaceae
White yam	Dioscorea rotundata (Poir.)	2n = 40	Dioscoreaceae
Lesser yam	Dioscorea esculenta (Lour.) Burk.	2n = 30-100	Dioscoreaceae
Elephant foot yam	Amorphophallus paeoniifolius (Dennst.) Nicolson	2n = 28	Araceae
Taro	Colocasia esculenta (L.) Schott.	2n = 28, 42	Araceae
Tannia	Xanthosoma sagittifolium (L.) Schott.	2n = 26	Araceae
Giant taro	Alocasia macrorrhiza (L.) G. Don.	2n = 28	Araceae
Swamp taro	Cyrtosperma chamissonis (Schott.) Merr.	2n = 26	Araceae
Chinese potato	Plectranthus rotundifolius (Poir.) Spreng.	2n = 60	Lamiaceae
Yam bean	Pachyrhizus erosus (L.) Urban	2n = 26	Fabaceae
West Indian arrowroot	Maranta arundinaceae L.	2n = 48	Marantaceae
Queensland arrowroot	Canna edulis (Ker-Gawler).	2n = 18	Cannaceae
East Indian arrowroot	Curcuma angustifolia Roxb.	2n = 42	Zingiberaceae

Table 1: List of major tropical tuber crops in India

low cost technologies the molecular markers are developed from available tuber crops genome sequences which can be used to accelerate plant breeding programmes. The first molecular markers used in cassava were random amplified polymorphisms (RAPDs) and restriction length polymorphisms (RFLPs), in cassava in 1993 to study the genetic variation. Later the first genetic linkage map of cassava was developed using these markers. These markers were replaced by simple sequence repeat (SSR) markers. Later simple sequence repeat (SSR) markers which was developed from expressed sequence tags (ESTs) replaced all these markers and were still used by several research groups. In 2005 the Diversity Array Technology (DArT) is developed for the first time in cassava. The DArT was tested against cassava SSR marker system and proved with restricted application for cassava germplasm characterization. Later the identification of SNPs made significant progress in cassava breeding through genomics. Overall in cassava the molecular markers were used for the identifications of various traits associated with markers and identification of genes. Resistance gene candidates (RGCs) were isolated and identified in cassava for diseases resistance. About NBS-LRRtype R genes of 500 partial sequences in cassava and other Manihot spp. by comparative genomics approach. Molecular markers associated with disease and pest resistance was identified and being used for developing resistant varieties. Molecular markers were also developed for identification of genes in yams. Dioscorea varieties with improved yield were also developed globally with the aid of molecular markers by various genetic improvement programs.

Application of Genetic Modification of Technology used in Tropical Tuber Crops

The application of transgenic and genomics technologies were recently used in tuber crops for the development

of desirable traits. Various economically important traits were developed in tuber crops by transgenic technology. The Agrobacterium tumifaciens transformation studies of cassava was started in 1993-1994 and successful genetic transformation was first reported at ETH Zurich in Potrykus laboratory in 1996. Somatic embryogenesis and friable embryogenic callus (FECs) were produced in Indian cassava cultivars by genetic transformation methods for cassava mosaic virus resistance. Gene engineering technology was already reported in sweet potato to develop various biotic and abiotic stresses. An efficient Agrobacterium-mediated transformation protocol was established for developing resistance against Dasheen Mosaic Virus (DsMV) in elephant foot yam. The Agrobacterium-mediated transformation was the widely used technique for gene transfer in yams.

Omics Technology for Unraveling Gene Function and Regulation in Tropical Tuber Crops

Cassava (Manihot esculenta) is most important among tropical crop which is cultivated globally. Cassava brown streak disease (CBSD) and Cassava mosaic disease (CMD) are the two major diseases which affect the production of the crop, livelihoods of farmers and lead to significant yield losses. Developing host plant resistance against pathogen is one of the alternate strategy and modern genomics approaches can speed up the process of developing resistant varieties (Lyons et al., 2022). Due to the complex genome size a reference genome sequence data is important for molecular breeding in all tuber crops. The sweet potato genome sequencing was difficult due to the highly large complex heterozygous hexaploid genome. The first sweet potato genome sequence was reported for carotenoidrich cultivar (Yang et al., 2017). Crop wild relatives (CWRs) posses many economically important traits and have been used in many breeding programmes. About 900 species

of wild *Ipomoea* are slackly considered to be the CWRs of cultivated sweet potato. The genome sequences of several *Ipomoea* spp. and database about these CWR of sweet potato are available for the crop improvement programme (Yan *et al.*, 2022).

Gene Editing Approaches in Tuber Crops

The gene editing technique, the clustered regularly interspaced short palindromic repeats (CRISPR/Cas9) system is most recent method for genome editing in many plants. This genome editing technique was applied to cassava, sweet potato and yams for developing various important traits related to nutritional aspects (Ntui *et al.*, 2024).

Conclusion

Biotechnology tools have been applied for the development of tropical tuber crops from past 20 years and the complex genome of various tuber crops was studied with the application of whole genome sequencing techniques. These modern techniques created opportunities for understanding the complexity of major tuber crops for improved yield and nutritional quality. However these findings are yet to be utilized for the advancement of underutilized minor tuber crops. Moreover in the near future the application of plant biotechnology research should be focused for studying the novel traits of CWR of the tropical tuber crops which will significantly help to unlock their unknown genetic potential for improvement of tropical tuber crops.

References

FAO, 2022. World Food and Agriculture - Statistical Yearbook 2022. In: *FAO Statistical Yearbook - World Food and Agriculture*. FAO, Rome, Italy. p. 382. DOI: https://doi. org/10.4060/cc2211en.

- Lyons, J.B., Bredeson, J.V., Mansfeld, B.N., Bauchet, G.J., Berry, J., Boyher, A., Mueller, L.A., Rokhsar, D.S., Bart, R.S., 2022. Current status and impending progress for cassava structural genomics. *Plant Molecular Biology* 109, 177-191. DOI: https://doi.org/10.1007/s11103-020-01104-w.
- Ntui, V.O., Tripathi, J.N., Kariuki, S.M., Tripathi, L., 2024. Cassava molecular genetics and genomics for enhanced resistance to diseases and pests. *Molecular Plant Pathology* 25(1), e13402, DOI: https://doi. org/10.1111/mpp.13402.
- Yan, M., Nie, H., Wang, Y., Wang, X., Jarret, R., Zhao, J., Wang, H., Yang, J., 2022. Exploring and exploiting genetics and genomics for sweetpotato improvement: Status and perspectives. *Plant Communications* 3(5), 100332. DOI: https://doi.org/10.1016/j.xplc.2022.100332.
- Yang, J., Moeinzadeh, M.H., Kuhl, H., Helmuth, J., Xiao, P., Haas, S., Liu, G., Zheng, J., Sun, Z., Fan, W., Deng, G., Wang, H., Hu, F., Zhao, S., Fernie, A.R., Boerno, S., Timmermann, B., Zhang, P., Vingron, M., 2017. Haplotype-resolved sweet potato genome traces back its hexaploidization history. *Nature Plants* 3, 696-703. DOI: https://doi.org/10.1038/s41477-017-0002-z.