AgriCos e-Newsletter
ISSN: 2582-7049
AgriCos e-Newsletter
Open Access Multidisciplinary Monthly Online Magazine
Volume: 03 Issue: 06 June 2022 Article No: 24

DNA Fingerprinting of Safflower (*Carthamus tinctorius*) Crop

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SUMMARY

The various studies done on genetic diversity had provided us the information that safflower originated from different geographical regions have similarity between the genotypic clusters. Currently the DNA fingerprinting techniques have helped to identify drought responsive gene in safflower and many other genes responsible for the agro– morphological traits that help in improving the agronomic traits. DNA fingerprinting of the safflower has helped in determining the individual DNA characteristic of various species of safflower. Thus, the DNA finger printing helps in the study of the genetic diversity of the safflower.

INTRODUCTION

Carthamus tinctorius (2n = 2x = 24), commonly known as safflower, is a member of the tribe *Cynareae*, sub-family *Tubulifloreae*, and family *Asteraceae*. The eastern part of the Mediterranean region is regarded *asthe* centre of origin of the genus. India ranks first in the production of safflower oil (50% of total world production) with ~0.4 million hectares under cultivation. In the past few decades, many promising cultivars have been released by the All India Coordinated Research Projects on Oilseeds (AICORPO). These cultivars cover ~90% of the total acreage of cultivation in various agro-climatic regions of India. Safflower is a traditional oilseed crop in the world. Its seed oil is a healthy edible oil containing high amount of unsaturated fatty acids. Genetically diverse exotic cultivars are valuable germplasm for introducing new diversity in safflower improvement programmes. Safflower (*Carthamus tinctorius L.)* is an annual oilseed crop adapted chiefly to the warm climatic areas of Iran, which recently commercialize to become and concentrated to produce oil.

Fig.1. Genomics of safflower

In 1985 the concept of a "DNA fingerprinting" was introduced as a means of evaluating human identity and relatedness . The possible forensic and legal applications of DNA evidence were quickly appreciated and such data are now frequently presented in court cases involving serious crimes such as murder and rape. DNA evidence is also used in establishing paternity, in determining relatedness in immigration and inheritance disputes, and in identifying disaster victims. Such cases, especially those involving famous people, are widely reported in the media and are of interest to the general population. DNA fingerprinting technology has now been extended from humans to even plants. In plants, identification of cultivars is one area where DNA fingerprinting is being used routinely and has applications in protection of plant breeders' and farmers rights. Before the advent of DNA fingerprinting by various molecular DNA markers, the precise cataloguing of the cultivars was an impossible task. In the present study, we assayed various regions of the genome of released safflower cultivars by RAPD, ISSR, and AFLP markers with a view to not only fingerprint the cultivars and assess their relative diversity but also to identify the primer(s) most suitable for fingerprinting safflower cultivars as well.

Fig.2.DNA fingerprinting of safflower

Development of non-spiny safflower crop:

Realizing that safflower harvesting is done manually, to facilitate its introduction in non-traditional areas, A.R. Sawant, working at the College of Agriculture of the Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV) in Indore, Madya Pradesh, embarked on a project to breed high-yielding spineless safflower. In this endeavor, he was assisted for some years by a grant by the International Development Research Centre (IDRC) from Canada. JSI-7, the first-ever spineless cultivar in India, was released in 1990. A decade later, in 2000, the spineless NARI-6 was released by NARI, providing a dual income to farmers, as the florets can easily be collected from non-spiny safflower after the crop matures and is thus sold for food and textile dye.

Improvement of oil content:

The efforts for improving oil content in safflower resulted in the development of a non spiny safflower cultivar, NARI-6, containing 35% oil in its seeds. It was released for commercial production in 2001 and the development and release of a genetic male sterility based, non spiny hybrid, NARI-NH-1, giving seed oil contents of 35%, was released in 2002. In addition, a thermo sensitive genic male sterile (TGMS)-based hybrid NARI-H-23, having 35% oil in its seeds, has been developed and was released for commercial cultivation in 2014. Continued efforts to further enhance oil content have paid rich dividends and as a result NARI has developed a safflower variety, NARI-57, giving oil contents as high as 38–39%. This cultivar has been released for commercial production in India in 2015.

Introducing disease resistant plants:

Wilt-resistant varieties of safflower viz. NARI-38 and NARI-57, were developed for commercial production in India during 2007 and 2015, respectively. The development of wilt-resistant cultivars has made safflower production, in areas endemic to wilt, highly sustainable because of an enhanced yield due to a lack of wilt compared with wilting of up to 80% in wilt-susceptible cultivars.

Introducing pest resistant plants:

Aphid resistance in safflower is reported to be under the control of both additive and non additive gene actions with a predominance demonstrated for non additive gene action (Singh and Nimbkar,1993). Breeding for aphid resistance has been initiated recently in India since it is the most economical, time-tested, and eco-friendly method for controlling aphids. Aphid-tolerant safflower reduces the usage of harmful chemicals. This in turn helps to reduce the cost of crop production and keeps the environment safe by way of avoiding chemical usage. This all leads to a more sustainable production of safflower.

Development of Short-Duration Safflowers:

In India, the high suitability and profitability of the extra early variety, JSI-99, under non conventional areas of safflower production has been demonstrated (Deshpande et al., 2005). Ramamurthy (2013) indicated that short-duration varieties maturing in 70–100 days need to be developed in safflowers since this is the length of the growing period in most safflower-growing areas. The reduced length of growing period adversely affects the seed yield of presently grown varieties with 125–130 days to maturity.

In view of the above, short-duration safflowers developed at NARI are able to meet their requirements of nutrient and moisture from poor soils. Improvement of yielding ability of short-duration safflowers would further enhance their profitability and sustainability over other crops grown in such soils.

CONCLUSION

Recent years witnessed an interest from the industrial sector in safflower for production of plant made pharmaceuticals and industrial proteins through molecular farming. However, crop breeding programmes are not being complemented adequately with the biotechnological tools. The structural genetic map of safflower is not available till date. Safflower has enormous variability and several traits could be genotyped through the available molecular marker systems. Genotyping should invariably be carried out along with phenotypic trait evaluation for maximizing gain from selection. Rich genomic resources are available for other taxa of *Asteraceae* viz., *Lactuca sativa* and *Helianthus spp*. and safflower could be an ideal candidate crop to have advancements in genomics through comparative mapping. Safflower is amenable to manipulations in vitro and genetic transformation protocols through vector mediated gene transfer are in place providing scope for development of transgenic for desirable traits. In safflower, anthers and microspores are known to have great susceptibility for shoot regeneration in vitro and this offers possibilities in marker assisted breeding through development of doubled haploid population. Wild Carthamus species constitute a rich range of genes for biotic and abiotic stresses besides oil quality traits and need to be utilized. Pre-breeding through intra specific and inter specific genetic enhancement coupled with marker aided selection will accelerate the breeding programmes. Nevertheless, safflower research is scattered and there is an immediate need for determining regional and international priorities and forming core work groups as in other crops for tapping the idle potential of safflower.

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