

2. Towards improvement of oil content in safflower (*Carthamus tinctorius* L.)

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Safflower (*Carthamus tinctorius* L.) is a multi-purpose oilseed crop grown for vegetable oil, animal feed, natural dyes and medicinal uses globally (Knowles 1989; Li and Mündel 1996). It is a traditional oilseed crop of India, primarily known for its healthy cooking oil containing more than 80% of polyunsaturated fatty acid (PUFA), the highest among edible oils (Kostik *et al.* 2012). Despite economic importance, safflower cultivation is declining in India, from 10 lakh ha. in 1988 to 1.5 lakh ha. in 2013 (FAOSTAT 2013). Seed oil content in the popular cultivars remains low (~28-32%), which is a concern for increasing the profitability of safflower cultivation. Increase of oil content in the cultivar would eventually lead to increase in oil yield, which would make safflower a commercially competitive crop for the farmers and attract the vegetable oil industry to take up safflower promotion in the country. We are exploring various strategies including the introduction of exotic high oil germplasm/ varieties, conventional and molecular breeding to enhance oil content coupled with high seed yield in safflower.

A total of 38 genotypes (30 from Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias-INIFAP, Mexico; 8 from United States Department of Agriculture-USDA) were imported through NBPGR, New Delhi and they were evaluated for oil content

along with Indian check varieties at research farm of DOR, Hyderabad. Twenty varieties recorded more than 35% oil content with the maximum of 41% (EC 736516-Centennial, a USDA variety) compared to the checks: A-1 (26%), Bhima (31%) and NARI-57 (37%). High oil content in the Mexican varieties was also confirmed in multi-location trials conducted by AICRP-safflower centres at Indore, Parbhani, Phaltan and DOR. The mean oil content of Mexican varieties ranged from 35.1% to 37.8% whereas the high oil check variety NARI-57 recorded 35.8% at four locations. In order to further establish the potential of the exotic varieties, genetic distance between Indian and Mexican safflower cultivar groups was analyzed by SSR markers. Sixty cultivars (30 from Mexico; 30 from AICRP-safflower centres in India) were genotyped using 48 randomly chosen SSR loci. Cluster analysis based on Neighbour-Joining (NJ) tree method clearly showed that Indian and Mexican safflower cultivars were genetically distinct ($F_{ST} = 0.396$). Overall, the phenotypic and molecular characterization of Mexican safflower varieties suggested that they provide genetically diverse sources of seed yield and high oil traits for Indian breeding programmes.

We have initiated a breeding programme to develop cultivars with high oil yield potential by

crossing the exotic high oil germplasm sources with Indian safflower varieties *viz.*, A-1, Bhima, PBNS-12 and NARI-57. Currently, the cross between NARI-57 and Centennial has been analyzed for inheritance and selection of desirable breeding progenies. The oil content of F_3 seeds of 248 F_2 progenies of this cross ranged from 19% to 44% with an average of 35% indicating quantitative nature of inheritance. The seed yield per plant of these 248 F_2 progenies ranged from 1.5 g to 82 g while the seed yield per plant of NARI-57 and EC 736516 were 38.3 g and 12.4 g, respectively. A set of F_3 and F_4 families that showed high seed yield coupled with high oil content (~40%) have been identified through pedigree method of selection, which are under field evaluation. Development of multi-parent advanced generation intercross (MAGIC) population (Bandillo *et al.* 2013) is in progress to facilitate genetics research and selection of breeding lines with high oil content coupled with high seed yield.

Historically, combining high oil content with high seed yield has been a challenge in safflower (Ranga Rao *et al.* 1977). Molecular markers offer promise for dissecting genetic basis of complex quantitative traits such as seed yield and

oil content and further combining desirable genes/alleles to achieve high oil yield. Nothing is known about genes controlling seed yield components and oil content in safflower except some reports on molecular tagging of genes for oil quality *viz.*, *li* - high linoleic acid content, *tph2* - high tocopherol content and *ol* - high oleic acid content (Hamdan *et al.* 2008; García-Moreno *et al.* 2011; Hamdan *et al.* 2012; Liu *et al.* 2013). We are exploring a combination of traditional QTL mapping and candidate gene based allele mining approaches, using bi-parental/MAGIC populations and germplasm panels, to detect genes and alleles contributing to increased oil content in safflower. Our initial characterization of 148 safflower accessions representing morphological and geographical diversity using 50 SSR loci revealed very weak population structure in the germplasm collection suggesting that genetic diversity is randomly distributed and not constrained by geographical locations/origins. We also observed very low SSR allelic diversity, which is a concern and there is a need to design SNP markers. Currently, lack of reference genome sequence and high density genetic linkage map are the major limitations, which need to be addressed to expedite trait mapping and marker-assisted selection in safflower.

