

RESEARCH PAPER

Discrimination of castor (*Ricinus communis* L.) genotypes through SSR marker

AMAR A. SAKURE¹, H.L. DHADUK², D.R. MEHTA² AND R.B. MADARIA²

¹Department of Biotechnology, Anand Agriculture University, ANAND (GUJARAT) INDIA

²Department of Agricultural Botany, Junagadh Agriculture University, JUNAGADH (GUJARAT) INDIA

Email : sakure.amar455@gmail.com

Castor (*Ricinus communis* L.) is one of the most ancient, non-edible oilseed crop. It is a highly polymorphic due to higher percentage of cross pollination. New genetic approaches have been developed, like molecular marker technology which adopted to map the castor genome, in order to select better cross combinations for popular hybrids. Genetic diversity in twenty two castor genotypes were assessed using SSR marker which gave higher percentage (90.90%) of polymorphic loci, higher heterozygosity (52%) and a greater range of genetic diversification for discriminating among them. In SSR analysis, a total 29 alleles were generated. The data revealed from ten markers, that genotypes JI-220, JI-353, JP-102 and JI-377 showed high genetic dissimilarity so, it is very important to improve the castor crop with the help of hybridization and crop improvement programme. The information gathered here would be helpful in genomic mapping studies with wider and diverse genetic background to obtain improved crop productivity.

Key words : Castor, SSR, Genetic diversity, Molecular marker

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INTRODUCTION

Castor (*Ricinus communis* L., $2n = 2x = 20$, Euphorbiaceae), is one of the most ancient, non-edible oilseed crops of the world valued for its medicinal and industrial application. Though castor oil is the chief commercial commodity, castor cake is also a good source of nitrogen (5.5 %) and widely used as manure but it is unfit for cattle feed due to presence of ricin. Dried stalks of castor are used for fuel in rural areas. Castor oil is chiefly used as a lubricant in high-speed engines, for the production of paints and varnishes, synthetic resins, fibre and nylon and in pharmaceutical due to its laxative properties and has many other industrial uses. The area, production and productivity of castor in India 10.54 lakh tones during 2007-2008 from area 7.87 lakh hectares with productivity level of 1339 kilogram per hectare contributing about 40 per cent of the world requirement (Anonymous, 2009). The other castor growing countries in the world are Brazil, China, Russia, Thailand, U.S.A. and a group of African countries. Castor is a highly polymorphic normally monoecious with pistillate flowers are situated on the upper part and

staminate flowers on the lower part of raceme. Though it is a cross-pollinated crop, most of the cultivars have been developed through hybridization followed by selection. New genetic approaches like molecular marker technology have been adopted to map the castor genome, in order to select better cross combinations to develop popular hybrids. Genetic markers have polymorphic genetic properties which can be used to distinguish the parental origin of alleles (Andersen and Lubberstedt, 2003). This genetic marker can be used to identify the genes that are responsible for genetic variation of economically important traits. Most traits and of interest in plant breeding such as productivity and resistance to biotic and abiotic stresses are determined by more than one gene or even large number of genes that are called quantitative traits. The identification of the major loci influencing these traits can be used to assist in the selection of desired plants (Masojc, 2002). Among the various DNA-based markers, amplified fragment length polymorphism (AFLP), random polymorphic DNA (RAPD) and restriction fragment length polymorphism (RFLP) have been used to study genetic diversity. These markers elucidate the phylogenetic relationships among various lines, for their efficient use in breeding and genetic