

Research Paper :

Genetic diversity among different *Ricinus communis* genotypes for Fusarium wilt through molecular markers



RASHMIN M. DHINGANI, RUKAM S. TOMAR, MANOJ V. PARAKHIA AND B. A. GOLAKIYA

International Journal of Plant Protection, Vol. 4 No. 2 (October, 2011) : 390-396

SUMMARY

Castor (*Ricinus communis* L.) is an important plant for production of industrial oil. The systematic evaluation of the molecular diversity encompassed in castor offers an efficient means of exploiting the heterosis in castor as well as for the development of disease resistant varieties. Three DNA-based molecular marker techniques, viz., random amplified polymorphism DNA (RAPD), simple sequence repeat (SSR) and inter simple sequence repeat (ISSR), were used to assess the genetic diversity in castor genotypes. Out of 27 RAPD, 15 SSR and 17 ISSR primers screened, a total of 29 polymorphic primers (11 RAPDs, 8 SSRs and 10 ISSRs), were used in this study. Amplification of genomic DNA of 9 genotypes, using RAPD analysis, yielded 83 fragments, of which 64 were polymorphic, with an average PIC value of 0.59. Number of amplified fragments with RAPD primers ranged from 2 to 13, with the size of amplicons ranging from 100 to 3000 bp in size. The polymorphism ranged from 54.54 to 100.0, with an average of 81.81 per cent. Similarly, SSR analysis yielded 10 fragments, of which 5 were polymorphic, with an average PIC value of 0.14. The 10 ISSR primers produced 71 bands across 9 genotypes, of which 54 were polymorphic, with an average PIC value of 0.25. The number of amplified bands varied from 3 to 15, with size of amplicons ranging from 100 to 2500 bp. The percentage of polymorphism using ISSR primers ranged from 38 to 100.0, with an average of 76.02 per cent. Clustering of genotypes within the groups was not similar when RAPD, SSR and ISSR derived dendrograms were compared, whereas, the pattern of clustering of the genotypes remained akin in RAPD and combined data of RAPD, SSR and ISSR. The similarity coefficient ranged from 0.61 to 0.98, 0.66 to 1.00, 0.62 to 0.83 and 0.65 to 0.85 with RAPD, SSR, ISSR, and combined dendrogramme, respectively. Knowledge on the genetic diversity of castor can be used to future breeding programs for increased oil production to meet the ever increasing demand of castor oil for industrial uses as well as for biodiesel production.

See end of the article for authors' affiliations

Correspondence to :
RUKAM S. TOMAR
Department of
Biotechnology,
Junagadh Agricultural
University,
JUNAGADH
(GUJARAT) INDIA

Key words :

Genetic diversity,
Ricinus communis,
Fusarium wilt,
Molecular marker

Received :

July, 2011

Revised :

August, 2011

Accepted :

September, 2011

Dhingani, Rashmin M., Tomar, Rukam S., Parakhia, Manoj V. and Golakiya, B. A. (2011). Genetic diversity among different *Ricinus communis* genotypes for Fusarium wilt through molecular markers. *Internat. J. Plant Protec.*, 4(2): 390-396.

Castor plant is a tropical plant that belongs to family Euphorbiaceae and is grown for its non-edible oilseed. In scientific terms, this plant is also termed as *Ricinus communis*. It is cultivated around the world because of the commercial importance of its oil. India is the world's largest producer of castor seed and meets most of the global demand for castor oil. India contributes 750,000 tons annually, and accounting for over 60 per cent of the entire global production.

Castor is an industrial oilseed crop. Because of its almost unlimited industrial applications, castor oil enjoys tremendous world demand. India is the world's top producer and

exporter of castor. Wilt (*Fusarium oxysporum* f.sp.*ricini*) is the major disease of castor (*Ricinus communis*) in India and it can cause 80–100% crop damage. Fusarium wilt is a common fungal vascular wilt disease. The pathogen that causes Fusarial wilt is *Fusarium oxysporum*. It affects a wide variety of hosts of any age and generally produces symptoms such as wilting, chlorosis, necrosis, premature leaf drop, browning of the vascular system, stunting, and damping-off.

Characterization of the genetic basis of resistance to *F. oxysporum* in castor germplasm based on molecular marker-assisted selection strategies will allow easier effective