

# Current Perspectives on Application of Biotechnology to Assist the Genetic Improvement of Rubber Tree (*Hevea brasiliensis* Muell. Arg.): An Overview

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# ABSTRACT

*Hevea* rubber clones are intensively cultivated in tropical regions of the world as main sources for Natural Rubber (NR) production which is one of the important raw materials for many industries. However, the heterozygous nature, long breeding time of trees and the prolonged period required for evaluation of mature traits are strong limitations for conventional breeding and selection methods. The development of methods for *in vitro* culture and genetic engineering has increased the possibility of producing rubber genotypes with improved latex yield, tolerance to tapping panel dryness (TPD) syndrome, growth rate and wood quality or reduction in undesirable traits. The combination of conventional breeding and molecular techniques will help to develop rubber trees with positive effects on the environment. However, the risks associated with the biotechnological applications should be carefully evaluated and field trials are to be performed with transgenic rubber tree. Genomic technologies were taken up by various research groups working on *Hevea* to identify new targets for breeding and/or complementary genetic transformation. In addition, molecular markers can provide simultaneous and sequential selection of agronomically important genes in *Hevea* breeding programs and effectively replace time consuming bioassays in early generation screens. With the advent of molecular techniques, several genes involved in rubber biosynthetic pathway have been characterized. Both HMGR and HMGS are essential enzymes involved in early steps of rubber biosynthesis. Among the genes identified, *REF* is a key rubber biosynthetic gene involved in polymerization of isoprene chain. However, further research is needed to use these identified genes for genetic manipulation of rubber tree. Most recently, a set of genes associated with TPD has been identified by SSH analysis. This review provides a comprehensive picture on rubber biotechnological research achievements in the last two decades.

Keywords: biotechnology, genetic engineering, molecular markers, tapping panel dryness, tissue culture, rubber biosynthesis related genes

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# INTRODUCTION

Natural rubber (cis-1,4-polyisoprene), an isoprenoid polymer composed of 320 to 35,000 isoprene molecules, is produced in about 2000 plant species with varying degrees of quality and quantity. At present, the Brazilian rubber tree (*Hevea brasiliensis* Muell. Arg., 2n=36) is one of the most important commercial sources due to its high rubber content

and quality (Backhaus 1985). Natural rubber is considered a vital raw material by developed countries and is valued for its high-performance characteristics. Synthetic rubber, derived from petroleum is not as elastic or resilient and does not have the heat transfer properties of natural rubber. Although synthetic rubber is often blended with natural rubber, various products, such as airplane tires require natural rubber. Also, synthetic rubber is obtained from a nonrenewable resource, whereas natural rubber is available indefinitely from renewable plant sources. Rubber tree is a perennial crop which belongs to the genus Hevea and to the botanical family Euphorbiaceae. The genus Hevea encompasses ten species, all originated from the Amazon region and all are strongly outcrossing and monoecious (Schultes 1990). Only one species, H. brasiliensis, is cultivated commercially for latex biosynthesis (rubber production). Among the other nine species, only H. benthamiana produces latex of reasonable quality, but this species has rarely been used in breeding programs. In H. brasiliensis, rubber biosynthesis takes place on the surface of rubber particles suspended in the latex (the cytoplasm of laticifers). The laticifers are specialized vessels that are located adjacent to the phloem of the rubber tree. When severed during tapping, the high turgor pressure inside the laticifers expels latex containing 30-50% (w/w) cis-1,4-polyisoprene.

In breeding and selection method of any crop species, one of the most important parameters is to bring together traits of agronomical interest. Genetic improvement of Hevea has been very slow and time-consuming, as in many other perennial crops, the major limitations being its very narrow genetic base, non-synchronous flowering, low fruit set, long gestation period, heterozygous nature, insufficient availability of land for field experiments and the absence of fully reliable early selection parameters. Furthermore, conventional breeding is rather difficult due to the heterozygous nature of the crop and its long juvenile phase that includes 6-7 years before latex collection. Cultivated clones are propagated vegetatively by grafting. As a rule, the rubber tree displays inbreeding depression, making it difficult to develop appropriate progenies for classical studies (Lespinasse et al. 2000a). Therefore, the most appropriate process is the selection of suitable genotypes. At any rate, the selection or breeding scheme of superior Hevea clones addresses important questions regarding the choice of traits, the methodology and how the results should be interpreted in order to provide farmers with new, superior clones. To this end, we should also take into consideration the climatic conditions and the tree variability. In spite of all these difficulties, rubber breeding programmes are in progress to develop improved clones in various rubber growing countries including India. Nowadays, a selection scheme of clones or individuals is underway using rapid genetic selection techniques and variability identification. Even though the number of laboratories working on rubber is restricted mainly to tropical countries, molecular markers have been established in less than a decade to set the basis in order to distinguish, characterize or identify clones, to estimate germplasm variability and to trace Hevea origin. Moreover, a number of genes involved in rubber biosynthesis have been recently isolated. This has helped to shed light on the regulation of rubber biosynthesis of this important crop. However, since we are only at the beginning, we need further investigation in order to find clues on how the rubber biosynthesis and the variability of quantitative and qualitative latex yield traits are regulated.

Although, traditional breeding of *Hevea* has limitations, improved clones have been produced by using conventional methods and there is a strong need for additional methods for genetic improvement. In concert with traditional plant breeding practices, biotechnology is contributing towards the development of novel methods to genetically alter and control plant development, plant performance and plant products. Conventional breeding utilizes domestic crops and related genera as a source of genes for improvement of existing cultivars, and this process involves the transfer of a set of genes from the donor to the recipient. In contrast, biotechnological approaches can transfer defined genes from any organism, thereby increase the gene pool available for improvement. The improvement of Hevea by biotechnological approaches primarily involves introduction of exogenous genes in a heritable manner, and secondarily, the availability of genes that confer positive traits when genetically transferred into Hevea. The development of in vitro technologies has thus complemented the conventional methods of *Hevea* breeding in generating elite clones via somatic embryogenesis. The genetic improvement of Hevea has received considerable attention over the years from plant breeders with the purpose of increasing the latex yield and to minimize crop loss due to various stresses including tapping panel dryness syndrome. The introduction of foreign genes encoding for useful agronomic traits into commercial clones has resulted in saving precious time required for introgression of the desired trait from the wild relatives by conventional practices (Jayashree et al. 2003; Sobha et al. 2003a). Therefore, in recent years, Hevea improvement efforts have been focused on raising genetically altered plants with high yield potential, capable of producing value added products such as recombinant protein and tolerant to abiotic stresses such as TPD (tapping panel dryness) according to the regional requirement of the crop. Though considerable progress has been made to improve the latex yield in *Hevea* in the recent past, TPD is one of the important physiological factors to limit the latex production in rubber plantations across world. It is estimated that 20-40% of annual rubber production was affected by the TPD syndrome (Chen et al. 2003). Therefore, development of new clones tolerant to TPD is one of the prerequisites in *Hevea* improvement.

The ever increasing demand for natural rubber has made it imperative to develop in vitro techniques for rapid propagation of elite H. brasiliensis. Also tissue culture and genetic manipulation are potential techniques that could be used in selection of elite plants for Hevea improvement. Initially attempts were made to propagate Hevea via shoot tip culture and haploid plants via anther culture. However, the difficulties associated with plantlet regeneration from microspores have compelled researchers to look for alternate target explants with better regeneration capabilities. Therefore, attention shifted to somatic embryogenesis and embryogenic callus cultures derived from tissues of immature anther and inflorescences. Detailed information on tissue culture, haplogenesis, somatic embryogenesis, protoplast culture of Hevea from different explants is available in various reviews and so has not been dealt with in detail here (Carron et al. 1989, 1995a, 1995b, 2001, 2005) (Table 1). In recent years, with the development of suitable regeneration protocols, somatic embryogenic calli derived from immature anthers and inflorescences are emerging as suitable target tissues for genetic transformation experiments (Kumari Jayashree et al. 1999; Sushamakumari et al. 2000a). The last two decades have witnessed the widespread use of micropropagation approaches for development of 'true-to-type' clones in Hevea. Isolated embryos cultured in vitro on suitable solid culture medium could develop into normal plantlets. In Hevea, successful plant regeneration from immature anther explants via somatic embryogenesis has been demonstrated by Kumari Jayshree et al. (1999). However, there are still some difficulties due to low efficiency of regeneration. To date, the Agrobacterium-mediated approach has been the most successful method for delivering foreign genes into Hevea (Jayashree et al. 2003; Sobha et al. 2003a).

In conventional breeding, molecular genetic markers are powerful tools that could enhance the speed and effectiveness of rubber breeding. General advantages of DNA markers include their ability to reveal the sites of variation in DNA segments among many individuals, their abundance and distribution over the whole genome and their independence from the variations of the environment. The process of using such markers as selection criteria is called Marker-Assisted Selection (MAS), the methodology of which is still at research level in rubber. There are several types of molec-

Table 1 Sum	mary of in	vitro research	applied to	Hevea	brasiliensis.
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Table 1 Summary of <i>in vitro</i> research applie		
Explants used	Results	References <sup>a</sup>
Micropropagation		
Shoot apices	PD, RD	Paranjothy and Ghandimathi 1975, 1976
Somatic embryos	PD	Carron and Enjalric 1982
Axillary buds from young trees	PD, RD	Enjalric and Carron 1982
Rubber rootstocks	PD	Carron and Enjalric 1983
Shoot tips from immature seedling	PD	Gunatilleke and Samaranayake 1988
Shoot tips, internodes	PD, RD	Te-chato and Muangkaewngam 1992
Apices from mature shoots	PD, RD	Perrin et al. 1994
Axillary buds	PD, RD	Seneviratne et al. 1995
Nodal explants from juvenile plants	PD, RD	Seneviratne and Flegmann 1996
Shoot tips	PD	Seneviratne 1991
Axillary buds from mature clones	PD, RD	Perrin et al. 1997
Axillary buds	PD	Seneviratne and Wijesekara 1996
Axillary buds	PD	Lardet et al. 1999
Nodal explants	PD	Lardet <i>et al.</i> 1999
Axillary buds	PD, RD	Mendanha <i>et al.</i> 1998
Shoot tips	PD	Kala <i>et al.</i> 2004
Organogenesis	10	
Cotyledon, hypocotyls, epicotyl	RD	Paranjothy and Ghandimathi 1975, 1976
Mature embryonic axes	PD	Paranjothy and Ghandimathi 1975, 1976
Young stem	CD, RD	Wilson and Street 1974
Stamens		Wilson and Street 1974
	CD, PD	
Leaves	CD, ED	Carron and Enjalric 1982
Leaves	CD, PD	Mendanha <i>et al.</i> 1988
Callus from inner integument	ED	Blanc <i>et al.</i> 2002
Anther/microspore culture	~-	~
Anther	CD	Satchuthananthabale and Irugalbandra 1972
Anther	CD	Satchuthananthabale 1973
Anther	CD, ED	Paranjothy 1974
Anther	CD, CD	Ghandimathy and Paramjothy 1975; Paranjothy and Ghandimathy 1975, 1976
Anther	CD, ED, PD	Paranjothy and Rohani 1978
Anther	CD, ED, PD	Chen et al. 1978, 1979, 1981, 1982; Chen 1984
Anther	CD, ED, PD	Shijie et al. 1990
Anther	CD, ED	Das et al. 1994
Isolated microspore culture	CD	Jayashree et al. 2005
Isolated microspore	CD	Jayashree et al. 2005
Somatic embryogenesis		
Anther	CD, ED, PD	Paranjothy 1974
Anther	CD, ED	Paranjothy and Ghandimathi 1975
Anther	CD, ED, PD	Paranjothi and Rohani 1978
Anther	CD, ED	Wang <i>et al.</i> 1980, 1984
Anther		Carron and Enjalric 1982
	CD, ED	5
Anther	CD, ED, PD	Wan et al. 1982
Integument tissue	CD, ED, PD	Carron and Enjalric 1985
Integument tissue	CD, ED	EI Hadrami <i>et al.</i> 1991, 1992
Integument tissue	CD, ED, PD	Etienne <i>et al.</i> 1993a, 1993b
Integument tissue	CD, ED	Montoro <i>et al.</i> 1993
Integument tissue	CD, ED	Veisseire et al. 1994a, 1994b
Integument tissue	CD, ED, PD	Asokan et al. 1992
Stamens	CD, ED, PD	Wang and Chen 1995
Immature anthers	CD, ED, PD	Kumari Jayasree et al. 1999
Immature inflorescence	CD, ED, PD	Sushamakumari et al. 2000a, 2000b
Leaf	CD, ED, PD	Kala et al. 2005
Roots	CD, ED, PD	Sushamakumari et al. 2006
Protoplast culture		
Immature leaves	PI, PF, FD	Cailloux and Lleras 1979
Stem pith cell suspensions	PI, FD	Rohani and Paranjothy 1980
Stem tissues	PI, FD	Wilson and Power 1989
Anther callus and cell suspension	PI, PF	Haris <i>et al.</i> 1993
Embryonic callus	PI, PPD, MCF	Cazaux and d'Auzac 1994
Stem tissues	PI, FD	Cazaux and d'Auzac 1994 Cazaux and d'Auzac 1995
Embryogenic cell suspension	2	
	PPD	Sushamakumari <i>et al.</i> 2000b
Embryogenic cell suspension	PPD	Sushamakumari et al. 2002
Genetic transformation		· · · · · · · · · · · · · · · · · · ·
In vitro and in vivo derived seedlings	Developed tumour cells	Arokiaraj and Wan 1991
Anther callus	TPR	Arokiaraj <i>et al.</i> 1994
Anther callus	TPR	Arokiaraj <i>et al.</i> 1996
Anther callus		Arokiaraj <i>et al.</i> 1998
Friable callus from inner integument of	TC	Montoro et al. 2000
immature fruit		
Anther callus	TPR	Arokiaraj <i>et al.</i> 2002
Anther callus	TPR	Jayashree et al. 2003
Anther callus	TPR	Sobha <i>et al.</i> 2003a, 2003b
Embryogenic callus from inner	TPR	Montoro et al. 2003
integument of immature fruit		
Embryogenic callus from inner	TPR	Blanc <i>et al.</i> 2005
integument of immature fruit		
Embryogenic callus from anther	TCD	Rekha et al. 2006
		halam et al. 2006a, Clement-Demange et al. 2007.

<sup>a</sup> For more information refer to reviews by Thulaseedharan *et al.* 2000, Venkatachalam *et al.* 2006a, Clement-Demange *et al.* 2007. Abbreviations: CD, callus development; ED, embryo development; MCD, micro calli development; PI, protoplast isolation; PD, plant development; PPD, protoplast division; RD, root development; TCD, transgenic callus development; TPP transgenic plant production.

ular genetic markers currently used: Restriction Fragment Length Polymorphism (RFLP), Random Amplification of Polymorphic DNA (RAPD), Amplified Fragment Length polymorphism (AFLP), Single Sequence Repeats (SSR) or Sequence Tagged Microsatellite Sites (STMS), DNA Amplification Fingerprinting (DAF), Microsatellite Primed-PCR (MP-PCR), and Single Nucleotide Polymorphism (SNP).

Recent reviews have been published on agricultural practices (Thulaseedhran *et al.* 2000; Priyadarshan 2003), breeding (Priyadarshan *et al.* 2004), genetics (Clément-Demange *et al.* 2007) and transformation (Venkatachalam *et al.* 2006a) of *Hevea*, so this review will concentrate on biotechnology and molecular biology of this species. An attempt to give an overview on the most important topics related to *Hevea* biotechnology is made, but due to the broad spectrum of the review, some omissions are unavoidable.

#### APPLICATIONS OF TISSUE CULTURE

#### Shoot tip culture

As the conventional method of propagation may lead to undesirable stock-scion interactions, the clonal propagation of Hevea by tissue culture is a relevant technique to a greater extent. The production of uniform individual plants is one of the main objectives for in vitro propagation of Hevea. Several reports are available on *in vitro* propagation of Hevea using different explants, mostly derived from seedlings (Seneviratne 1991; Seneviratne and Wijeskara 1996). Initially, Paranjothy and Ghandimathi (1975, 1976) made an attempt to culture shoot apices from 2-3-weeks old aseptically grown seedlings and rooted plantlets were obtained within four weeks in liquid MS (Murashige and Skoog 1962) medium. Also, Enjalric and Carron (1982) achieved shoot sprouting from the stem nodes of young green house plants. Carron and Enjalric (1983) also reported that the propagation of elite Hevea clonal stock material from stem cuttings was a failure due to inadequate rooting system, which is necessary for the tree stability. Later, Carron et al. (1989) obtained full plantlets from seedlings. Gunatilleke and Samaranayake (1988) cultured shoot tip explants from aseptically grown seedlings for microprapagation. Further, Te-Chato and Muangkaewngam (1992) produced multiple shoots from different explants derived from in vitro seedlings. Shoot apices collected from mature trees of two Hevea genotypes were micro grafted onto 3 week old seedlings grown in vitro by Perrin et al. (1994). This indicates that the physiological juvenility of the explants is important for successful micropropagation. Seneviratne et al. (1995) described that the regenerated shoots did not produce tap root system, however, the growth of these plants was similar to the plants developed by bud grafting or embryo culture. Seneviratne and Flegmann (1996) reported multiple shoot production from the nodal explants of juvenile origin and elongated shoots produced roots. Seneviratne and Wijesekara (1996) also demonstrated that the axillary bud development was enhanced with the application of cytokinins. Mendanha et al. (1998) described plant development from the axillary buds cultured on MS medium supplemented with growth hormones. At Rubber Research Institute of India (RRII), in vitro propagation of Hevea clone was attempted where the shoot tips were cultured on a medium containing indole-3-acetic acid (IAA) (1.5-3.0 mg/l) and Kinetin (0.5-1.5 mg/l) and fully developed plantlets were obtained and rooted plantlets were established in the field (Thulaseedharan et al. 2000). Carron et al. (2000) evaluated the rooting ability of in vitro propagated plants in Hevea. The in vitro plantlets had a well developed tap root system with lateral roots similar to that of plants obtained from seeds. The effect of different fungicides and antibiotics to control microbial contamination in Hevea cultures were also examined (Kala et al. 2004).

#### Organogenesis

In vitro organogenesis from various explants has been attempted by earlier workers, but the success rate was very low. Initial attempt was made to develop callus and suspension cultures in Hevea by Wilson and Street (1974). Paranjothy and Ghandhimathi (1975) described a method for full plantlet regeneration from dehusked seeds or freshly fallen seeds. Cotyledon, epicotyl or hypocotyl explants produced compact callus with roots but failed to regenerate plants (Paranjothy and Ghandhimathi 1975). Carron and Enjalric (1982) demonstrated callus induction from the leaf explants but no organogenesis was noticed. Muangkaewngam and Te-Chato (1992) evaluated the effect of low temperature on zygotic embryo culture in vitro. Perrin et al. (1997) compared the ability for in vitro axillary shoot organogenesis and rhizogenesis between mature and rejuvenated clones of H. brasiliensis. Mendanha et al. (1998) reported abundant callus initiation from the leaf explants however, no regeneration was noticed when they were subcultured onto medium.

#### **Protoplast culture**

Protoplast culture is now widely applied in cell biology and in association with molecular characterization of genes. It is a fundamental tool for the genetic improvement of plants by somatic hybridization and genetic engineering. The reports on protoplast culture of Hevea are scanty. Initially, Cailloux and Lleras (1979) isolated protoplasts from young leaves and stem tissues but no division was observed. Rohani and Paranjyothi (1980) made an attempt to isolate protoplasts from different tissues of Hevea and reported that pith from young shoots and suspension cultures of anther derived calli were the most promising sources for obtaining viable protoplasts. Even though cell wall regeneration was noticed within 7 days, no cell division was observed. Wilson and Power (1989) obtained protoplasts from stem tissues of Hevea and they were successful in cell wall regeneration and divisions, but rapid degeneration of the protoplasts was recorded. Haris et al. (1993) isolated protoplasts from cell suspensions derived from anther calli while Cazaux and d'Auzac (1994) used embryogenic calli for protoplast isolation and obtained microcalli from Hevea protoplasts. Later, Cazaux and d'Auzac (1995) reported that He*vea* stem protoplasts were found to be recalcitrant to division due to high ethylene production. Sushamakumari et al. (1999a) successfully isolated protoplasts from 2 month old embryogenic cell suspensions derived from immature inflorescence. Further, cell division and microcalli formation were also obtained. Subsequently, Sushamakumari *et al.* (2000a) regenerated plants from protoplast derived callus via somatic embryogenesis. Also a detailed study was conducted to examine the effect of nitrogenous compounds on plant regeneration from protoplast derived callus by Sushamakumari et al. (2000a). It is reported that the amino acids arginine, proline (50-100 mg/l), glutamine (400 mg/l) stimulated embryo induction while plant regeneration was enhanced by glutamine. They also observed that GA3 increased the percentage of embryogenesis (1.45  $\mu M$ ) as well as plant regeneration (2.9  $\mu$ M). The addition of glucose along with sucrose had beneficial effect on embryo induction and plant regeneration.

#### Anther and microspore culture

Haploid plants can play an important role in the study of quantitative traits, in the removal of deleterious recessive genes and in speeding up selection in conventional breeding. Anther culture and isolated pollen culture offers the possibility of easy production of homozygous haploid lines. Microspore culture is an elegant system for gene mapping and genetic transformation. However, the long juvenile phase and the requirement of many generations of inbreeding make this approach impractical. *In vitro* approaches to

induce haploids in Hevea have only limited success in comparison with other plant species. Satchuthananthavale and Irugalbandra (1972) cultured Hevea anthers for the first time, with the aim of obtaining haploid plants. Satchuthananthavale (1973) and Paranjothy and Gandimathi (1976) noticed callus formation as well as continued growth from anther tissues and pollen grains after 4-5 weeks in culture. Chen et al. (1978, 1979, 1981, 1982) and Chen (1984) reported the production of pollen plantlets in Hevea and reported the establishment of pollen plantlets in the soil. Das et al. (1994) obtained callus induction from several clones on a medium with 6% sucrose. No report is available on the isolated microspore culture of *Hevea*. Jayasree et al. (2005) reported microcalli formation from isolated microspores. Though anther culture was the first significant success of *in vitro* culture applied to rubber tree, this approach did not receive much attention in research after the end of the 1980s because of difficulties in achieving new elite clones via haplogenesis.

#### Somatic embryogenesis

Somatic embryogenesis is one of the powerful tissue culture techniques for mass propagation of elite Hevea clones. In recent years, the utilization of this system also opens up new avenues for molecular farming through genetic transformation. Hevea somatic embryogenesis was first developed in China and Malaysia, using the anther wall as initial mother tissue explant. Paranjothy (1974) induced embryoids from anther wall derived calli and subsequently shoot development of the embryoids was also achieved (Paranjothy and Ghandimathi 1975; Paranjothy and Rohani 1978). Since then, Wang et al. (1980, 1984) and Wan et al. (1982) succeeded in plant development via somatic embryogenesis from anther wall calli. Carron and Enjalric (1982) induced calli and embryoids from anther wall. Later, Wang and Chen (1995) developed plantlets from stamen cultures. At CIRAD, the inner integument of immature seeds was chosen as explant for developing somatic embryogenesis through four successive phases: (1) callogenesis (2) differentiation of embryos (3) multiplication of embryos and (4) germination of embryos and development into plantlets (Carron and Enjalric 1982). Carron and Enjalric (1985) used integumental tissue of immature fruits for somatic embryogenesis and regenerated plantlets were successfully established in the soil. The effect of various factors on somatic embryogenesis was studied in detail by EI Hadrami et al. (1989, 1991, 1992), Michaux-Ferrier and Carron (1989), Auboiron et al. (1990) and Etienne et al. (1991). Etienne et al. (1993a, 1993b) described that a slow desiccation or maturation with 351 mM sucrose supplemented with 1mM ABA strongly improved germinability and conversion to plantlets. Role of ABA on embryo development was also reported by Veisseire *et al.* (1994a, 1994b). Montoro *et al.* (1993, 1995) reported that a higher level ( $351 \mod m^{-3}$ ) of sucrose and 12 mM calcium promoted embryogenesis. Somatic embryogenesis from integument tissues and subsequent plant regeneration has been reported by Te-Chato and Chartikul (1994). Carron et al. (1995a) made a qualitative and quantitative comparison on somatic embryogenesis in 4 different Hevea clones (PB260, PR107, RRIM600, and PB235). Cailloux et al. (1996) established a long term embryogenic line with recurrent embryogenesis. Etienne et al. (1997a, 1997b) also reported enhanced somatic embryogenesis by the use of a temporary immersion technique with addition of higher concentration of CaCl<sub>2</sub> in embryo induction medium. Etienne et al. (1997b) standardized a pulsed-air temporary immersion system for enhancing embryo production, through culturing embryogenic callus under immersion in an autoclavable filtration unit RITA<sup>®</sup>. Engelmann et al. (1997) observed a rapid regrowth as well as production of somatic embryos with cryopreserved callus using freezing protocols. Wang et al. (1998) identified suitable temperature requirement for callus and embryo induction as well as for

plant regeneration. Martre et al. (2001) explained that temporary immersion generates potentially stressful conditions for explants which may enhance somatic embryo production. Blanc et al. (1999) investigated the role of carbohydrates and reported that somatic embryo production was significantly higher with maltose. A comparative study between somatic and zygotic embryos was conducted by Lardet et al. (1999). Although plant regeneration via somatic embryogenesis was successful in Hevea, this regeneration system is still a fleeting phenomenon because of low germination percentage and plant conversion (Cailloux et al. 1996; Linossier et al. 1997) as in many other tree species. Charbit et al. (2004) identified 28 differentially expressed cDNAs during induction in the embryogenic regenerating line (ER) in Hevea by DD-RTPCR analysis. Most recently, Lardet et al. (2007) reported that calli pre-cultured on 1 mM CaCl<sub>2</sub> displayed better regeneration ability than those pre-cultured on 0 mM  $CaCl_2$  medium. Further they showed that some non-regenerant lines became regenerant after cryopreservation, indicating that cryopreservation improves morphogenetic competence of embryos derived from cryopreserved callus. The authors also demonstrated that embryos derived from cryopreserved tissues led to plant recovery with no phenotypic differences between cryopreserved and non- cryopreserved calli

Substantial progress has been achieved in this direction in the recent years (Thulaseedharan et al. 2000). Somatic embryogenesis remains difficult due to the occurrence of low frequency plant regeneration from different Hevea genotypes. Futher, reliable embryo formation is limited to only a few genotypes (PB 260, PR 107, PB 235, RRII 105 and RRIM 600) and embryo formation is also fugacious (Carron et al. 1989; Kumari Jayasree et al. 1999). Molecular mechanism of embryogenic callus formation, embryo induction and differentiation were poorly understood (Etienne et al. 1993a). In fact, somatic embryogenesis needs further improvement for the commercial application of the system. There has been an ever-increasing interest in the development of plantlets through somatic embryogenesis especially by the advent of genetic transformation (Kumari Jayasree et al. 1999). Since 1990, research has been initiated for in vitro plant regeneration via somatic embryogenesis especially for Indian Hevea clones at the Rubber Research Institute of India (RRII). Both immature anthers (Kumari Jayasree et al. 1999) and inflorescence (Sushamakumari et al. 2000b) explants were found ideal for somatic embryogenesis and plant regeneration for the high yielding Indian Hevea clone RRII 105 (Fig. 1A-C, 1G). In depth studies were carried out to find out the nutritional and hormonal requirements as well as other environmental conditions like light for maximum induction of calli, embryos and subsequent plantlet regeneration (Kumari Jayasree et al. 1999). With immature anthers, optimum callus induction was noticed on medium supplemented with 2.0 mg/l 2,4-D combined with 0.5 mg/l KIN. On subsequent culturing to modified MS medium with 0.7 mg/l KIN and 0.2 mg/l NAA induced embryos and plantlet regeneration achieved on hormone-free medium. Also the diploid nature of the regenerated plantlets was further confirmed by cytological analysis. Somatic embryo derived plants were successfully planted in field at Rubber Research Institute of India (Fig. **1H**). Further, plantlet development was enhanced by induction of multiple shoots from germinative embryos (Sushamakumari et al. 1999b). Sushamakumari et al. (2000b) studied the role of sucrose and ABA on callus development, embryo induction and plant regeneration and somatic embryo-derived plants were established in RRII experimental field. Later, a detailed study was undertaken with immature anthers for enhancing embryo induction and plant development (Kumari Jayasree et al. 2001). Accordingly, initial preculture of anthers in liquid medium for 10 days prior to culturing onto solid medium promoted callus induction as well as reduced the time requirement. Polyamines had no significant effect except with spermidine (0.5 mg/l). Addition of 150-200 mg/l glutamine and 400 mg/l casein hyd-

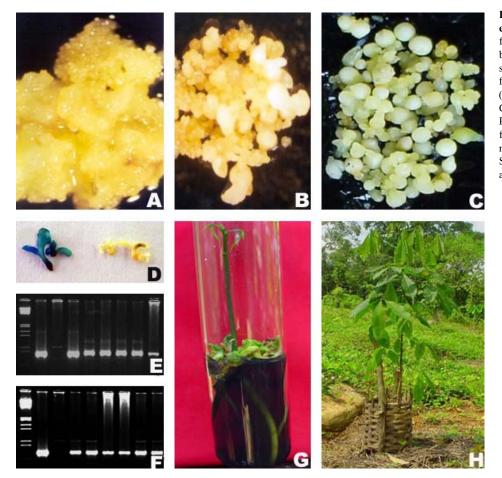


Fig. 1 Rubber propagation via somatic embryogenesis. (A) Callus initiation from immature anther explants; (B) Embryogenic callus formation; (C) Different stages of somatic embryos; (D) Transformed embryos with GUS expression (left) and control embryos (right); (E) Confirmation of *npt*II gene (800 bp) by PCR; (F) Amplification of *uid*A gene fragments (600 bp), (G) Embryo germination and plantlet development and (H) Somatic embryo derived plant established at RRII experimental field.

rolysate enhanced embryo induction rate. Kumari Jayasree and Thualseedharan (2001) reported that the incorporation of 2.0 mg/l GA<sub>3</sub> increases embryo induction as well as germination percentage. Repetitive embryogenesis was also induced from primary somatic embryos derived from integumental tissue (Asokan *et al.* 2002). An isozyme study during different developmental stages of somatic embryogenesis revealed a marked difference between embryogenic and non embryogenic calli (Asokan *et al.* 2001).

Kumari Jayasree and Thulaseedharan (2004) observed long-term embryogenesis from embryogenic callus and the embryogenic potential was retained for a period of 3 years. Inclusion of 100 mg/l proline increased the regeneration potential and activated charcoal was found to be essential for high frequency plant regeneration up to 80%. Among 4 cytokinins [6-benzylaminopurine (BA), zeatin (ZEA), kinetin (Kn) and thidiazuron (TDZ)] tested, TDZ at 0.25 mg/l was found to be superior for somatic embryogenesis followed by BA and ZEA (0.25 mg/l) (Kumari Jayasree and Thulaseedharan 2005). Recently attempts were also made to induce somatic embryos from leaf and root ex-plants (Kala *et al.* 2005, 2006; Sushamakumari *et al.* 2006). Yellow, friable callus induced from leaf explants on modified MS medium (Kumari Jayasree et al. 1999) containing 2,4-D, NAA and BA as growth hormones was differentiated into embryos. Embryo maturation occurred on woody plant medium (WPM) (Lloyd and McCown 1980) supplemented with BA (0.3 mg/l), TZD 0.5 mg/l and GA<sub>3</sub><sup>-1</sup>(1.5 mg/l). Further, organic supplements (100 mg/l malt extract and 150 mg/l banana powder) enhanced embryo maturation and the regenerated plantlets were established in polybags (Kala et al. 2006). Friable embryogenic calli derived from root explants were differentiated into somatic embryos on WPM medium fortified with the combination of  $\dot{G}A_3$  (4.35  $\mu$ M) and BA (8.84  $\mu$ M) and the maximum frequency of plant regeneration obtained was 65%. Regenerated plants were successfully initially transferred to small polybags filled with autoclaved soil rite and kept in the glass house at controlled environment. Subsequently, the

acclimatized plantlets were transferred to larger poly bags and maintained in the filed under shade before planting in the experimental field (Sushamakumari *et al.* 2006).

# **Genetic engineering**

Conventional rubber breeding takes more than 25 years to obtain a new clone. Genetic transformation offers a potential tool to breeders for adding valuable traits to crop plants, leading to the development of elite clones in a relatively short period of time. The rubber tree is a good candidate for manipulation by genetic transformation due to the long breeding cycle and heterozygous nature. Furthermore, in vitro techniques including plant regeneration via somatic embryogenesis have been established. Thus, the basic technology for genetic manipulation of rubber plant at the cellular and molecular levels is available. Many agronomic traits that could be considered for rubber improvement biotechnology programme include TPD tolerance, high yield potential, resistance to diseases, production of recombinant protein and timber wood quality improvement. Genetic engineering of crop plants integrated with specific genes has been achieved either by direct gene transfer or by Agrobacterium tumefaciens mediated genetic transformation. Although, genetic transformation and stable integration of foreign genes have been successful in many annual crop plants, the success in perennial tree crops is rather limited in general and Hevea in particular. The possibility of genetic transformation in Hevea brasiliensis was first explored in 1991 by Agrobacterium-mediated transformation (Arokiaraj and Wan 1991). Later Arokiaraj et al. (1994) succeeded in developing the first transgenic Hevea plants using anther derived calli from the clone GL 1, by the particle gun method. Subsequently, A. tumefaciens-mediated transformation was achieved with anther derived calli as initial explant and transgenic Hevea plants were produced (Arokiaraj et al. 1996, 1998). Montoro et al. (2000) reported that the transformation efficiency was significantly enhanced when CaCl<sub>2</sub> (9 mM)-treated friable callus was cultured on calcium-free medium. Montoro *et al.* (2003) used callus from inner integument tissues of immature fruits (clone PB260) for genetic transformation. Recently, Blanc *et al.* (2005) developed transgenic plants of *Hevea* (clone PB 260) via *Agrobacterium*-mediated transformation. In order to find out the most suitable explant for genetic transformation, an experiment was performed with different explants such as immature anther and ovule, sixty day old callus and embryogenic callus derived from immature anther and ovule explants and maximum transformation frequency (62%) was obtained with anther derived embryogenic callus (Rekha *et al.* 2006). Further, histochemical GUS assay revealed the expression of the *uid*A gene in the transgene integration with *Hevea* genome was also confirmed by polymerase chain reaction (PCR).

Arokiaraj et al. (1998) used Agrobacterium GV2260 (p35SGUSINT) that harboured the β-glucuronidase (gus) and neomycinphosphotransferase (nptII) genes for genetic transformation. Subsequently, Montoro et al. (2000, 2003) developed transgenic calli cocultivated with Agrobacterium (EHA105) containing binary vector pCAMBIA2301 using inner integument tissues of immature fruits (clone PB260) and led to high transient GUS activity in callus. Blanc et al. (2005) produced transgenic plants of Hevea (clone PB 260) via Agrbacterium-mediated transformation where pCAMBIA2301 with strain EHA105 was used for all the experiments. Its T-DNA construct harbours both a uidA gene interrupted by a Catalase-intron and a nptII gene conferring resistance to neomycin, each of them under the control of a CaMV35S RNA promoter. Although, earlier transformation studies in Hevea were performed with various marker genes, recent experiments are mainly focused on transferring various agronomically important genes into Hevea for the production of transgenic plants with enhanced tolerance to abiotic stresses including TPD, high latex and timber yield and for the production of recombinant proteins. In rubber tree, TPD syndrome is considered to be a physiological disorder which greatly affects latex yield. Once the TPD occurs, the tapping incision is partly or entirely blocked and the amount of latex production is significantly decreased or stops completely. The incidence of TPD occurs in 20-40% of rubber trees in almost every rubber growing country. Under normal conditions, active oxygen species (AOS) are efficiently scavenged by detoxifying enzymes such as superoxide dismutase (SOD). The presence of excessive AOS results in severe latex yield losses. It has been reported that SOD activity protected plants from oxidative and other stresses. In order to overcome this TPD problem, an attempt was made to increase the SOD enzyme activity by over expression of this gene in Hevea transgenic plants. Transgenic plants were produced with the SOD gene under the control of CaMV 35S and FMV 34S promoters (Jayashree et al. 2003; Sobha et al. 2003a). Two-month-old callus derived from immature anther was co-cultivated with Agrobacterium strain EHA 101 harbouring a plasmid vector containing the HbSOD gene under the control of CaMV 35S promoter, uidA gene for screening and *npt*II for selection. Transformed callus surviving on medium containing 300 mg/l kanamycin was selected and used for somatic embryo development. Subsequently, mature embryos germinated and developed into plantlets. Histochemical GUS assay revealed the expression of *uidA* gene in embryos (Fig. 1D, 1F) as well as leaves of transgenic plants. The presence of the uidA, nptII, and HbSOD genes in the Hevea genome was confirmed by molecular analysis (Fig. 1E). In another study, the HbSOD gene fused under the control of the Figwort Mosaic Virus (FMV) 34S promoter was used for genetic transformation and biochemical studies indicated that the superoxide dismutase, catalase and peroxidase enzyme activities increased significantly in transgenic embryogenic callus lines as compared to the control (Sobha et al. 2003a, 2003b). Transgenic Hevea plants have been successfully developed and established in soil at the Rubber Research Institute of

India for further evaluation (Jayashree *et al.* 2003). At present, rubber transgenic plants with SOD gene were multiplied by bud-grafting and established in the field. It would be interesting to study the tapping effect on overexpression of SOD enzyme in these plants but it will take 6 years for initiation of tapping.

Venkatachalam et al. (2006a) described an efficient protocol for Agrobacterium-mediated genetic transformation in rubber. As in the case with most other crops, major improvements have been made over the last century in the productivity of rubber, as the yield of dry rubber per acre have been increased significantly by releasing elite clones. There is no doubt that conventional breeding will lead to increased latex production in rubber trees. However, it is quite possible that the rate of rubber biosynthesis within the tree becomes the limiting factor (Arokiaraj 2000). At this point, latex yield could only be enhanced either by treatments or by over-expression of rubber biosynthesis genes in transgenic Hevea plants. It was reported that the constitutive level of HMGR1 enzyme may be a limiting factor in rubber biosynthesis. Based on this hypothesis, Arokiaraj et al. (1995) initiated genetic transformation experiment to overexpress HMGR1 in Hevea where, hmgr1 activity of transformed callus ranged from 70-410% of the value of wild type control and the activity is transformed embryos obtained ranged from 250-300%. However, they failed to produce transgenic plants. Among the latex associated proteins, the amount of REF in the whole latex is proportional to the rubber content. As such, REF protein amount is shown to be correlated simultaneously with rubber yield, there is a possibility to enhance rubber yield by over expression of REF gene which is involved in rubber biosynthesis. At present, the author's laboratory has initiated a research project in which rubber biosynthesis genes such as HMGR1, FDP, REF and CIS are cloned into binary vectors and transformation work is in progress to develop transgenic plants. Currently transgenic callus lines were obtained and further multiplication and production of transgenic plants via somatic embryogenesis is under way.

Rapid progress in molecular biology and physiology makes it possible to modify wood quality in tree species. Until now, the most important product of the rubber tree was its latex, however, rubber wood (non-latex product) is increasingly being sought as a commercial commodity for the furniture industry (Arokiaraj 2000). With the depletion of tropical forests leading to a shortage of timber for many industrial and engineering uses, attention has moved on to rubber wood as an alternative source of timber for markets (Arokiaraj et al. 2002). As the composition of wood is important for the pulp industry, lignin genetic engineering is a very active area of research that has been stimulated in recent years by the characterization of important genes controlling lignification. The reports of rubber-wood from Malaysia rose from RM900 million in 1993 to RM3.7 billion in 1998 and subsequently to RM5.2 billion in 2001 (Arokiaraj et al. 2002). This figure clearly indicates how rubber wood is gaining importance for making furniture, sawn rubber wood and new plywood material. In trees, little is known about the process of differentiation and development that are involved in wood formation. Knowledge on what determines the pathway of differentiation of cambial cells is essential for any attempt to design better wood characteristics. In rubber tree, the homeobox (HB) gene has been isolated and it is presumed that HB genes may be involved in differentiation of cambium cells to form latex vessels (Arokiaraj et al. 2002). However, till date there is no report on transgenic plant development to enhance wood quality in rubber tree.

In many plants, foreign proteins can be produced easily, but their purification is a real problem. Alternatively, the *para* rubber tree, which synthesizes an enormous volume of latex upon tapping could be exploited without any destruction for large-scale production of foreign protein in the latex throughout the year. Depending upon the promoters used, recombinant proteins will be sequestered throughout the plant or in specific parts of the plants or in specific organelles within a given plant cell. Already, human serum albumin proteins were expressed in transgenic *Hevea* plant (Arokiaraj *et al.* 2002). Two hevein promoters (*Hev1* and *Hev2*) were cloned and promoter-*gus* constructs were introduced into rice callus tissues by *A. tumefaciens* for functional analysis (Pujade-Renaud *et al.* 2005). Also in this respect, the Rubber Research Institute of India has been working on the isolation of laticiferous-specific promoters which will eventually enhance recombinant protein production in transgenic rubber trees. Recently, the promoter sequence of a rubber elongation factor gene was cloned and characterized from high latex yielding Indian *Hevea* clone RRII105 (Priya *et al.* 2006). Further work is in progress to insert this promoter into a binary vector for the production of recombinant proteins in *Hevea*.

#### Applications of molecular markers

Molecular markers have served as useful aids in understanding the genetics of *H. brasiliensis* in the recent past. They can play an important role in assisting Hevea clonal identification and origin. For the last two decades, a large number of molecular markers and techniques have been applied in Hevea breeding. Nowadays many types of molecular marker techniques are available, the most widely used include RAPD (random amplified polymorphic DNA), RFLP (restriction fragment length polymorphism), AFLP (amplified fragment length polymorphism), minisatellite fingerprints and microsatellites or SSR (simple sequence repeats) (reviewed in Teixeira da Silva et al. 2005). These markers differ in the type and amount of variability they express, in their suitability for each particular question and in the ease and costs of their development and application. Among these, three major molecular marker techniques were applied to cultivar identification: random amplified polymorphic DNA (RAPD), restriction fragment length polymorphism (RFLP) and amplified fragment length polymorphism (AFLP). In addition to these methodologies, microsatellite markers, otherwise known as simple sequence repeat length polymorphisms (SSRLP) are generated by highly specific PCR amplification. Simple sequence repeats (SSR) are regions of short tandemly repeated DNA motifs (generally less than or equal to 4 bp) with an overall length in the order of tens of base pairs. SSR have been reported to be highly abundant and randomly dispersed throughout the genomes of many plant species. Thus, SSRLP may occur even between closely related individuals. Microsatellite markers have been used in plants for fingerprinting, mapping, and genetic analysis. Though RFLPs are powerful for studying genetic diversity and mapping, this technology is not preferred now since it is labour intensive and requires large DNA samples. Its marker index value (expressed as the number of polymorphic products per sample) is also low with only 0.10 compared to PCR based marker systems like RAPDs (0.23), SSRs (0.60) and AFLPs (6.08) (Low et al. 1996). Initially, isozymes were utilized for clonal identification (Chevallier 1988); subsequently other tools like minisatellites (Besse et al. 1993a), RFLPs (Besse et al. 1993b, 1994), mitochondrial and chloroplastic RFLPs (Luo et al. 1995), RAPDs and DAFs (Low et al. 1996; Varghese et al. 1997; Venkatachalam et al. 2001, 2002, 2006b), AFLPs (Lespinasse et al. 2000a), and SSRs (Besse et al. 1993a; Atan et al. 1996; Low et al. 1996; Bindu Roy et al. 2004) were developed and used in detection of molecular markers in H. brasiliensis.

#### **Isozyme markers**

In conventional plant breeding, many morphological traits were used as markers for analysing genetic traits and identifying cultivars, but specific genetic information on Mendelian traits has been rare in *Hevea*. In the 1980s, isozymes have been used in rubber as genetic markers for cultivar identification, genetic diversity analysis, control of progenies issued from hand pollination, and reproductive biology (Chevallier 1988; Leconte et al. 1994; Paiva et al. 1994a; Sunderasan et al. 1994). Analysis of isozymes was developed at CIRAD with a set of 13 polymorphic isozymic systems to formulate a diagnostic kit associated with a clonal identification database. This kit was able to differentiate a large set of cultivated clones (Leconte et al. 1997). Subsequently, a study was carried out to estimate the distance *H. brasiliensis* pollen dispersed under natural conditions by using isozyme markers. Esterase isozyme markers were used to determine if the seeds had been derived from self- or cross-pollination. The incidence of cross-pollination was then examined in relation to the distance from the inter-clonal boundary. A logarithmic model suggested that pollen could travel distances in the order of  $0\pm 3$  to  $1\pm 1$  km (Yeang and Chevallier 1999). Moreover, isozyme-based analyses are limited by the rather small number of marker loci available and a general lack of polymorphism for these loci.

#### **RAPD** markers

Though considerable progress has been made to increase the yield in Hevea clones in the last two decades, satisfactory resistance to biotic and abiotic stress has not been achieved because of limited genetic resources within the Hevea gene pool. Wind damage is one of the serious problems in rubber-growing countries, each year a considerable number of rubber trees were lost due to wind damage in rubber plantations. The incorporation of the dwarf character into high-yielding Hevea clones would be useful for generating a high-yielding tree with a desirable architecture (dwarf stature) and high density planting (Venkatachalam et al. 2004). Using RAPD analysis, Varghese et al. (1997) evaluated 24 cultivated Hevea clones to estimate genetic distances. Subsequently, Venkatachalam et al. (2002) described the genetic relationships for 37 Hevea clones by using RAPD markers (Fig. 2A, 2D). This molecular information concurs with the reported high morphological variability in Hevea and a dendrogram was constructed based on the RAPD markers, which showed that 69% of the bands observed were polymorphic between the 37 Hevea clones. The clones were classified into seven major groups based on DNA markers. The phenogram showed that RRII105 (India) and RRIM600 (Malaysia) were nearly identical. Three clones belonging to Thailand have been included in the same cluster. The two clusters formed by the Indian clones were distinct with one group (RRII201, RRII204, RRII205, RRII207, and RRII209) clustering with one Malaysian clone. Clones PB312 and PB314, which were issued from the same cross (RRIM600  $\times$  PB235) appear genetically very close. RAPD analysis therefore reflects genetic differences and geographical origin of the Hevea clones. The Indian RRII203 clone was very dissimilar to the Malaysian PB255 clone (similarity index: 0.692). From the dendrogram it is intriguing to note that several primary clones developed in different countries, such as TJIR1, GI1, PB86, Mil3/2, AVROS255, and BD10 were closely clustered. In most cases, clones with common ancestors, such as RRII105, RRIM600, PB311, PB312, PB314, KRS128, KRS163, PB217, PB255, PB260, RRII204, RRII209 were observed to cluster together.

Venkatachalam *et al.* (2004) identified a dwarf genome-specific randomly amplified polymorphic DNA (RAPD) marker in rubber tree. The primer OPB-12 generated a 1.4-kb DNA marker from both natural and controlled  $F_1$  hybrid progenies (dwarf stature) derived from a cross between a dwarf parent and a normal cultivated clone as well as from the dwarf parent; it was absent in the other parent (RRII118). To validate this DNA marker, 22  $F_1$  hybrids (13 with a dwarf stature and nine with a normal stature) were analyzed; the dwarf genome-specific 1.4-kb RAPD marker was present in all dwarf-stature hybrids and absent in all normal-stature hybrids. This DNA marker was cloned

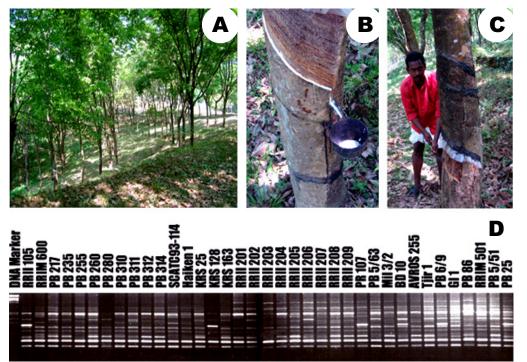


Fig. 2 Rubber plantation and molecular markers. (A) A view of rubber plantation at Rubber Research Institute of India (RRII, Kottayam); (B) A healthy rubber tree producing latex; (C) TPD affected tree with no latex production at tapping panel (tree is being tapped by tapper); (D) RAPD marker profile generated by OPC-05 prime.

and its locus specificity was further confirmed by Southern blot hybridization. More recently, Venkatachalam *et al.* (2006b) identified two DNA markers with OPB-12 primer in *Hevea* and the size of these two polymorphic bands was 1.2 kb and 1.4 kb. The 1.4 kb RAPD marker was cloned and nucleotide sequence revealed certain homology with *Saccharomyces cerevisiae* proline-specific permease gene. Further, to validate this RAPD marker, SCAR primers were designed and the SCAR marker was amplified from 14 clones among 37 clones tested. Therefore accumulated data on *Hevea* RAPD analysis from different clones give information on genetic relations, *Hevea* origin and could provide the initial basis for clonal distinction and germplasm evaluation of agronomical interest. The data can be also used as tools in *Hevea* improvement programs.

#### **RFLP** markers

In Hevea, Low et al. (1996) used RFLPs for identification of progenies with two common parents and Besse et al. (1993a) reported the ribosomal DNA variations among genotypes. Identification of 73 Wickham clones was carried out with 13 probes associated with restriction enzyme Eco RI (Besse et al. 1993b). Besse et al. (1994) studied the genetic diversity of 92 Amazonian and 73 Wickham clones using RFLP analysis. One clone from Rondonia, RO/C/8/9, showed eight specific restriction fragments and a unique malate dehydrogenase (MDH) allele indicating its interspecific origin (Besse et al. 1994). Application of microsatellites to genetic diversity analysis confirmed that wild accessions were more polymorphic than cultivated Wickham clones. Some accessions such as RO/OP/4 20/16 and RO/ A/7 25/133 seem unique since they do not fall under any cluster due to their high level of specific alleles (Lekawipat et al. 2003a, 2003b). A high mt DNA polymorphism was found in Amazonian accessions while no such variation was noticed in the Wickham population except GT 1 (Luo et al. 1995). Sequencing of a highly polymorphic mt DNA fragment from 23 genotypes showed real potential for phylogenetic analysis in Hevea (Luo and Boutry 1995). Chloroplast cp DNA analysis was carried out over 217 accessions representing 126 mitochondrial genotypes and only two cp DNA RFLP profiles were found, thus showing a much lower polymorphism and this indicate the high level of conservation of this chloroplast genome (Luo et al. 1995). The mt DNA of Wickham population has lesser variation since their female progenitors are restricted to a

very small set of primary clones. Cytoplasmic donors of most of the improved clones were either PB56 or Tjir1. Obviously, this may be one of the reasons for the mt DNA profile showing only two clusters (Priyadarshan and Goncalves 2003). A possible explanation for greater polymerphism in mt DNA of wild accessions is that they might have been evolved through interspecific hybridization. Seguin *et al.* (2003) proposed a general organization of *H. brasiliensis* germplasm with 6 genetic groups.

## **AFLP** markers

The first comprehensive genetic linkage map of Hevea brasiliensis was constructed by using RFLP, AFLP, microsatellites and isozyme markers (Lespinasse et al. 2000a). The parents used were PB260 (PB5/51 × PB49) and RO38  $(F4542 \times AVROS363)$  and homologous markers segregating in both parents were ascertained for consensus map construction. F4542 was a clone of H. benthamiana species. The  $F_1$  synthetic map of 717 markers was distributed in 18 linkage groups corresponding to the 18 chromosomes and consisted of 301 RFLP, 388 AFLP, 18 microsatellite and 10 isozyme markers. The genetic length of the 18 chromosomes was fairly homogeneous with an average map length per chromosome of 120 cM. Many AFLP markers were seen in clusters, which were attributed as reduced recombination frequency regions. Though the RFLP markers were well distributed all over the 18 linkage groups, these were insufficient to saturate the map. AFLPs and few microsatellites together contributed to saturating the map (Lespinasse et al. 2000a). A genetic approach developed on the cross PB260  $\times$  RO38 was targeted to identify the resistance allele or loci to South American Leaf Blight (SALB) disease (Lespinasse et al. 2000b). Eight different QTLs were identified as resistance to different SALB strains in RO38 and it was further rationalized that the resistance (alleles) of RO 38 have inherited from wild grandparent (H. benthamiana) and no favourable alleles came from AVROS 363, the Wickham parent (Lander and Botstein 1989). Field evaluation against the pool of Microcyclus strains was per-formed under the real infestation conditions and the pre-sence of the predominant QTL in g13 previously found was confirmed by Le Guen et al. (2003). Most recently, Le Guen et al. (2007) investigated the genetic resistance components of the H. brasiliensis  $\times$  H. benthamiana RO 38 cultivar to Microcyclus ulei disease by inoculating isolates which succeeded in partially or completely infecting genotypes of a

mapping population. Among eight QTLs tested, only one contributed to the partial resistance against a highly pathogenic isolate, and no QTL was detected for resistance against the most pathogenic isolate.

## Microsatellite markers (SSRs)

Simple sequence repeats or microsatellites (SSRs), issued from PCR developed from specifically designed primers, appeared very powerful due to their high polymorphism (between 15 and 20 alleles per marker). Polymorphism in microsatellites was detected also in H. pauciflora, H. guianensis, H. camargoana, and H. benthamiana (Low et al. 1996). Microsatellite-enriched libraries were produced and led to the identification of large numbers of microsatellite markers (Atan et al. 1996; Seguin et al. 2003; Saha et al. 2005); sequences were deposited in the EMBL/Genbank databases. Microsatellite markers from rubber pathogens can also be used for distinguishing the genetic differences between the races, such as was made with 11 markers for Microcyclus (Le Guen et al. 2004). For methodological purposes, one seed garden made up with 50 Amazonian genotypes and GT1 clone, planted at CNRA (Ivory Coast) was subjected to the analysis of gene flux and paternity identification with isozymes and microsatellites (Blanc et al. 2001; Lidah 2005). A high level of confidence was found for paternity identification carried out with 8 microsatellite markers. Paternity identification with microsatellites was carried out with the Cervus software (Marshall et al. 1998).

Genetic mapping was developed with a set of 247 microsatellite markers complemented by 198 AFLPs in order to study the genetic basis of different factors related with latex production (Prapan et al. 2004). Lekawipat (2003a, 2003b) performed a genetic diversity analysis of H. brasiliensis germplasm over 66 Amazonian and 40 Wickham accessions, by using both non-expressed molecular genetic markers (12 microsatellites) and 17 markers of expressed genes. Bindu Roy et al. (2004) described the simple sequence repeats (SSRs) or microsatellites from genomic library of Hevea, derived from a clone GT1 and RRII105. Different types of repeat motifs comprising dinucleotides (TG/AC, AG/TC, TA/AT), trinucleotides (AAG, AGG, ATT), tetranucleotides (GAAA, AAGG, pentanucleotide TAAA, AAAT) and one ATCC. (GAAAT) were detected. It was reported that about 67 microsatellites having characteristic simple and compound repeats, out of which 59 were from GT1 and eight from RRII105. Subsequently, Saha et al. (2005) used a combination of four microsatellite markers to discriminate uniquely all the 27 Hevea clones and some clone-specific allelic profiles were generated. Further, cross-species amplification of the markers developed in H. brasiliensis had also been demonstrated with two other Hevea species, H. benthamiana and H. spruceana, indicating a high degree of sequence homology at the flanking regions. Also, sequence analysis of the SSRs at the 3'-UTR of the hydroxymethylglutaryl-coenzyme A reductase gene, revealed the existence of two alleles based on the repeat length polymorphisms. It is obvious that the results obtained from the above mentioned molecular marker techniques have contributed to the understanding of clonal relations and are potential tools in germplasm evaluation and genetic characterization of traits with agronomical interest.

#### Applications of molecular biology

*Hevea* rubber tree (*H. brasiliensis*) is the only plant species being cultivated for commercial production of rubber in the world. It is therefore of great interest to study the regulation and the expression of the genes involved in natural rubber biosynthesis. To meet the ever increasing rubber demand, it is necessary to increase the latex production substantially by genetic manipulation (Priya *et al.* 2006). Rubber biosynthesis in *Hevea* has become a major field of research to understand the isoprenoid pathway. The general metabolic pathway of rubber biosynthesis is as follows: Sucrose from photosynthesis is actively transported into laticiferous cells through the plasmalemmic membrane, and is then hydrolyzed into glucose and fructose by invertase. These sugars are then converted into acetyl-CoA through glycolysis. Three molecules of acetyl-CoA are condensed into mevalonic acid which is converted to IPP. Polymerization of thousands of IPP molecules assisted by the action of the enzyme rubber transferase in association with REF, a molecule fixed on the rubber particles membranes leads to the formation of high molecular weight rubber. Genes expressed in the latex of Hevea can be divided into three groups based on the proteins they encode: (1) rubber biosynthesis-related proteins such as REF (rubber elongation factor), HMGR (hydroxymethylglutaryl-coA reductase), HMGS (hydroxymethylglutaryl-coA synthase), CIS (cisprenyltransferase), GGPP (geranylgeranyl diphosphate) synthase, SRPP (small rubber particle protein), IPP (isopentenyl diphosphate) isomerase; (2) defense/stress-related proteins such as MnSOD, hevein, chitinase,  $\beta$ -1,3-glucanase and HEVER; and (3) latex allergen proteins such as Hev.b.3, Hev.b.4, Hev.b.5, Hev.b.7 etc.. Biological functions of the allergenic proteins are largely unknown (Oh et al. 1999).

#### **Rubber biosynthesis-related genes**

Rubber biosynthesis is a side-branch of the ubiquitous isoprenoid pathway (Fig. 3). Natural rubber is made almost entirely of isoprene units derived from the precursor isopentenyl pyrophosphate (IPP). Also, trans-allylic pyrophosphates are essential for rubber formation as they are used to initiate all new rubber molecules. Both the HMGS (3-hydroxy-3-methylglutaryl coenzyme A synthase) and HMGR have been shown to be involved in the early steps of rubber biosynthesis by forming HMG-CoA (3-hydroxy-3methyl glutaryl coenzyme A) using HMGS. The HMGS catalyses the condensation of acetyl CoA and acetoacetyl-CoA to form HMG-CoA (Suwanmanee et al. 2002, 2004; Sirinupong et al. 2005). According to Suwanmanee et al. (2002) HMGS mRNA transcripts accumulation was more in laticifers than in leaves. Moreover, a positive correlation has been observed between the activity of HMGR and HMGS and the dried rubber content of the latex from tappings. Two members of HMGS (1.8 Kb and 1.9 Kb cDNAs) from H. brasiliensis called hmgs1, and hmgs2, were cloned and characterized by Suwanmanee et al. (2002) and Sirinupong et al. (2005). The expression of hmgs1 was found to be higher in laticiferous cells than in leaves whereas the abundance of *hmgs2* gene transcripts was more in laticifer and petiole than in leaves. In plants, HMG-CoA was reduced by HMGR to mevalonate and was subsequently converted into IPP. It was reported that there were three genes encoding HMGR in Hevea namely, hmg1, hmg2 and hmg3. The hmg1 gene is likely to be involved in the rubber biosynthesis, whereas the *hmg3* is possibly involved in isoprenoid biosynthesis of another nature (Chye et al. 1992). The first step in rubber biosynthesis is the isomerisation of IPP to DMAPP (dimethylallyl diphosphate) by IPP isomerase. The successive head-to-tail condensation reactions of the five carbon intermediates, catalyzed by the enzyme "rubber transferase", have been assumed to yield rubber.

Moreover, Oh *et al.* (2000) have isolated and characterized a cDNA clone encoding IPP isomerase from *Hevea* and showed by *in vitro* rubber assay that the recombinant IPP isomerase was required for rubber biosynthesis. Subsequently, Takaya *et al.* (2003) described the role of GGPP synthase gene in rubber biosynthesis in *Hevea*. Based on their investigation, GGPP synthase would catalyse the condensation of IPP with allylic diphosphates to give (all-E)-GGPP. Natural rubber is predicted to be made almost entirely of *cis*-isoprene units derived from IPP, and the enzyme responsible for polymerization is believed to have characteristics similar to the *cis*-prenyl diphosphate syntha-

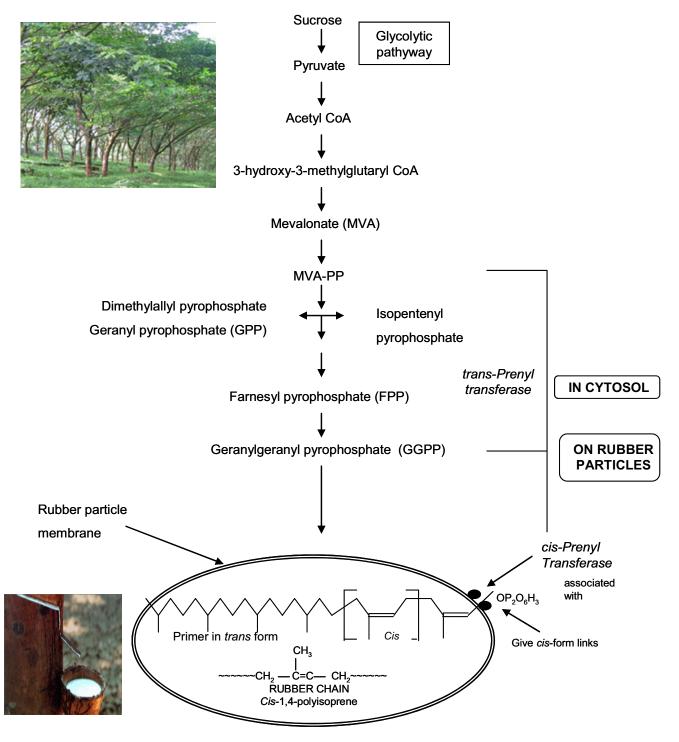


Fig. 3 General rubber biosynthesis pathway.

ses. Further, the gene responsible for the cis-1,4-polymerization of isoprene units has been isolated and characterized in Hevea by Asawatreratankul et al. (2003). It was suggested that rubber biosynthesis in Hevea is mediated by the association of a soluble trans-prenyltransferase with the REF, a 14.6 kDa protein, tightly bound to the rubber particles in the laticifers (Dennis and Light 1989). FPP (farnesyl diphosphate) is a key intermediate in the biosynthesis of at least 20,000 isoprenoids. FPP is also the allylic diphosphate initiator of rubber biosynthesis in plants. FPP is synthesized by the enzyme FPS (farnesyl diphosphate synthase), which has been cloned and characterized from Hevea by Adiwilaga and Kush (1996). REF protein was isolated and studied extensively and the results indicate that the FPS and REF complex was responsible for the *cis*-1,4-polyprenol condensations observed in isolated rubber particles (Light et al. 1989). The REF gene was isolated and the involvement of REF on rubber formation was analysed by Attanyaka *et al.* (1991) and Goyvaerts *et al.* (1991). Also, Oh *et al.* (1999) reported a novel *Hevea* cDNA of a protein called small rubber particle protein (SRPP) associated with small rubber particles and the sequence analysis revealed that this protein is highly homologous to the REF. Recently, Priya *et al.* (2006) described cloning and characterization of REF gene from genomic DNA which was isolated from a high yielding clone RRII105. REF gene (1367 bp) has three exons interrupted by two introns and encoded a 138 amino acid peptide containing an open reading frame of 414 bp with a calculated  $M_W$  of 14,700 Da. Nucleotide sequence analysis showed that 1.3 kb genomic DNA showed 100% homology to REF cDNA from *Hevea*. RNA blot analysis indicated that REF transcript is highly expressed in high yielding clone than in low yielder. Our ultimate goal is to produce transgenic Hevea plants with enhanced latex yield by over-expression of REF protein. It is possible that the rubber biosynthesis pathway is coordinately regulated by these enzymes. Transcripts involved in rubber biosynthesis are 20 to 100 times greater in laticifers than in leaves (Kush et al. 1990). On the other hand, transcripts for chloroplastic and cytoplasmic forms of glutamine synthetase are restricted to leaves and laticifers respectively (Kush et al. 1990), indicating thereby that the cytoplasmic form of glutamine synthetase plays a decisive role in amino acid metabolism of laticifers. According to the reports on EST analysis from Hevea, rubber biosynthesis-related genes are highly expressed in latex (Han et al. 2000). Subsequently, Ko et al. (2003) used cDNA-AFLP technique to analyse the ESTs in Hevea. The results revealed that the most abundant ESTs were the genes encoding REF and SRPP, comprising 29% of the total ESTs.

#### **Defense/stress-related genes**

Several defense/stress related genes from latex of Hevea have also been identified. One of the stress related genes, MnSOD was isolated by Miao and Gaynor (1993). MnSOD transcripts were found in all tissues examined (leaf, petiole, root, latex, callus) and young leaves exhibited the highest levels in intact plants. Also, the transcript level of MnSOD in embryogenic callus was nearly 50-fold higher than in mature leaves. Sivasubramaniam *et al.* (1995) cloned and characterized a novel stress-induced gene, HEVER from the rubber tree, which was found to be developmentally regulated and expressed at basal levels in Hevea tissues. Chye and Cheung (1995) described the isolation and characterization of  $\beta$ -1,3-glucanase gene from Hevea cDNA library prepared from the latex of Hevea brasiliensis. Nucleotide sequence analysis revealed that the 1.2 kb cDNA encoding a basic  $\beta$ -1,3-glucanase showed 68% nucleotide homology with other glucanase genes in the database and was expressed at higher levels in latex than in leaf. Te-Chato and Chartikul (1995) identified resistant callus lines to Phytophthora spp. culture filtrate in rubber. Subsequently, Thanseem *et al.* (2003, 2005) cloned and characterized  $\beta$ -1,3-glucanase gene from Indian *Hevea* clone. Further, they also demonstrated that a prolonged accumulation of  $\beta$ -1,3-glucanase mRNA transcripts was noticed with abnormal leaf fall (ALF) tolerant RRII105 clone compared with susceptible one. Another defence related protein is Hevein (a chitin-binding protein) that play a crucial role in the protection of wound sites from fungal attack and is also involved in the coagulation process. It belongs to a multigene family and the specificity of its expression in the latex is under investigation (Broekaert et al. 1990; Pujade-Renaud et al. 2005). Chrestin et al. (1997) described that over-expression of chitinase (hevein) gene was due to the partial deglycosylation of the hevein receptor and the resulting delay in coagulation. The level of hevein and chitinase expression in the latex is regulated by ethylene.

## Laticifer-specific promoters

Recently there has been growing interest in using plants for the production of biopharmaceutical proteins and peptides because they are easily transformed and provide a cheap source of protein. In this aspect the commercial rubber tree has great potential to produce foreign proteins in the latex, which can be easily purified from the serum phase of the latex. The availability of regulatory sequences or promoters to target expression to laticifers is an essential component for engineering traits in transgenic *Hevea* plants as the constitutive expression of foreign proteins is deleterious to the plants. One way to identify such promoters would be to study the upstream region of genes like REF, HMGCoA reductase etc. that are highly expressed in latex. Besides promoters, other regulatory elements like introns and enhancers also play important roles in gene expression. Pujade-Renaud et al. (2005) reported the isolation of promoter regions from two hevein genes of Hevea and analyzed them in rice. Although both were functional, only the longest promoter sequence (PHev2.1) conferred a high level of expression to the transgene in various tissues of this heterologous host plant. Most recently, promoter sequence of REF gene was cloned and characterized by Priya et al. (2006). The cloned 5' promoter region has a putative TATA element at -150 and CAAT box at the -221 position. To identify the regulatory role of REF promoter, chimaeric fusion between REF promoter sequence and the  $\beta$ -glucuronidase (GUS) coding, *uidA* gene was constructed and used to transform tobacco and Arabidopsis. Expression of the *uidA* reporter gene was detected histochemically in the transformed tobacco plants where, GUS activity was detected in the leaf and petiole of transformed plants. The stable integration of REF:uidA fusion into the tobacco genome was further confirmed by PCR amplification and Southern blot analysis. A histochemical study of stable transformants demonstrated that the 5' upstream region of REF can drive strong GUS gene expression specifically in the vascular tissues (xylem and phloem) of leaf, stem and midribs of transgenic Arabidopsis. GUS staining revealed that REF:GUS expression was also induced by wounding. The results suggested that the cloned REF promoter is capable of directing gene expression.

#### **Tapping Panel Dryness (TPD) syndrome**

Tapping panel dryness (TPD) syndrome ultimately leads to the partial or complete stoppage of latex biosynthesis in high latex yielding rubber trees. Different approaches have been used to describe and study the development of the TPD syndrome in the recent past. It had been previously reported that the latex from trees displaying the TPD syndrome exhibited different protein patterns compared to healthy trees (Dian et al. 1995). Accumulation of three polypeptides in the latex cytosol of TPD affected trees were also considered as protein markers (Sookmark et al. 2002). However these protein markers have been yet utilized neither for early detection nor for diagnosis of TPD syndrome in rubber tree. Subsequently, studies aimed to identify genes associated with TPD have also been attempted. Chen et al. (2003) reported that the expression of HbMyb1 was likely associated with TPD syndrome. Recently, Venkatachalam et al. (2005, 2007) described the identification of TPD responsive genes by Suppression Subtractive Hybridization (SSH) technology using mRNA from latex samples of healthy and TPD trees (Fig. 2B, 2C). To identify the genes involved in this process, two SSH cDNA libraries were constructed. For forward subtracted cDNA library, healthy RNA was used as 'tester' and TPD RNA served as 'driver', whereas TPD RNA was 'tester' and healthy RNA was 'driver' for reverse subtracted cDNA library. A total of 1079 putatively positive clones were screened from these two libraries; 352 of these clones were found to be positive by differential screening with forward and reverse subtracted probes and were selected for further sequencing analysis. The putative functions of clones were predicted by BLASTX/BLASTN analysis. Among these, 64 clones were genes whose function had been previously identified while the remaining clones were genes with either unknown protein function or insignificant similarity to other protein/ DNA/EST sequences in existing databases. Differentially expressed genes selected by subtractions were classified into 12 broad categories according to their putative functions generated by BLAST analysis. Two genes, i.e. Myb transcription factor and TCTP (Translationally Controlled Tumor induced Protein) that were up-regulated in the forward SSH library, were selected for expression analysis. Results from Northern analysis confirmed that the expression of these two genes was down-regulated in TPD frees. Some other known genes identified in this study might provide new insights into the TPD triggered PCD development in rubber tree (Venkatachalam et al. 2007).

#### **Risks and concerns**

The introduction of transgenic crops into the existing natural system has generated a number of questions about the possible negative consequences. Biosafety considerations, including the impact of transgene dispersion through pollen and unexpected effects on non-target organisms, are now receiving attention. The issues on *Hevea* rubber transgenic plants can be broadly grouped into concerns about:

#### Damage to human health and natural environment

Since *Hevea* is not used as a food crop, there is no such food safety issue with transgenic *Hevea* plants. Gene flow from transgenic crops to others requires: 1) the presence of sexually compatible wild relatives close to the crop, 2) an overlap of flowering times between the crop and wild relatives and 3) the presence of a pollinating agent such as a bird or an insect unless, the likelihood that transgenes will spread can be different for each crop and wild combination in each area of the world. Unlike other crops, there are no wild relatives of *Hevea* in the nature. If pollen grains from transgenic *Hevea* plants are released in these areas they do not encounter any compatible plants to pollinate, so there is no risk of gene flow. Also rubber seedlings are developed via budgrafting technique, so the risk of gene transfer is much insignificant.

# Concerns about damage to current farming practices

Hybridization of transgenic crops with nearby conventional crops raises concerns on several fronts. Movement of pollen from a transgenic field to an organic field involves farmers in discussions about the distance required between fields to ensure purity of a crop, and about who must pay if unwanted genes move into a neighbour's crop. It is important to ensure that hybridization is not occurring in the field. Many agencies publish recommended minimum separation distances for a variety of crops. These distances have been developed to maintain a level of purity that has been acceptable to the agricultural community in the past. When there is a danger of gene flow to nearby fields, it is possible to prevent contamination of nearby crops by planting tall barrier plants to physically block the flow of pollen. If GM pollen pollinates plants in neighbouring field, then the issue of genetic trespass may arise. These issues have already prompted several lawsuits and they will continue to be a factor in the development and use of transgenic plants for years to come. As far as Hevea transgenic plants are concerned, it takes about 6 years for the first flowering, so the crop suitability can be assessed before pollen production. The main objective of Hevea transformation is to produce plants for enhanced latex yield, TPD tolerance, disease resistance and recombinant protein production. Therefore the impact of any gene escape to the environment or neighbor field is expected to be remote with transgenic Hevea plants. Also, the ultimate product from transgenic *Hevea* plant is latex with protein and it is to be purified from latex so neither the inserted gene not the selection marker gene is thus available to the consumer.

#### CONCLUSIONS AND FUTURE PROSPECTS

In *Hevea* rubber tree species, there has been tremendous progress in *in vitro* culture research. In the last decade several protocols have been developed for *in vitro* mass propagation of *Hevea*. Micropropagation of superior rubber clones via somatic embryogenesis has had considerable impact on production of uniform plants. Few protocols are available for micropropagation by using immature anther and inflorescence explants from elite mature rubber trees. In these reports it is evident that there is a possibility to overcome some of the inherent problems of large scale production and establishment of rubber plants. However, in many instances the extent of rejuvenation through tissue culture techniques is insufficient to permit commercial propagation. The importance of selecting the appropriate explants of rubber tree for the initiation of in vitro cultures should receive more attention. Moreover, the techniques are not yet sufficiently refined for commercial application. A number of large-scale field trials with in vitro derived clones are in progress and it is expected that these will reveal whether commercial application is possible or not. The field trials will determine the current potential of micropropagation techniques for commercial scale cultivation of rubber. In vitro approaches are presently being applied to Hevea rubber tree to achieve genetic transformations. These techniques are likely to play a vital role in future tree-improvement programs. More refinement in the protocols is essential in understanding the requirements for efficient plant regeneration. With recent research developments, molecular biology provides tools that may allow genetic improvement to make up lost ground. The genetic transformation provides opportunities for creating new clones with important agronomic traits otherwise unavailable, such as TPD tolerance, improvement of growth, latex biosynthesis, and wood quality and a reduction in the expression of endogenous genes that encode undesirable traits. It is obvious that the results obtained from the above mentioned molecular marker techniques have contributed to the understanding of clonal relationships, origin and distribution and are potential tools in germplasm evaluation and genetic characterization of traits with agronomical interest. Molecular investigations provide a basis for understanding the regulation of various genes and their potential involvement in the complex rubber biosynthetic pathway. Using the identified genes, it is possible to determine the rate limiting steps and the regulation points or controlling events in latex biosynthesis at least at the transcriptional level. Although considerable progress was achieved in annual crops during the last decade, many biotechnological approaches are at a preliminary stage in rubber tree. Moreover, the application of biotechnology to rubber tree requires further investigations on the risk of genetic instability in transgenic plants and on potential escapes of transgenes into wild plants.

A combination of tissue culture and molecular biology may synergistically provide great benefit to the improvement of rubber tree. All available biotechnological tools must be employed to meet the challenges of sustainable agriculture and rubber security in the world. Scientists are investigating new biotechniques that may have great applications in the genetic enhancement of rubber tree. However, biotechnology should be integrated along with other existing techniques in current Hevea improvement programs. Today, biotechnology offers to Hevea improvement programs clean and fast multiplication of clones via micropropagation, and genetic markers for assisted selection. Rubber biotechnology has made a first phase impact. If current progress in in vitro culture and genetic transformation combined with molecular biology applications continues, the future may witness superior Hevea tree species tailored for special agronomic and economic characteristics.

#### ACKNOWLEDGEMENTS

We wish to thank Drs. James Jacob, Director, Annamma Vargheese, (Joint Director), RRII for their constant encouragement.

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