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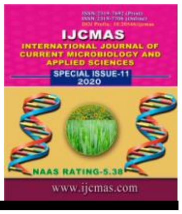

Review Article

Forest Biotechnology: Current Trends and Future Prospects

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ABSTRACT

The application of biotechnology to forestry and in particular to plantation forestry in countries, holds considerable promise to: provide increased genetic gain, make forestry operations more economic, yield higher returns, and provide environmental benefits. Genetically improved trees are playing a greater role in meeting the world's wood requirements. Genetically engineered trees, created by asexual means, offer potential to provide higher-quality and lower-priced wood as well as environmental benefits. Modern biotechnology tools provide a range of options in which the advances made in plant improvement. Recent developments in forest tree biotechnology suggest that this is already occurring and that there is no longer a significant bottleneck to some of the barriers of traditional forest tree improvement. Combined with the genetic advances made by the tree breeding, a new dimension to forest tree enhancement initiatives has been introduced with the advent of new biotechnological methods covering the fields of plant developmental biology, genetic transformation, and the discovery of genes associated with complex multigenic traits. With reference to future energy, pulp, food and construction uses, the role of 'tree technology' using changed practises or genetic components in tree breeding is defined. The present and future leading edge prospects for biotechnological breakthroughs are explored in manipulating rapid growth, expanding geographical ranges, flowering production control, carbohydrate involvement, 'omics innovations, and biotic and abiotic stress resistance. It addresses the potential of forest biotechnology to contribute to the global delivery of economic, societal and environmental benefits. In the near future, the commercialization of planting stocks as new varieties developed by clonal propagation and advanced breeding programmes or as high-value transgenic trees is anticipated, and these trees will increase the quality and productivity of our plantation forests.

Keywords

Biotechnology, Forestry, Micropropagation, Tissue culture, Tree Improvement

Introduction

The domestication of various plants and animals for provision of food, and making articles for everyday use, has contributed significantly to the welfare of mankind. Many of these domesticated species no longer resemble their original ancestors. Over recent decades, we have witnessed waves of innovation that have led to significantly increased agricultural production and an improvement of the quality of products derived from plants and animals. The use of modern biotechnology, which many have termed the second green revolution, has in the last 6-8 years, demonstrated a strong capability to produce even more food, more economically, and with a reduced environmental impact (James, 2003; Gianessi *et al.*, 2002).

The world population now could be 6.7 billion and is foreseen to achieve nine billion by 2050 (Von Braun, 2010). Such a speedy growing population has enormously accumulated the challenge for food security. Obviously, it's not possible for ancient agriculture to confirm the food security, whereas plant biotechnology offers sizeable potential to comprehend this goal (Fedoroff, 2010). The term "biotechnology" has been accustomed seek advice from several biological processes that turn out helpful product, together with some quite ancient ones like fermentation in brewage, wine and cheese (Coombs, 1992; Zaid *et al.*, 1999, Vikas Kumar *et al.,* 2015a). However, most often nowadays the term is employed to seek advice from information concerning the natural processes of DNA replication, breakage, ligation, and repair that has created possible a deeper understanding of the mechanics of cell biology and therefore the hereditary method (McCouch, 2001). Biotechnology provides vital tools for the sustainable development of agriculture, fisheries and forestry and may be of great facilitate in meeting an essential half within the rise of human civilization. It so usually thought-about united of the fields of research during which the foremost speedy advances are created in recent years (Vikas Kumar *et al.*, 2015a).

Forest biotechnology analysis and application is actually world in scope with activities known in seventy six countries. a big majority of cited activities happens in developed countries (68 percent), with the United States (14 percent), France (9 percent) and Canada (8 percent) the foremost active participants diagrammatic within the knowledge set (percentages are of total citations of main biotechnology activities). India (9 percent) and China (6 percent) were way and away the foremost active of the developing countries and countries in transition. Regionally, forest biotechnology activities were most varied in Europe (39 percent), Asia (24 percent) and North America (23 percent), and least varied in Oceania (6 percent), South America (5 percent), Africa (3 percent) and therefore the Near East (less than one percent). Whereas, forest biotechnology analysis and application has unfold to a minimum of one hundred forty genera, the good majority of activity (62 percent) has been targeted on solely six genera (*Pinus*, *Eucalyptus*, *Picea*, *Populus*, *Quercus* and *Acacia*, in dropping order of activity).

Forestry has been tremendously benefited from the event and implementation of improved silvicultural, forest management practices and breeding techniques, that have contributed considerably to the advance of forest tree species within the past, and can still have a considerable impact on the genetic gain and productivity of economically vital tree species by providing higher germplasm and improved management practices for plantation forests. though smart progress has been created in breeding trees for altered xylem-fibre lengths and polymer content, that is efficacious to the paper and pulp industries (Turnbull 1999, Heilman 1999), a lot of less progress has been created in rising timber quality, exactly as a result of the wood formation is thus poorly understood (Lev-Yadun and Sederoff, 2000; Plomion *et al.*, 2001).

It's most likely one in all the foremost advanced phenomena facing plant biologists these days, with maybe 40,000 genes being concerned (Lorenz and Dean 2002), thus while not biotechnological tools to realize a far better understanding of the method, markers for wood quality traits can stay a foreign prospect. Traditional breeding strategies are typically unnatural by the long procreative cycles of most tree species and also the problem in achieving important enhancements to the advanced traits like wood properties, disease and pest control, and tolerance to abiotic stresses. The state of food and agriculture reported that biotechnology is quite Genetic Engineering (FAO, 2004). In fact, eighty one of all biotechnology activities in forestry over the past 10 years weren't associated with genetic modification (Wheeler, 2004).

The 1995 Convention on Biodiversity defines biotechnology as ‘any technological application that uses biological systems, living organisms, or derivatives thence, to create or modify product or processes for specific use’. Any product or processes derived from trees or alternative forest ecosystem organisms might so usefully be thought-about as forest biotechnology. However, intensive forestry has become the order of the day once the provision of land and alternative factors are creating traditional forestry practices progressively unsustainable. Trees with shorter rotations, and genetically improved for disease and pest resistance, superior kind etc., are deployed in plantations in several of the developed nations wherever genetic improvement programmes has been initiated. The arrival of biotechnology within the past twenty years, however, broadened the scope of genetic improvement of trees, chiefly by removing the hurdles encountered in standard breeding programmes. Partly because of the environmental issues and conjointly because of the increasing realization of the benefits of intensively managed plantations of quick growing tree crops, the interest in application of biotechnology to forest crops has been enkindled (Fig. 1 and 2; Table 1).

Desirable effects

Biotechnology in forestry offers a number of attractive possibilities such as increased productivity, reduced pressure on the land base, preservation of genetic diversity, and better biological control of pests. The various biotechnologies each offer their own benefits. In general, genetic gains generated over a number of generations from classical breeding programs vary between 5 and 20% and higher (Dane, 1991). One should expect the gains generated by forest biotechnology to be a minimum of as great as, and possibly faster than, those obtained from conventional genetics. This can be achieved through vegetative propagation of valuable genotypes (Mullin and Park 1992) and enhanced tree growth (von Arnold *et al.*, 1991). Enhanced tree growth are often attained by manipulating the genes controlling the synthesis of growth regulators (von Arnold *et al.*, 1991), as has been done with tobacco using a gene that encodes an enzyme involved in ethylene biosynthesis (Medford *et al.,* 1989). Tree growth could also be increased through improved tolerance to environmental stresses. Results suggest that plants have genes controlling heat tolerance (Mansfield and Key 1987, Ottaviano *et al.*, 1991), drought tolerance (Seiler and Johnson 1988, Teskey *et al.*, 1987), and low-nutrient tolerance (Crawford *et al.*, 1991). The optimist may speculate that the insertion of such genes into trees and their subsequent expression may increase tree growth generally, and maybe enable tree planting on some poor forest sites which couldn't be intensively managed otherwise.

Undesirable effects

Potentially, the appliance of biotechnology in forestry could lead on to four sorts of undesirable effects: acquired resistance to regulate agents, non-target pest emergence, reduction of biodiversity, and genetic pollution. Not all biotechnological applications lead to each of these undesirable effects. Many of the effects of biotechnology on natural ecosystems can also arise from other human interventions such as, for example, classical breeding and silvicultural programs (Mikola, 1991). Acquired resistance to regulate agents has relevancy to all or any biotechnological activities aimed toward pest control. Adaptation of pests to pesticides is commonplace (Forgash, 1984) particularly because the utilization of all groups of pesticides, including *B. thuringiensis* on crop plants but not trees, has led to the emergence of resistant biotypes (McGaughey, 1985; Raffa, 1989). It is important to know that the rapidity of emergence of resistant biotypes may be a function of the intensity and nature of the choice pressures applied on pest populations. Pests adapt faster to single resistance factors than to multiple resistance genes (Ellingboe, 1981, Van der Plank, 1968). For this reason, large-scale out planting of trees with engineered resistance may favour -pest populations if this resistance is predicated on single resistance genes and if the choice pressures are exerted intensively over the length of stand rotation. Therefore, pest management should be based on multigenic resistance when trees themselves are the carrier of the resistance genes (Hubbes, 1987). Transgenic resistance in trees and other intensive sorts of control of forest pests using biotechnology may exert new evolutionary pressures on non-target pests through removal of their natural enemies or by freeing ecological niches. Raffa (1989) noted that the sole major outbreak of the spruce spider mite *Oligoizcy husununguis* reported in natural forests followed a DDT spray for the control of western spruce budworm *Choristoneura occidentalis* (Furniss and Carolin, 1977). It so happened that DDT did not affect the mites but killed their natural enemies. So, as can be seen, the control of some forest pests may favour the emergence of new pests. Due to a scarcity of knowledge on natural populations of potential pests, it's difficult to predict the occurrence of latest pests in response to biotechnology (Niemela and Neuvonen, 1983).

Clonal forestry

Clonal forestry can be defined as afforestation with a restricted number of vegetatively propagated clones, which have been tested and selected in clonal tests, the best being subsequently mass produced (Menzies and Aimers-Halliday, 2004). Although implementation has been slow with conifers, there are numerous successful eucalyptus clonal forestry programmes, some of which have been active for many years (Zobel, 1993; Griffin *et al.*, 2000). The potential benefits of clonal forestry have often been cited (e.g. Libby, 1982; Libby and Rauter, 1984 and Carson, 1986) including

- gains arising from testing and selection of clones,
- clone/site matching to increase genetic gains both from capture of favorable genotype by environment effects (G X E), and from targeting expression to existing site properties
- greater *uniformity*, which may have little impact on growth and yield traits, but can be extremely valuable for log and wood quality and disease resistance traits, and for harvesting and processing, and
- greater *repeatability*, which provides benefits in yield prediction and planning.

There are a number of risk factors that need to be addressed in clonal forestry programmes (e.g. Kube and Carson, 2004), principal among these being the potential risk to ‘genetic monocultures’ from damaging losses to pests and diseases.

In vitro culture

This technique involves propagating plant tissues (units as small as a cell) in a controlled environment free of microorganisms. Approximately 34% of all biotechnology activities reported in forestry over the past ten years related to propagation (Chaix and Monteuuis, 2004; Wheeler, 2004). An entire tree is often regenerated from one cell. *In vitro* culture can be used to reproduce seedlings and to cryopreserve cell lines from which it will be possible to regenerate other copies of the same seedlings in the future. In *in vitro* plant culture, regeneration occurs via two main pathways: organogenesis and somatic embryogenesis. Organogenesis is the regeneration of plants through organ formation on an explant or from cell masses, and for somatic embryogenesis it is done through the formation of embryo-like structures. Organogenesis has been the tactic of choice for species like poplar and eucalyptus, and embryogenesis has been used very successfully with conifers (Park *et al.,* 1998). Both processes provide the means to clonally propagate large numbers of elite trees for research and reforestation. One drawback of somatic embryogenesis is that it is fully applicable only using juvenile material as initial explants (embryos but difficult to carry out with needles). O capture maximum gains a two-step procedure must be established. Firstly, while testing new lines produced with replicated clonal trees, tissue lines must be cryopreserved. Secondly, once the simplest clone has been identified after a couple of years of testing, cryopreserved tissue of the simplest lines are replaced into *in vitro* culture for tree multiplication and propagation. *In vitro* culture is additionally essential to gene-splicing or transgenesis work because it provides the fabric on which the technology is often administered.

The new insights to be gained into the control of growth, differentiation, carbohydrate partitioning, reproductive control and both food- and non-food uses of trees will all play major parts in determining the precise nature of the longer term of forest biotechnology (Troggio *et al.*, 2012). The waves of latest epigenomic data now starting to emerge will undoubtedly provide increased understanding of the control of organic phenomenon, environmental stress responses and development. When put together, all of these enhancements will ensure that forest biotechnology makes a significantly larger contribution to meeting our global economic, environmental and societal needs for many decades to come.

Biotechnological approaches have begun to deliver new tools in combating threats to forest trees. For many of the threats posed to our forest trees by imported pathogens, other biotic or abiotic stresses like global climate change, biotechnology is perhaps the sole effective way to develop novel solutions. This is especially so where tree biodiversity is under threat, or for individual trees of significance, sometimes known as 'heritage trees'. Initial progress is encouraging and within the years ahead, the amount of examples where biotechnological tools are often wont to overcome threats to valuable biodiversity and key germplasm will increase.

Future deployment, on forest or landscape scales is going to be strongly influenced by the degree of public acceptability for such biotech trees. Dutch elm disease is caused by the fungus *Ophiostoma novo-ulmi*, transmitted by elm bark beetles (*Scolytus spp*.) has ravaged elms throughout the Northern Hemisphere, with so far limited outbreaks in New Zealand and Japan. Scientists have developed Agrobacterium mediated gene transfer techniques for English elm (*Ulmusprocera Salisbury*) and transferred a range of potential anti-fungal genes into the clonal SR4 genotype found in the southern British Isles (Gartland *et al.*, 2005). These candidate genes appear to limit fungal growth either by preventing spore germination or restricting hyphal growth. State University of New York (SUNY) scientists have used a similar delivery approach to successfully express a synthetic anti-microbial peptide ESF 39A, in American elm (*U. americana* L.). Promising results against the fungal pathogen *O. novo-ulmi*, have been obtained, whilst undertaking the first field trials of genetically modified American elms (Newhouse *et al.*, 2009).

Regulations controlling the use of biotechnology in forestry should not only include some regulations borrowed from those used for agricultural crops (Kalous and Duke, 1989), but they should also take into account the forest trees. Trees have rotation ages that are much longer than those of crops, and so the exposure of forest ecosystems to a particular biotechnologically-derived product is much longer than in agricultural ecosystems. These differences dictate that unique regulations should be applied to the use of biotechnology in Forest ecosystems. To date, the most thorough regulations controlling the use of genetically engineered and clonally propagated trees have been enacted by the Swedish and German governments (Muhs 1988). These regulations encompass the source, field testing, and final field use of improved trees.

DNA markers

DNA markers are just beginning to have a major impact in forest tree improvement programmes. DNA fingerprinting is being used as a tool for quality control (e.g. Wilcox *et al.*, 1997), for example in

- studying the genetic diversity of breeding population accessions from native provenance and land-race origins,
- verifying genetic identity of plus-tree candidates held in clonal archives
- Paternity testing of progeny in screening trials, and
- verifying genetic identity of seed orchard parents and production clones in tissue culture operations during stages of multiplication of elite stock for deployment.

Mapping, marker-assisted selection and genomics (MMG)

MAS are now being used extensively in agricultural crops. Although it has not yet been implemented in trees, MAS promises to be a powerful tool for obtaining genetic gains through bypassing the need for long-term field trials and shortening the time required for selection. MAS could now be applied directly for early screening of progenies and clones of radiata pine, and eucalypts (Devey *et al.*, 2003).

During the decade of the 1990s significant biotechnology activity centred on the development of molecular markers, test populations, genetic linkage maps, and statistical means of identifying Quantitative Trait Loci (QTLs). QTLs represent statistical associations between markers and genes that control some proportion of the genetic and phenotypic variation of a quantitative trait (generally but 10 percent per QTL). QTLs have several potential applications including (i) genetic dissection of complex quantitative traits, (ii) providing the idea for MAS, and (iii) providing guidance for selection and prioritization of candidate genes (discussed later). Linkage and QTL maps are created for over twenty-four tree species and though more maps are likely to seem, most current efforts appear to specialise in increasing the density and sort of markers located on these maps. The current trend in MAS is towards the selection of superior alleles in candidate genes directly controlling phenotypic variation in traits of interest. This approach, termed association genetics, differs in application from traditional QTL studies primarily within the sort of the test population being studied. Traditional methods use pedigreed populations for within-family selection while association studies believe populations of unrelated individuals. Though MAS using QTLs has found utility for specialized populations of commercial species in a few developed and developing countries, association genetics holds promise for application across many populations, species and countries following appropriate development.

Over the last six years tremendous resources have been invested in genomics sciences, though this may not yet be reflected in the activities compiled here. Genomics encompasses a wide range of activities including gene discovery (ESTs), gene space and genome sequencing, gene function determination (database blast searches, expression profiling using arrays and slides, etc.), comparative studies among species, genera and families, physical mapping and therefore the burgeoning field of bioinformatics. The ultimate goal of genomics is to spot every gene and its related function in an organism.

Transgenesis

A wide diversity of sources of transgenes and regulative parts, and supposed traits, are tested, as well as expression of communicator genes; insect, disease, and weed killer resistance; changed wood properties; changed flowering and fertility; and changed rate and stature (Viswanath *et al.,* 2011). Procedures for genetic transformation of forest trees dissent very little from those for different plant species and are chiefly confined to the utilization of Agrobacterium, with some reports on particle bombardment-mediated transformation. Differentiation of reworked cells could be a necessity to getting transgenic plants and 2 systems are being employed in forest trees: organogenesis and embryogenesis. Such transformation procedures, as well as the utilization of selectable markers and screening ways, are well established. It's potential to introduce one or additional absolutely characterised new characters while not, in theory, adversely poignant the general genetic make-up of the plant. This approach conjointly offers the likelihood of overcoming the genetic barrier between species, during a comparatively shorter timeframe than through typical tree breeding. the main obstacles to economical production of transgenic trees are: (i) difficulties in plant regeneration from Agrobacterium-infected or particle-bombarded explants; (ii) incomplete development on the far side the in vitro stage of unmoving plants for establishing field trials; and (iii) transgene instability throughout the long life-span of forest trees, as well as transgene silencing and somaclonal variation (Harfouche *et al.,* 2011). Once transgenesis is performed at the cell level, in vitro culture techniques are often accustomed regenerate the complete tree.

Micropropagation

Micropropagation is a term used here to explain strategies of *in vitro* vegetative multiplication together with rooted cuttings, organogenesis and somatic embryogenesis. Micropropagation is employed to make massive numbers of individual clones or genotypes. As a result of vegetative propagation bypasses the genetic mixture related to sexual reproduction, it represents a perfect due to deliver genetic gain: selected people are replicated exactly. The bulk of biotechnology activities excluding genetic modification compiled by Chaix and Monteuuis (42 percent) relate to micropropagation.

Micropropagation by rooted cutting is often employed in quite twenty species of commercial importance, the bulk of that are angiosperms. Several of the activities noted recommend the technology is advanced and commercially viable. Conifers are less simply rooted than angiosperms, though' modest programmes for many genera exist. Somatic embryogenesis is outlined by Associate in Nursing array of steps that end in the creation of embryos from somatic tissues (as against cell embryos from germinal cell lines). Though technically troublesome, the technology has the potential to supply virtually countless genetically identical individual plants. It's received right smart R&D attention for extremely valued gymnosperm tree species, primarily in developed countries, for several years. Though large-scale industrial plantings of somatic embryos don't nevertheless exist, progress within the technology seems promising and small-scale field testing is increasing (for example, on *Pinustaeda* within the United States). The delivery of somatic embryos to the sphere remains a big hurdle to reducing plantlet cost and, therefore, large-scale use. Glorious progress within the creation of factory-made seed seems to produce an answer to the present drawback, though' more analysis is probably going to be required.

Table.1 Tree genomics Records

Tree	Species	Indicative problem
Poplar	*Populus trichocarpa*	Gender determination Fate of transgenes model 41,377 genes
Amborellid	*Amborella trichopoda*	Earliest diverging angiosperm still extant Primitive tree Organ differentiation
Apple	*Malus x domestica*	'golden delicious' Fruit properties57,386 genes
Peach	*Prunus persica*	Selfing behaviour control 27,852 genes
Pear	*Pyrusbret schneideri*cv.	Dangshansuli Fruit flesh quality Processing properties
Papaya	*Caricus papaya*	Fruit colour and yield control 28,629 genes
Cocoa	*Theobroma cacao* 'Criollo'	Cocoa bean butter properties 35,000+ genes
Grape	*Vitis vinifera*'	Pinot Noir' Fruit processing properties 26,346 genes
Eucalypts	*Eucalyptus grandis*	Pulping properties40,000+ genes
Sweet orange 'ridge pineapple'	*Citrus sinensis*	Juice properties25,376 genes
Clementine Mandarin	*Citrus elementina*	Taste properties 25,385 genes

Fig.1 Plant improvement through tissue culture technology

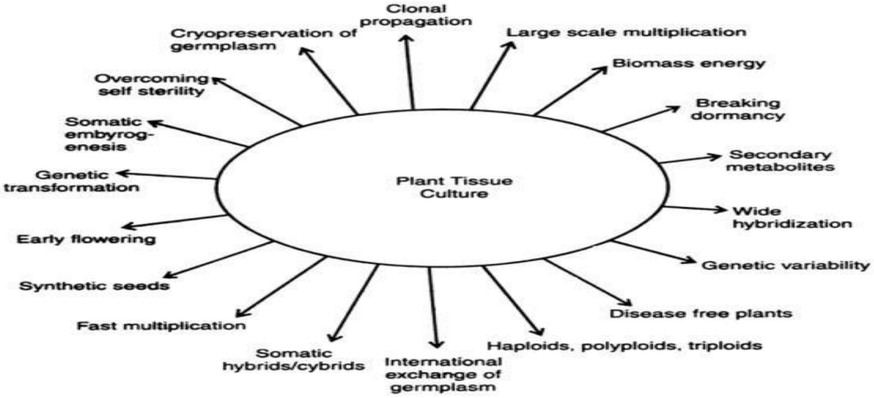
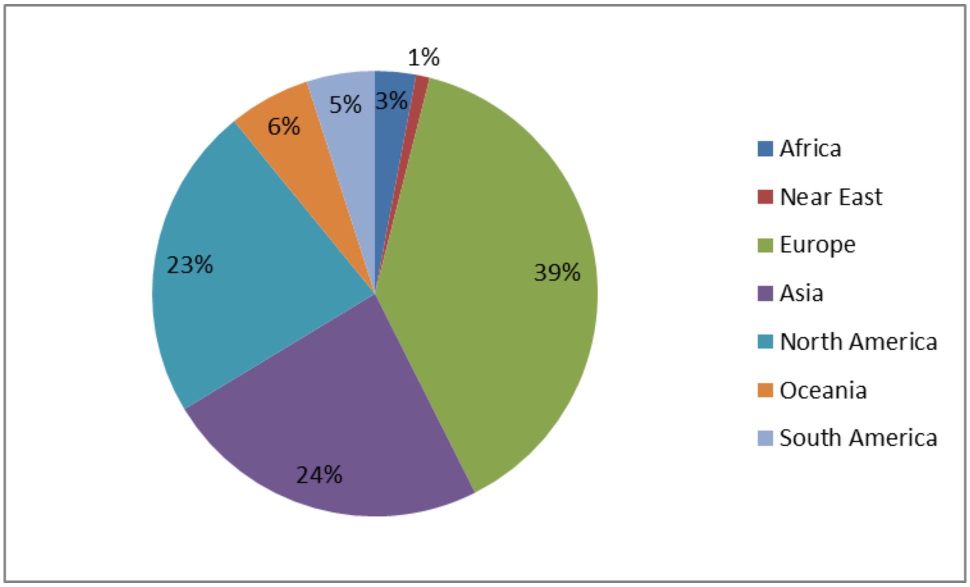


Fig.2



References

Anderson, J.B., Petsche, D.M. and Smith, M.L. 1987. Restriction fragment polymorphisms in biological species of *Artnillaria mellea*. Mycologia 79: 69-76.

Baxter, I, and Dilkes, B.P. 2012. Elemental profiles reflect plant adaptations to the environment. Science 336:1661–1663.

Carlson, J.E., L.K. Tulsieram, J.C. Glaubitz, V.W.K. Luk, C. Kauffeldt and Rutledge, R. 1991. Segregation of random amplified DNA markers in F1 progeny of conifers. Theor. Appl. Genet. 83: 194-200.

Carson, M.J. 1986. Advantages of clonal forestry for Pinus radiate – real or imagines? N.Z.J. For. Sc. 16: 403-415.

Chaix, G. and Monteuuis, O. 2004. Biotechnology in the Forestry Sector. In: Food and Agriculture Organization.

Connor, A. and Meredith, C. 1985. Strategies for the isolation and characterization of aluminum resistant variants from cell cultures of

Nicotiana plurnbuginifolia. Planta 166: 466-473.

Coombs, J.M. 1992. Macmillan Dictionary of Biotechnology. Hants, UK: Macmillan.

Crawford, D.T., B.G. Lockaby and Somers, G.L. 1991. Genotype-nutrition interactions in field-planted loblolly pine. Can. J. For. Res. 21: 1523-1532.

Danell, O. 1991. Possible gains in initial stages of a national tree improvement programme using different techniques. Forest Tree Improv. 23: 11-30.

Devey, M.E., K.D. Jermstad and Neale, D.B. 1991. Inheritance of RFLP loci in a loblolly pine three-generation pedigree. Theor. Appl. Genet. 83: 238-242.

Ellingboe, A.H. 1981. Changing concepts in host-pathogen genetics. Ann. Rev. Phytopathol. 19: 125- 143.

FAO. 2004. The State of Food and Agriculture 2003–2004. Agricultural biotechnology: meeting the needs of the poor? FAO Agriculture Series, No. 35. Rome.

Forgash, A. J. 1984. History, evolution, and consequences of insecticide resistance. Pest. Biochem. Physiol. 22: 178- 186.

Gartland, K.M.A., McHugh, A.T., Crow, R.M., Garg, A, and Gartland, J.S. 2005. Biotechnological progress in dealing with Dutch Elm disease. In Vitro Cell Dev Biol Plant 41:364–367.

Gianessi, L., Sivers, C.S., Sankula, S. And Carpenter, J.E. 2002. Plant Biotechnology: Current and Potential Impact for improving pest management in US agriculture – An analysis of 40 case studies. The National Centre for Food and Agricultural Policy, Washington.

Government of Canada. 1990. Canada's Green Plan. Dept. of Supplies and Services, Ottawa.

Griffin, R., harbard, J.L., Centurion, C. and Santini, P. 2000. Breeding *Eucalyptus grandis* x globules and other inter-specific hybrids with high inviability – Problem analysis and experience with Shell Forestry projects in Uruguay and Chile. Symposium on hybrid breeding and genetics, Noosa, Queensland, April 2000.

Harfouche, A., Meilan, R. and Altman, A. 2011. Tree genetic engineering and applications to sustainable forestry and biomass production. Trends in Biotechnol., 29(1): 9-17.

Heilman, P.E. 1999. Planted forests: poplars. New Forest, 17: 89-93.

James, C. 2003. Global status of commercialization of transgenic crops. ISAAA briefs No. 30.

Kremer, A, Vincenti, B, Alia, R, Burczyk, J, Cavers, S, Degen, B, Finkelde, R, Fluch, S, Gomory, D, Gugerli, F, Koelwijn, H.P., Koskela, J, Lefevre, F, Morgante, M, Mueller-Starck, G, Plomion, C, Taylor, G, Turok, J, Savolainen, O, and Ziegenhagen B. 2011. Forest ecosystem genomics and adaptation. Tree Genet Genomes 7:869–875.

Kube, P. and Carson, M. 2004. A review of risk factors associated with clonal forestry of conifers. In: Walter, C. And Carson, M.J. (Eds) plantation forest biotechnology for 21st century. Research Signpost, Kerala, India.

Landry, B.S. and R.W. Michelmore. 1987. Methods and applications of restriction fragment length polymorphism analysis in plants. Pages 35-44. In: G. Breuning, J. Harada, T. Ksuge and A. Hollaender (eds.). Tailoring genes for crop improvement. Pleunum Press, New York.

Larkin, P.J. and Scowcroft, W.R. 1989. Somaclonal variation of eyespot toxin tolerance in sugarcane. Plant Cell Tissue Organ Cult. Plant Cell Tissue Organ Cult. 2: 11-121.

Larkin, P.J., P.M. Banks, R. Bhati, R.I.S. Brettell, P.A. Davies, S.A. Ryan, W.R. Scowcroft, L.H. Spindler and G.J. Tanner. 1989a. From somatic variation to variant plants: mechanisms and applications. Genome 3(1): 705-711.

Larkin, P.J., S.A. Ryan, R.I.S. Brettell, and Scowcroft, W.R. 1989b. Heritable somaclonal variation in wheat. Theor. Appl. Genet. 67: 443-455.

Lev-Yadun, S. and Sederoff, R. 2000. Pines as model gymnosperms to study evolution, wood formation and perennial growth. J. Plant Growth Regul., 19: 290–305.

Libby, W.J. 1982. What is a safe number of clones per plantation? In: Resistance to disease and pests in forest trees. In: Heybroek, H., Stephen, B., and Weissenberg, K. (Eds.) proceedings of the 3rd International Workshop on the Genetics of Host parasite Interactions in Forestry September 1980. Wageningen, Netherlands, pp. 342-360.

Libby, W.J. and Rauter, R.M. 1984. Advantages of clonal forestry. For. Chron. 60: 145-149.

Mansfield, M.A. and Key, J.L. 1987. Synthesis of the low molecular weight heat shock proteins in plants. Plant Physiol. 84: 1007-1017.

Mantell, S.H., J.A. Matthews and McKee, R.A. 1985. Principles of plant biotechnology. Blackwell Scientific Publications, Oxford. McGaughey, W.H. 1985. Insect resistance to the biological insecticide Bacillus thuringiensis. Science 229: 193- 195.

McCouch, S.R. 2001. Is biotechnology an answer? In Who Will Be Fed in the 21st Century?, ed. K Wiebe, N Ballenger, P Pinstrup-Andersen, pp. 29–40.

McHughen, A. 1987. Salt tolerance through increased vigor in a flax line (STS-II) selected for tolerance in vitro. Theor. Appl. Genet. 74: 727-732.

Medford, J.I., R. Horgan, Z. ElSawi and Klee, H.J. 1989. Alterations of endogenous cytokinins in transgenic plants using a chimeric isopentenyl transferase gene. Plant Cell 1: 403-413.

Menzies, M.I. and Aimers-Halliday, J. 2004. Propagation options for clonal forestry with conifers. pp. 255-274, in: C. Walter and M. Carson (editors). Plantation forest biotechnology for the 21st century. Research Signpost, Trivandrum, Kerala, India.

Mikola, J. 1991. Consequence of modern tree breeding techniques on breeding strategies of the main tree species in Finland. Forest Tree Improv. 23: 81-103.

Muhs, H.J. 1988. Rules governing the release of forest reproductive material derived by in vitro culture. Pages 211-219.

Mullin, T.J. and Park, Y.S. 1992. Estimating genetic gains from alternative breeding strategies for clonal forestry. Can. J. For. Res. 22: 14-23. In: M.R. Ahuja (ed.) Somatic cell genetics of woody plants. Kluwer Academic Publishers, Dordrecht, The Netherlands.

Niemela, P. and Neuvonen, S. 1983. Species richness of herbivores on hosts: how robust are patterns revealed by analyzing published host plant lists? Ann. Entomol. Fenn. 49: 95-99.

Nybom, H. and Schaal, B.A. 1990. DNA fingerprint reveal genotypic distributions in natural populations of blackberries and raspberries (*Robus* L. Rosaceae). Am. J. Bot. 77: 883-888.

Park, Y. S., Barrett, J.D. and Bonga, J.M. 1998. Application of somatic embryogenesis in high-value clonal forestry: deployment, genetic control, and stability of cryopreserved clones. In Vitro Cell. Dev. Biol. Plant, 34(3): 231-293.

Plomion, C., Leprovost, G. and Stokes, A. 2001. Wood formation in trees. Plant Physiol., 127: 1513-1523.

Raffa, K.F. 1989. Genetic engineering of trees to enhance resistance to insects. Bioscience 39: 524-534.

Seiler, J.R. and Johnson, J.D. 1988. Physiological and morphological responses of three half-sib families of loblolly pine to waterstress conditioning. Forest Sci. 34: 487-495.

Shaner, D., T. Malefyt and Anderson, P. 1985. Herbicide resistant maize through cell culture selection. British Crop. Council Monogr. 32: 45-50.

Smith, M.L., L.C. Duchesne, J.N. Bruhn, and Anderson, J.B. 1990. Mitochondria1 genetics in a natural population of the plant pathogen Armillaria. Genetics 126: 575-582.

Stern, N. 2007. The economics of climate change. Cambridge University Press, Cambridge.

Sticklen, M.B., M.G. Bolyard, R.K. Hajela, and Duchesne, L.C. 1991. Molecular and cellular aspects of Dutch elm disease. Phytoprotection 72: 1 - 13.

Teskey, R.O., B.C. Bongarten, B.M. Cregg, P.M. Dougherty and Hennessey, T.C. 1987. Physiology and genetics of tree growth response to moisture and temperature stress: an examination of the characteristics of loblolly pine (*Pinus taeda* L.) Tree Physiology 3: 41-61.

Turnbull, J.W. 1999. Eucalypt plantations. New Forest, 17: 37-52.

Van der Plank, J.E. 1968. Disease resistance in plants. Academic Press, London.

Vikas Kumar, Vikram, H.C., Pradhan, D., Thushima, P.S., Aiswarya, C.P., Mahitha, P.V., Lishamol Poulose and Jiji, K.S. 2015b. Micropropagation techniques for the regeneration of plant species. Van Sangyan, 2(8): 13-19.

Viswanath, V., Albrectsen, B.R. and Strauss, S.H. 2011. Global regulatory burden for field testing of genetically modified trees. Tree Genetics and Genomes. 8: 221-226.

Von Arnold, S., D. Clapham and I. Ekberg. 1991. Has biotechnology a future in fores; tree breeding? fore st Tree Improv. 23: 31-47.

Von Braun, J. 2010. Food insecurity, hunger and malnutrition: necessary policy and technology changes. N Biotechnol., 27: 449-452.

Wallace, D.R. 1990. Forest entomology or entomology in the forest? Canadian research and development. For Chron. 66: 120-125.

Wang, B.S.P., B. Downie and Charest, P. J. 1993. *Er* situ storage of pollen, and seeds, and in vitro cultures of perennial woody plant species. FA0 report (in press).

Wheeler, N. 2004. A snapshot of the global status and trends in forest biotechnology. In: FAO, Washington State, USA.