Assessing recovery of humid tropical forests after selective logging in the Western Ghats of Kerala, India

Selective logging is the popular and widely employed approach for commercial timber production in the tropical forests[1]. However, the impacts of selective logging on forest structure, composition and regeneration dynamics are large, which is of great concern to forest managers and forest ecologists[2]. Although the forest department officials undertake periodic census in selectively logged forests, such investigation is generally aimed to document the regeneration of commercially important species and not to analyse the changes in compositional and structural aspects of other associated trees. Thus to provide the fundamental knowledge required to undertake sustainable management of the forests, both silviculturally and ecologically, more precise studies are needed to clarify the effects on overall stand structure and floristic composition[3]. Tropical evergreen forest species can be categorized into primary (whose seedlings establish in closed canopy area but need small canopy gaps for growth), late secondary (whose seedlings establish in small gaps but need small to medium size gaps for growth) and early secondary (whose seedlings need larger canopy gaps for both establishment and growth)[4,5]. When the forest is disturbed, number and density of secondary species would increase and the increase would depend on intensity and frequency of disturbance[6]. As the forest recovers from the disturbance, contribution by secondary species to the total species number, density and basal area is expected to decline and the rate of decline may be influenced by the extent and scale of the disturbance. Therefore, this study in the wet evergreen forests in the Western Ghats of India was aimed to obtain an estimate of the time required for the selectively logged forests to recover from the disturbance and to resemble undisturbed forests in terms of seedling and tree density and basal area distribution among three successional plant categories.

The study was undertaken in the wet evergreen forest tract of Nelliampathy, under Nenmara Forest Division of the Western Ghats in Kerala (10°30′N and 76°40′E) located at an altitude of 950 m. During the year 2000, we selected an unlogged forest patch as a benchmark (primary) forest. We also selected three selectively logged forest patches, each one to represent a patch logged in 1986, 1982, and 1979. Thus the post-logging age of these patches was 14, 18 and 21 years respectively. These selectively logged patches, located about 2 to 3 km apart from each other, were studied again after two years and thus their post-logging ages were now 16, 20 and 23 years respectively. In the primary forest patch, three plots, each of 1 ha in size were marked. The mean distance between plots was 500 m. Twenty-five quadrats each of 10 m × 10 m in size were randomly established in each replicate plot. In each selectively logged forest patch, three replicate plots, each of 4–5 ha in size, with mean distance between them being 500 m, were marked. In each replicate plot, 25 quadrats each of 10 m × 10 m were randomly established. However, the quadrats established in a selectively logged plot in the years 2000 and 2002 were different. All trees (individuals with gbh above 10.1 cm; gbh was measured with tape at 1.37 m from the ground) located in the quadrats were marked, identified and their gbh was recorded. In each quadrat, one sub-quadrat of size 2 m × 2 m was marked and used to study the tree seedlings (individuals with girth <10.0 cm and height <1 m). The total number of stems on a hectare basis was estimated separately for tree seedlings and trees in the primary forest patch as well as in selectively logged forest patches of different post-logging ages. Similarly, basal area of all stems of a species was calculated. Following the definition given in refs 4 and 5, species encountered in the study area were grouped into three successional categories, namely primary, late secondary and early secondary. Species-wise data obtained for density and basal area were used to estimate the total stem density and basal area in seedling and tree phases in each successional category.

To compare the values of parameters studied across undisturbed sites and sites representing different post-logging ages, we conducted the ANOVA, with means compared using Bonferroni-adjusted multiple t-tests. The analysis revealed that the mean seedling density of primary species in the selectively logged patches (Table 1) was significantly less ($P < 0.05$) than those in the primary forest. In addition, compared with the primary forests, selectively logged forests have structural characteristics typical of secondary forests, such as significantly more ($P < 0.05$) density and basal area of late and early secondary species.

It is reported that a selective-logged, moist evergreen forest in the Western Ghats of India gradually recovered and 10–15 years after logging, became similar to primary forests in terms of growing stock (density and basal area)[7]. However, time required for the selectively logged forests to have growing stock of trees belonging to different successional species comparable to that in unlogged primary forests can differ. Therefore, in the present study the regression equations were derived to find out the relationship between density and basal area of seedlings and trees of different successional categories and post-logging age (Table 2). Wherever the R^2 of regression equations were statistically significant, equations were used to estimate the time required for a given parameter to reach the mean value equal to that in the undisturbed forest plots. In the regressions of seedling and tree basal area of primary species on post-logging age, the regression coefficients were significant ($P < 0.05$). The expected time for the basal area of seedling and trees of primary species in selective logging forests to become equal to that in primary forests is around 25 and 19 years respectively. Contrary to the earlier report[7], seedling and tree density of primary species remained lower than that in unlogged forest even 23 years after logging. When plots of different post-logging age were compared, the density of seedlings and trees and basal area of seedlings of late secondary species declined significantly with age ($P < 0.05$). Thus the seedling and tree density of late secondary species in the selectively logged forests is expected to become equal to that in primary forest when the post-logging age is around 27 and 37 years respectively. However, the tree basal area of late secondary species in the logged forests would be more than that in primary forest till around 53 years after logging. The present study thus demonstrated that

Table 1. Mean density (individuals ha^{-1}) and basal area (cm^2 ha^{-1}) of primary, late secondary and early secondary species in seedling and tree phases in the primary forest and in selectively logged sites in a humid tropical evergreen forest at Nelliampathy, Kerala, India[†]

		Post-logging age (years)					
	Primary forest	14	16	18	20	21	23
Density of primary species							
Tree seedlings	5973[a]	2380[b]	2733[c]	3840[d]	3703[de]	3480[e]	3757[de]
Trees	1405[a]	834[b]	899[c]	1090[d]	1097[d]	958[e]	1047[f]
Basal area of primary species							
Tree seedlings	23265[a]	9282[b]	11351[c]	15936[d]	15488[d]	18508[a]	18508[a]
Trees	549967[a]	309180[b]	353032[b]	545628[a]	561204[a]	674772[c]	848561[d]
Density of late secondary species							
Tree seedlings	19[a]	224[b]	175[c]	92[d]	79[d]	48[e]	43[e]
Trees	54[a]	227[b]	211[c]	204[c]	167[d]	164[d]	118[e]
Basal area of late secondary species							
Tree seedlings	5[a]	645[b]	558[c]	382[d]	359[d]	222[e]	227[e]
Trees	2977[a]	13606[b]	14244[b]	24004[c]	21821[d]	24096[c]	16393[e]
Density of early secondary species							
Tree seedlings	12[a]	426[b]	358[c]	328[d]	300[e]	224[f]	207[f]
Trees	7[a]	246[b]	270[c]	74[d]	113[e]	162[f]	128[g]
Basal area of early secondary species							
Tree seedlings	56[a]	1576[b]	1660[c]	1942[d]	1800[e]	1420[f]	1147[g]
Trees	333[a]	13421[b]	15391[c]	9414[d]	14927[ce]	24660[f]	14589[e]

[†]Values within any row followed by the same letter are not significantly different at $P < 0.05$.

Table 2. Curvilinear regression equations derived for different parameters against post-logging age in wet evergreen forest of Nelliampathy, Kerala, India

	Regression equation
Primary species	
Tree seedlings	Density (individuals ha^{-1}) = $1283.6e^{0.05 \times \text{post-logging age (years)}}$ $R^2 = 0.7002^{ns}$
	Basal area (cm^2 ha^{-1}) = $3278.1e^{0.0793 \times \text{post-logging age (years)}}$ $R^2 = 0.8893*$
Trees	Density (individuals ha^{-1}) = $634.52e^{0.0234 \times \text{post-logging age (years)}}$ $R^2 = 0.4867^{ns}$
	Basal area (cm^2 ha^{-1}) = $62619e^{0.1131 \times \text{post-logging age (years)}}$ $R^2 = 0.9619*$
Late secondary species	
Tree seedlings	Density (individuals ha^{-1}) = $3599.4e^{-0.1967 \times \text{post-logging age (years)}}$ $R^2 = 0.9601*$
	Basal area (cm^2 ha^{-1}) = $3995.6e^{-0.1278 \times \text{post-logging age (years)}}$ $R^2 = 0.9202*$
Trees	Density (individuals ha^{-1}) = $627.15e^{-0.0675 \times \text{post-logging age (years)}}$ $R^2 = 0.8811*$
	Basal area (cm^2 ha^{-1}) = $4693.7e^{0.0777 \times \text{post-logging age (years)}}$ $R^2 = 0.811*$
Early secondary species	
Tree seedlings	Density (individuals ha^{-1}) = $1338.8e^{-0.0805 \times \text{post-logging age (years)}}$ $R^2 = 0.9328*$
	Basal area (cm^2 ha^{-1}) = $2802.8e^{-0.0311 \times \text{post-logging age (years)}}$ $R^2 = 0.3046^{ns}$
Trees	Density (individuals ha^{-1}) = $638.94e^{-0.0775 \times \text{post-logging age (years)}}$ $R^2 = 0.277^{ns}$
	Basal area (cm^2 ha^{-1}) = $8071.4e^{0.0324 \times \text{post-logging age (years)}}$ $R^2 = 0.122^{ns}$

[ns]R^2 value not significant ($P > 0.05$); *R^2 value significant ($P < 0.05$).

in the selectively logged forests, the basal area of primary species may become equal to that in a primary forest within 19–25 years after logging. However, even 23 years after logging, the forest structure and composition of logged forest had not recovered as evidenced by a relatively high growing stock of late and early secondary species. It is also possible to conclude that the degree of disturbance caused by selective logging is so severe that the forest may require more than 50 years to recover from the logging disturbance. Thus the prescribed 40–45-year felling cycle may not be enough for a primary forest to completely recover. In this context, the decision of the Indian Government to abandon selective logging operations in natural forests since 1987 is commendable. Thus it seems appropriate to conclude that if the forests were once again subjected to selective logging before they resemble a primary forest both structurally and floristically, they would experience arrested succession and the resultant vegetation would be dominated by late secondary or early secondary species depending on the severity of disturbance.

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ACKNOWLEDGEMENTS. We thank Dr J. K. Sharma, Director, Kerala Forest Research Institute, Peechi for his keen interest and encouragement. Thanks are due to the Divisional Forest Officer and staff of Nenmara Forest Division for extending full support to conduct field studies. This investigation is part of a project funded by the State Committee on Science, Technology and Environment, Government of Kerala, India.

Received 27 July 2005; revised accepted 12 April 2006

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Long-term effect of *Pseudomonas aeruginosa* GRC_1 on yield of subsequent crops of paddy after mustard seed bacterization

Worldwide, the population depends on rice as staple food. Demand for rice is gradually increasing day-by-day. To meet demand, growers apply additional nutrient input in the form of chemical fertilizers[1]. But these chemicals disturb the environment, subvert ecology, degrade soil and mismanage water resources[2]. Nowadays, it is an endeavour to blend ecology and economy in a cost–benefit framework; hence considerable attention has been paid to use plant growth promoting rhizobacteria (PGPR) in the field[3].

Pseudomonads are well-known PGPR, which control deleterious pathogens through production of siderophore, antibiotics and HCN[4]. Gu and Mazzola[5] reported the improved root colonization of non-legumes by pseudomonads. Lumsden *et al.*[6] reported that rhizosphere-competent antagonistic microorganisms are ideal biological control agents, as the rhizosphere provides the frontline defence for roots against infection by the pathogens, which results in increased plant growth and productivity[7]. The objective of this work was to assess the residual effect of *Pseudomonas aeruginosa* $GRC_1^{rif+str+}$ on crops of paddy grown for two subsequent years.

Plant growth promoting activities of *P. aeruginosa* GRC_1 such as phosphate solubilization, production of IAA, HCN and siderophore, and biological control activity against *Macrophomina phaseolina* were evaluated earlier[8]. When *P. aeruginosa* $GRC_1^{rif+str+}$ bacterized mustard seeds were sown in the field during 2000, it enhanced the growth and yield of *Brassica campestris* compared to control. *Pseudomonas*-bacterized seeds increased 151% mustard grain yield per plant (Table 1). At that time rhizosphere population of *P. aeruginosa* $GRC_1^{rif+str+}$ was 4.5 ($\log_{10}$ cfu). After one year (2001) of harvesting, paddy seedlings were raised in the same field. The field was not given any exogenous treatment of fertilizer, except irrigation whenever required. To determine root colonization, paddy plants were carefully uprooted with shovel and 1 g of the root segments was serially diluted in sterile distilled water (SDW) to determine cfu per gram. The serially diluted root suspension was spread on tryptic soy agar medium (TSM) containing streptomycin (100 $\mu g\ ml^{-1}$) and rifampicin (100 $\mu g\ ml^{-1}$). The plates were incubated at 28 ± 1°C for 24 h. Plates without antibiotics were used to determine the total indigenous bacterial population. All vegetative parameters of the plant, such as seedling fresh weight, dry weight, shoot length, root length and grain yield per plant were recorded at the time of harvesting. Data were analysed statistically using analysis of variance (ANOVA) and LSD.

Residual effect of *P. aeruginosa* $GRC_1^{rif+str+}$ after a period of one year significantly enhanced fresh weight, dry weight of seedlings, shoot and root length of paddy compared to control. After a gap of two years (2002), *P. aeruginosa* GRC_1 also showed significant increase in seedlings of paddy compared to control. Grain yield per plant was enhanced by 105 and 267% respectively, more in the first year and second year compared to respective control (Table 1).

Root colonization study revealed that the population of *P. aeruginosa* GRC_1 and indigenous bacteria increased by 17.7 and 18.3%, respectively, in paddy compared to mustard crops. There was 15% more grain yield per paddy plant compared to the yield during the first year. Cfu of *P. aeruginosa* GRC_1 in the second year (2002) population was 11.3% greater than the first year (2001) population. Indigenous bacterial population in rhizosphere also increased by 8.6% compared to the first year population (Figure 1).

IAA production and phosphate solubilization activities of *P. aeruginosa* $GRC_1^{rif+str+}$ have increased the importance of these bacteria because such activities improved plant growth as well as productivity of non-legumes[9]. Better root colonization confirmed that *Pseudomonas* GRC_1 has capability to survive in rhizosphere of paddy and increase its population successively for two years. Also, it enhanced growth and grain yield of paddy every year. De La Fuente *et al.*[10] reported that inoculation with *Pseudomonas fluorescens* did not affect the symbiosis between rhizobia and forage legumes. They also reported that *Mesorhizobium loti* B816 with UP16 increased dry weight of lotus plant compared to *M. loti* B816 as control. Such observations give support that biocontrol *Pseudomonas* strains may be unaffected by other beneficial bacteria.

Rewari[11] observed that substantial increase in yield was often obtained with