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Role of Protected Area in Conserving the Population and Genetic Structure of Economically Important Bamboo Species

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ABSTRACT

Due to widely expanding threats to the forests, protected areas may offer the best approach and prospect to conserve the biological diversity. However, there have been few studies that have emphatically demonstrated the role of protected areas in conserving the genetic diversity of plant species. We examined the population structure and genetic diversity of two economically important bamboo species, *Bambusa arundinacea* and *Dendrocalamus strictus*, in the core, buffer and the peripheral regions of the Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS) at central Western Ghats, India. Our results indicate that the proportion of human disturbance on both the bamboo species were significantly less in the core and buffer regions of the BRTWS as compared to periphery. In both the bamboo species, the core and buffer regions maintained a better population stand. The frequency distribution of the genetic similarity indices of the core populations were found to be more widely distributed as compared to the peripheral populations. Our results strongly indicate the relevance of protected areas in maintaining the population structure and the genetic diversity of economically important plants such as bamboos that are otherwise prone to heavy extraction pressures.

Keywords: *Bambusa arundinacea*, *Dendrocalamus strictus*, genetic diversity, human disturbance, population structure

INTRODUCTION

Bamboo forms an important component of the tropical forests of the south and south-east Asia. With nearly 24 genera and 130 species of bamboo, India forms the second richest source of bamboo in the world, the first being China, with an estimated total area of 9.6 million ha (Sharma 1985; Seethalakshmi and Kumar 1998; Uma Shaanker *et al.* 2004). Owing to rare physical properties of elasticity, flexibility, natural resistance to impacts, etc., bamboo constitutes one of the most important non-timber forest product species (NTFPs) in the economy of the indigenous communities in India. More than half a million people are involved in the bamboo cottage industry (Chaluvaraju *et al*. 2001). Besides the traditional user groups, bamboo is much sought after by the paper and pulp industry which uses about 5 million tons annually (Varamah and Bahadur 1980; Chaluvaraju 1999; Seethalakshmi 2001; Uma Shaanker *et al*. 2004).

The demand on the bamboo resources is substantive and it is projected that in the years to come the demand would soon out-score the stock. This is particularly true in countries, such as India, where almost all the requirements of bamboos are met from the natural populations (Kumar 1991; Seethalakshmi 2001; Uma Shaanker *et al*. 2004). In recent years, due to the intense and often indiscriminate extraction of these resources from the natural populations, coupled with extensive changes in the land-use patterns, the bamboo resources are increasingly threatened (McNeely 1995; INBAR 1997; Chaluvaraju 1999). This has presumably led to considerable pressure on the bamboo resources of the country. It is feared that the large-scale destruction of habitats and over-harvesting of bamboo could lead to irreversible loss of biological diversity at the species level as well as for unique populations (Chaluvaraju *et al*. 2001; Uma Shaanker *et al*. 2004).

In the light of such increasing pressures on forests and forest products, it is believed that the protected areas (PAs) could form an important network of landscapes to serve as repositories of intra-specific genetic diversity for economically important species such as bamboo along with other species (Hogbin *et al*. 2000; Woodford 2000; Brunner *et al*. 2001; Nageswara Rao *et al*. 2001a; Theilade 2001; Uma Shaanker *et al*. 2003). More than 12,700 PAs have been established around the world accounting to 13.2 million km^2 (IUCN 1992). Despite the obvious importance of PAs in serving as refugia for the world's biological diversity, there have been several concerns about its effectiveness. One of the main apprehension is that PAs might not reflect the conservation concerns of specific non-target taxa as most often they are established based on large charismatic animal species (Rodgers and Panwar 1988; Brunner *et al*. 2001). Reports also indicated that only less than one quarter of declared national parks, wildlife refugia, and other PAs in the 10 key forested countries were well managed, and many had no management at all (IUCN 1992; Ramesha 2003). It is not uncommon that due to the pressures of livelihoods, often the PAs in the developing countries, such as India, are threatened from anthropogenic pressures (Liu *et al*. 2001; Wickneswari and Boyle 2000; Suchitra 2001; Uma Shaanker *et al*. 2001; Nageswara Rao *et al*. 2001b; Padmini *et al*. 2001; Ravikanth *et al*. 2002; Uma Shaanker *et al*. 2003). Notwithstanding the criticisms, PAs of the world may provide the last hope of conservation for a number of critically endangered species that are not found anywhere else (Noss 1996; Brunner *et al*. 2001; Kutty and Kothari 2001).

In this paper, we examine the effectiveness of PA in conserving the genetic resources of two economically important species of bamboos. The study has focused on addressing if indeed the PA a) facilitates a better demographic profile of bamboos within PA than outside and b) facilitates

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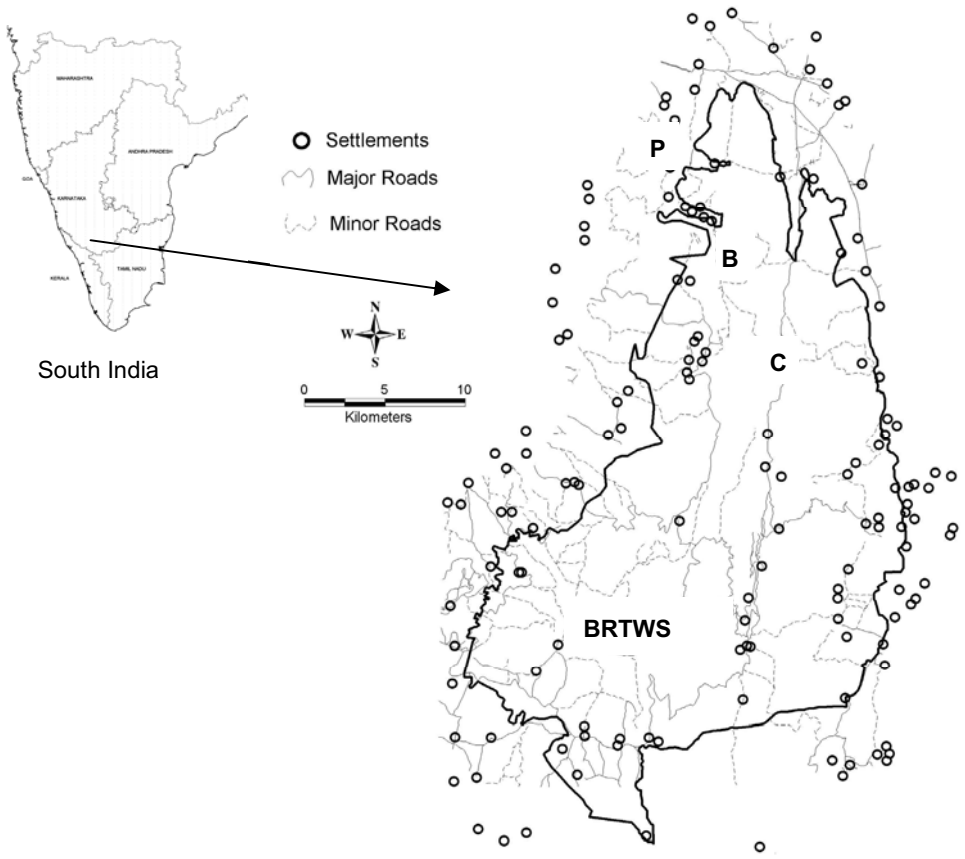

Fig. 1 Thematic map depicting study sites (C = Core, B = Buffer, P = Periphery) in Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS), central Western Ghats, India.

the maintenance of higher genetic diversity within than outside the PA. We discuss our results to assess the threats to bamboo genetic resources along with the role of PA in conserving them. We highlight that the PA could, in fact, form an important conservation approach for other non-target species that are highly threatened.

MATERIALS AND METHODS

Study site

The study was conducted at Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS; 11-13° N and 77-78° E) in the central Western Ghats (one of the 18-biodiversity hot-spots of the world; Myers *et al*. 2000), Karnataka, India. BRTWS (**Fig. 1**) is one of the richest sources of bamboos in the central Western Ghats. The "Soligas" (indigenous tribes of South India), have been living in this forest for centuries. They derived their name from the bamboo thickets. 'Soliga', meaning "people emerging from the bamboo or from the thickets", an obvious reference to the thickets bamboo groves that were once widely prevalent in these hills. They live in groups of small huts made out of bamboo, wild woods and grass. Bamboo is being used by them for walls, roof, doors and for fencing. They also make bamboo articles for household purposes, for barter purposes and derive substantial income from them (Hegde *et al*. 1996; Murali *et al*. 1996). The sanctuary has also been under pressure from people at the foothills who depend upon the forest for a number of resources (Hegde *et al*. 1996). According to Ganeshaiah and Uma Shaanker (1998) in the northern part of BRTWS, over 90% of the area under bamboos has been lost during the past 50 years.

System

The study was carried-out using two most economically important species of bamboos, *viz*., *Bambusa arundinacea* and *Dendrocalamus strictus*. These species are heavily extracted for use both by the traditional weaving community as well as the paper and pulp industries (Uma Shaanker *et al*. 2004) leading to a substantial reduction in their natural populations (Chaluvaraju *et al*. 2001). In certain regions of the Western Ghats, the populations have been rendered locally extinct (Kumar 1991).

Population and genetic structure of bamboo in BRTWS

For both the bamboo species, based on the information obtained from the local forest division/ranges, the approximate spatial occurrence of bamboo was mapped and sampling strategy was designed. Based on the administrative boundary of the PA, a site each in the core, buffer and periphery was identified for sampling. For *B. arundinacea*, the three sampling sites selected were Raikallamadu (core), Karigundanahalla (buffer) and Biligiri Ranganathaswamy temple sites (periphery). For *D. strictus*, Dodda Betta (core), Karibetta (buffer) and Ketamarana Gudi (periphery) were selected for collection of samples. The average distance separating the three study sites were about 4-5 km (in a linear array core > buffer > periphery). Though, PAs are supposed to be insulated from human and cattle interferences, often because of the heavy pressures, the peripheral regions of the sanctuary tend to be more open to disturbance than the core of the PA. Accordingly, sites from core to periphery were assumed to offer decreasing levels of immunity to human disturbance/extraction and to decreasing levels of protection.

In order to assess the population structure in both the bamboo species, 15 to 20 quadrants (10 m × 10 m) were randomly laid at each of the study sites and the data on number of clumps in each quadrant as well as the average number of culms per clump were recorded. The mean density of clumps and mean culms per clump were arrived at by pooling the data site-wise and were statistically tested using student's *t*-test. As a measure of disturbance index, the number of cut and broken stems of *B. arundinacea* and *D. strictus*

were also assessed. The values of the total percent stems harvested were arcsine transformed and statistically tested using student's *t*-test.

For *B. arundinacea* and *D. strictus* population genetic variability assessment, leaf samples were collected from 12 randomly selected individual clumps across the core, buffer and peripheral populations in BRTWS. Care was taken to ensure that only one collection was made from each clump. The harvested leaves were air dried and stored until required for the genomic DNA (g-DNA) isolation. Dry leaf tissue (1 g) was used for bamboo g-DNA extraction following CTAB method (Doyle and Doyle 1987). For population genetic variability study, 35 Inter Simple Sequence Repeat (ISSR) primers (*Operon technologies Inc*, USA) were initially screened, of which 10 primers (UBC 807, UBC 830, UBC 844, UBC 848, UBC 855, UBC 880, UBC 888, UBC 889, ISSR 4 and ISSR 5) yielded consistent and reliable PCR amplification and hence were retained for further population diversity analysis. The PCR amplification was carried out in 25 µL of reaction mixture containing 25 ng template DNA, 2.5 µL 10X reaction buffer containing 15 mM $MgCl_2$, 3 µM of each dNTP, 0.25 µM ISSR primer and 0.5 U *Taq* DNA Polymerase (*Bangalore Genei*, India). The thermocycler (MJ Research, USA) program was set for 3 min at 94°C for initial denaturation, followed by 35 cycles of 45 s denaturing at 94°C, 45 s annealing at 45°C and 2 min extension at 72°C and a final extension cycle of 8 min at 72°C. ISSR-PCR amplification products were resolved electrophoretically on 1.5% agarose gel. Gels were stained with ethidium bromide and bands were visualized and photographed under UV light. Binary coding was used to score the gels (Wendell and Weeden 1989). Considering the bands of DNA as an allele, each allele was given a score of '0' (for absence) or '1' (for presence). All the distinct bands were designated with numbers, starting from the lowest migrating (cathodal) to the fastest migrating (anodal) bands and used in all the genetic diversity parameter estimations.

The data was subjected to population genetic analysis using POPGENE software (Yeh and Boyle 1997). In order to assess the polymorphic percentages, the proportion of polymorphic amplification product for each population of both the bamboo species was estimated. An amplified PCR product was considered polymorphic only if the frequency of the most frequent ISSR product was below 95%. Nei's gene diversity index (Nei 1972), which is equivalent to the diversity of amplified gene products within an infinite population, was computed as $h = 1 - S\ Pi^2$, where Pi is the frequency of the occurrence of the i^{th} amplified product over individuals within a population. The data was subjected to student's *t*-test. Based on the Squared Euclidean Distance between individuals, cluster analysis was performed following UPGMA algorithm (Sneath and Sokal 1973). A dendrogram was then constructed. A principal component analysis (PCA) was also performed using statistiXL (Version 1.7) to display the genetic relationships among individuals across each study sites in both the bamboo species. The genetic similarity index between all possible pairs of individuals within each species was computed (Sneath and Sokal 1973). POPGENE (Yeh and Boyle 1997) was also used to obtain an estimate of the total genetic diversity from all the populations (H_t) and the mean diversity within population (H_s). From the H_t and H_s values, the proportion of total genetic diversity residing among populations (G_{st}) was calculated as $G_{st} = (H_t\text{-}H_s)/H_t$ (Nei 1973). Based on the presence or absence of the amplification products, NC_2 pairs of similarity indices (n = 93 for *B. arundinacea* and n = 91 for *D. strictus* similarity indices) were computed for within each site and across all the three sites. The mean similarity, over all pairs of individuals of core, buffer and periphery was arrived at. The mean similarity was compared across the sites using student's *t*-test. The frequency distribution of similarity index was developed for core, buffer and peripheral populations. The frequency distribution of the similarity indices across (for unlike pairs only i.e. NC_2-N) the sites were then analyzed by performing a K-S test (Siegel and Castellan 1988).

RESULTS

Population structure

For both species of bamboo, *B. arundinacea* and *D. strictus*, the mean number of clumps was higher in the core (4.27 ± 1.39 for *B. arundinacea*; 5.8 ± 1.32 for *D. strictus*) than in the adjoining buffer and peripheral populations (**Table 1**). The density distribution of clumps of *D. strictus* population in the core was significantly higher when compared to that in buffer and periphery (core vs buffer, $p = 0.00013$; core vs periphery, $p = 0.0014$, **Table 1**), indicating a better status of bamboo population in the core region of their distribution at BRTWS. In contrast, for *B. arundinacea*, though the core population had the highest mean number of clumps than in the buffer and the peripheral populations, they were not significantly different from each other.

To assess the population stability, the mean culms per clump (per 100 m^2) was also calculated across all the three regions for both the bamboo species. In *B. arundinacea*, the core populations had a significantly greater mean density of culms per clump (23.76 ± 10.87, **Table 1**) as compared to the buffer and peripheral populations (core vs buffer, $p = 0.007$; core vs periphery, $p = 0.035$, **Table 1**). However, in *D. strictus*, the buffer population had the highest mean culms per clump (24.21 ± 10.05, **Table 1**). The peripheral population was found to have significantly less mean number of culms per clump as compared to buffer populations (Buffer vs Periphery, $p = 0.029$, **Table 1**). However, the difference was found to be non-significant with respect to core population. In summary, the population status of the two bamboo species was found to be better maintained in the core and buffer region of the PA than in the peripheral regions at BRTWS.

As a measure of disturbance index or the intensity of bamboo harvest at each of the study sites (core, buffer and periphery), the proportion of cut and broken stems of bamboos, *B. arundinacea* and *D. strictus*, were recorded. For

Table 1 Demographic parameters of *Bambusa arundinacea* and *Dendrocalamus strictus* in core, buffer and peripheral regions of the Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS) in the central Western Ghats, India.

Demographic parameters	Study sites	Mean ± SD[a]	*t*-test	
			Pairs	*p*-value
Bambusa arundinacea				
Mean clump/100 m^2	Core	4.27 ± 1.39	Core vs Buffer	ns
	Buffer	4.1 ± 1.44	Buffer vs Periphery	ns
	Periphery	3. 93 ± 0.80	Periphery vs Core	ns
Mean culms/clump/100 m^2	Core	23.76 ± 10.87	Core vs Buffer	0.007
	Buffer	13.80 ± 7.66	Buffer vs Periphery	ns
	Periphery	16.15 ± 7.74	Periphery vs Core	0.035
Dendrocalamus strictus				
Mean clump/100 m^2	Core	5.8 ± 1.32	Core vs Buffer	0.00013
	Buffer	3.9 ± 1.06	Buffer vs Periphery	ns
	Periphery	4.2 ± 1.15	Periphery vs Core	0.0014
Mean culms/clump/100 m^2	Core	20.74 ± 6.90	Core vs Buffer	0.0280
	Buffer	24.21 ± 10.05	Buffer vs Periphery	0.029
	Periphery	16.34 ± 8.70	Periphery vs Core	ns

[a] SD = Standard deviation; ns = non-significant

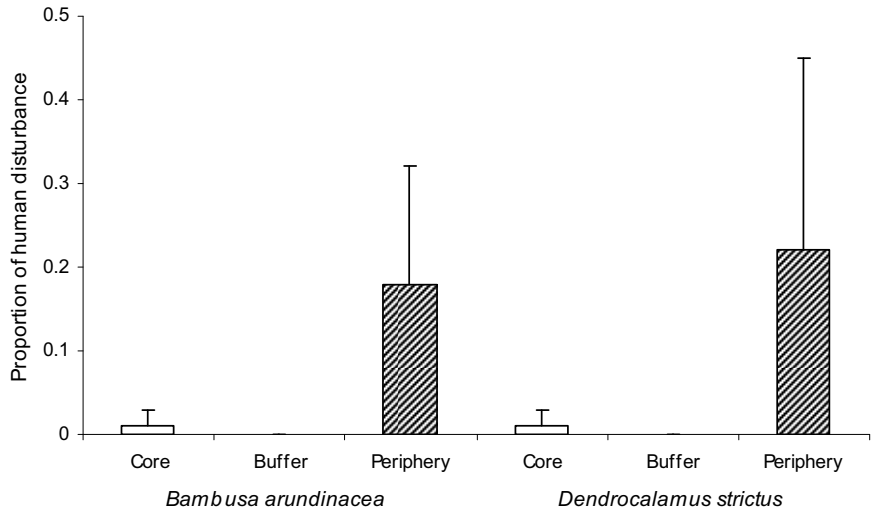

Fig. 2 Proportion of bamboo culms harvested by humans in Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS), central Western Ghats, India. (*Bambusa arundinacea*; Core vs Buffer, $p = 0.165$; Buffer vs Periphery, $p = 0.00005$; Core vs Periphery, $p = 0.00002$ and *Dendroclalmus strictus*; Core vs Buffer, $p = 0.07$; Buffer vs Periphery, $p = 0.001$; Core vs Periphery, $p = 0.0017$).

both the bamboo species studied, the peripheral populations had significantly larger proportion of cut and broken stems (0.18 ± 0.14 for *B. arundinacea*; 0.22 ± 0.23 for *D. strictus*) as compared to core region (0.01 ± 0.02 for *B. arundinacea* and *D. strictus*) in the BRTWS (**Fig. 2**). The proportion of human disturbance on bamboo resources was significantly higher in and around the fringes (periphery) of the PA than that of the core regions at BRTWS (**Fig. 2**).

Genetic diversity and structure

The total number of loci analyzed over all the ten ISSR primers in BRTWS was 93 for *B. arundinacea* and 91 for *D. strictus*. In *B. arundinacea,* the loci analyzed for each primer ranged from seven alleles for UBC 848 to 11 alleles each for UBC 807, UBC 844 and UBC 855, while it ranged from six alleles from ISSR4 to 12 from UBC 807 in *D. strictus* (**Table 2**). Nei's genetic diversity for *B. arundinacea* at BRTWS was high for the core and buffer populations than the peripheral population (**Table 3**). In *D. strictus*, the buffer population had the highest Nei's genetic diversity (0.125 ± 0.196) followed by core and the peripheral populations (**Table 3**). The differences in the genetic diversity across the regions for both the bamboo species were non-significant. Based on the ISSR analysis on all the proportions of polymorphic amplified ISSR–PCR products, the percentage of polymorphic loci for *B. arundinacea* and *D. strictus* were computed. The percentage polymorphism was highest for the buffer (35.19% in *B. arundinacea* and 34.48% in *D. strictus*) population followed by core and peripheral populations (**Table 3**). It appears that, at BRTWS, for both bamboo species over all the ISSR loci analyzed, a higher genetic diversity was maintained in the core and buffer populations than those of the peripheral population.

Table 2 Primer sequences for inter simple sequence repeats (ISSR's) and number of PCR amplified products obtained in *Bambusa arundinacea* and *Dendrocalamus strictus*.

Primers	Sequence (5'→3')	№ of PCR amplified products (*B. arundinacea*)	№ of PCR amplified products (*D. strictus*)
ISSR4	$HVH(CA)_7$	10	6
ISSR5	$(TCC)_5RY$	9	11
UBC807	$(AG)_8T$	11	12
UBC830	$(TG)_8G$	8	8
UBC844	$(CT)_8RC$	11	11
UBC848	$(CA)_8RG$	7	11
UBC855	$(AC)_8YT$	11	9
UBC880	$(GGAGA)_3$	8	8
UBC888	$BDB(CA)_7$	8	7
UBC889	$DBD(AC)_7$	10	8

B=C, G, T; D=A, G, T; R=A, G; Y=C, T; H=A, C, T; V=A, C, G

Table 3 Population genetic parameters of *Bambusa arundinacea* and *Dendrocalamus strictus* in core, buffer and peripheral regions of the Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS) in the central Western Ghats, India.

Population study sites	Sample size (N[a])	Nei's genetic diversity		Polymorphic loci (%)
		Mean	SD[b] (±)	
Bambusa arundinacea				
Core	12	0.133	0.206	31.48
Buffer	11	0.134	0.205	35.19
Periphery	12	0.129	0.190	33.33
Dendrocalamus strictus				
Core	12	0.103	0.189	24.14
Buffer	12	0.125	0.196	34.48
Periphery	11	0.097	0.178	31.03

[a] N = Number of individuals genetically screened; [b] SD = Standard deviation

Based on the presence or absence of the amplified ISSR–PCR products, mean genetic similarity index among all unlike pairs of individuals within a site (core, buffer or periphery) was computed and compared. The mean genetic similarity increased from core to buffer and peripheral populations in *B. arundinacea*, while for *D. strictus* it increased from periphery to buffer and the core populations (**Fig. 3**). The mean genetic similarity differences among the study sites, in both the bamboo species were not significantly different. However, in both the bamboo species, the frequency distribution of the similarity indices of the core population was more widely distributed within a smaller mean compared to the population from the periphery (KS test; *B. arundinacea*, $p = 0.01$; *D. strictus*, $p = 0.009$, **Fig. 4A, 4B**). The total genetic diversity (H_T) when all populations (core, buffer and periphery) were considered was estimated to be 0.154 (for *B. arundinacea*) and 0.107 (for *D. strictus*). The proportion of total diversity residing among populations (G_{ST}) was 0.237 for *B. arundinacea* and 0.276 for *D. strictus*.

Besides assessing genetic diversity, attempt was also made to address the genetic structure of the *B. arundinacea* and *D. strictus* populations from each of the three regions at BRTWS. Based on ISSR–PCR products, Nei's genetic distance was computed and the dendrogram of clustering was constructed for each of the study site. At all the three sites, the membership of a cluster was found to be non-randomly occupied by individuals from the core, buffer or periphery for both the bamboo species indicating a fine degree of

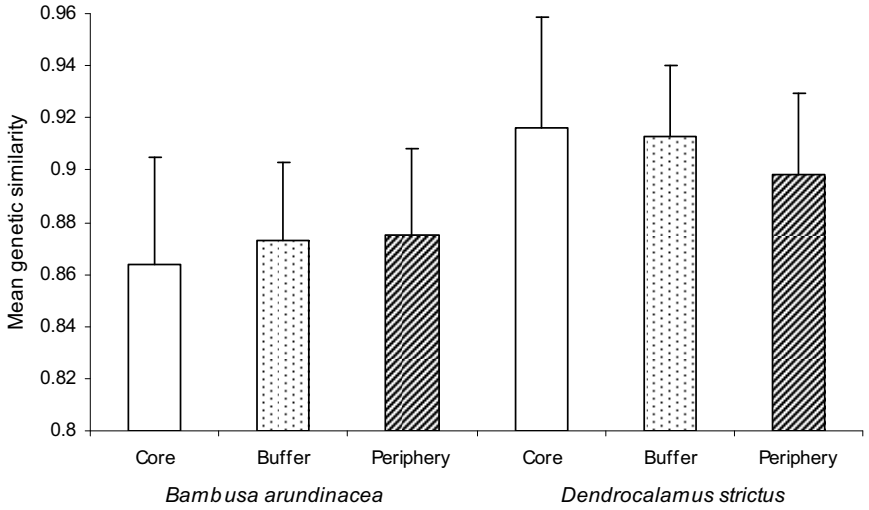

Fig. 3 Mean similarity index of *Bambusa arundinacea* and *Dendrocalamus strictus* at Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS), central Western Ghats, India.

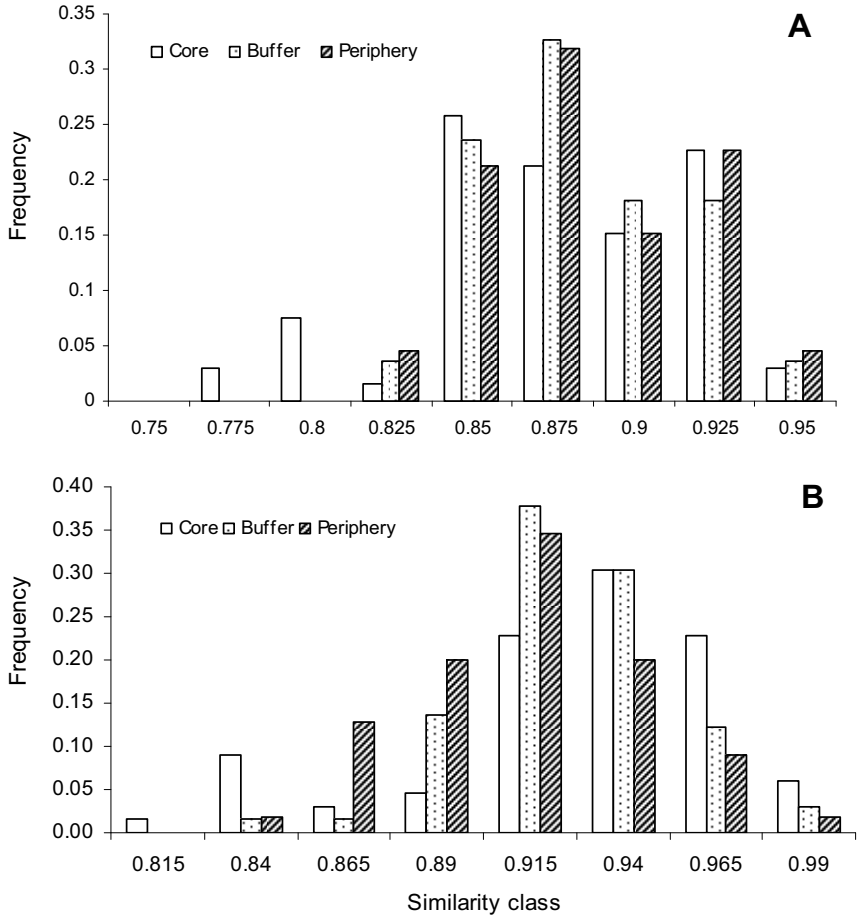

Fig. 4 Frequency distribution of similarity indices for core, buffer and periphery populations at Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS), central Western Ghats, India in (A) *Bambusa arundinacea*; (B) *Dendrocalamus strictus.*

genetic structuring among the various populations at BRTWS (**Fig. 5**). This was also evident from the principal component analysis (PCA) of the bamboo populations; individuals tended to group based on their sites of origin (**Fig. 6**). Thus those from core region grouped into a nearly cohesive cluster as did those from the buffer and peripheral region. The first two axes of the PCA for *B. arundinacea* explained 71.62% of the total variance, while for *D. strictus* the principal component axes explained 69.9%. Thus, in each of the three sites, the core individuals grouped predominantly into a separate cluster or at best grouped with individuals from the buffer region, but not with the peripheral individuals.

DISCUSSION

Due to widely expanding threats to the forests, it has been realized that PAs including national parks, sanctuaries, biosphere reserves and their networks may perhaps offer the best approach and prospect to conserve the biological diversity and by default the genetic resources of the species (Brunner *et al*. 2001). By legislation, PAs are completely protected from external pressures, including harvesting of NTFPs (Kutty and Kothari 2001). Their clear insulation from external pressures, both direct and indirect, could serve as "control" in evaluating the impacts of harvesting, or other disturbances on the community structure and gene-

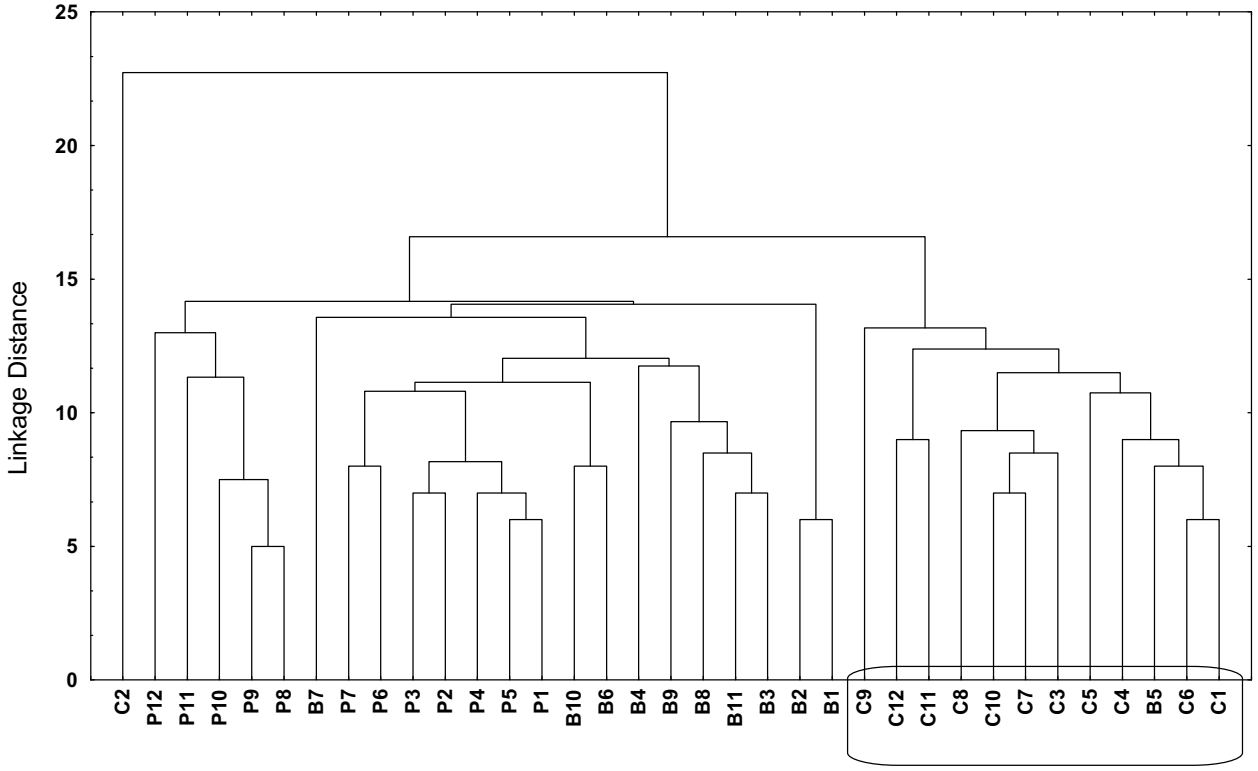

Fig. 5 Clustering of individuals based on dendrogram analysis of *Bambusa arundinacea* in core (C), buffer (B) and peripheral (P) regions at Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS), central Western Ghats, India.

tic diversity of bamboos as well as other species. Several studies have shown that the PAs could in fact form the last footholds for conserving biological diversity and are the safest strongholds of wilderness around the globe (Pimm and Lawton 1998; Brunner *et al*. 2001; Uma Shaanker *et al*. 2003; Nageswara Rao 2004). However, there have been few studies that have emphatically demonstrated the role of PAs in conserving the genetic diversity of focal species. We examined the role of PA in maintaining the population and genetic structure of economically important species such as bamboos.

At BRTWS, the population structures of bamboos are different between protected and least protected (peripheral) populations. The mean clumps and mean number of culms per clump in both the bamboo species, *B. arundinacea* and *D. strictus*, were found to be higher in the core and buffer populations as compared to the periphery of the PA. The observed results seem to be explicable considering that the core and buffer regions of the PA harbor a good population stand (**Table 1**), than those at the periphery, reflecting a lesser level of human disturbance (**Fig. 2**). It is feared that the extremely small sizes of the fragmented bamboo populations in the peripheral regions are more likely to be prone to extinction (Chaluvaraju *et al*. 2001; Uma Shaanker *et al*. 2004). Our results clearly reinforce that either due to their relative inaccessibility or their higher protection status, the regions with-in the PA (core and buffer) help in conserving genetic resources of bamboos better than the peripheral regions. The extent of disturbance and fragmentation of the existing bamboo stands in peripheral region might also adversely affect the genetic diversity of natural populations at BRTWS. There are also several unambiguous agreements that the larger the population the better would be the status of the genetic resources (Gilpin and Soule 1986; Prober and Brown 1994; Young *et al*. 2000; Cruse-Sanders and Hamrick 2004; Nageswara Rao *et al*. 2007). Irrespective of the pollination and dispersal modes and the breeding system of the species, small populations on an average suffer more from mating constraints than large populations and that may lead to low genetic diversity over the time (Nageswara Rao 2004; Cruse-Sanders and Hamrick 2004; Uma Shaanker *et al*. 2004). These effects result from increased drift, increased inbreeding, and reduced gene flow between populations and local population extinction (Frankham and Ralls 1998; Young *et al*. 2000; Uma Shaanker *et al*. 2004). Positive correlations between population density and gene diversity have been reported earlier for several forest species and have underlined the importance of demography in maintaining the population genetic diversity (Godt and Hamrick 2001; Nageswara Rao *et al*. 2001a; Lonn and Prentice 2002; Ramesha 2003). For *B. arundinacea* as well as *D. strictus*, it clearly appears that the core as well as buffer of the sanctuary may perhaps be well endowed with mating partners than the populations towards the fringes. Our results reinforce that the management of PAs has important implications on the demographic status of the forest species.

We also examined population genetic parameters of bamboos in the core, buffer and periphery of the PA, BRTWS. Nei's genetic diversity index indicated that the core and buffer populations for both the bamboo species maintained higher genetic diversity compared to the peripheral population (**Table 3**). This was further reinforced by the fact that the frequency distribution of similarity indices was widely distributed for the core and the buffer populations as compared to that for the peripheral population (**Fig. 4A, 4B**). In American ginseng (*Panax quinquefolius* L.), a medicinal plant belonging to the family Araliaceae, significant increase in genetic diversity was observed among the protected populations as compared to populations in which harvesting was permitted (Cruse-Sanders and Hamrick 2004). Nageswara Rao *et al*. (2001b) reported that populations of *Santalum album* L., a tree extensively harvested for its heartwood and heartwood oil in India, had a higher genetic diversity in the populations maintained within the national parks and sanctuaries. The higher genetic diversity in the core and buffer of BRTWS could also be expected to reflect a higher fitness of these populations compared to those at the periphery. This has been well demonstrated in many other systems (Oostermeijer *et al*. 1994; Nageswara Rao *et al*. 2001a; Padmini *et al*. 2001; Ramesha 2003; Uma Shaanker *et al*. 2003; Cruse-Sanders and Hamrick 2004; Nageswara Rao 2004). Several workers

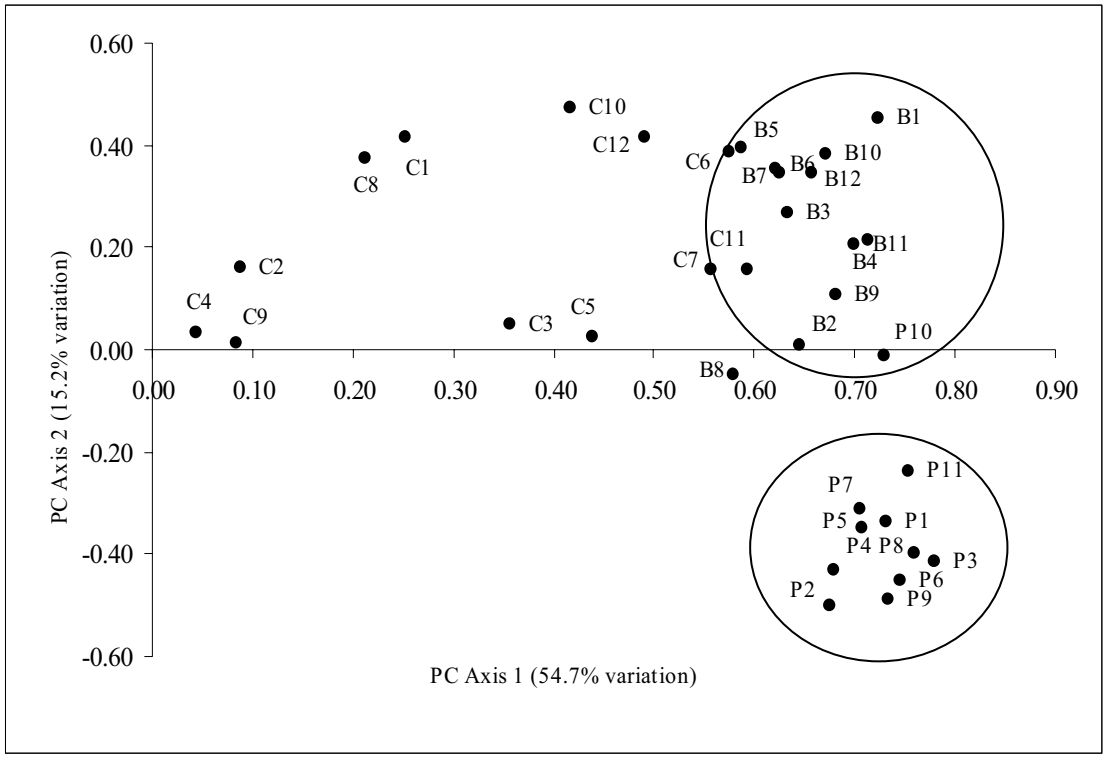

Fig. 6 Principal component analysis of individuals of *Dendrocalamus strictus* in core (C), buffer (B) and peripheral (P) regions at Biligiri Ranganathaswamy Temple Wildlife Sanctuary (BRTWS), central Western Ghats, India.

have reported the decline in abundance and in the levels of genetic diversity of populations subjected to extraction (Frankham and Ralls 1998; Gillies *et al*. 1999; Wickneswari and Boyle 2000; Suchitra 2001; Uma Shaanker *et al*. 2001). In fact, interest to maintain the genetic diversity of the populations that are harvested or exploited by humans are motivated in general by the need to conserve the range of gene assemblages that have evolved over millennia. In the present context, it is important to note that the core and buffer populations are able to maintain higher densities of the species and therefore by default have implications for the conservation of genetic diversity. Through cluster and principal component analysis it was clear that the individuals from the core and buffer regions tend to cluster separately from those of periphery, indicating that there could be a genetic structuring of the bamboo populations (**Figs. 5, 6**). The population differentiation (G_{ST}) values for *B. arundinacea* and *D. strictus* are in concordance with the earlier studies on bamboos (Chaluvaraju 1999; Lee and Chung 1999; Uma Shaanker *et al*. 2004). For both the bamboo species, there appeared to be genetic differentiation of the populations along the gradients of disturbance suggesting that individuals from different region (core to buffer to periphery) may have assorted themselves with specific allelic configurations. While such clustering may be due to assortative mating (as opposed to random mating; Gerard *et al*. 2006) among the individuals within each of the study sites, it is rather intriguing considering the fact that both the species exhibit mass flowering and hence could easily span the distances separating the three regions. The observed results on population structure and genetic diversity across the study sites seems to confirm the well recognized pattern that maintenance of the genetic diversity of a population is contingent upon the availability of good population stand. Good bamboo population stands with higher levels of genetic diversity in the core and buffer populations were also observed in another PA (Dandeli Wildlife Sanctuary) at the central Western Ghats (unpublished data).

Our results seem to strongly indicate the relevance of PAs in maintaining the population structure and thereby, the genetic diversity of economically important plants such as bamboo that otherwise are prone to heavy extraction pressures. In fact, the PAs could serve as *in situ* sites for conserving the genetic diversity of other economically important plant species besides bamboo and should form a central component of conservation strategies. This is particularly true considering that future pressures of harvesting could only be expected to distend the separation between protected (core) and non-protected (periphery) areas. By creating more PAs as well as protecting the existing areas against immediate and perceived threats would make a significant contribution for long-term conservation of genetic resources of bamboos along with other non-targeted species as well. Our results are an important indicator of the conservation status of the natural resources and may be used by people from different backgrounds including forest officers, scientists and policy makers to safeguard these resources.

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