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Ground insect community responses to habitat restoration efforts in the Attappady hills, Western Ghats, India

Ravi Ramalingam* and Priyadarsanan Dharma Rajan

Ashoka Trust for Research in Ecology and the Environment (ATREE), Royal Enclave, Srirampura, Jakkur Post, Bangalore 560 064, India

A reconnaissance survey was undertaken to assess the responses of ground insect communities to habitat restoration efforts in the Attappady hills, Western Ghats. Diversity patterns of various ground insect assemblages such as ants, beetles, etc. were compared across an age trajectory of restored sites. The diversity of these assemblages was correlated with age trajectory of sites. Also, patterns of recolonization by different insect trophic guilds and ant functional groups were comparable with earlier studies from different biogeographic areas.

Keywords: Ants, diversity, ecological restoration, recolonization, Western Ghats.

WIDESPREAD loss of production and conservation values of natural habitats due to various anthropogenic activities makes large-scale ecosystem restoration an increasingly urgent task[1]. Ecological restoration is often undertaken as a compensatory mitigation for degraded, damaged or destroyed ecosystems. A properly planned restoration project attempts to fulfil clearly stated goals by pursuing specific objectives[2]. The specification of goals for restoration projects is frequently described as the most important component of a project, because it sets expectations, drives the detailed plans for actions, and determines the extent of post-project monitoring[3]. To ascertain the achievement of specific goals, project monitoring is undertaken as an integral part of such restoration projects. The success of restoration programme is based on the scientific evaluation of the natural ecosystem, restoration practice and its regular monitoring. Monitoring involves measuring ecosystem attributes such as diversity, vegetation structure or ecological processes[4]. Though many projects aim at restoring the total ecological fidelity, i.e. structural/compositional, functional and durability, attempts to evaluating the success of restoration efforts should not be limited to revegetation alone.

Other than monitoring vegetation growth, invertebrates like insects are often included because they represent many different trophic groups, e.g. predators, herbivores, parasites and parasitoids, pollinators and decomposers[5]. Arthropod groups have been used to track restoration success in many contexts; for example, arthropod com-

*For correspondence. (e-mail: raviram@atree.org)

munities have been used for monitoring in the appraisal of strip mine reclamation[6], butterflies in ponderosa pine forest restoration[7], arthropods in Spartina salt marsh[8] and forest litter invertebrates in Colombian Andes[9].

Ant species richness, and community structure in particular, is widely used in assessing recolonization patterns in restored sites due to their great abundance and functional importance, the great variety of interactions they have with the rest of the ecosystem, and their ability to integrate a wide range of ecological variables[6]. A recent feature of monitoring studies using ants is the use of functional groups, in relation to environmental stress and disturbance[10], to assist in the prediction and interpretation of the responses of ant communities to land use. In insect communities, functional groups are typically 'guilds', sets of species exploiting a common pool of resources, usually trophically based. Most ant species have similar foraging requirements; thus, trophically based guilds are of limited use in ant community studies[11]. So ant genera are classified into functional groups based on their response to environmental stress and disturbance, where stress is defined as any factor limiting productivity (e.g. low temperature, nest site availability, food supply and microhabitat structure and resource capture), and disturbance as any factor removing biomass[12]. Thus, the ant functional group classification is analogous to those of plant functional group models that are based on a broad range of ecological characters, including life-form, morphology, reproductive behaviour and colonization ability[11,12]. In the context of restoration ecology, a broad consensus on the indicator of successful restoration is that the composition of ant functional group changes over time indicating different stages of vegetation succession. Other than in Australia, these protocols are adopted in Brazil[13], South Africa[14] and recently in Italy[15].

In order to design long-term experiments and monitoring protocol using ground insect communities in assessing the efficiency of restoration efforts in the Attappady hills, Western Ghats, a reconnaissance survey was undertaken. Presently, a large scale ecological restoration of the degraded forest landscape is being undertaken by Attappady Hills Area Development Society (AHADS), an autonomous body set up exclusively for the purpose under the aegis of the Kerala State Government. Attappady plateau with an area of 745 km^2 (10°55′N and 11°15′N; 76°21′E and 76°48′E) forms a part of the Nilgiris Biosphere reserve (NBR) in the Western Ghats. Attappady shares its boundaries with the reserve forests of Nilgiris South and Coimbatore forest divisions of Tamil Nadu State to the North and East, Mannarkad Taluk to the South and Silent Valley National Park to the West. The terrain of Attappady is quite undulating, with a large number of very steep hillocks of varying elevation ranging from 450 to 2300 m msl (mean sea level). The eastern slopes are in the rain shadow region with rainfall less than 1000 mm per annum whereas the western half of the Attappady receives close to 3000 mm per annum. Dry winds during summer months, with erratic rainfall along with poor soil moisture retention have rendered these lands an erosional landscape leading to desertification. Historically, the forest types occurring in Attappady hills are Southern Euphorbia Scrub, Southern Tropical Dry Deciduous Forest, Southern Moist Mixed Deciduous Forest, West Coast Semi-evergreen Forest and West Coast Tropical Evergreen Forest[16]. A significant cause as well as indication of the ecological imbalance of Attappady is the widespread destruction of the natural vegetation cover of the area.

Current restoration management by AHADS includes fencing to remove grazing pressure, followed by active techniques like frequent de-weeding of invasive and native weeds, intensive planting of drought-resistant tree species to minimize soil erosion and to facilitate regeneration of native tree species. However, in each site under restoration, the frequency and intensity of on-site activities like de-weeding and planting is reduced along the temporal trajectory. For example, frequency and intensity of de-weeding and planting are higher in a 2-year-old site compared to a 5-year-old site after restoration efforts began.

For this survey, we focused on changes occurring in the ground insect community assemblages across a gradient of restored sites, with particular reference to the ground insect diversity patterns, insect feeding guilds and ant functional groups. For the purpose of assessing the recolonization pattern by ground insect communities, the Substitution of Space for Time Method[17] was adopted. On the basis of this method, sites were selected according to the chronological sequence representing a trajectory of age after restoration efforts began. Hence, the age trajectory was considered as surrogate of habitat features representing structure and composition of the vegetation. Five sites were selected in the following order: (i) PLO, a pre restored site with sparse vegetation cover representing a degraded patch of land, (ii) sites under restoration; PL2 (two years after restoration efforts began), PL3 (three years after restoration efforts began) and PL4 (four years after restoration efforts began) representing different degrees of vegetation structural and diversity attributes, and (iii) a nearby relatively less disturbed forest as a reference site (F). All the sites including the reference site lie within the same watershed with an altitude ranging from 500 to 700 m msl. Hence, the variation arising due to the topographical and climatic factors was minimized. However, the vegetation structure and diversity varied due to the ongoing restoration efforts.

The ground insects were sampled using pitfall traps from 21 to 28 September 2006. Plastic jars of 500 ml capacity, 12.5 cm in height and 6 cm diameter were used as pitfall traps. The traps were sunk into the soil so that the mouth was level with the soil surface. 50% alcohol mixed with a drop of glycerol was used as preservative in

Table 1. Summary statistics for number of species, individuals and point diversity per trap and nonparametric ANOVA results for different ground insect assemblages, insect guilds and ant functional groups

	Mean ± SD					Nonparametric ANOVA	
Assemblages	PL0	PL2	PL3	PL4	F	$\chi^{2\$}$	*P*-Value
Ground insects (all)							
No. of species	8.4 ± 5.05	7.3 ± 4.5	10 ± 2.7	8.7 ± 2.7	9.6 ± 2.6	5.65	0.22
Individuals	171.5 ± 98.4	39.2 ± 35.3	36.9 ± 19.2	22.7 ± 14.1	56.8 ± 22.1	18.88	0.008**
Shannon index	1.33 ± 0.67	1.38 ± 0.56	1.83 ± 0.33	1.80 ± 0.41	1.68 ± 0.39	11.36	0.02*
Ground insects (excluding Collembola)							
No. of species	8 ± 4.6	8.2 ± 3.3	9 ± 2.5	8.6 ± 2.6	8.2 ± 2.6	3.02	0.72
Individuals	35 ± 26.2	43.6 ± 32.2	26.9 ± 13.2	21.8 ± 14.1	33.1 ± 14.6	9.70	0.04*
Shannon index	1.46 ± 0.62	1.30 ± 0.51	1.77 ± 0.34	1.79 ± 0.41	1.58 ± 0.41	11.56	0.02*
Ground insects (excluding Collembola and ants)							
No. of species	5.5 ± 3.6	5.6 ± 2.7	6.2 ± 2.1	5.6 ± 2	4.4 ± 1.7	6.00	0.19
Individuals	16.1 ± 14.8	13.9 ± 17.3	12.9 ± 6.3	11.1 ± 5.3	14.9 ± 6.9	4.56	0.33
Shannon index	1.26 ± 0.66	1.33 ± 0.46	1.54 ± 0.40	1.45 ± 0.40	0.95 ± 0.49	14.28	0.006**
Ants							
No. of species	2.2 ± 1.1	2.9 ± 0.9	2.7 ± 1.1	3 ± 1.1	3.6 ± 1.5	5.28	0.2
Individuals	22.2 ± 24.7	32.2 ± 28.3	15.0 ± 11.5	10.7 ± 13.6	18.6 ± 10.6	17.19	0.001**
Shannon index	0.65 ± 0.37	0.66 ± 0.32	0.7 ± 0.48	0.76 ± 0.48	0.91 ± 0.43	4.41	0.35
Ants (excluding *A. gracilipes*)							
No. of species	2 ± 0.9	2 ± 1	1.8 ± 1.1	2.6 ± 1.3	3.3 ± 1.6	12.78	0.01*
Individuals	8.7 ± 5.7	7.7 ± 6.3	9 ± 8.6	9 ± 13.8	13 ± 9.5	5.48	0.24
Shannon index	0.85 ± 0.63	0.41 ± 0.43	0.41 ± 0.52	0.70 ± 0.44	0.89 ± 0.57	10.91	0.02*
Beetles							
No. of species	3.8 ± 2.5	3.3 ± 1.9	3.6 ± 1.6	3.6 ± 1.7	3.1 ± 1.4	1.73	0.78
Individuals	13.4 ± 13.7	9.8 ± 16.3	8.8 ± 4.2	8.94 ± 4.3	13.5 ± 6.7	11.77	0.01*
Shannon index	0.93 ± 0.57	0.81 ± 0.5	0.99 ± 0.51	0.98 ± 0.54	0.68 ± 0.44	5.02	0.28
Insect guilds							
Detrivores	2.7 ± 2.0	5.9 ± 10	4 ± 4.7	2.2 ± 1.1	1.7 ± 0.9	4.74	0.31
Herbivores	2.2 ± 1.8	3.4 ± 1.8	2.4 ± 1.3	1.8 ± 1.1	1.5 ± 0.8	12.93	0.01*
Omnivores	26.5 ± 34.8	8.7 ± 6.3	15.5 ± 11.7	6.0 ± 4.0	34.8 ± 15.6	23.81	0.008**
Predators	6 ± 6.6	3.9 ± 8	2.6 ± 2	3.4 ± 2.1	2.2 ± 1.2	7.50	0.11
Ant functional groups							
C	–	–	–	1.2 ± 0.4	–	na	na
CCS	7.3 ± 4.9	2.8 ± 2.9	8.0 ± 10.9	10.5 ± 13.4	5 ± 5.1	4.18	0.38
DD	3 ± 1.6	6.4 ± 8.9	2.7 ± 1.5	1.6 ± 0.5	7.1 ± 6.3	3.31	0.51
GM	3 ± 2.6	6.5 ± 3.1	4.3 ± 1.7	7.1 ± 16.4	4.2 ± 4.8	8.71	0.08
HCS	20.3 ± 26.7	26.3 ± 28.7	9.1 ± 7.9	4.4 ± 4	11.8 ± 8.8	15.88	0.003**
SC	2 ± 1.4	1 ± 0.2	–	1.25 ± 0.5	–	na	na
SP	1.8 ± 1.3	1 ± 0.3	2.1 ± 1.1	2.5 ± 2.8	5.8 ± 7.3	7.58	0.10
TCS	–	2.8 ± 1.9	8.2 ± 12.9	3.3 ± 2.3	–	na	na

χ^2, χ^2-Value; *$P < 0.05$; **$P << 0.05$. Statistical significance at $\alpha = 0.05$; SD, Standard deviation; C, Cryptic species; CCS. Cold climate specialist; DD, Dominant Dolichoderinae; GM, Generalized Myrmicinae; HCS, Hot climate specialist; SC, Subordinate Camponotus; SP, Specialist predator; TCS, Tropical climate specialist; na, Not applicable.

the pitfall traps. In each site, 20 pitfall traps were laid (30 m between successive traps) along a 600 m linear transect and were retrieved after five days. The collected insects were preserved in 70% alcohol and were identified in the lab.

As it is not possible to identify every insect to species level in a multitaxon approach, a more practical morphospecies or the Recognisable Taxonomic Unit (RTU) approach was adopted. A morphospecies is a morphologically distinct and recognizable organism that represents an assumed species and is a relatively robust indicator of true species identity[5]. The collected insects were identified to Order, Family and then sorted to morphospecies. Further, the insects were identified based on the feeding guilds, i.e. predators, herbivores, omnivores and detrivores and the ants to functional groups, i.e.

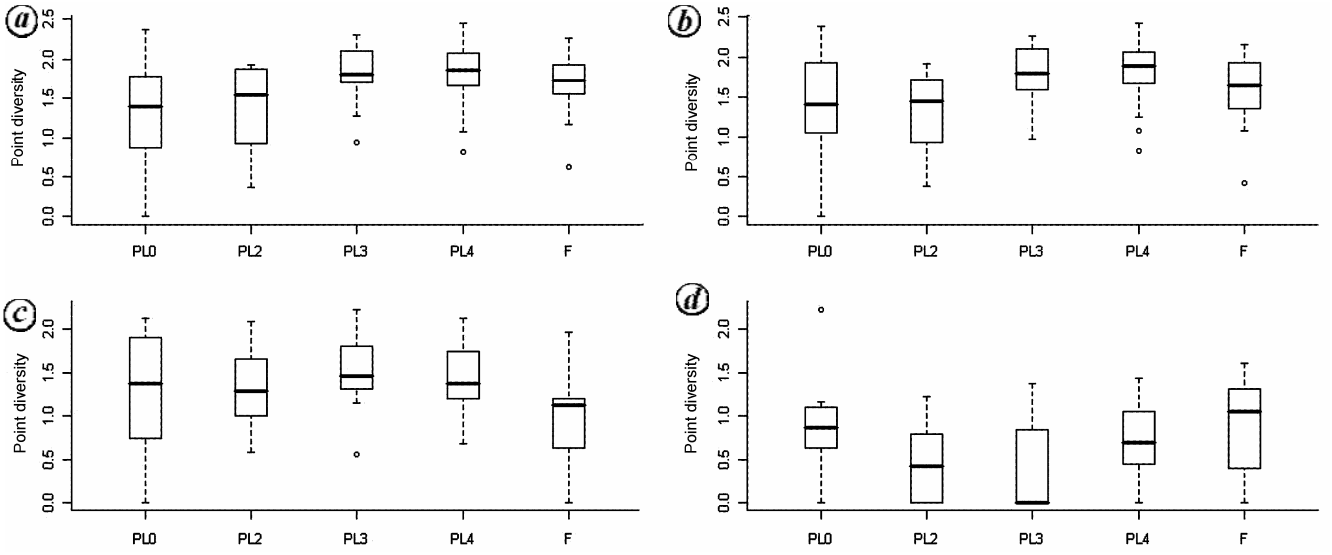

Figure 1. Comparison of point diversity of different insect assemblages across the trajectory of sites. ***a***, Ground insects; ***b***, Ground insects excluding Collembola; ***c***, Ground insects excluding Collembola and ants; ***d***, Ants excluding *A. gracillpes*.

Table 2. Diversity values for different assemblages of ground insects along the trajectory of restored sites

Assemblages	PL0	PL2	PL3	PL4	F
Ground insects					
Species richness	49	47	52	54	47
Abundance	3416	777	728	454	1086
Shannon diversity	1.07	2.23	2.83	3.06	2.57
Chao 1 estimator	53.04	57.11	65.78	65.97	59.88
Ground insects (excluding Collembola)					
Species richness	47	45	49	53	43
Abundance	698	694	528	437	654
Shannon diversity	2.5	2.11	2.92	3	2.51
Chao 1 estimator	51.97	56.38	62.08	66.49	51.82
Ground insects (excluding Collembola and Ants)					
Species richness	36	32	37	30	31
Abundance	299	209	257	194	290
Shannon diversity	2.45	2.73	2.69	2.53	1.53
Chao 1 estimator	40.4	41	50.84	36.12	40.5
Ants					
Species richness	12	13	12	22	12
Abundance	393	485	271	215	355
Shannon diversity	1.35	0.96	1.79	2.14	2.05
Chao 1 estimator	12.02	14.5	12.59	26.69	11.95
Ants (excluding *A. gracilipes*)					
Species richness	11	12	11	21	11
Abundance	158	116	162	162	247
Shannon diversity	1.69	1.72	1.87	2.1	2.06
Chao 1 estimator	10.97	13.5	11.74	24.69	10.99
Beetles					
Species richness	25	22	21	16	19
Abundance	255	147	177	170	270
Shannon diversity	2.07	2.22	1.97	1.84	1.12
Chao 1 estimator	28.37	29	23.65	18.25	20.99

dominant Dolichoderinae, generalized Myrmicinae, subordinate *Camponotus*, hot climate specialist, tropical climate specialist, cold climate specialist, specialist predator and cryptic species based on functional groups designated to genera[18]. As the data did not represent site replicates, statistical analysis was limited to the number of species and relative abundance along with point diversity for different insect assemblages using the nonparametric rank ANOVA, computed using R software[19]. The insect feeding guilds and the ant functional groups were compared based on their relative abundance using nonparametric rank ANOVA. The sites were compared for differences in morphospecies richness and diversity of different insect assemblages using Chao 1 estimator and Shannon diversity index, computed using EstimateS[20].

A total of 6532 individuals belonging to 104 morphospecies representing 40 families and 12 orders were captured during the study from a total of 100 pitfall traps (Appendix 1). Collembolans and Hymenopterans (mainly ants) together accounted for 80% of the total catch. Of these, 1726 individuals and 27 morphospecies were ants with the yellow crazy ant (*Anoplolepis gracilipes*), an invasive species, the most abundant representing 51%. Another well represented insect order was Coleoptera (15.60%). Orders – Orthoptera, Heteroptera, Blattaria and Isoptera were represented with individuals between 25 and 120, whereas Thysanura and Dermaptera were represented with fewer than 20 individuals.

The difference in the number of species among sites was not significant for all the insect assemblages except ants when *A. gracilipes* was excluded (Table 1). Relative abundance differed significantly for all insect assemblages except ants when *A. gracilipes* was excluded,

Appendix 1. Number of morphospecies and individuals belonging to each of the families of ground insect communities collected by pitfall trapping from a trajectory of restored sites at Attappady hills

	Trajectory									
	PL0		PL2		PL3		PL4		F	
Taxa	Sp. rch	Ab	Sp. rch	Ab	Sp. rch	Ab	Sp. rch	Ab	Sp. rch	Ab
Blatellidae[B] (D)	1	4	1	2	2	2	1	1	1	1
Blattidae[B] (D)	1	2	1	6	1	15	3	9	1	6
Anthecidae[CO] (H)	1	1	1	1	2	4	0	0	0	0
Carabidae[CO] (P)	3	8	3	3	2	8	3	16	1	6
Circulionidae[CO] (H)	2	3	1	2	0	0	0	0	2	3
Cupedidae[CO] (O)	0	0	1	1	0	0	0	0	0	0
Dermestidae (D)	1	4	1	4	0	0	0	0	1	1
Elateridae[CO] (O)	3	80	2	18	3	6	2	6	2	6
Histeridae[CO] (P)	2	100	1	36	1	23	1	29	1	13
Hybosoridae[CO] (D)	0	0	0	0	1	1	0	0	0	0
Lucanidae[CO] (D)	1	3	1	1	2	5	0	0	1	3
Nitidulidae[CO] (O)	1	2	2	6	2	16	2	13	1	15
Pselapidae[CO] (O)	1	2	0	0	0	0	0	0	0	0
Pterodactylidae[CO] (O)	0	0	0	0	1	4	1	2	0	0
Ptiliidae[CO] (D)	0	0	0	0	1	4	1	2	0	0
Scarabaeidae[CO] (D)	4	9	2	5	2	25	2	20	2	6
Silvanidae[CO] (D)	0	0	0	0	0	0	0	0	1	1
Staphylinidae[CO] (O)	5	39	3	11	3	79	3	79	3	209
Tenebrionidae[CO] (D)	1	4	1	4	1	1	2	5	1	3
Entomobryiidae[C] (O)	1	38	2	83	2	195	1	17	2	352
Isotomitidae[C] (O)	1	2680	0	0	1	5	0	0	2	114
Labiduridae[D] (O)	1	6	0	0	0	0	0	0	0	0
Drosophyliidae[DI] (D)	1	1	0	0	0	0	0	0	0	0
Musciidae[DI] (D)	1	4	0	0	0	0	0	0	0	0
Phoridae[DI] (D)	1	3	0	0	0	0	0	0	0	0
Sciaridae[DI] (D)	0	0	0	0	1	1	0	0	1	1
Cydneidae[HE] (H)	0	0	1	1	0	0	1	1	0	0
Lygaeidae[HE] (L)	2	7	2	4	4	5	1	4	1	1
Aphididae[HO] (H)	0	0	0	0	0	0	0	0	1	1
Cicadellidae[HO] (H)	1	17	1	7	1	3	1	3	1	2
Formicidae[HY]	12	400	13	485	12	271	22	215	12	355
Scelionidae[HY] (P)	2	5	1	4	2	10	0	0	2	7
Scottidae[HY] (P)	0	0	0	0	0	0	0	0	1	1
Scottilidae[HY] (P)	1	1	0	0	0	0	0	0	0	0
Kalotermitidae[I] (D)	0	0	1	8	1	16	1	3	1	3
Meropeidae[M] (O)	0	0	0	0	1	1	0	0	0	0
Acrididae[O] (H)	1	1	0	0	2	3	3	6	1	1
Gryllidae[O] (H)	3	6	2	30	3	30	3	24	3	11
Lepismatidae[TY] (D)	0	0	1	4	1	5	1	1	1	9
(B) Ant sub-family or genera[HY]										
Aenictus (TC)	0	0	1	13	2	41	2	26	0	0
Amblyopone (C)	0	0	0	0	0	0	1	1	0	0
Anochetus (SP)	0	0	1	1	0	0	0	0	0	0
Anoplolepis (HC)	1	108	1	242	1	369	1	109	1	53
Camponotus (SC)	2	10	1	2	0	0	1	5	0	0
Cerapachys (C)	0	0	1	1	0	0	2	3	0	0
Crematogaster (GM)	1	10	1	32	1	11	2	4	1	61
Dolichoderus (DD)	2	12	1	32	1	11	2	5	2	71
Formicinae (GM)	0	0	1	2	0	0	1	4	1	2
Leptogenys (SP)	2	9	2	3	2	13	2	12	2	94
Meranoplus (HC)	1	22	0	0	1	47	0	0	1	10
Monomorium (CC)	2	96	2	17	2	24	1	17	2	30
Myrmicinae (GM)	1	6	1	44	2	21	5	81	2	22
Tetraponera (TCS)	0	0	1	1	0	0	1	1	0	0

[B]Blattaria; [C]Collembola; [CO]Coleoptera; [D]Dermaptera; [DI]Diptera; [HE]Hemiptera; [HO]Homoptera; [HY]Hymenoptera; [I]Isoptera; [M]Mecoptera; [O]Orthoptera; [TY]Thysanura.

D, Detrivores; H, Herbivores; O, Omnivores; P, Predators; DD, Dominant Dolichoderinae; SC, Subordinate Camponotini; GM, Generalised Myrmicinae; HC, Hot climate specialists; TC, Tropical climate specialists; CC, Cold climate specialists; SP, Specialists predators; C, Cryptic.

whilst point diversity significantly differed for most insect assemblages except for ants and beetle assemblages. The abundance of *A. gracilipes* significantly decreased among sites under restoration efforts (nonparametric rank ANOVA, $\chi^2_{(\alpha=0.05)} = 21.58$, d$f = 4$, $p = 0.0002$). Although the number of species and abundance differed significantly among sites, no particular trend along the trajectory could be found. The point diversity of most insect assemblages except for ants, indicated relatively higher diversity in sites under restoration (PL2, PL3, and PL4) compared to pre-restored (PL0) and reference sites (F).

Chao 1 and Shannon diversity indices based on random resampling were comparable across the restored sites for various insect assemblages of the ground insects (Table 2). The species richness and diversity for ground insects and for ant assemblages increased with time since restoration, while that for beetles decreased. Also, the pattern remained the same when the most abundant taxa such as Collembolans and the invasive ant, *A. gracilipes* were removed from analysis.

The results indicate that the species richness and diversity for various insect assemblages were lower in sites PL0 and F, where PL0 represents the upper limit of disturbance which is frequent while F represents the lower limit of disturbance which is rare. This pattern of increased diversity in the sites under restoration efforts (Figure 1) is indicative of the intermediate disturbance hypothesis. Intermediate disturbance hypothesis proposes that the diversity is highest when disturbance is neither too rare nor too frequent[21]. This could be an attribute of ground insect community response to the local disturbance such as de-weeding and planting activities in these sites.

Among the insect feeding guilds, relative abundance of herbivores and omnivores differed significantly among sites whereas no such significance was found for detrivores (Orders: Coleoptera, Dermaptera, Isoptera and Blattaria) and predators (Order: Coleoptera) (Table 1). Though omnivorous insects (Orders: Coleoptera, Collembola) differed significantly, no particular trend was found. The very high abundance of omnivores is attributed to that of four morphospecies from two families of Collembola (Appendix 1). Relative abundance of herbivorous insects (Orders: Orthoptera, Heteroptera and Coleoptera) decreased along the trajectory (Appendix 1).

The composition of ant functional groups varied across the restored sites (Table 1). Among the sites, the relative abundance of hot climate specialists (HCS) such as *A. gracilipes* and *Meranoplus* spp. significantly decreased while no significant differences in relative abundance of other ant functional groups were found. The relative abundance of dominant Dolichoderinae decreased, whereas the abundance of cold climate specialists (CCS) such as *Monomorium* spp. and specialist predators such as *Leptogenys* spp. increased with time since restoration. As expected, the subordinate Camponotus (SC) were present mostly in the early stages of restoration and cryptic species (C) of Ambyloponinae and Cerapachyinae appeared in the later stages. These patterns are comparable to many studies that have used the ant functional group protocol in monitoring restoration success[10–15]. A similar pattern was not observed for generalized Myrmicinae and tropical climate specialists.

Restoration ecology is built upon the succession theory where simpler communities are built upon to attain complexity over time. Many studies have adopted a Substitution of Space for Time Method or chronological sequence approach[16] based on the comparison of restored areas of different ages that represent different stages of succession. We find this method feasible and effective in understanding the dynamics of succession in ecological communities subjected to restoration. However, there are two limitations in the study. First, as this was a reconnaissance survey, we felt classification of restored sites based on a trajectory of chronological sequence is sufficient to explain the recolonization patterns seen in the ground insect communities. Measuring vegetation structure and diversity in these sites would have helped better in explaining the recolonization patterns observed in these ground insect communities. Secondly, quantifying on-site restoration activities such as de-weeding and planting with respect to its frequency and intensity would have better explained the observed diversity patterns with respect to intermediate disturbance hypothesis. Also, we opine that long-term monitoring programme using insect responses to habitat restoration efforts in Attappady hills should include detailed studies on vegetation structure/composition and management techniques involving sufficient replicates of sites.

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Overlap index: a measure to assess flowering synchrony among teak (*Tectona grandis* Linn. f) clones in seed orchards

Rajesh P. Gunaga[1,2] and R. Vasudeva[1,*]

Department of Forest Biology and Tree Improvement, College of Forestry, University of Agricultural Sciences, Sirsi Campus, Dharwad 581 401, India
[2]Present address: College of Forestry, Dr BSKKV, Dapoli 415 712, India

One of the most important aspects in a seed orchard is the synchrony among the clones for reproductive phenology. This will decide the extent of random mating among the constituent clones and hence the genetic gain in the resultant progeny. In the present study, synchrony among clones for flowering and peak flowering was estimated through the phenogram as well as through a novel overlap index. Rating of an entire orchard for its relative degree of flowering synchronization is effective with this new measure. The present study was conducted in teak clonal seed orchard (CSO), Manchikere, Karnataka using 25 clones to study the clonal variation for flowering phenology. There are two peak periods in flowering. The first period during early May to July corresponds mainly to the clones of central and southern origin; the second period during July to August corresponding to those of northern origin. Further, these two peaks are also more apparent considering the peak flowering periods of clones. Perhaps, this is the first empirical evidence among the CSOs of teak in India where asynchrony has been documented and quantified through meticulous observations as well as by developing a new index.

Keywords: Geographic variation, genetic gain, panmixis, phenology, teak clones.

THE knowledge of reproductive phenology is a fundamental requirement for the successful operation of any seed orchard because it affects the extent of gene exchange between clones and consequently, the genetic composition of the seeds produced[1]. Clonal seed orchard (CSO) is a plantation where phenotypically superior individuals of a species are deployed as vegetatively propagated plants, in isolation, to achieve a big genetic gain through the process of random mating. Since superior genotypes identified from diverse regions are used in a CSO, understanding the flowering phenology of the constituent clones becomes imperative to achieve maximum synchrony. A large number of reports are available for temperate species, which document asynchronous flowering among the clones in a seed orchard, especially among monoecious species[2].

*For correspondence. (e-mail: vasukoppa@gmail.com)