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Species-abundance distribution (SAD) of sarcosaprophagous fly population guild

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Abstract

The present study analyzes lognormal and log series distribution of meta-communities of sarcosaprophagous fly species of a large area. The carrion fly species contain numerous individuals and analysis of their diversity is the central theme of the present study. The fly populations of three families (Parasarcophagidae, Calliphoridae and Muscidae) form a guild and are potentially competing in a local area for common resource utilization. The sampling data of sarcosaprophagous fly species from twelve study sites are analyzed with logarithmic series, lognormal distribution, Whittaker plots as well as canonical correlation analysis (CcorA) and CCA to show their relationships in distribution pattern over a large area. The analysis of these fly species corresponds to their synanthropic association with human population. The outcome of the analysis of γ -diversity shows that the distributions of this fly guild are not uniform; instead exhibit patchiness, show wide range of variation in species richness due to possible variation in microhabitat.

Keywords: Alpha guild, CCA, Community analysis, lognormal, log-series, Whittaker plot

Introduction

Biodiversity can be measured most simply by counting the number of species in an area ^[1]. A combination of a number of species and their relative abundance defines species diversity which is organized hierarchically and the central of ecological study. The industrialization has a great effect on the species diversity ^[2, 3]. It is examined that the differences of species diversity of moss dwelling amoeba depend on the moss genera as they inhabit in mostly same type of habitat ^[4]. The local or ecological community is defined as a group of trophically similar, sympatric species that actually or potentially compete in a local area for the same resources ^[5, 6]. The meta-communities of a large region contain numerous individuals that are slowly lost and infrequent events of speciation can maintain the high species diversity ^[7]. It is found that species diversity is higher in complex environments, and intermediate levels of disturbance promote higher diversity. Log series analysis is proposed by Fischer *et al.* ^[8] to arrive at an unsaturated habitat at random intervals of time. Log normal distribution is a continuous probability of a random variable whose logarithm is normally distributed. Preston ^[9] proposed species-abundance distribution (SAD) model and argued that species-abundance obeys a Gaussian (Normal) distribution, partly as a result of the Central Limit Theorem.

The most important property of the lognormal process is that it represents a product of independent random variables. Normally, lognormal process abstracts variable of interest from many independent random variables multiplied together. Whittaker ^[10] introduced abundance-species rank order plots to explain the species richness. Ghorbani *et al.* ^[11], while studying the species richness in grassland and shrub land in Iran, preferred Modified Whittaker plot ^[12] over the original Whittaker plot. There are controversies whether lognormal distribution fits to the analysis of species distribution ^[13, 14]. Ulrich *et al.* ^[15] after assessing three types of abundance analyses (lognormal, log series and power law) favors Whittaker over Preston plots.

Flies are commonly regarded as noxious agents and transmit or cause various diseases like dysentery, myiasis, poliomyelitis, etc. These flies, such as, blow flies, blue bottle flies, green bottle flies, and flesh flies are of medical, veterinary, and sanitary importance, and found in almost all the zoogeographical realms. Root ^[16] defined an ecological guild as a group of species who exploit the same environmental resources in a similar manner. The sarcosaprophagous flies form an ecological guild (group) because they exploit the same resources in an identical way and may be classified within alpha guild ^[17] because all the family Calliphoridae, Parasarcophagidae, and Muscidae enjoy similar food niche as well as form an ecological group ^[18].

The female flies are filth-inhabiting dipterans; feed on rotten flesh of vertebrate source, as well as carcasses, thus called carrion flies or sarcosaprophagous flies, Synanthropy of these flies from different districts of West Bengal were documented [19, 20]. Majumdar *et al.* [21] analyzed the diversity of carrion flies in relation to human habitation. In their study, the authors used 19 types of analytical procedures to assess the diversity of sarcosaprophagous fly community. Further, the authors studied niche breadth and overlap of these sarcosaprophagous flies [18].

Jana *et al.* [22] found that insect community in industrial and non-industrial areas exhibit lognormal distribution. The authors also recorded that x and N/S values of the logarithmic series indicate good relationship between the insect community and its diversity. The present study is based on relative abundance (cf. Table 2; Majumdar *et al.* [20]) with the

aim that this may unravel some further important aspects of sarcosaprophagous fly community, hitherto not explored. Based on their data, the present communication dealt with analyses of logarithmic series and lognormal distribution along with Whittaker plot. The hypothesis of the present work is that the relationship among sarcosaprophagous fly species corroborates SAD as analyzed using five different analytical methodologies.

Material and Methods

The recent survey work was conducted in twelve selected study sites of three districts of West Bengal *viz.*, North 24 Parganas, Hooghly and Midnapore.

Altogether 12 study spots were selected for trapping the carrion flies. However, following spots were considered for analysis of synanthropy.

Districts	Town	Village	Uninhabited place
North 24 Parganas	Naihati (Nai) (Lat. 22.88815, Long. 88.45231)	Balivara (Bali)	Rajendranagar (Rajen)
Hooghly	Chinsurah (Chin) (Lat. 22.891891, Long. 88.3967446)	Simlipal (Simli)	Baidyabati (Baidya)
Midnapore	I Contai town (Con)	Serpur (Ser)	Kalamdan (Kalam)
	II Monoharchalk (Mono) III Haripara (slum area) (Hari)	Raghurampur (Raghu)	

Sampling procedure

For trapping the fly carrion traps [23, 24] were used. To attract the fly species different types of fresh and rotten foods were used. The detail procedure of collection and catching of flies are given Majumdar *et al.* [20].

Data analysis

In the study the analysis of obtained data was involving logarithmic series [8], lognormal distribution [25], Whittaker plot [10], Canonical correlation analysis [26] and canonical correspondence analysis [27]. Both log-series and lognormal distribution were plotted using ECOLOGICAL

METHODOLOGY 7.1 program and Canonical analyses were done by XLSTAT 2015.1.01.

Results

Table 1 represents the abundance data of all the collected fly species from the study sites. Logarithmic series parameters of sarcosaprophagous flies were estimated all the study sites (Table 2). The table also expressed x of logarithmic series. It shows that α value is highest in Haripara and lowest in Kalamdan, whereas x is highest in Contai and lowest in Rajendrapur. Figure 1 compares that α (alpha) of logarithmic series in all the study sites; of which Haripara exhibit maximum value.

Table 1: Abundance data of fly species from 12 study sites.

Fly species	Nai	Bali	Rajen	Chin	Simli	Baidya	Cont	Hari	Mono	Ser	Raghu	Kalam
Calliphoridae												
<i>Chrysomya megacephala</i>	1837	945	371	2029	571	217	3438	1846	1501	2235	621	231
<i>C. rufifacies</i>	346	342	74	150	59	60	530	1117	671	489	72	206
<i>Hemipyrellia sp.</i>	153	89	43	813	156	123	363	435	112	173	40	38
<i>Lucilia cuprina</i>	162	65		43	48	6	13	10	16	24	3	0
<i>L. illustris</i>	158	95	0	96	154	0	54	58	53	76	0	0
<i>L. sericata</i>	0	0	0	34	50	0	0	0	0	0	0	0
Parasarcophagidae												
<i>Parasarcophaga albiceps</i>	97	189	212	141	165	152	143	319	288	148	108	234
<i>P. ruficornis</i>	78	145	171	44	89	209	96	171	217	67	136	159
<i>P. brevicornis</i>	65	92	110	16	54	111	52	254	123	58	78	162
<i>P. misera</i>	0	0	0	0	60	97	7	20	54	20	9	30
<i>Sinonipponia hainanensis</i>	0	0	0	0	0	0	0	8	0	0	0	0
Muscidae												
<i>Musca domestica</i>	1175	1087	7	1372	303	9	2552	1589	1598	1274	28	0
<i>M. sorbens</i>	745	796	19	452	103	37	1001	643	386	597	30	0
<i>M. ventrosa</i>	67	66	12	35	10	5	98	472	427	28	32	0
<i>M. lucens</i>	0	0	0	54	82	2	243	46	49	199	22	0
<i>Atherigona orientalis</i>	126	70	3	141	120		204	168	262	216	39	40
<i>Ophyra chalcogaster</i>	108	132		36	51	0	53	93	55	46	6	8
<i>Orthellia sp.</i>	0	0	0	0	0	0	10	0	0	0	0	0
<i>Graphomya sp.</i>	0	0	0	0	0	0	0	3	0	0	0	0
<i>Gymnodia tonitruui</i>	0	0	0	0	0	0	0	4	0	0	0	0
<i>Limnophora sp.</i>	0	0	0	0	0	0	0	0	0	9	0	0
<i>Myospila bina bina</i>	0	0	0	0	0	0	0	9	0	0	0	0
<i>Synthesiomyia nudiseta</i>	0	0	0	0	0	0	11	7	0	0	0	0

Observed and expected lognormal distribution of species of all the sampling sites was plotted. Observed distribution of species in octaves shows similar to that of expected pattern (Table 3). More or less similar pattern of observed and expected distribution pattern is observed in Mono, Nai, Raghu, Bali and Cont. Estimated mean of lognormal distribution of species in

all the 12 study sites show that the mean distribution is minimum in uninhabited places like, Rajen, Baidya and Kalam (Figs. 2E, F, 3F). Figures 4-5 show the observed and expected lognormal distribution of major fly species in twelve study sites. Most of the fly species corroborate log-normal distribution pattern.

Table 2: Estimation of Logarithmic series parameters of the flies trapped from 12 study sites.

Study sites	Total individuals	Total species	Alpha (α)	Variance of α from Anscombe (1950)	S.E. of α	95% CL for α	x of logarithmic series
Naihati	1696	13	1.9152	0.0397	0.1991	1.5249 - 2.3055	0.9988720
Balivara	1183	12	1.8578	0.0433	0.2080	1.4502 - 2.2655	0.9984320
Rajendranagar	178	10	2.2904	0.1412	0.3758	1.5539 - 30.269	0.9872960
Chinsurah	1830	15	2.2353	0.0476	0.2181	1.8078 - 2.6627	0.9987800
Simlipal	698	16	2.9186	0.1009	0.3177	2.2959 - 3.5413	0.9958360
Baidyabati	345	12	2.4149	0.1066	0.3266	1.7748 - 3.0549	0.9930490
Contai	3124	17	2.3636	0.0428	0.2069	1.9581 - 2.7691	0.9992440
Haripara	2415	20	2.9862	0.0638	0.2526	2.4910 - 3.4813	0.9987650
Monoharchalk	1899	15	2.2206	0.0465	0.2057	1.7978 - 2.6434	0.9988320
Serapur	2049	16	2.3631	0.0493	0.2220	1.9280 - 2.7982	0.9988480
Raghurampur	423	14	2.7829	0.1191	0.3452	2.1064 - 3.4594	0.9934640
Kalamdan	342	9	1.6941	0.0633	0.2516	1.2010 - 2.1871	0.9950710

Table 3: Fitting a continuous lognormal distribution of common noxious fly species in twelve study sites.

Study sites	Number of species in sample	Total numbers of individuals in samples	Estimated mean of lognormal distribution	Estimated variance of lognormal	Estimated total number of species in community
Naihati	13	1696	1.8257	0.23153	13
Balivara	12	1183	1.7715	0.18697	12
Rajendranagar	10	178	0.9751	0.29092	10.1
Chinsurah	15	1830	1.6100	0.42162	15
Simlipal	16	698	1.4929	0.12461	16
Baidyabati	12	345	1.1837	0.36323	12.1
Contai	17	3124	1.5585	0.75898	17.3
Haripara	20	2415	1.4068	0.86762	20.7
Monoharchalk	15	1899	1.7610	0.33447	15
Serapur	16	2049	1.6240	0.50192	16.1
Raghurampur	14	423	1.1291	0.32053	14.1
Kalamdan	9	342	1.3840	0.24476	9

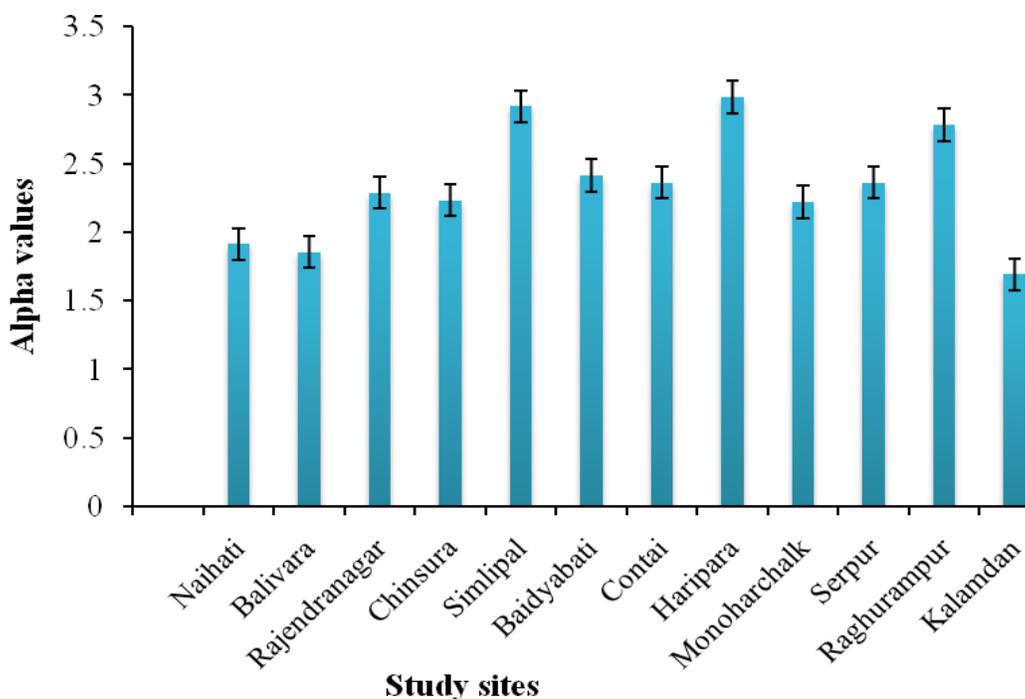


Fig 1: Graphical representation of alpha (α) values of twelve study sites.

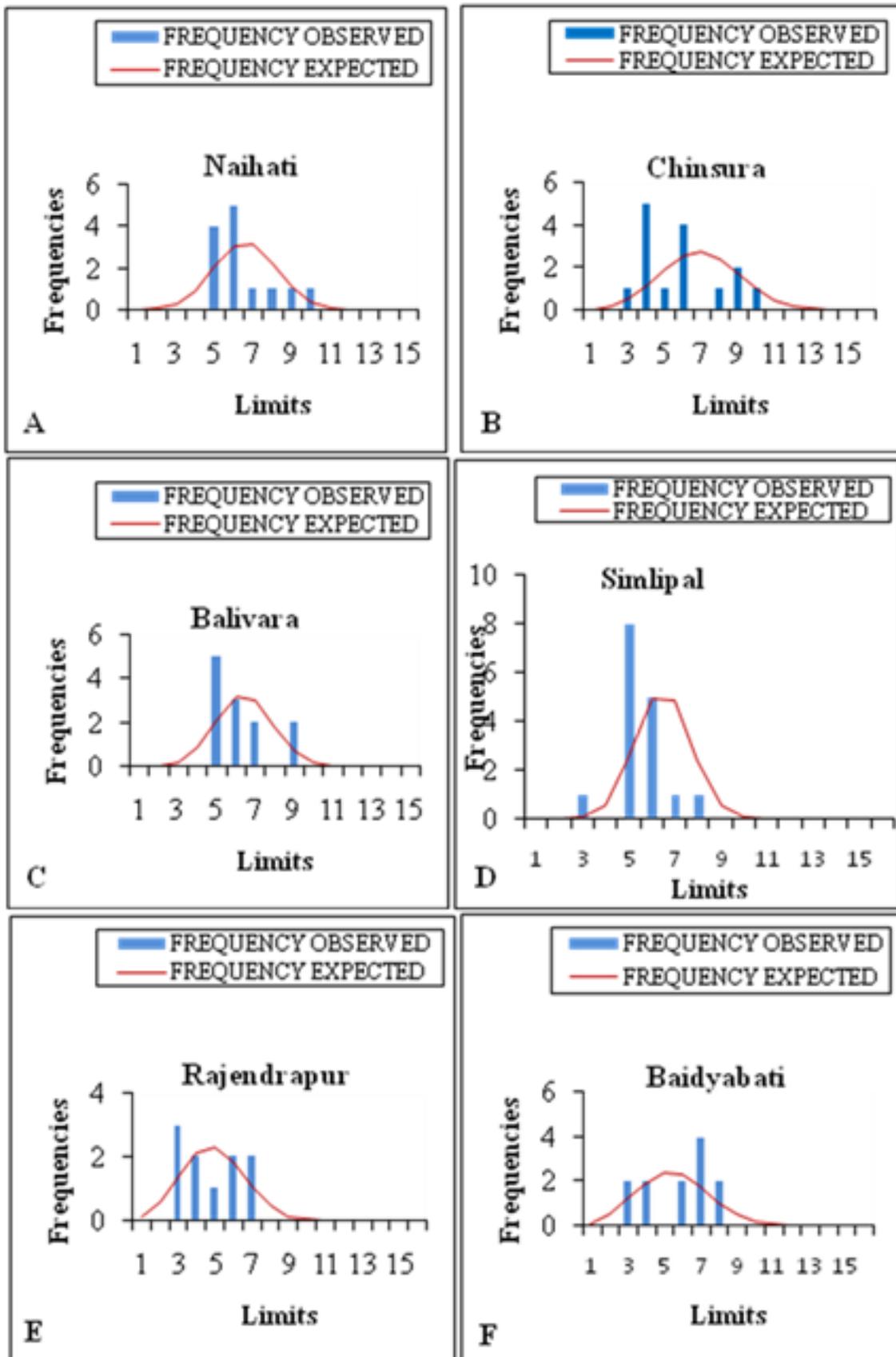


Fig. 2(A-F). Lognormal distribution of species abundances for different study sites of North 24 Parganas (2A, C, E) and Hooghly (2B, D, F).

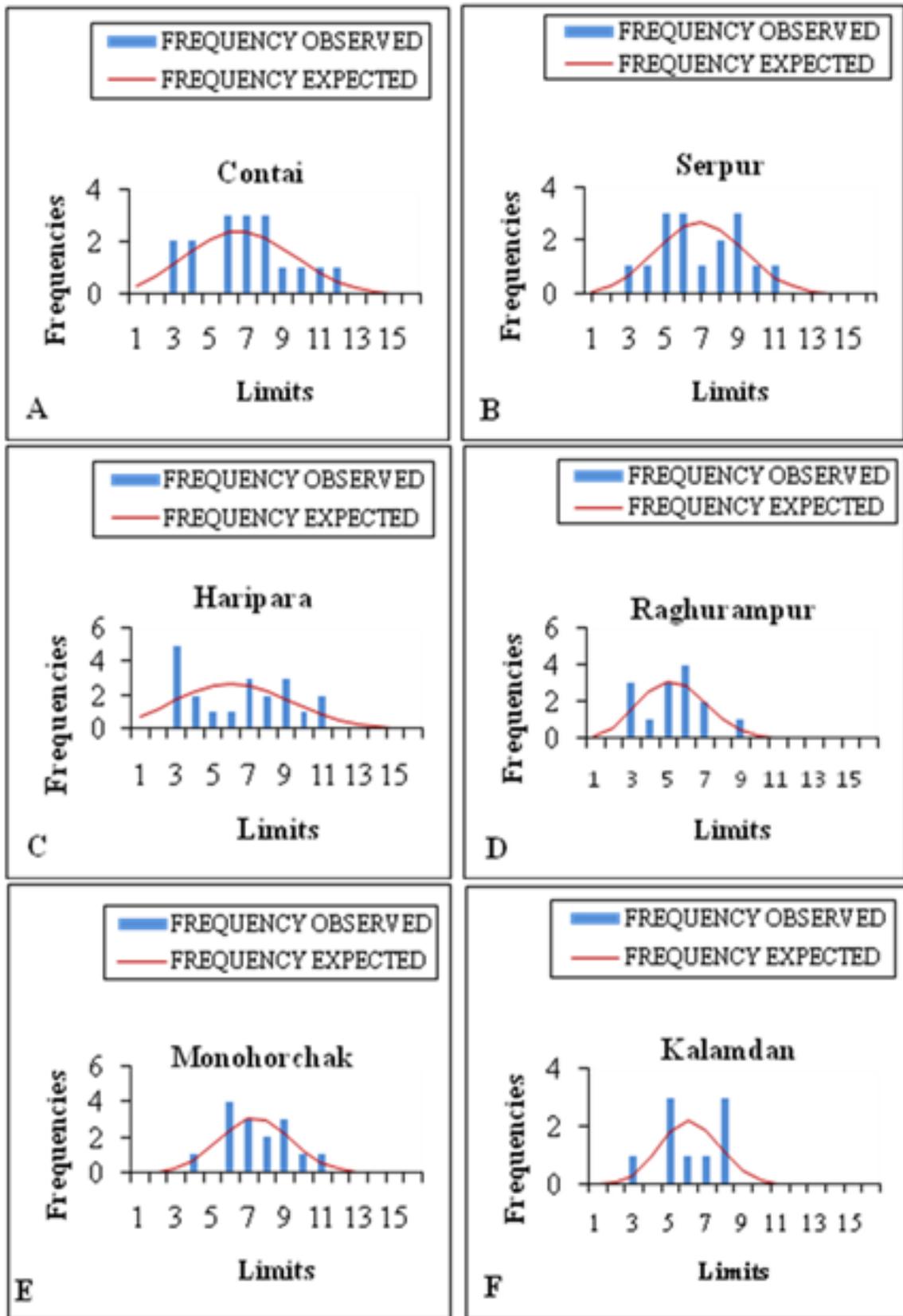


Fig. 3(A-F). Lognormal distribution of species abundances for different study sites of Midnapore.

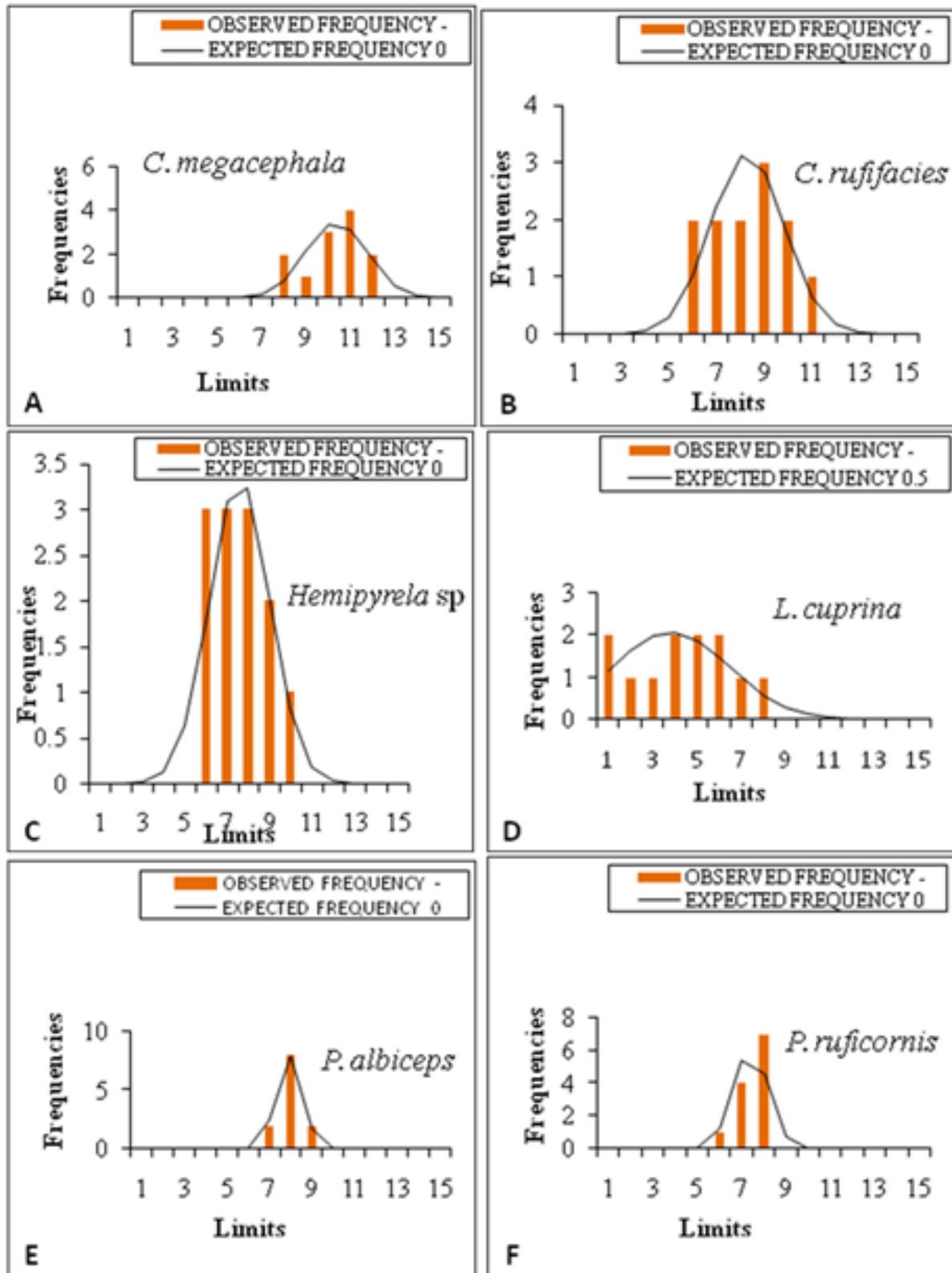


Fig. 4(A-F). Graphical representation of log-normal distribution of six fly species on twelve study sites. A-D, family Calliphoridae; E-F, family Parasarcophagidae.

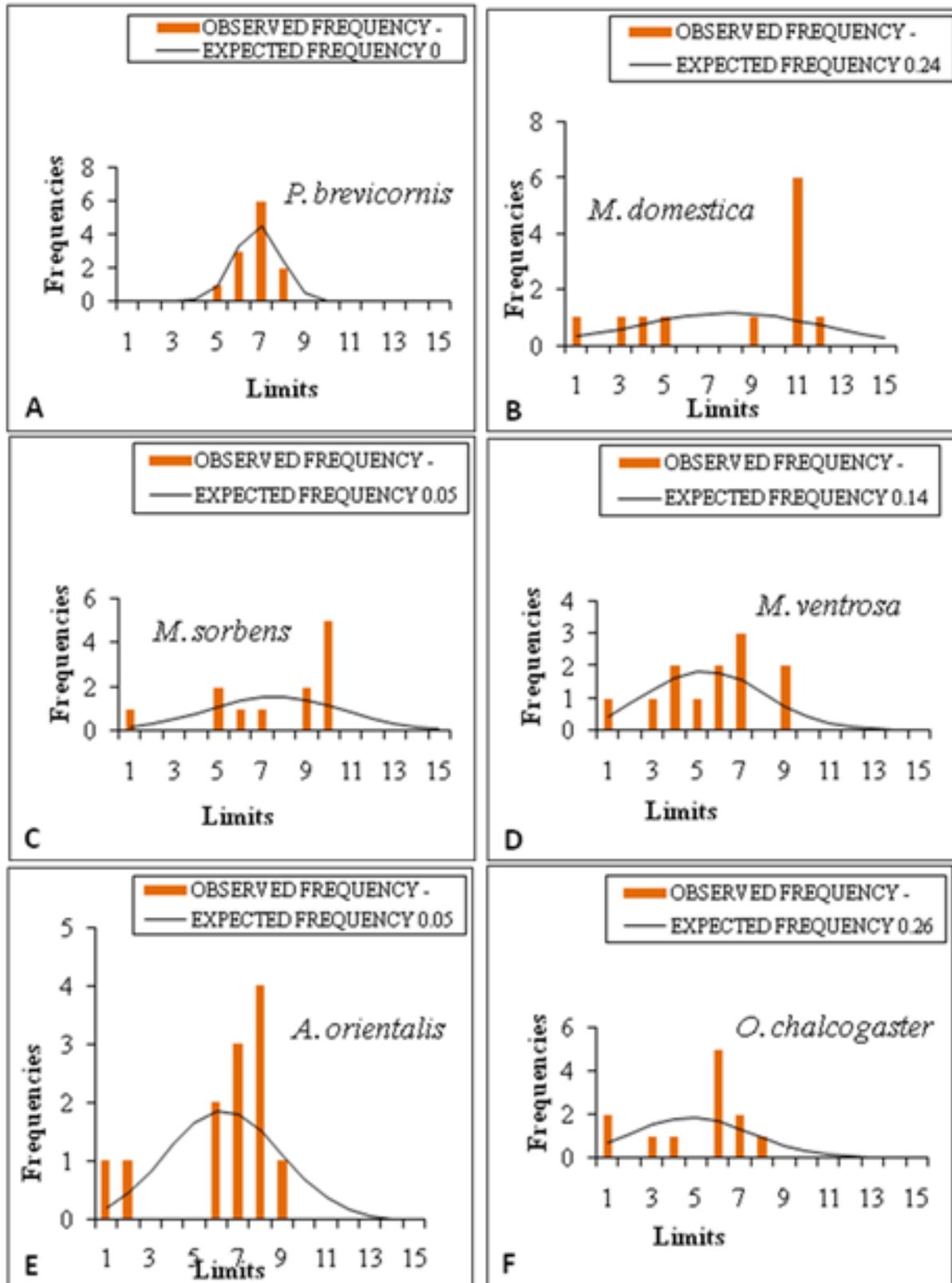


Fig. 5(A-F). Graphical representation of log-normal distribution of six fly species on twelve study sites. A, family Parasarcophagidae; B-F, family Muscidae.

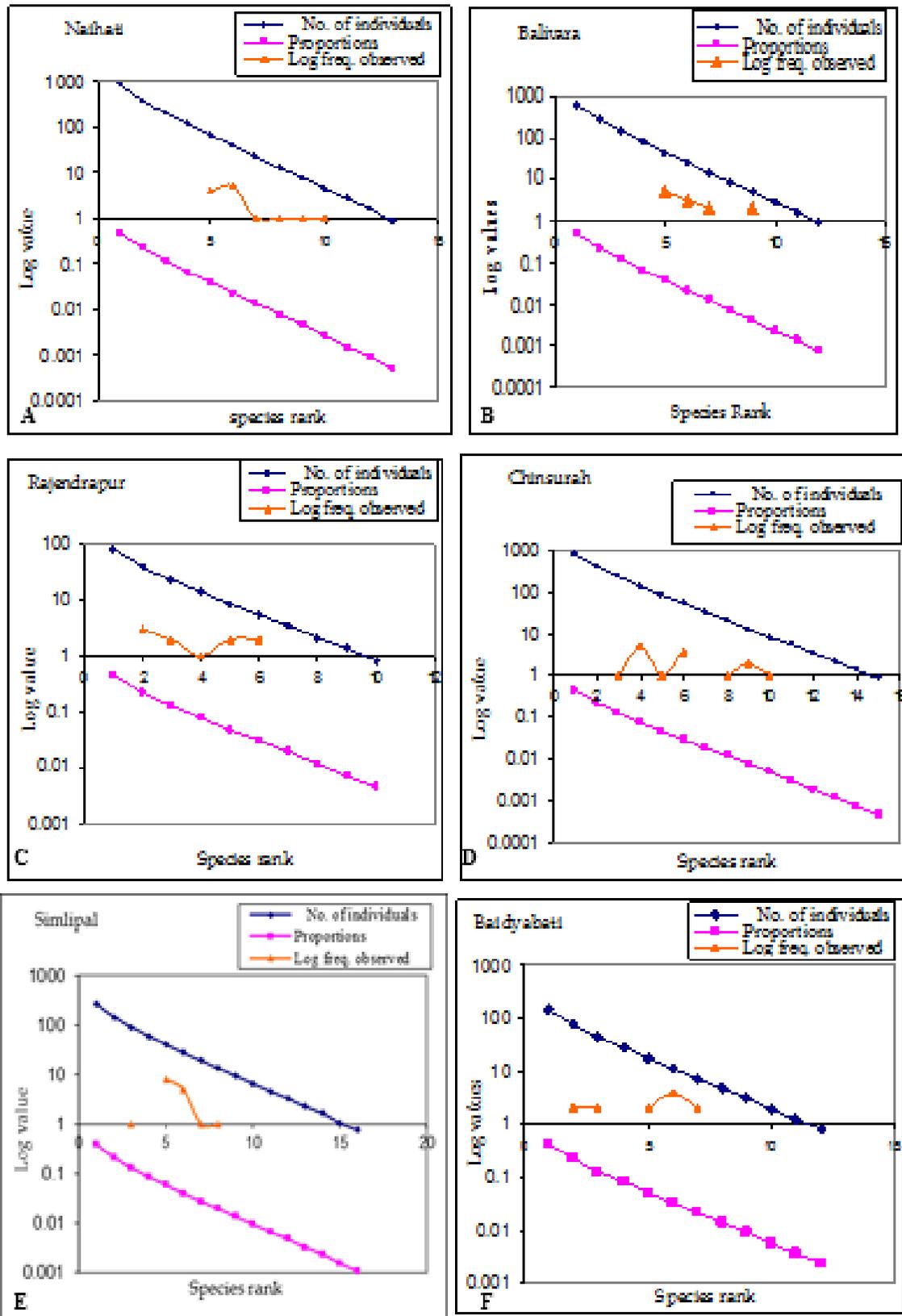


Fig. 6(A-F). Theoretical Whittaker Plot of species abundances for different study sites of North 24 Parganas (6A-C) and Hooghly (6D-F).

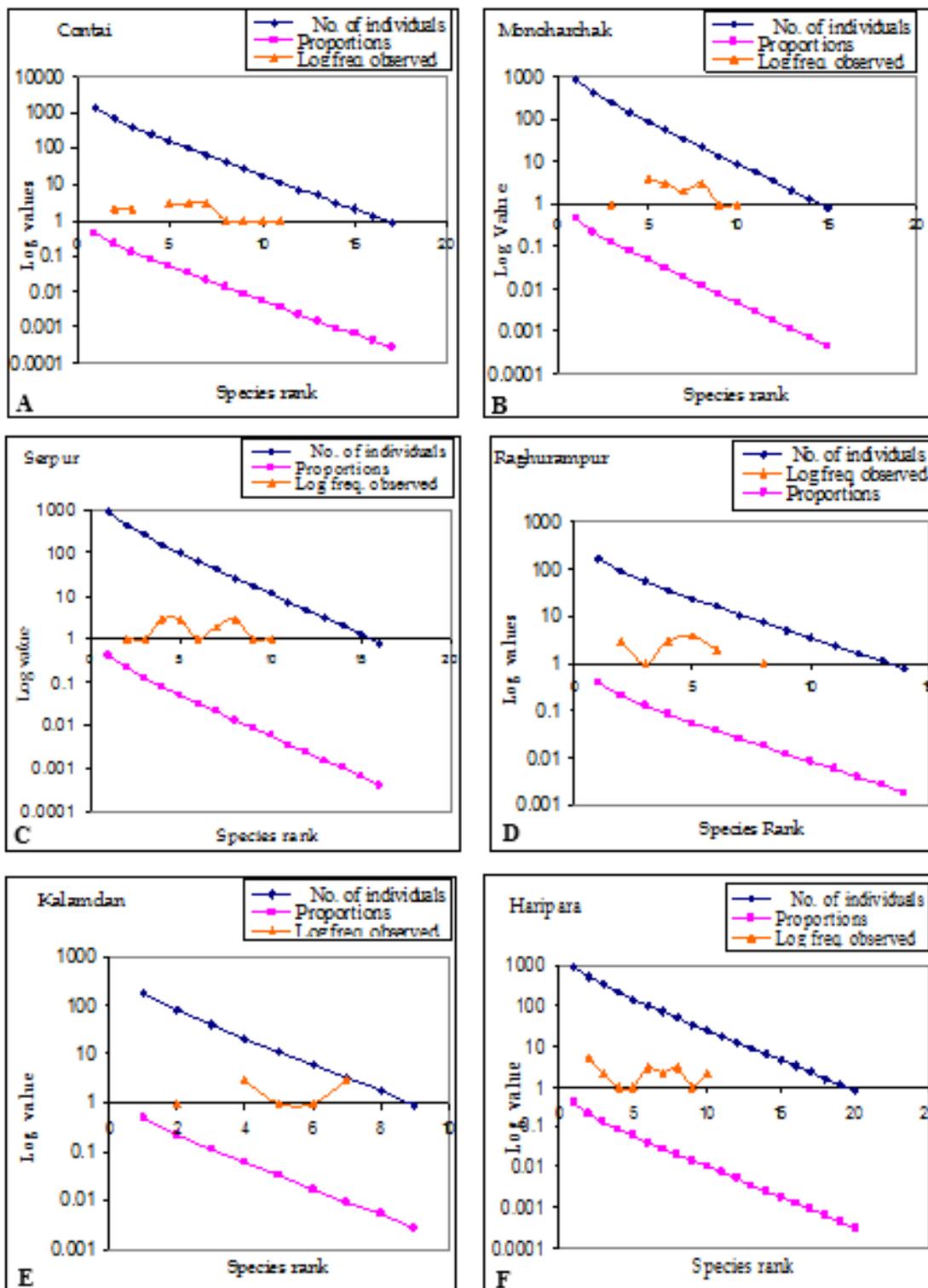


Fig. 7: (A-F). Theoretical Whittaker Plot of species abundances for different study sites of Midnapore.

Figures 6-7 represent the Whittaker plot for 12 sites where species rank is compared to their proportions in log scale. It is to be noted that both the curves follow typical straight-line appearance. Observed log frequency of the species is also added in the figures for comparison. This log frequency plot attains typical dome shape in Simlipal (Fig. 6E).

Figure 8 shows the relationship between the calculated values of x and those of N/S of the logarithmic series. The jackknife estimate for the species richness of the insect samples from the 12 study sites was 28.5 (confidence limit = 20.3–36.7), and the number of unique species was 6.

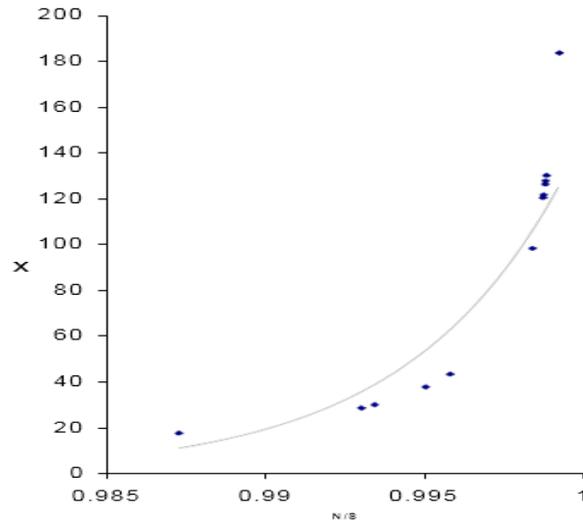


Fig 8: Values of x in relation to N/S of the logarithmic series; x = value of logarithmic series, S = total number of species in the sample, N = total number of individuals in the sample.

Figure 9 shows the Canonical Correlation Analysis (CcorA) between abundant fly species on twelve study sites. The CcorA expression is most fitted in this relationship among sarcosaprophagous flies. The figure clearly shows that there is

also a linear relationship between fly species on all sampling areas. The relationship between Parasarcophagidae and other two fly families were shown in figure 10 (A – B).

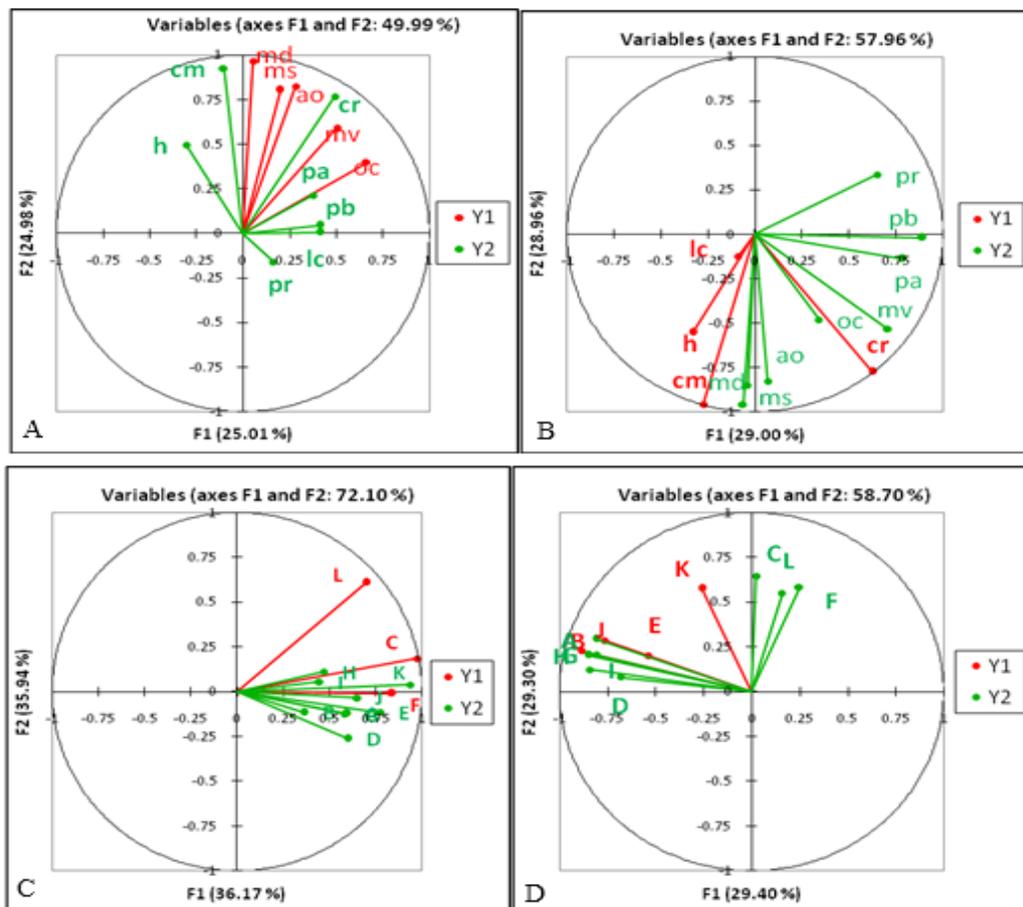


Fig. 9.(A-B). Canonical correlation analysis (CcorA) between fly families (Calliphoridae, Parasarcophagidae and Muscidae); A- Muscidae and others, B-Calliphoridae and others.

cm- *C. megacephala*, cr- *C. rufifacies*, lc- *L. cuprina*, h - *Hemipyrellia* sp, pa- *P. albiceps*, pr- *P. ruficornis*, pb- *P. brevicornis*, md- *M. domestica*, ms- *M. sorbens*, mv- *M. ventrosa*, ao- *A. orientalis*, oc- *O. chalcogaster*. (C-D). CcorA between study sites (uninhabitat, village and town); C- uninhabitat area and others, D- village and others.

A- Nai, B- Bali, C- Rajen, D- Chin, E- Simli, F- Baidya, G- Cont, H- Hari, I- Mono, J- Ser, K- Raghu, L- Kalam.

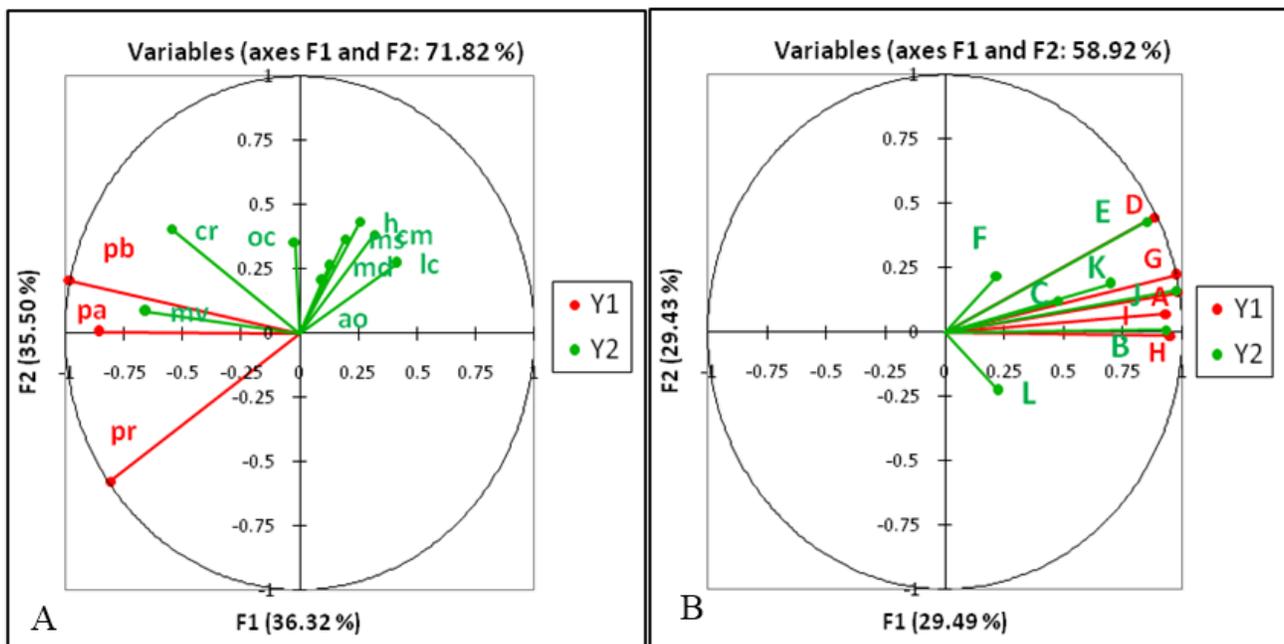


Fig. 10. A. Canonical correlation analysis (CcorA) between Parasarcophagidae and others. **B.** CcorA between town area and others; cm- *C. megacephala*, cr- *C. rufifacies*, lc- *L. cuprina*, h - *Hemipyrellia* sp, pa- *P. albiceps*, pr- *P. ruficornis*, pb- *P. brevicornis*, md- *M. domestica*, ms- *M. sorbens*, mv- *M. ventrosa*, ao- *A. orientalis*, oc- *O. chalcogaster*.
 A- Nai, B- Bali, C- Rajen, D- Chin, E- Simli, F- Baidya, G- Cont, H- Hari, I- Mono, J- Ser, K- Raghu, L- Kalam.

Figure 11 represents the Canonical Correspondence Analysis (CCA) that expresses the relationship between study sites of village area and others (uninhabited and town areas). The relationship between variables with objects and sites is shown in figure 12 (A – B).

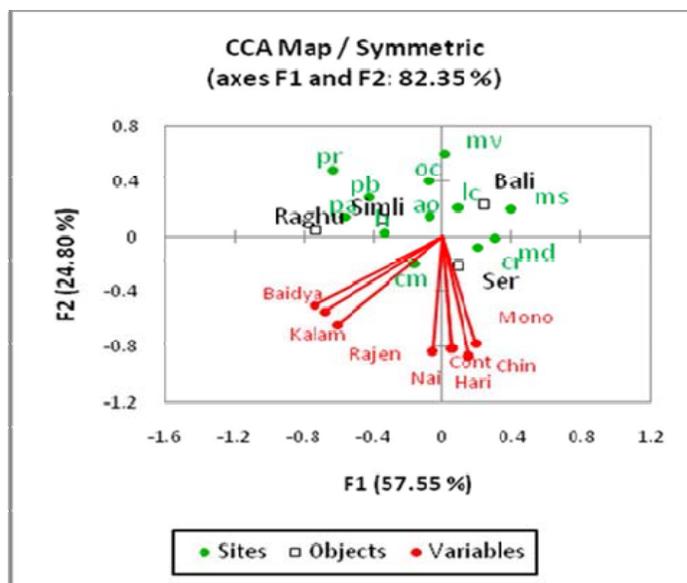


Fig 11: Canonical correspondence analysis (CCA) between village and other study sites. cm- *C. megacephala*, cr- *C. rufifacies*, lc- *L. cuprina*, h - *Hemipyrellia* sp, pa- *P. albiceps*, pr- *P. ruficornis*, pb- *P. brevicornis*, md- *M. domestica*, ms- *M. sorbens*, mv- *M. ventrosa*, ao- *A. orientalis*, oc- *O. chalcogaster*.

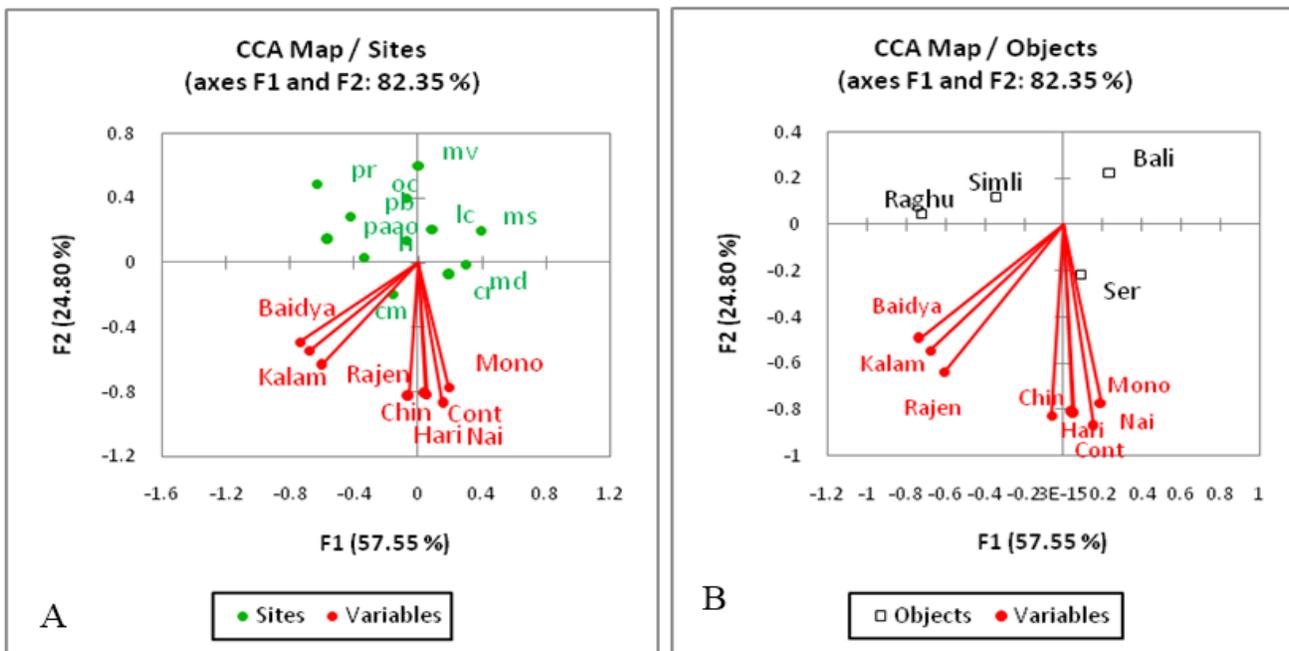


Fig 12: A and B. Canonical correspondence analysis (CCA) between village and other study sites.

Discussion

There are controversies whether H' should be used as heterogeneity measure. It is proposed that α of the logarithmic series is a better diversity statistic than H' [28]. Pielou [29] recommended Brillouin's index for measuring species diversity. Application of Brillouin's index (H) is under scrutiny [30]. Margalef [31] was in favour of using Brillouin's index as a measure of diversity. In the present analysis, Simlipal shows maximum Brillouin's index of 2.9186 followed by Haripara (2.9862) [21]. A similar close value for α was also obtained for these two sites. Thus, whatever are the limitations of the three non-parametric measures, the present data fit very well for all the three measures to describe species heterogeneity.

Three categories of species diversity are considered to analyse a community. Diversity of species within a community or habitat is α -diversity, while β -diversity considers the rate and extent of change in species along a gradient i.e. from among habitats. The richness of species in a range of habitats in a geographical area is termed as γ -diversity (the study sites of three districts differ in Latitude and Longitude scale). Thus, the γ -diversity is the value of S in an area and it combines point diversity (α -diversity) with the effect of having many habitats in space (β -diversity). The relationship species number (S) and abundance of individuals (N) explains species richness as well as evenness. Among the models of S : N relationship, logarithmic series and lognormal distribution models are employed in the present study. The log series is regarded as the convenient approximation to gamma model with maximal variance [32]. Originally Fisher *et al.* [8] put forward the analysis and later theoretical justification of the analysis was given by May [33]. The present species abundance plot was constructed taking $\text{Log}(y)$ – arithmetic (x) as is called Whittaker plots. The index of diversity (α) is highest in Haripara followed by Simlipal, whereas x log is highest in Contai followed by Naihati, Monoharchak, and Serpur. According to Krebs [30], the value of α is low when the number of species is less, and high when the number of species is high. Thus, Haripara having 20 species exhibits

highest α value, whereas Kalamdan with the lowest number of species (9) shows lowest α value. Therefore, the α can be considered as one of the best measures of diversity. As per x value is considered, N/S is lowest in Raghurampur (between 28.58 and 32.38) and highest in Contai i.e. N/S is 175.1. This relationship measure is important for assessing the community structure. However the graph differs from the studies on insect diversity inhabiting *Calotropis procera* [22]. Acceptance of logarithmic series is critically discussed in a number of articles [28, 34]. However, Wolda [35] concluded that α of the logarithmic series is probably the best measure of the species diversity. Krebs [30] recommended Whittaker plot as the standard species abundance plot, which utilizes log-relative abundance (y)–arithmetic species rank as (x). And the expected form of this plot would be nearly a straight line. In the present Whittaker plot, observed log frequency is also included. The Whittaker plots for all the study sites are ideal and maximum diversity is observed in Haripara. Thus logarithmic series together with Whittaker plots are good measures for species diversity and can be used in community analysis.

According to Preston [9, 36], the lognormal distribution fits a variety of data from diverse communities. The graphical configuration derived from lognormal distribution is termed as canonical distribution [36, 37], which explains commonness and rarity. In the present study, the lognormal distribution to species abundance data using the maximum likelihood method is followed as proposed by Cohen [25]. Estimated mean of lognormal distribution (μ) to species abundance showed distinct variation among city areas, village and uninhabited places. Maximum estimated variance of lognormal (σ^2) is observed in Contai and Haripara, where estimated species number ($\hat{S}T$) is also highest. Observed and expected distributions fit very well in Simlipal, where both diversity and evenness measures were also found to be maximum than those of other sites. It is found that species-abundance distributions in all the study sites are lognormal and estimate of total number of species in the community shows that there might be some rare species not yet been collected. Sites like, Rajendrapur, Baidyabati, Contai, Haripara, Serpur and

Raghurampur have some hidden sectors of lognormal distribution, where some rare species may exist. Gotelli and Colwell [38] stated that most biodiversity metrics are sensitive to sampling intensity and is an underestimate biased against rare species. In the present analysis of log-normal distribution of abundant fly species from all the study sites represents the expected number of individuals are slightly lower than the observed numbers in Muscidae family. This clearly reflects that flies in each study sites are log- normally distributed and sampling is good. It is prominently shown from the analysis that, the dominant sarcosaprophagous fly families are Calliphoridae and Parasarcophagidae in all the study areas. The probable reason of this dominance is the habitat and the availability of resource. The abundance of fly species is higher in village and town areas than uninhabited areas. In uninhabited sites the flies of Muscidae family are either very low or absent than other fly families. The estimated mean of lognormal is abundant in *Chrysomya megacephala* than other fly species on twelve study sites. The above relationship of these flies corroborates to that of their synanthropic index [20]. Thus, it can be inferred that species abundance study using logarithmic series and lognormal distributions has certainly strengthened the analysis of the carrion fly communities. These two analytical parameters may be used in the analysis of communities to explain γ - diversity. In the present study, α -diversity for each site is explained, and β -diversity was studied by considering different habitats (such as urban, village and uninhabited areas with different types of population density, sanitation, etc.).

The canonical correlation analysis (CcorA) is a multivariate statistical method which are used to examine the relationships among variable sets [39, 40]. The CcorA represents the involvement of fly species with their environmental factors. The CcorA expression is almost linear among sarcosaprophagous flies on all sampling areas, however, this expression significantly differ between uninhabited areas and human settlement. It may be due to the availability of same type of food sharing by them which help to form alpha guild community. The canonical correspondence analysis (CCA) also elucidates the relationship between biological assemblages of species and their corresponding environment [41, 42]. The present analysis expresses a symmetric representation of CCA between the study sites and fly species. The present analysis of γ - diversity shows that the distribution of these fly species are not uniform, instead exhibits patchiness and reflects wide range of variation in species richness due to reasonable variation in microhabitat, and the probable existence of hidden rare species [21]. It is mentioned earlier that previous survey on Calliphoridae, Muscidae and Parasarcophagidae recorded higher number of species.

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