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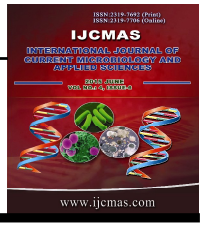

Original Research Article

Studies on the Loss of Biodiversity due to Parasitic Adaptation in Selected Fungi - An Overview

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A B S T R A C T

Fungi are eukaryotes which occur in nature as symbionts, saprophytes and parasites with their host on the basis of their mode of nutrition. The present study deals with the parasitic mode of adaptation of some selected members of fungi in different ecological conditions and their effect for the silent loss of biodiversity. Fungi show an wide range of host specificity from algae to human beings. Oomycetes and Chytrids occur mostly in marine ecosystems and parasitize on different algal host ranging from green algae to diatoms. The Zygomycetes fungi *Piptocephalis virginiana* is a mycoparasite of another zygomycetes fungi *Choanephora cucurbitarum.* Fungi parasitize on bryophytes, pteridophytes and gymnosperms in different ecological conditions. Angiosperms are the largest host of fungi. *Beauveria bassiana* is an entomopathogenic fungus but act as a host of a mycoparasitic fungus *Syspastospora parasitica. Batrachochytrium dendrobatidis* causing Chytridiomycosis of amphibians results in dramatic population decline of amphibian species. When fungi parasitize on human cause severe diseases like aspergillosis, candidiasis, coccidiomycetes, etc. About 15 species of Oomycota parasitize on algae and diatoms. Green alga *Chaetomorpha media* showed infection up to 5% by the fungus *Pontisma lagenidioides*. About 30% of amphibians of world is declined by the infection of *B. dendrobatidis* (Longcore *et al.,* 1999). The major, chronic, invasive and allergic form of aspergillosis account for around 600,000 death annually worldwide (Denning *et al.,* 2013). The mortality rate in human due to systemic candidiasis is 30-50%.From the observation it can be concluded that the studied group of fungi play an important role causing different diseases by their parasitic mode of adaptations following the silent loss of biodiversity.

Keywords

Parasitic adaptation, Biodiversity loss, Fungi

Introduction

Parasitism is one of the most common adaptation among eukaryotes and the world wide distribution of fungal parasites with their remarkable evolved modification plays an important role in nature. There are approximately 100,000 described species of fungi (Kirk *et al.,* 2008), which only represent a fraction of its diversity,

estimated to be between 1.5 and 5 million species (Hawksworth and Rossman, 1997, Blackwell 2011). Importantly, one of the hallmarks of fungi is their propensity to form intimate interactions/associations with other groups of life on Earth (Vega and Blackwell, 2005). As per latest statistics in 2010 according to IUCN Red list which incorporates the global amphibians assessment and subsequent updates focuses that about 30% of amphibians of world is declined by the infection of *B. dendrobatidis* (Longcore *et al.,* 1999). The major, chronic invasive and allergic form of Aspergillosis account for around 600,000 death annually worldwide (Denning *et al.,* 2013). The mortality rate in human due to systemic candidiasis is 30–50% (Williams and Lewis, 2011). Our present research paper deals with the investigation of the pattern of adaptation of different fungal parasites, their infectivity, aggressivity and their gradual modification showing which the silent biodiversity loss. The nature of fungal parasites and their gradual evolution indicates their adaptability runs from simple to complex organism. It is seen under investigation that the selection of host and their morphogenetic coevolution are closely related. Infectivity, aggressively, dominance and choice of host are not occurred randomly, selection of all the things is momental and modification for their evolution runs forever.

Materials and Methods

Study of organisms and their populations

The parasitology of different fungus were studied and recorded. Approximately 45 different fungal populations among which 30 major are chosen for consideration on the basis of the IUCN and published recorded data for year wise infection rate. It has also been focused on the behavioral characteristics of different parasitic fungus according to their host range from lower algal group to complex human system. On the basis of our objective we are trying to record the estimation of biodiversity loss by some of the selective parasitic fungus.

Application of various statistical tools - We calculated the derived data into the following pattern of analysis-

PDI = (No. of aggressive population) / (Total no of population) □ 100

RD = $(X/n_1) - (Z/n_2)$

RR = $(X/n_1) / (Z/n_2)$

A = PDI / 12

DEP = Differential extinction Point (Considered as a hidden factor for biodiversity loss.)

(PDI -Parasitic domain incidence, RD -Risk difference, RR- Risk ratio, X- Previous year PDI, Z= Next year PDI, n_1-Previous year aggressive population, n_2- Next year aggressive population, A- Aggressivity)

We are going through software analysis (plotting data on the respect of PDI, A, RD, DEP (as an unknown factor)) by using some statistical tools like Descriptive analysis, Clusture analysis, Ward linkage and Centroid linkage analysis between derived data, Cross correlation, Auto-correlation, Partial correlation, Frequency analysis, Proximities, Dendrogram analysis, Exploration of model and so on. The following mentioned analysis is necessary for tracing any link to biodiversity loss or extinction for future forecasting.

Establishment of proper 3d-diffractive model by software application

To make the 3D diffractive model for analysis of biodiversity loss and finding the correlation in between species richness (SR), Aggressivity index (AI), Parasitic domain

incidence (PDI), Differential extinction point (DEP), so that we are going through ORIGIN 17.0 SOFTWARE and MICROORISIS (developed by Michigan university) modern software tools. We are plotting species richness in 0.1 to 1 scale of SINCLAIR, 1997. Establishment of model is necessary for real estimation of biodiversity loss.

Parasitic fungus and their host: Some selected parasitic fungus and their host ranging from the primitive algal groups to complex carnivorous level (Table 1.1).

According to SINCLAIR 0.9 SCALE we are distributing parasitic fungal density with the relative aggressivity to different host from 2005 to 2013 and the data is plotted in the following graph.

Results and Discussion

Year wise population of different parasitic fungus with their derived aggressivity is recorded and their PDI, RD, RR & A is calculated in following manner:

The following table shows the Correlation & Descriptive analysis between PDI and Aggressivity with Anova analysis

The Wilcoxon signed rank sum test is the non-parametric version of a paired samples t-test. We are using the Wilcoxon signed rank sum test for assuming the difference between the two variables i.e. either they are in interval or normally distributed (where the difference is ordinal). We will use the same example as above, but we will not assume that the difference between read and write is either in interval or normally distributed. Correlation is significant at the 0.01 level. The significant level between the two variables is 0.008.

In the above mentioned cases we are getting the valid cluster level is 9 and it is distributed in between 4 and 5 level in two clusters and mentioned here. At first we assumed that there is something missing or hidden data as DEP but our calculation indicates that all the including data are valid.

Ward's minimum variance criterion minimizes the total within the cluster variance. At each step the pair of clusters with minimum distance between the clusters is merged. To imply this method, at each step we find the pair of clusters that leads to minimum increase in total within the cluster variance after merging. This increase is a weighted squared distance between cluster centers. At the initial step, all clusters are in singletons (clusters containing a single point). To apply a recursive algorithm under this function, the initial distance between individual objects must be proportional to squared Euclidean distance.

In Centroid Linkage Clustering, a vector is assigned to each pseudo-item, and this vector is used to compute the distances between this pseudo-item and all remaining items or pseudo-items using the same similarity metric as were used to calculate the initial similarity matrix. The initial cluster distances in Ward's minimum variance method are therefore defined to be the squared Euclidean distance between points:

$$d_{ij} = d(\{X_i\}, \{X_j\}) = \|X_i - X_j\|^2.$$

In all the upper nine cases we are analyzing by hierarchical cluster analysis and making dendrogram using centroid method and shows highest proximity (level 0 to 25) in case 3 and case 4. The minimum level of proximity is found in case 5. Zero to five level of proximity cluster is found in case of

case 5, case 8, case 6, case 1, and case 2. Five to ten level of proximity cluster is found in case 7 and case 9.It is mentioned here that the highest proximity cluster shows closest correlation and the smallest proximity cluster shows distant correlation between two clusters. Cluster proximity analysis is important for measuring significance level between two consecutive data.

Here in the following table, we are considering two variables as VAR00001 as PDI and VAR00002 as Aggressivity, and connecting the two with cross correlation to find out the significance level.

VAR00001 considering as PDI and VAR00002 considered as aggressivity and create auto correlation, and partial correlation between the two. The Ljung–Box test (named for Greta M. Ljung and George E.P.Box) is a type of statistical test of whether any of a group of autocorrelations of a time series are different from zero. Instead of testing randomness at each distinct lag, it tests the "overall" randomness based on a number of lags, and is therefore a portmanteau test.

The Ljung–Box test can be defined as follows.

H_0: The data are independently distributed (i.e. the correlations in the population from which the sample is taken are 0, so that any observed correlations in the data result from randomness of the sampling process).

H_a: The data are not independently distributed

$$Q = n(n+2)\sum_{k=1}^{h}\frac{\hat{\rho}_k^2}{n-k}$$

where n is the sample size, $\hat{\rho}_k$ is the sample autocorrelation at lag k, and h is the number of lags being tested. Under H_0 the statistic Q follows a $\chi^2_{(m)}$. For significance level α, the critical region for rejection of the hypothesis of randomness is –

$$Q > \chi^2_{1-\alpha,h}$$

In case of ANOVA analysis we are getting convergence. Convergence is due to small change or static in cluster centers. The maximum absolute coordinate changes for any centres are 0. The minimum distance between initial centres is 26.085.Box-Ljung shows that all the correlated data are positively significant. Partial auto-correlation reflects that in case of PDI and A, some data are positively significant and some are negatively correlated with A, so therefore we can assume that (A) is inversely proportional to PDI. In case of one sample correlation or paired sample correlation (with PDI and A) we are getting positively related data (where correlation is significant in 0.01 level). Non parametric correlation with Kendall's tau b and spearmann's rho shows a significant positive result. Wilcoxon signed ranked test gives the positive emphasis and shows sometimes VAR00002 > VAR00001 and sometimes VAR00002 < VAR00001 (where VAR00002 denoting A, VAR00001 denoting PDI), so we can clearly turn into the indication that (A), is an independent factor, correlation comes in different dome through phylogenetic evolved line. The 'F' tests should be used only for descriptive processes. Proximity analysis between RD and A, showing 100% valid data, and close cross linkage between the two (RD □ A). We are getting by this analysis 4 valid clusters. At a time we considered DEP as a hidden factor, now it is under valid cluster. So, therefore we are going through 3D

diffractive model and get some point of traces of DEP, which forecasts the silent biodiversity loss.

Table.1 Parasitic fungus and their host: Some selected parasitic fungus and their host ranging from the primitive algal groups to complex carnivorous level

Name Of The Parasitic Fungus	Name Of The Host
PARASITIC FUNGUS	**ALGAL HOST**
Chytridium polysiphoniae	*Centroceros clavulatum* (Raghukumar 1987a&b)
Coenomyces sp.	*Cladophora sp, Rhizoclonium* sp (Raghukumar,1994)
Ectrogella perforans	*Lichmorpha sp* (LI Wei *et al.*, 2010)
Lindra thalasiae	*Sargassum sp.* (Sharma *et al.*, 1994)
Labyrinthula sp.	*Rhizoclonium* (Raghukumar, 1994)
Olphidium rostriferum	*Cladophora frascatti* (Raghukumar 1986a, 1987a)
Olphidiopsis porphyrae	*Bangia, Porphyra* (LI Wei *et al.*, 2010)
Pontisma lagenioides	*Chaetomorpha media* (Raghukumar, 1987a & b)
Petersenia pollagaster	*Chondrus crispus.* (LI Wei *et al.*, 2010)
Pythium porphyrae	*Porphyra sp.* (LI Wei *et al.*, 2010)
Schizochytrium	*Thalassonema nitzchioides* (Gaertner,1979)
PARASITIC FUNGUS	**FUNGAL HOST**
Piptocephalis virginiana	*Choanephora cucurbitarum* (Manochaand Roya Golesorkhi, 1979)
Syspastospora parasitica	*Beauveria bassiana* (Humber et al 2004)
Verticillium biguttatum	*Rhizoctonia solani* (Van Den Boogert and Velvis, 1991)
PARASITIC FUNGUS	**BRYOPHYTEAN HOST**
Lamprospora carbonicola	*Funaria hygrometrica* (Benkert D. 1976)
Lamprospora miniata	*Barbula convoluta* (Benkert, 2009)
Neottiella albocincta	*Atrichum undulatum* (Benkert, 1987c)
Neottiella vivida	*Polytrichum strictum* (Benkert, 1995)
Octospora grimmiae	*Grimmia pulvinata* (Benkert, 2009)
Octospora humosa	*Pogonatum aloides* (Dobbeler & Itzerott,1981)
Octospora ithacaensis	*Marchantia polymorpha* (Benkert, 2009)
Octospora leucoloma	*Bryum argenteum* (Benkert, 1998c)
Typhrocybe palustris	*Sphagnum sp.* (Peck, 1872)
PARASITIC FUNGUS	**PTERODOPHYTEAN HOST**
Mixia osmundae	*Osmunda regalis, O. Cinnamomea* (Kramer,1958)
PARASITIC FUNGUS	**GYMNOSPERMEAN HOST**
Gymnosporium juniper-verginianae	*Juniperus virginiana* (Peterson, 1967)
PARASITIC FUNGUS	**ANGIOSPERMIC HOST**
Armillaria mellea	Forest and fruit trees (O'Reilly, 1963)
Albugo candida	Crucifers (Alexopoulosn *et al.*,1996)
Alternaria sp	Potato, Tomato (Rotem, 1994)
Cryphonectria parasitica	Chestnut tree (Roane *et al.*, 1986)

Helminthosporium oryzae	Rice (Alexopoulosn *et al.*,1996)
Phytophthora infestans	Potato (Ingram and Williams, 1991)
Puccinia graminis	Wheat (Roelfs and Bushnell, 1985)
Polyporus sp	Woody trees (Alexopoulosn *et al.*,1996)
Ustilago sp	Corn,Wheat (Christensen,1963; Joshi *et al.*,1983)
PARASITIC FUNGUS	**INSECT HOST**
Beauveria bassiana	Termites,White flies,Thrips,Aphids and Beetles (Bassi, 1835)
Ophiocordyceps unilateralis	*Camporotus leonardi* (Wallace, 1859)
PARASITIC FUNGUS	**AMPHIBIAN HOST**
Batrachochytrium dendrobatidis	Frogs (Longcore *et al.*, 1999)
PARASITIC FUNGUS	**HERBIVOROUS HOST**
Pithomyces chartarum	Callttle, sheep, deer, goats etc (Di Menna *et al.*, 2010)
PARASITIC FUNGUS	**CARNIVOROUS HOST**
Microsporum canis	Dogs and Cats
PARASITIC FUNGUS	**HUMAN HOST**
Aspergillus fumigatus	Bronchopulmonary of human(Jean Paul Latge,1999; Smith and Denning, 2011)
Aspergillus niger	Human ear (Vrabee *et al.*, 2006)
Candida albicans	Oral and Gastrointestinal tract (Williams and Lewis, 2011)
Coccidioides immitis	Human body (Dickson,1937)
Trychophyton rubrum	Human foot,hair,skin,nail (Kane, 1997)

Table.2 Showing year wise population of different fungus and their PDI, RD, RR and A

RESULT

YEAR	POPULATION	RANGE OF AGGRESSIVE EFFECTIVE POPULATION	PARASITIC DOMAIN INCIDENCE (PDI)	RISK DIFFERENCE(RD)	RISK RATIO (RR)	AGGRESIVITY	PEARSONS CORRELATION [BETWEEN PDI AND AGGRESIVITY]	DIFFERENTIAL EXTINCTION POINT (DEP)
2005	12000 [j.capelle & c.neema]	8075	67.292	-	-	5.607	r = 0.999999926	we are considering differential extinction point as a hidden data, so we are ploting it as an unknown factor for biodiversity loss
2006	13000 [knogge et.al]	9345	71.885	0.00064	1.08322	5.99		
2007	14500 [Barron et.al]	10000	68.966	0.00079	1.11449	5.747		
2008	16000 [Berger et.al]	12765	79.781	0.00065	1.104	6.648		
2009	16987 [voyles et.al]	14567	85.754	0.00036	1.06112	7.146		
2010	18742 [Bromenshenk et.al]	15678	83.652	0.00055	1.103	6.971		
2011	19567 [Evens & Hughes et.al]	17456	89.211	0.00023	1.04501	7.434		
2012	22675 [Huger et.al]	19800	87.321	0.0007	1.15873	7.276		
2013	23000 [Meirinho.P.A et.al]	21456	93.287	0.00006	1.01379	7.773		

(* PDI –Parasitic Domain Incidence. RD – Risk Difference. RR- Risk ratio. A- Aggessivity.)

Table.3 Showing Correlation & Descriptive analysis between PDI and Aggressivity with Anova analysis

```
T-TEST
  /TESTVAL=0
  /MISSING=ANALYSIS
  /VARIABLES=VAR00001 VAR00002
  /CRITERIA=CI(.95).
```

```
CORRELATIONS
  /VARIABLES=VAR00001 VAR00002
  /PRINT=TWOTAIL NOSIG
  /STATISTICS DESCRIPTIVES XPROD
  /MISSING=PAIRWISE.
```

T-Test

[DataSet0]

One-Sample Statistics

	N	Mean	Std. Deviation	Std. Error Mean
VAR00001	9	80.7943	9.38679	3.12893
VAR00002	9	6.7324	.78218	.26073

One-Sample Test

	Test Value = 0					
					95% Confidence Interval of the Difference	
	t	df	Sig. (2-tailed)	Mean Difference	Lower	Upper
VAR00001	25.822	8	.000	80.79433	73.5790	88.0097
VAR00002	25.822	8	.000	6.73244	6.1312	7.3337

Correlations

[DataSet0]

Descriptive Statistics

	Mean	Std. Deviation	N
VAR00001	80.7943	9.38679	9
VAR00002	6.7324	.78218	9

Correlations

		VAR00001	VAR00002
VAR00001	Pearson Correlation	1	1.000**
	Sig. (2-tailed)		.000
	Sum of Squares and Cross-products	704.894	58.737
	Covariance	88.112	7.342
	N	9	9
VAR00002	Pearson Correlation	1.000**	1
	Sig. (2-tailed)	.000	
	Sum of Squares and Cross-products	58.737	4.894
	Covariance	7.342	.612
	N	9	9

** Correlation is significant at the 0.01 level (2-tailed).

(VAR00001- PDI, VAR00002- Aggressivity)

Table.4 Showing Non-parametric Correlations between PDI & A

```
NONPAR CORR
  /VARIABLES=VAR00001 VAR00002
  /PRINT=BOTH TWOTAIL NOSIG
  /MISSING=PAIRWISE.
```

Nonparametric Correlations

[DataSet0]

Correlations

			VAR00001	VAR00002
Kendall's tau_b	VAR00001	Correlation Coefficient	1.000	1.000**
		Sig. (2-tailed)	.	.
		N	9	9
	VAR00002	Correlation Coefficient	1.000**	1.000
		Sig. (2-tailed)	.	.
		N	9	9
Spearman's rho	VAR00001	Correlation Coefficient	1.000	1.000**
		Sig. (2-tailed)	.	.
		N	9	9
	VAR00002	Correlation Coefficient	1.000**	1.000
		Sig. (2-tailed)	.	.
		N	9	

**. Correlation is significant at the 0.01 level (2-tailed).

```
NPAR TESTS
  /WILCOXON=VAR00001 WITH VAR00002 (PAIRED)
  /MISSING ANALYSIS.
```

NPar Tests

[DataSet0]

Wilcoxon Signed Ranks Test

Ranks

		N	Mean Rank	Sum of Ranks
VAR00002 - VAR00001	Negative Ranks	9[a]	5.00	45.00
	Positive Ranks	0[b]	.00	.00
	Ties	0[c]		
	Total	9		

a. VAR00002 < VAR00001

b. VAR00002 > VAR00001

c. VAR00002 = VAR00001

Test Statistics[b]

	VAR00002 - VAR00001
Z	-2.666[a]
Asymp. Sig. (2-tailed)	.008

a. Based on positive ranks.

b. Wilcoxon Signed Ranks Test

Table.5 Showing Cluster analysis between PDI & A

```
QUICK CLUSTER VAR00001 VAR00002
  /MISSING=LISTWISE
  /CRITERIA=CLUSTER(2) MXITER(10) CONVERGE(0)
  /METHOD=KMEANS(NOUPDATE)
  /SAVE  DISTANCE
  /PRINT INITIAL ANOVA CLUSTER DISTAN.
```

Quick Cluster

[DataSet0]

Initial Cluster Centers

	Cluster	
	1	2
VAR00001	67.29	93.29
VAR00002	5.61	7.77

Iteration History[a]

	Change in Cluster...	
Iteration	1	2
1	4.705	5.461
2	.000	.000

a. Convergence achieved due to no or small change in cluster centers. The maximum absolute coordinate change for any center is .000. The current iteration is 2. The minimum distance between initial centers is 26.085.

Number of Cases in each Cluster

Cluster	1	4.000
	2	5.000
Valid		9.000
Missing		.000

Cluster Membership

Case Number	Cluster	Distance
1	1	4.705
2	1	.096
3	1	3.025
4	1	7.827
5	2	2.098
6	2	4.207
7	2	1.371
8	2	.526
9	2	5.461

Final Cluster Centers

	Cluster	
	1	2
VAR00001	71.98	87.85
VAR00002	6.00	7.32

Distances between Final Cluster Centers

Cluster	1	2
1		15.919
2	15.919	

ANOVA

	Cluster		Error			
	Mean Square	df	Mean Square	df	F	Sig.
VAR00001	559.259	1	20.805	7	26.881	.001
VAR00002	3.884	1	.144	7	26.899	.001

The F tests should be used only for descriptive purposes because the clusters have been chosen to maximize the differences among cases in different clusters. The observed significance levels are not corrected for this and thus cannot be interpreted as tests of the hypothesis that the cluster means are equal.

Table.6 Showing Cluster analysis through Ward Linkage and Centroid Linkage

```
CLUSTER  VAR00001 VAR00002
  /METHOD WARD
  /MEASURE=SEUCLID
  /PRINT SCHEDULE
  /PRINT DISTANCE
  /PLOT DENDROGRAM VICICLE.
```

Cluster

```
[DataSet0]
```

Case Processing Summary[a]

Cases					
Valid		Missing		Total	
N	Percent	N	Percent	N	Percent
9	100.0	0	.0	9	100.0

a. Ward Linkage

Proximity Matrix

Case	Squared Euclidean Distance								
	1	2	3	4	5	6	7	8	9
1	.000	21.242	2.822	157.059	343.214	269.510	483.780	403.946	680.432
2	21.242	.000	8.580	62.780	193.685	139.425	302.275	239.924	461.225
3	2.822	8.580	.000	117.776	283.794	217.177	412.706	339.244	585.616
4	157.059	62.780	117.776	.000	35.925	15.089	89.543	57.246	183.678
5	343.214	193.685	283.794	35.925	.000	4.449	12.034	2.472	57.139
6	269.510	139.425	217.177	15.089	4.449	.000	31.117	13.555	93.476
7	483.780	302.275	412.706	89.543	12.034	31.117	.000	3.597	16.729
8	403.946	239.924	339.244	57.246	2.472	13.555	3.597	.000	35.840
9	680.432	461.225	585.616	183.678	57.139	93.476	16.729	35.840	.000

Ward Linkage

Agglomeration Schedule

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	5	8	1.236	0	0	3
2	1	3	2.647	0	0	5
3	5	7	7.445	1	0	6
4	4	6	14.990	0	0	7
5	1	2	24.460	2	0	8
6	5	9	50.379	3	0	7
7	4	5	119.529	4	6	8
8	1	4	709.789	5	7	0

Centroid Linkage

Agglomeration Schedule

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	5	8	.000	0	0	3
2	1	3	.001	0	0	4
3	5	7	.008	1	0	6
4	1	2	.018	2	0	8
5	4	6	.019	0	0	6
6	4	5	.047	5	3	7
7	4	9	.096	6	0	8
8	1	4	.434	4	7	0

Table.7 Showing Cross Correlation between PDI & A

```
CCF
  /VARIABLES=VAR00001 VAR00002
  /NOLOG  /MXCROSS 7.
```

VAR00001 with VAR00002

CCF

[DataSet0]

Model Description

Model Name		MOD_1
Series Name	1	VAR00001
	2	VAR00002
Transformation		None
Non-Seasonal Differencing		0
Seasonal Differencing		0
Length of Seasonal Period		No periodicity
Range of Lags	From	-7
	To	7
Display and Plot		All lags

Applying the model specifications from MOD_1

Case Processing Summary

Series Length		9
Number of Excluded Cases Due to	User-Missing Value	0
	System-Missing Value	0
Number of Valid Cases		9
Number of Computable Zero-Order Correlations After Differencing		9

Cross Correlations

Series Pair:VAR00001 with VAR00002

Lag	Cross Correlation	Std. Error[a]
-7	-.283	.707
-6	-.453	.577
-5	-.289	.500
-4	-.194	.447
-3	-.007	.408
-2	.387	.378
-1	.578	.354
0	1.000	.333
1	.578	.354
2	.387	.378
3	-.007	.408
4	-.194	.447
5	-.289	.500
6	-.453	.577
7	-.283	.707

a. Based on the assumption that the series are not cross correlated and that one of the series is white noise.

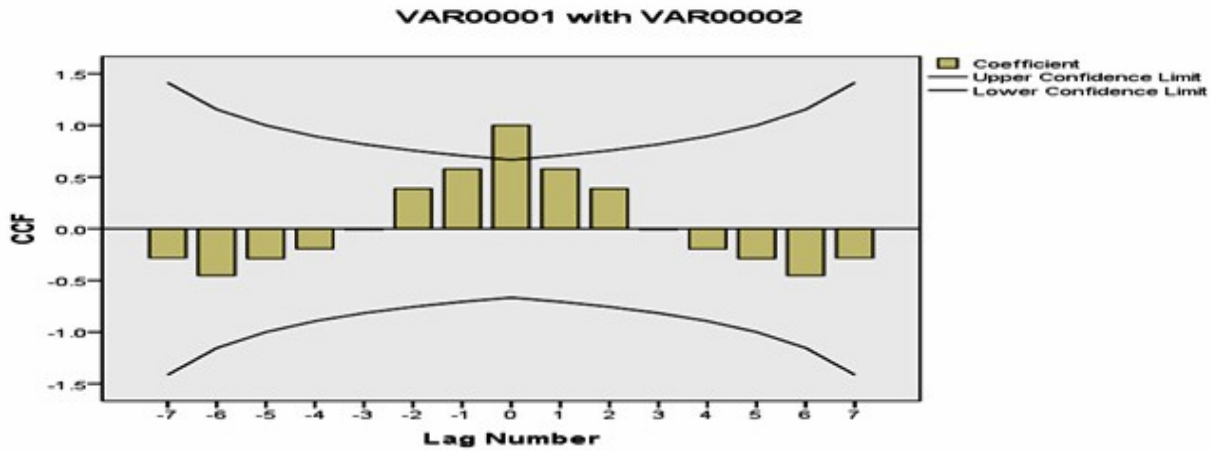


Table.8 Showing Auto Correlation between PDI & A

```
ACF VARIABLES=VAR00001 VAR00002
  /NOLOG
  /MXAUTO 16
  /SERROR=MA
  /PACF.
```

ACF

```
[DataSet0]
```

Model Description

Model Name		MOD_2
Series Name	1	VAR00001
	2	VAR00002
Transformation		None
Non-Seasonal Differencing		0
Seasonal Differencing		0
Length of Seasonal Period		No periodicity
Maximum Number of Lags		16
Process Assumed for Calculating the Standard Errors of the Autocorrelations		MA with the order equal to the lag number minus one (the Bartlett approximation is used)[a]
Display and Plot		All lags

Applying the model specifications from MOD_2

a. Not applicable for calculating the standard errors of the partial autocorrelations.

Case Processing Summary

		VAR00001	VAR00002
Series Length		9	9
Number of Missing Values	User-Missing	0	0
	System-Missing	0	0
Number of Valid Values		9	9
Number of Computable First Lags		8	8

VAR00001

Autocorrelations

Series:VAR00001

Lag	Autocorrelation	Std. Error[a]	Box-Ljung Statistic Value	df	Sig.[b]
1	.578	.333	4.132	1	.042
2	.387	.430	6.249	2	.044
3	-.007	.468	6.250	3	.100
4	-.194	.468	6.994	4	.136
5	-.289	.476	9.055	5	.107
6	-.453	.495	15.838	6	.015
7	-.283	.540	19.800	7	.006

a. The underlying process assumed is MA with the order equal to the lag number minus one. The Bartlett approximation is used.

b. Based on the asymptotic chi-square approximation.

VAR00001

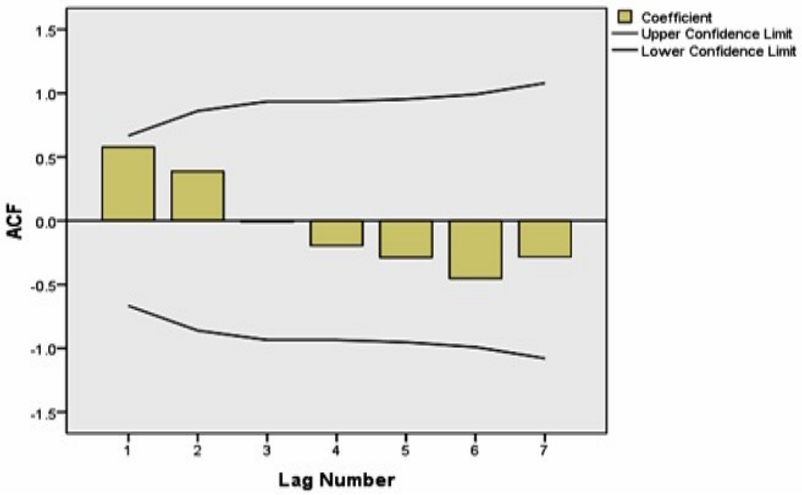
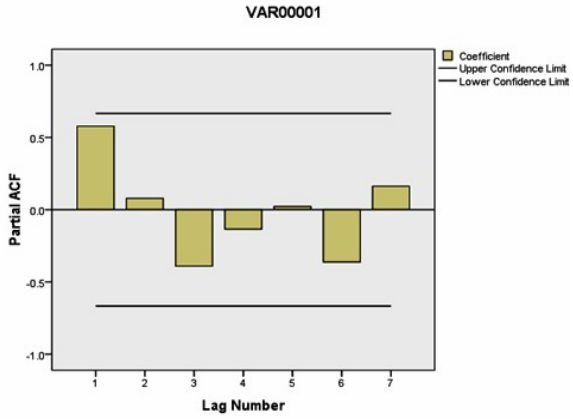


Table.9 Showing comparison between auto correlation and partial auto correlation of PDI & A

Partial Autocorrelations

Series:VAR00001

Lag	Partial Autocorrelation	Std. Error
1	.578	.333
2	.080	.333
3	-.391	.333
4	-.135	.333
5	.022	.333
6	-.362	.333
7	.163	.333



VAR00002

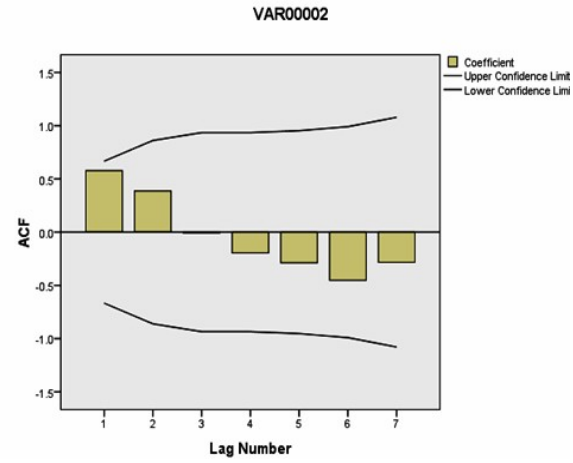
Autocorrelations

Series:VAR00002

Lag	Autocorrelation	Std. Error[a]	Box-Ljung Statistic		
			Value	df	Sig.[b]
1	.578	.333	4.133	1	.042
2	.387	.430	6.250	2	.044
3	-.007	.468	6.251	3	.100
4	-.194	.468	6.996	4	.136
5	-.289	.476	9.059	5	.107
6	-.453	.495	15.839	6	.015
7	-.283	.540	19.799	7	.006

a. The underlying process assumed is MA with the order equal to the lag number minus one. The Bartlett approximation is used.

b. Based on the asymptotic chi-square approximation.



Partial Autocorrelations

Series:VAR00002

Lag	Partial Autocorrelation	Std. Error
1	.578	.333
2	.080	.333
3	-.391	.333
4	-.135	.333
5	.022	.333
6	-.362	.333
7	.162	.333

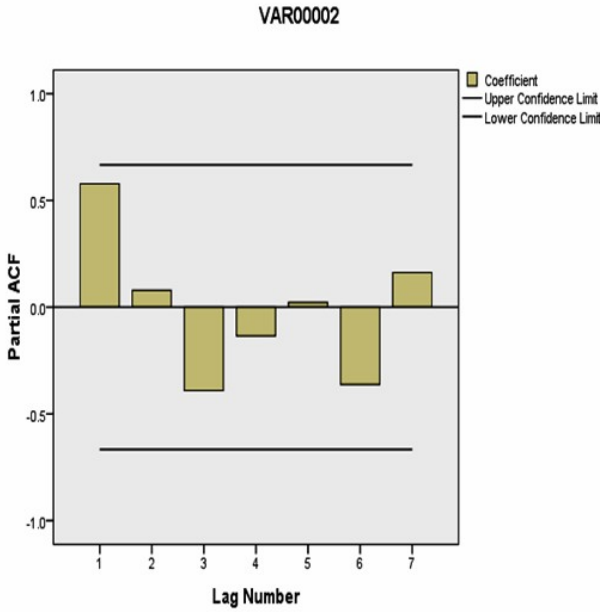


Table.10 Showing proximity analysis between RD & A

Frequency Table

VAR00001

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	-	1	11.1	11.1	11.1
	0.00006	1	11.1	11.1	22.2
	0.00023	1	11.1	11.1	33.3
	0.00036	1	11.1	11.1	44.4
	0.00055	1	11.1	11.1	55.6
	0.00064	1	11.1	11.1	66.7
	0.00065	1	11.1	11.1	77.8
	0.0007	1	11.1	11.1	88.9
	0.00079	1	11.1	11.1	100.0
	Total	9	100.0	100.0	

VAR00002

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	5.61	1	11.1	11.1	11.1
	5.75	1	11.1	11.1	22.2
	5.99	1	11.1	11.1	33.3
	6.65	1	11.1	11.1	44.4
	6.97	1	11.1	11.1	55.6
	7.15	1	11.1	11.1	66.7
	7.28	1	11.1	11.1	77.8
	7.43	1	11.1	11.1	88.9
	7.77	1	11.1	11.1	100.0
	Total	9	100.0	100.0	

```
PROXIMITIES   VAR00002
  /MATRIX OUT('C:\Users\sidd\AppData\Local\Temp\spss1404\spssclus.tmp')
  /VIEW=CASE
  /MEASURE=ABSOLUTE SEUCLID
  /PRINT NONE
  /STANDARDIZE=VARIABLE NONE.
```

Proximities

```
[DataSet0]
```

Case Processing Summary[a]

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
	9	100.0%	0	.0%	9	100.0%

a. Absolute Squared Euclidean Distance used

```
  /MATRIX IN('C:\Users\...AppData\Local\Temp\spss1404\spssclus.tmp')
  /METHOD BAVERAGE
  /PRINT SCHEDULE
  /PRINT DISTANCE
  /PLOT DENDROGRAM HICICLE.
```

Proximity Matrix

	Absolute Squared Euclidean Distance								
Case	1:Case 1	2:Case 2	3:Case 3	4:Case 4	5:Case 5	6:Case 6	7:Case 7	8:Case 8	9:Case 9
1:Case 1	.000	.147	.020	1.084	2.369	1.860	3.338	2.786	4.692
2:Case 2	.147	.000	.059	.433	1.336	.962	2.085	1.654	3.179
3:Case 3	.020	.059	.000	.812	1.957	1.498	2.846	2.338	4.105
4:Case 4	1.084	.433	.812	.000	.248	.104	.618	.394	1.266
5:Case 5	2.369	1.336	1.957	.248	.000	.031	.083	.017	.393
6:Case 6	1.860	.962	1.498	.104	.031	.000	.214	.093	.643
7:Case 7	3.338	2.085	2.846	.618	.083	.214	.000	.025	.115
8:Case 8	2.786	1.654	2.338	.394	.017	.093	.025	.000	.247
9:Case 9	4.692	3.179	4.105	1.266	.393	.643	.115	.247	.000

This is a dissimilarity matrix

Average Linkage (Between Groups)

Agglomeration Schedule

	Cluster Combined			Stage Cluster First Appears		
Stage	Cluster 1	Cluster 2	Coefficients	Cluster 1	Cluster 2	Next Stage
1	5	8	.017	0	0	3
2	1	3	.020	0	0	4
3	5	7	.054	1	0	6
4	1	2	.103	2	0	8
5	4	6	.104	0	0	7
6	5	9	.252	3	0	7
7	4	5	.438	5	6	8
8	1	4	2.185	4	7	0

Fig.1 X-axis with the average relative parasite richness & Y-axis with consecutive year

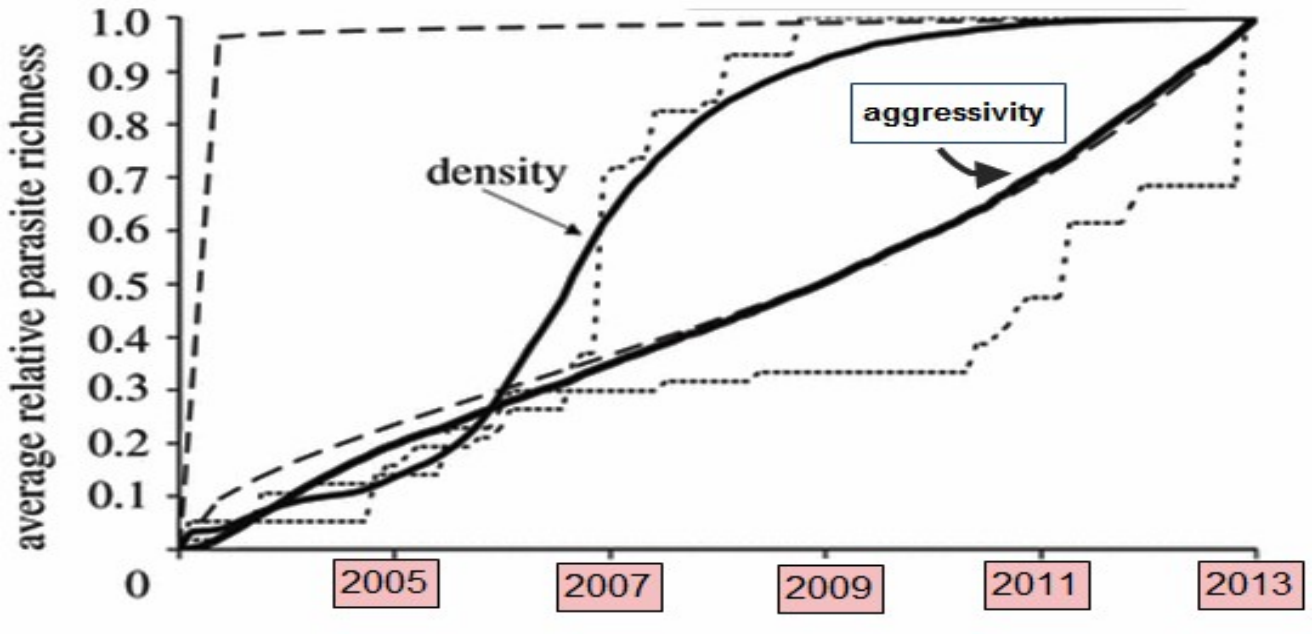


Fig.2 X-axis with two different variables i.e. Original Population (OP) & Expected Population (EP); Y-axis with consecutive year

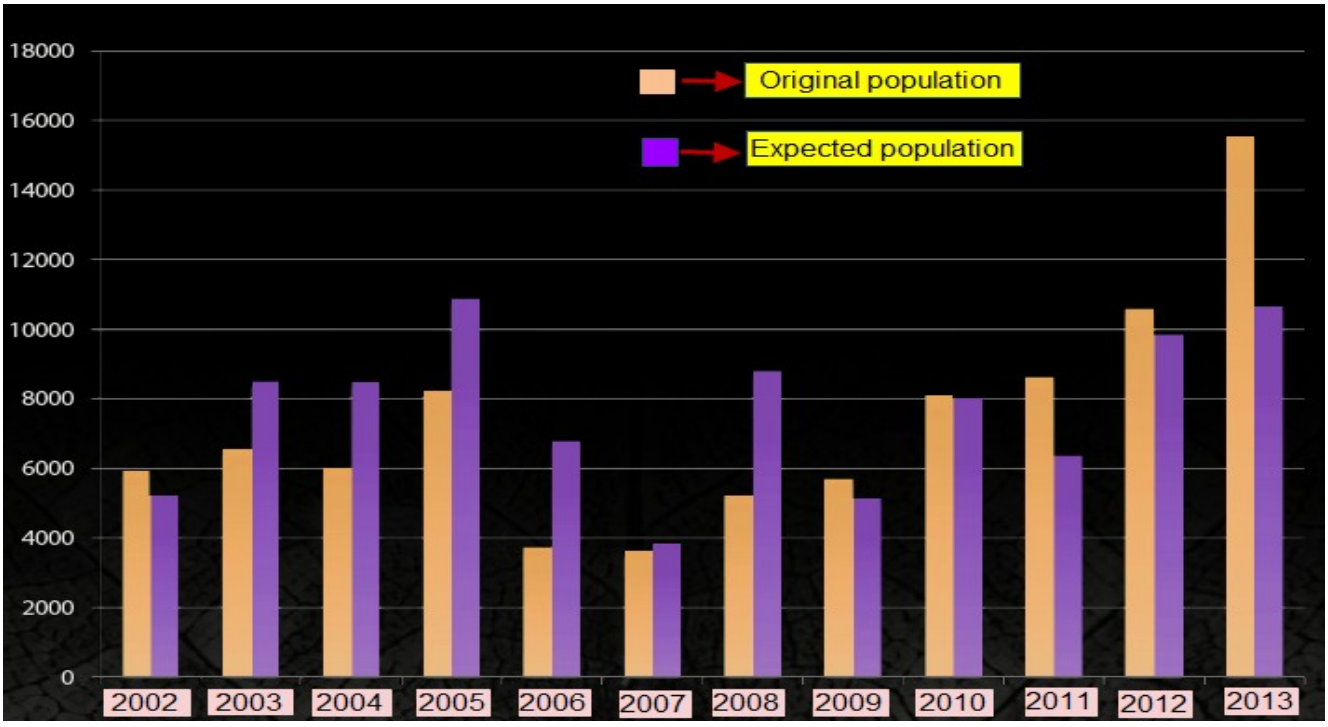
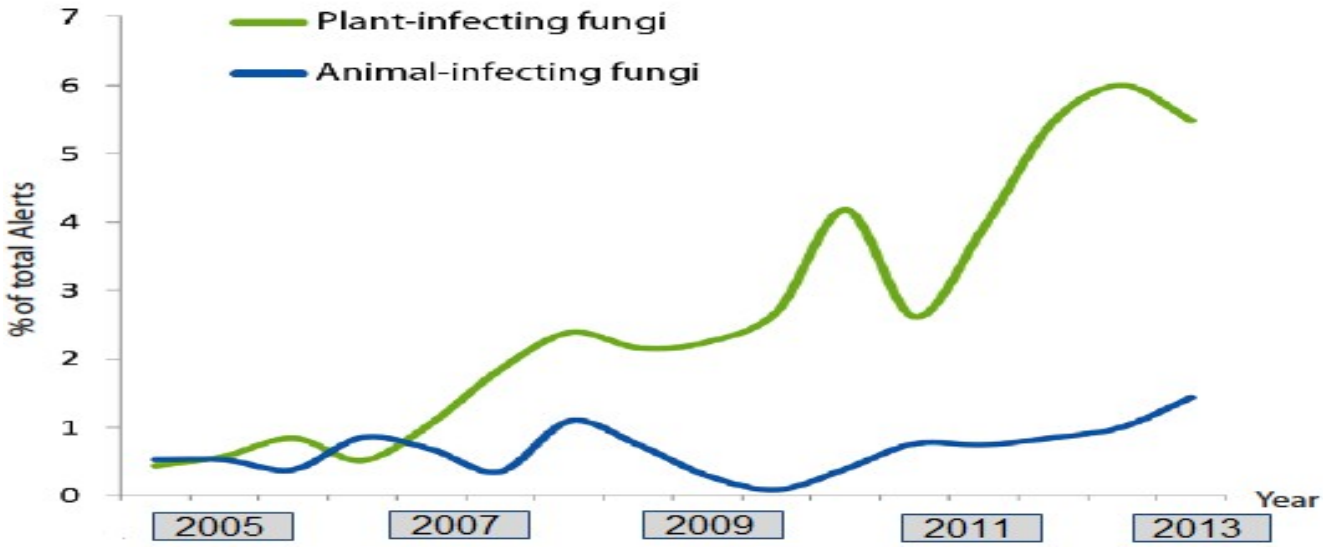
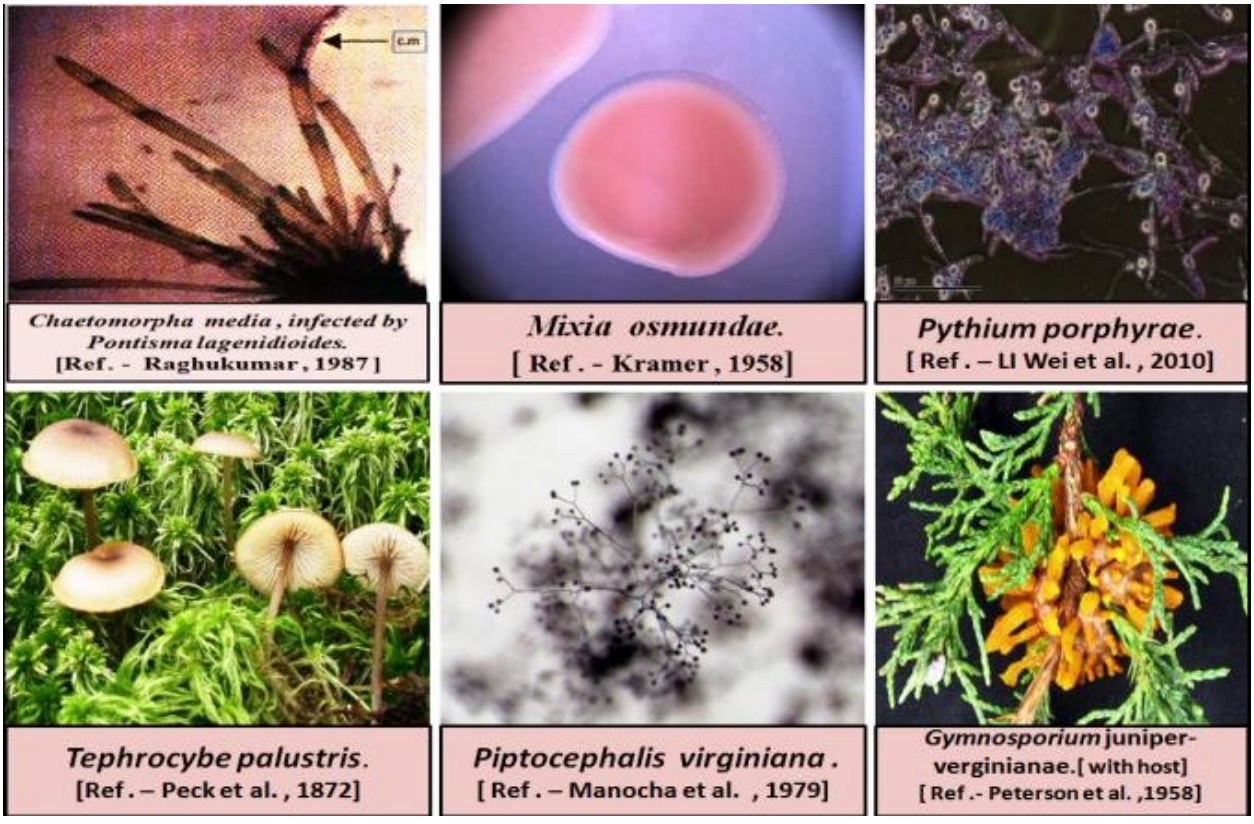
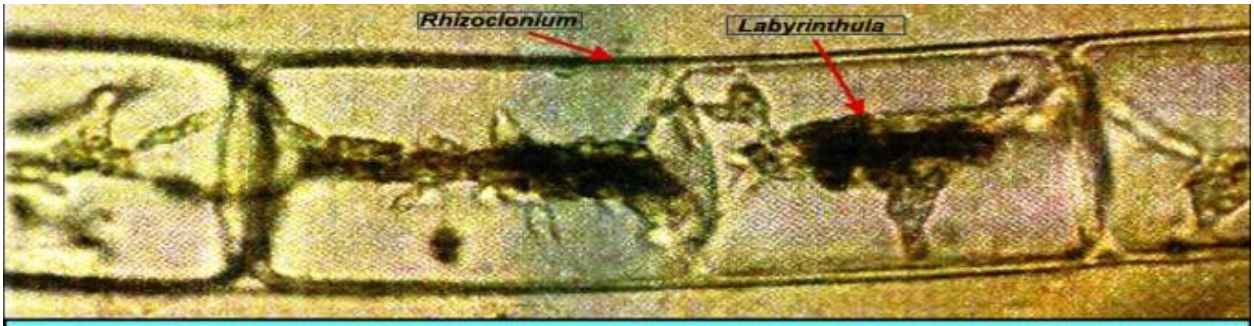


Fig.3 X-axis with rate of infection on plants and animals; Y-axis with consecutive year





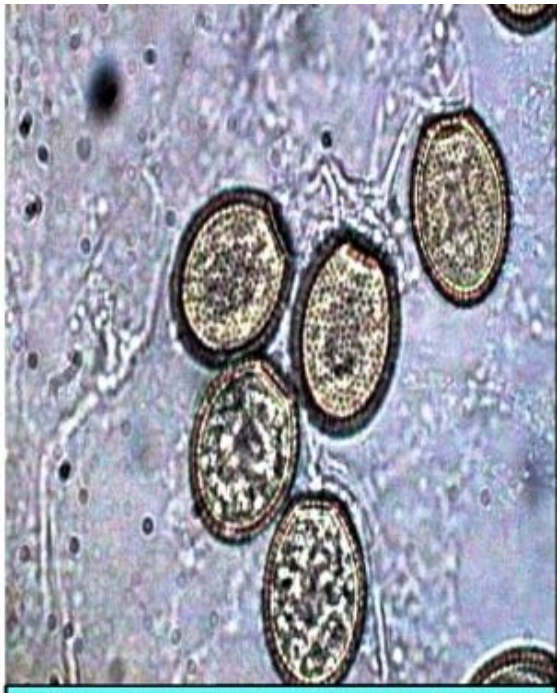


Labyrinthula sp. parasitize on ***Rhizoclonium*** . [Ref. – Raghukumar , 1994]

Cryphonectria parasitica. (ON CHESTNUT TREE.) [Ref. – Roane et al. ,1986]

Puccinia graminis . (CAUSES STEM RUST OF WHEAT.) [Ref. – Roelfs. et al. 1985]

INFECTION BY ***Batrachochytrichum dendrobatidis*** IN FROGS. [Ref. – Longcore et al.2010]

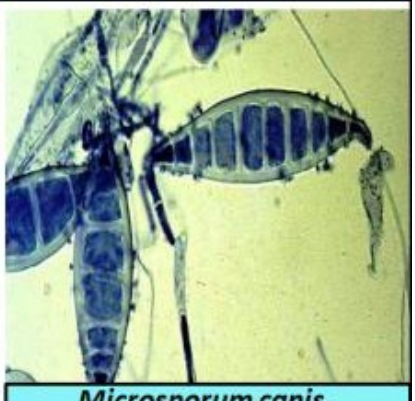


Batrachochytrichum dendrobatidis .
[Ref. – Longcore et al. , 2010]

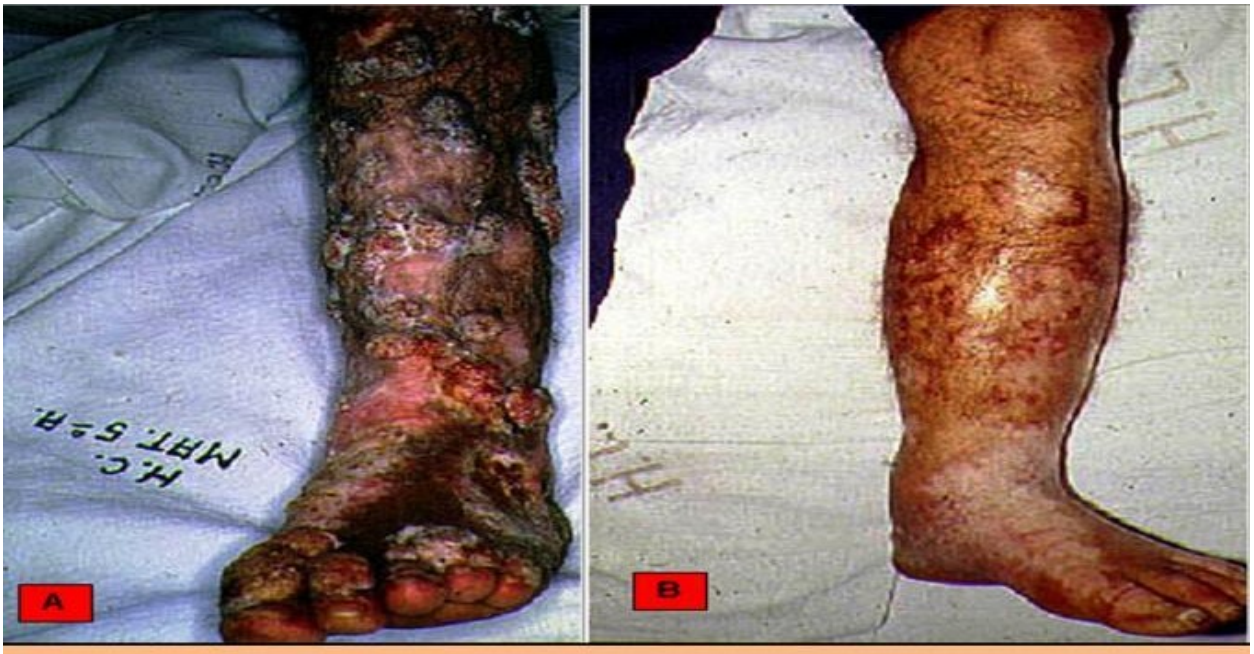
DEVASTATING OUTBREAK OF *Beauveria bassiana* ON LEPIDOPTERON INSECTS.
[Ref. – Bassi et al. , 1835]

Pithomyces chartarum .
(PARASITIZE ON HERBIVORES.)
[Ref. – Menna et al. , 2010]

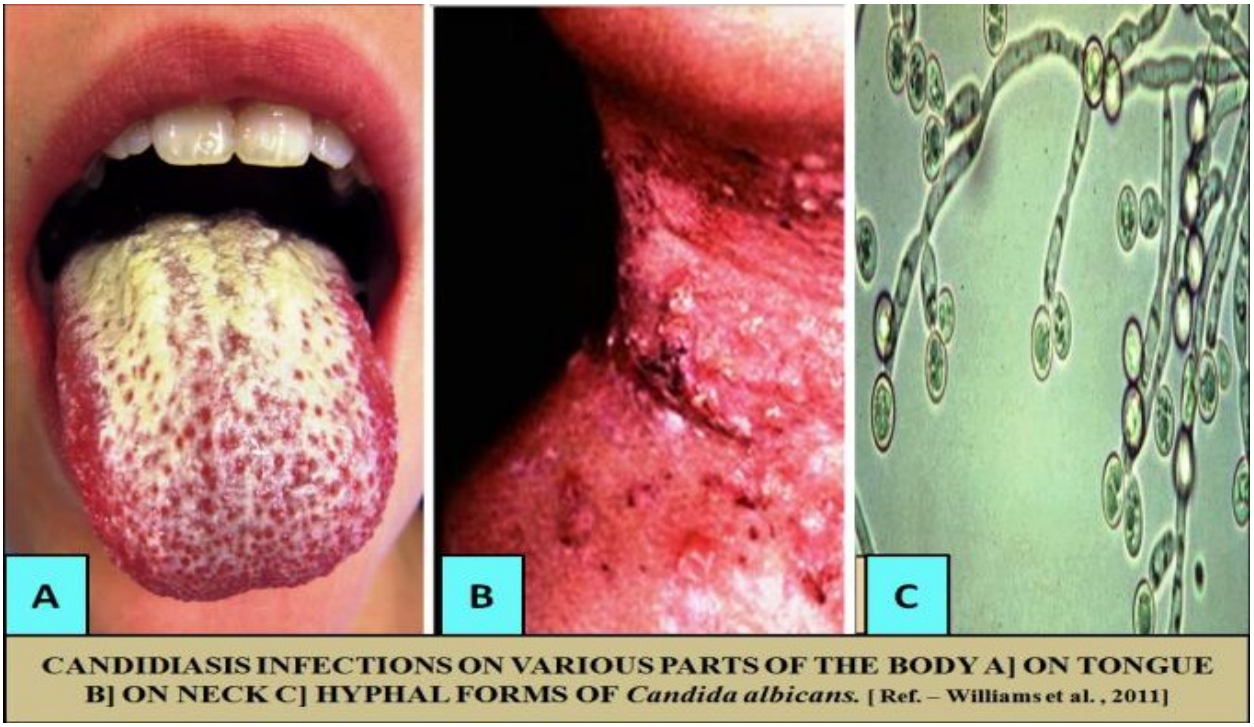
HOST -*Camporotus leonardi* (Carpenter ant) PARASITE -*Ophiocordyceps unilateralis.* [Ref. – Wallace, 1859]



Microsporum canis .
(PARASITIZE ON CARNIVORES)[Ref. – CNCM / www.provlab .ab.ca/mycol/tutorials/derm/ dermhome.htm]

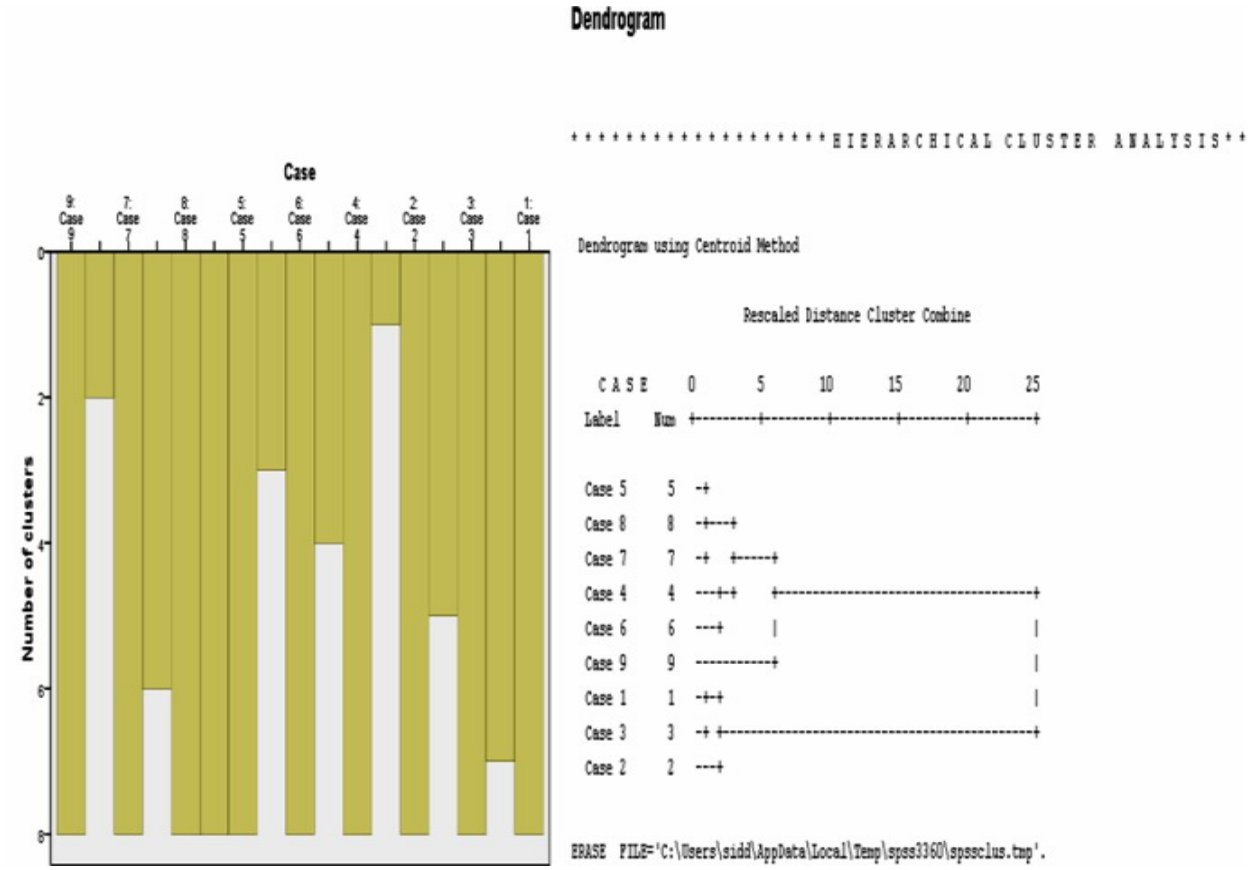


A] *Fonsecae pedrosoi* INFECT OF LEFT LEG . B] SAME LEG AFTER DAILY TREATMENT WITH INTRACONAZOLE. [Ref.- Glenn Bulmer, From www. Medicalmycology.net.]



CANDIDIASIS INFECTIONS ON VARIOUS PARTS OF THE BODY A] ON TONGUE B] ON NECK C] HYPHAL FORMS OF *Candida albicans*. [Ref. – Williams et al. , 2011]

Fig.4 Showing the Dendrogram analysis of the data



* H I E R A R C H I C A L C L U S T E R A N A L Y S I S * *

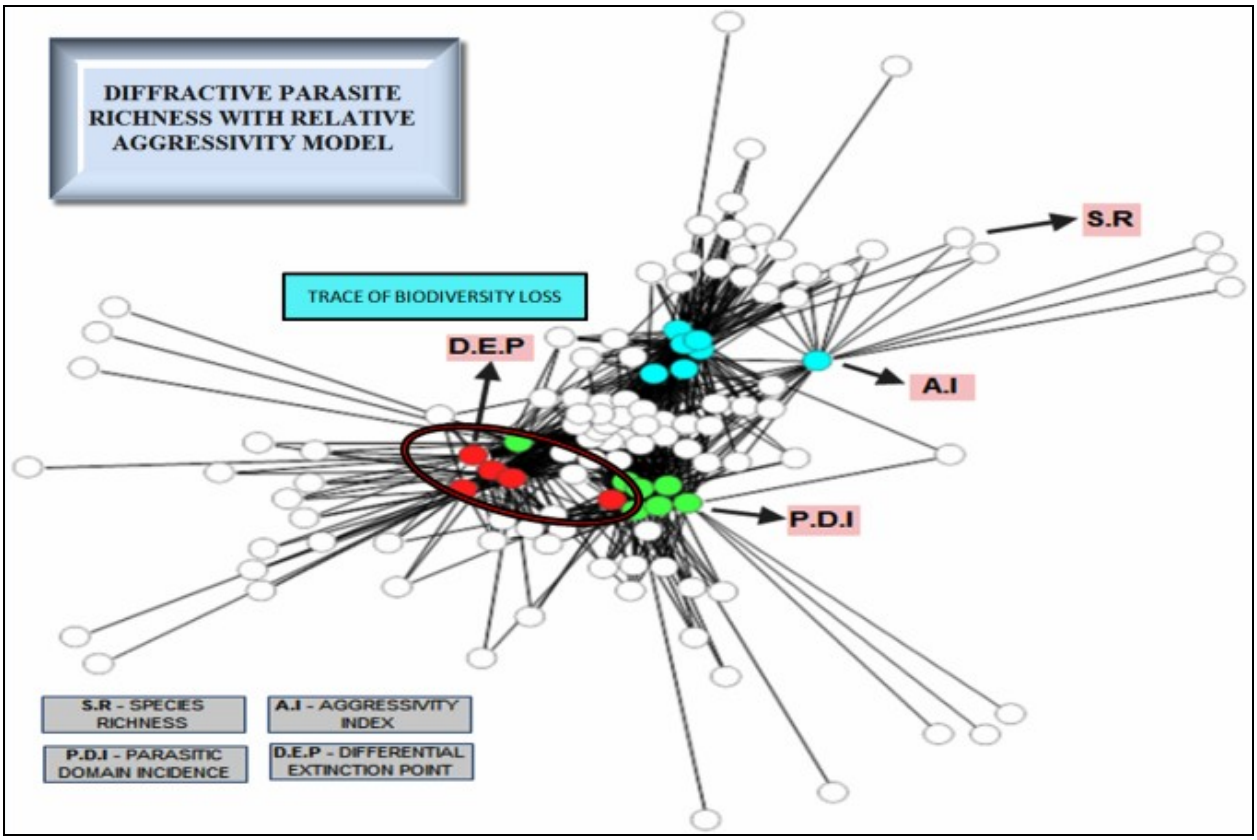
Dendrogram using Centroid Method

Rescaled Distance Cluster Combine

CASE Label	Num	0	5	10	15	20	25
Case 5	5	-+					
Case 8	8	-+---+					
Case 7	7	-+ +-----+					
Case 4	4	---+-+	+----------	----------	----------	----------	----------+
Case 6	6	---+	|				|
Case 9	9	----------+					|
Case 1	1	-+-+					|
Case 3	3	-+ +----------	----------	----------	----------	----------	----------+
Case 2	2	---+					

ERASE FILE='C:\Users\sidd\AppData\Local\Temp\spss3360\spssclus.tmp'.

Fig.5 Exploration of 3d-diffractive model and trace of silent biodiversity loss



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