STATISTICAL ANALYSIS OF APPLETON-WHITTELL RESEARCH RANCH INSECT COMMUNITY DATA

Prepared for

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January 2003

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Statistical Report
Appleton-Whittell Research Ranch Insect Community Data

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STATISTICAL ANALYSIS OF APPLETON-WHITTELL RESEARCH RANCH INSECT COMMUNITY DATA

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II. EXECUTIVE SUMMARY

This is a report of the results of statistical analysis of insect community data collected in grazed and ungrazed sampling sites on the Appleton-Whittell Research Ranch and nearby ranches. The data were received from the Dr. Sandy DeBano, OSU Hermiston Agricultural Research Station. Data to be analyzed were counts of species collected in pitfall traps and in sweep nets on the sampling sites. Questions of interest were defined after an initial consultation and discussion. A list of those questions of interest is included in this report.

The report includes a summary of the project and discussion of the structure of the data, the explanatory and response variables, and the statistical procedures employed in the analysis.

After reducing the number of species for analysis to those defined as not rare, the data were analyzed using multivariate techniques to discover patterns in the distributions of species. Specifically, the data were first analyzed using Principal Coordinate Analysis (ORD) and Principal Component Analysis (PCA) to find general ordination patterns of the sites in species space. The resulting ORD configurations were rescaled using Nonmetric Multidimensional Scaling (NMDS). The data were also inspected using cluster and Two-Way Indicator Species Analysis (TWINSPAN) techniques to find spatial relationships between logical groups sampling sites. The affinities of the members of the groups and distance relationships between groups were investigated using

Multigroup Discriminant Analysis. The results of these analyses are reported and statistical inferences discussed.

Data decks, analysis output files, and electronic copies of this report are provided on an accompanying CD. This work is in partial fulfillment of a Professional Services Contract 117077.

III. INTRODUCTION

Summary of the experiment and objectives

This was a study designed to investigate the patterns of insect diversity and species' distributions in grazed and ungrazed plots on several ranches in southeastern Arizona. The work was part of a PhD research project conducted in 1993 and 1994. The goal was to discover new information that would be useful in developing effective management plans for conservation grasslands and the species living in them.

Questions of Interest

1. What species characterize the community composition at grazed and ungrazed sites in southeastern Arizona?
2. What species of insects may be particularly sensitive to grazing pressure?
3. What is the strength of the association within groups?
4. What is the strength of the association between groups?
5. What insect species contribute to the variations between groups?

Populations of Interest

The populations of interest are the total counts of adult insect species collected in pitfall traps and sweep net samples on eight grazed and ungrazed ranch plots in southeastern Arizona.

Sampling Design

Four 30 X 30 m ungrazed sites (not grazed by livestock since 1968) on the Audubon's Appleton-Whittell Research Ranch were paired with 4 similar sites on adjacent active cattle ranches that completely surround it. Sites were paired based on similarities in elevation, topography, soil type, and vegetation type (except for those differences in vegetation due to grazing), and each pair of sites was separated by between 1.0 to 1.8 km. Two of the grazed sites (Sites 2-D and 4-D) were grazed using holistic range management practice, and the other two (Sites 1-D and 3-D) were grazed under more traditional grazing practices.

Insects were sampled at the 8 sites approximately biweekly with pitfall traps and sweep nets three times in 1993 (September-November) and four times in 1994 (June-August). Each site was sampled once with 8 pitfall traps per sampling session. Sweep net sampling efforts were made once a day for 4 days per sampling session, so that each site could be sampled once during 4 time periods throughout the day: mid-morning, late-morning, early afternoon, and late afternoon. Each sampling effort consisted of 100 arc-shaped sweeps. Ants were eliminated from the analysis.

Data Matrix

Insects sampled by pitfall traps and sweep net were separated to morphological species (i.e., based on morphological similarity) and data from both years were combined because of the non-overlapping temporal distribution of sampling (i.e., different parts of the season were sampled each year). All samples from pitfall traps were analyzed. Sweep net

sample analyses include all the most common species (greater than 50 individuals for all sampling sessions combined) for both years, all Acrididae (short-horned grasshoppers) for both years, and all insects collected in the first sampling session (September, 1993).

Two data sets were made from the samples, 1) pitfall trap species, and 2) sweep net species.

Structure of the Experiment

Experimental Units

Experimental units are eight plots.

Response variables

Counts of adult insect species in pitfall traps and in sweep net samples.

Explanatory variables

Grazed and ungrazed treatments

IV. STATISTICAL PROCEDURES

Summary Statistics

The original pitfall trap data set contained abundance information for 101 species. The total abundance of each species was tabulated from the data over the entire sampling period and species were sorted in descending order according to abundance.

The original sweep net data set contained abundance information for 239 species. The total abundance of each species was tabulated from the data over the entire sampling period and species were sorted in descending order according to abundance.

Dataset Reduction

Some of the species were present at very low abundance, an expected condition in biologically diverse communities. Low abundance may indicate truly rare species (i.e., those whose abundance is typically low in the sampled habitats) or species that occur temporarily or accidentally as migrating or vagrant species. Many forest-dwelling arthropods are vagile, and stragglers are often found in habitats where they perform no regular ecological function (or where they are not able to reproduce) (Niemelä 1997).

Non-abundant species are typically removed from data analyzed with multivariate techniques because the occurrences are usually due more to chance than some underlying ecological condition (i.e., the absence of a

"rare species" in site traps may be due to chance, not the absence of the species at that site). Sampling artifacts may influence analyses, because outliers (low abundance of rare or vagrant species) increase the statistical "noise", often masking underlying patterns (Gaston 1994).

Pilanka (1986) recommends eliminating non-abundant species from multivariate analyses, only after careful consideration and with standards applied to all species. After consultation with Dr. DeBano, it was decided to identify pitfall trap species whose average abundance was less than 1.5% of the total pitfall trap captures as non-abundant and candidates for removal from the multivariate analysis. Twenty species were left in the pitfall trap data. Three additional species were eliminated because they occurred at only one sampling site. Seventeen species were used in the Pitfall Trap Data analysis.

Sweep net species whose average abundance was less than or equal to 0.15% of the total sweep net captures were identified as non-abundant and candidates for removal from the multivariate analysis. Forty-one species were left for the sweep net data analysis.

Similarity Indices

Similarity indices measure the ecological relationship of sites based on the abundance of species collected at those sites. The measurements are expressed in the form of an association coefficient. The result is a site-by-site association matrix. More than four dozen similarity indices have been developed and the selection of which to apply is largely personal (Krebs 1989). The performance of similarity indices may be influenced by sample size, number of rare species, and species diversity, and some indices may perform better than others depending on the nature of the community information. Several reviews have described the application of similarity indices and offer guides for their use (e.g., Janson and Vegelius 1981, Wolda 1981, Hubalek 1982, Krebs 1989, Pimentel 1993).

The indices can be calculated from binary (presence/absence) data, from qualitative data with multistate variables, or from quantitative data, usually representing some form abundance of species within the sampling units. The data in this analysis are in the latter form, and the association matrices were formed from a site-by-species matrix with counts of the species in each of the eight plots.

There are several ecological indices that perform well for analysis of community data. The Percentage Similarity index values between sampling sites were calculated using the insect community data. Of the many quantitative similarity indices available, Percentage Similarity appears to perform very satisfactorily over a diverse set of ecological data sets (Gauch 1982, Ludwig and Reynolds 1988, Krebs 1989).

Percentage Similarity is one of the best quantitative indices. It was first proposed by Renkonen (1938) and is sometimes called Renkonen index (Krebs 1989). The index is calculated as:

$$P = \sum \text{minimum}\left(p_{1i}, p_{2i}\right)$$

where P = Percentage similarity between samples 1 and 2,

p_{1i} = Percentage of species i in sample 1

p_{2i} = Percentage of species i in sample 2

The index ranges from 0 (no similarity) to 100 (complete similarity). Sample size and diversity have only small effects on the performance of the index to measure actual similarity between sampling units (Krebs 1989).

Multivariate Analysis

Ordination

It is sometimes useful to sort sampling units into groups based on species composition. Communities of interest may then be designated for research and management purposes. Several techniques have been developed that group similar sampling units. Since low-cost computing has become available, calculation-intensive multivariate statistical analysis has been widely used to discover patterns or relationships between species, communities, and/or environmental factors. Comprehensive discussions of the techniques and their applications in ecological studies are available (e.g., Poole 1974, Gauch 1982, Pielou 1984, Digby and Kempton 1987).

Ordination is one of the many multivariate techniques used to analyze community data. Ordination is the collective term for multivariate analytical methods that arrange sampling units along axes such that similar sites are close together and dissimilar sites are far apart. The result is an objective summary of the relationships between sampling units in a low-dimensional species space. The goal is to reveal underlying structure in the data that represent patterns of species occurrence as determined by environmental variables.

Principal component analysis (PCA) is perhaps the most popular and widely used ordination technique. The method was developed by Pearson (1901) and refined by Hotelling (1933). It was first used to analyze ecological data by Goodall (1954) and has been used extensively since. Entomologists have successfully used PCA for a wide range of studies including analysis of forest canopy-arthropod community structure (e.g., Schowalter et al. 1988, Schowalter 1995).

In PCA, distance measures on component axes are Euclidean and the reduced space is no more than the original variable space with new coordinate axes. The maximum amount of variation is accounted for after minimizing distance distortions. The positions of the sampling units on the axes are determined from the data alone and hence, PCA is an objective rendition of the intrinsic ecological relationships in the data.

The method is most efficient when the data have a normal distribution although the method is robust to departures from the ideal structure (Hotelling 1933, Greig-Smith 1980, Gauch 1982). However, the results of

PCA are strongly influenced by non-linear relationships between sampling units (Gauch 1982). When habitat diversity is large and environmental gradients complex, the true ecological proximity between sampling units often lies along a curved response. In this situation, PCA ordination distorts ecological distances between sampling units, with some appearing much more closely related than they really are (Digby and Kempton1987). This "horseshoe effect" is compensated for in other analytical methods.

Principal Coordinate Analysis (ORD) is one such ordination method. The method was developed by Gower (1966) and is a generalization of Principal Component Analysis ordination (PCA). A sampling unit similarity matrix is the starting basis of comparison. The result of the method is a representation of sampling unit on axes that approximate total relationships between sampling units and that yields the "best" overall solution (Pimentel 1993). The method is useful in exploring gradients and ecological communities, and is less influenced by non-linear relationships than PCA (Gauch 1982, Pimentel 1993).

Appleton-Whittell Research Ranch insect community data were analyzed using ORD. Final configurations of three axes combinations showing sampling sites were plotted. The sampling site ORD scores for the first ten axes were output further analysis. The Final configuration was further evaluated using Nonmetric Multidimensional Scaling (NMDS).

NMDS is ordination technique that uses rank order information from a similarity matrix, rather than the metric information, to evaluate ordinal

relationships between sampling units. The intention is to eliminate the strong and problematic assumption of linearity of species responses to underlying environmental gradients made by other ordination methods. NMDS relies on a weaker assumption of monotonicity (i.e., $f(x_1) < f(x_2)$ for all $x_1 < x_2$). The goal of NMDS is to locate sampling units in a low-dimensional ordination space in such a manner that the interpoint distances in the ordination have the same rank order as do the interpoint similarities in the similarity matrix. NMDS is more robust when the input trial vectors are derived from another robust ordination method such as ORD. Use of randomly generated coordinates is not recommended because of the possibility of arriving at an invalid solution. Input trial vectors from ORD provide greater assurance of obtaining a global minimum solution. Random trial vectors are more likely to result in local minimum solutions (Pimentel 1993). Random trial vector results are also more susceptible to non-linear relationships between sampling units (like PCA results) and final configurations can suffer from "arch" distortion (Gauch 1982).

Trial vectors from ORD were analyzed using NMDS. Final NMDS configurations of three axes combinations showing sampling sites were plotted.

Classification

Classification is the grouping or clustering of sampling units based on some measure of their resemblance. The purpose is to summarize large data sets and aid in interpretation of community structure.

Two-Way Indicator Species Analysis (TWINSPAN) is a classification procedure designed for ecological studies (Hill 1979, Gauch and Whittaker 1981, Jongman et al., 1995). The procedure simultaneously forms groups of sites with similar species composition and groups of species with similar site distributions. The classification is accomplished by transforming each species abundance data into one or more pseudo-species presence/absence. The more abundant a species, the more pseudo-species are created. Dichotomies are created by ordinating the samples with correspondence analysis (Hill 1973), making the first division at the centroid. The result is a dendogram that illustrates the hierarchical relationships between the groups. The higher the order grouping, the more dissimilar are the groups. Only dendograms of the sampling site groups are shown for the analysis of the Appleton-Whittell Research Ranch insect community data.

Multigroup Discriminant Analysis (MDA) is another of the multivariate classification methods. The technique evaluates the within and between variation of *a priori* groups. MDA forms linear combinations of the variables (coordinate axes) that have the greatest between-group variation relative to their within-group variation (Digby and Kempton 1987). The resulting canonical axes represent combinations of variables,

the first canonical axis comprised of variables that maximize group differences.

The accuracy of community analysis using MDA relies on the validity of assumptions made about the distributional properties of the data. The assumptions are the same as those of ANOVA, and include 1) random sampling; 2) normality; 3) independence of errors; and 4) equality of population dispersions (homoscedasticity). Species-by-site abundance data rarely satisfy these assumptions, however a failure of one or more of the assumptions does not necessarily invalidate the analysis (Pimentel 1993, Manly 1986, Digby and Kempton 1987). The axes that result from ORD have standardized normal distributions and are therefore ideal for use in MDA.

Vectors from the first four principal coordinate axes from ORD were analyzed using MDA. Euclidean and Generalized (Standard Deviation) distances and 95% confidence radii about the group centroids were calculated. The treatment groups were classified by Geisser Classification into predicted groups and the results were compared to a priori group assignments.

V. RESULTS

A. PITFALL TRAP SPECIES

Species List

Table V-A.1. PITFALL TRAP Species List.
A list of the species in the PITFALL TRAP - Analytical Group 1, the total number of each species captures, and the proportion of the total number of individuals captured in pitfall traps.

Order	Species	Total	Proportion
Coleoptera	1	1	0.004
Coleoptera	2	5	0.019
Coleoptera	3	1	0.004
Coleoptera	4	3	0.012
Coleoptera	5	2	0.008
Coleoptera	6	4	0.015
Coleoptera	7	5	0.019
Coleoptera	8	1	0.004
Coleoptera	9	1	0.004
Coleoptera	11	5	0.019
Coleoptera	12	19	0.073
Coleoptera	13	1	0.004
Coleoptera	14	3	0.012
Coleoptera	15	1	0.004
Coleoptera	16	1	0.004
Coleoptera	17	2	0.008
Coleoptera	18	1	0.004
Coleoptera	19	1	0.004
Coleoptera	20	1	0.004
Coleoptera	21	1	0.004
Coleoptera	22	7	0.027
Coleoptera	23	1	0.004
Coleoptera	24	7	0.027
Coleoptera	25	1	0.004
Coleoptera	26	1	0.004
Coleoptera	31	1	0.004
Diptera	1	1	0.004
Diptera	2	1	0.004
Diptera	3	5	0.019
Diptera	4	1	0.004
Diptera	5	2	0.008

Order	Species	Total	Proportion
Diptera	6	4	0.015
Diptera	7	2	0.008
Diptera	8	5	0.019
Diptera	9	2	0.008
Diptera	10	2	0.008
Diptera	11	2	0.008
Diptera	12	1	0.004
Diptera	13	1	0.004
Diptera	14	1	0.004
Diptera	15	1	0.004
Diptera	16	1	0.004
Diptera	17	1	0.004
Diptera	18	1	0.004
Diptera	19	1	0.004
Diptera	20	1	0.004
Diptera	21	1	0.004
Diptera	22	1	0.004
Diptera	23	1	0.004
Diptera	24	3	0.012
Diptera	25	1	0.004
Diptera	26	1	0.004
Diptera	27	1	0.004
Diptera	28	1	0.004
Hemiptera	1	30	0.116
Hemiptera	2	1	0.004
Hemiptera	3	1	0.004
Hemiptera	4	1	0.004
Hemiptera	5	8	0.031
Hemiptera	6	1	0.004
Hemiptera	8	1	0.004
Homoptera	1	17	0.066
Homoptera	2	1	0.004
Homoptera	3	1	0.004
Homoptera	4	1	0.004
Hymenoptera	1	2	0.008
Hymenoptera	2	3	0.012
Hymenoptera	3	1	0.004
Hymenoptera	4	1	0.004
Hymenoptera	5	2	0.008
Hymenoptera	6	1	0.004
Hymenoptera	7	2	0.008
Hymenoptera	8	1	0.004
Hymenoptera	9	1	0.004
Hymenoptera	10	1	0.004

Order	Species	Total	Proportion
Hymenoptera	11	1	0.004
Hymenoptera	12	1	0.004
Hymenoptera	13	1	0.004
Hymenoptera	14	1	0.004
Lepidoptera	1	5	0.019
Lepidoptera	2	5	0.019
Lepidoptera	3	2	0.008
Lepidoptera	4	1	0.004
Orthoptera	1	8	0.031
Orthoptera	2	2	0.008
Orthoptera	3	5	0.019
Orthoptera	4	4	0.015
Orthoptera	5	1	0.004
Orthoptera	6	1	0.004
Orthoptera	7	1	0.004
Orthoptera	8	1	0.004
Orthoptera	9	4	0.015
Orthoptera	10	1	0.004
Orthoptera	11	2	0.008
Orthoptera	12	1	0.004
Orthoptera	13	1	0.004
Orthoptera	14	1	0.004
Orthoptera	15	1	0.004
Orthoptera	16	1	0.004
Orthoptera	17	1	0.004
Orthoptera	19	5	0.019

Table V-A.2. PITFALL TRAP Species List.
A list of the species from the PITFALL TRAP used for analysis in Analytical Group 1, the total number of each species captures, and the proportion of the total number of individuals captured in pitfall traps.

Order	Species	Total	Proportion
Hemiptera	1	30	0.116
Coleoptera	12	19	0.073
Homoptera	1	17	0.066
Orthoptera	1	8	0.031
Hemiptera	5	8	0.031
Lepidoptera	1	5	0.019
Coleoptera	2	5	0.019
Lepidoptera	2	5	0.019
Diptera	3	5	0.019
Orthoptera	3	5	0.019
Coleoptera	7	5	0.019
Diptera	8	5	0.019
Coleoptera	11	5	0.019
Orthoptera	4	4	0.015
Coleoptera	6	4	0.015
Diptera	6	4	0.015
Orthoptera	9	4	0.015

Similarity Indices

Percentage Similarity

Table V-A.3. PITFALL TRAP SPECIES Percentage Similarity Index. Site-by-site matrix of Percentage Similarity association coefficients calculated from Appleton-Whittell Research Ranch insect community data.

SITES	Site 1	Site 2	Site 3	Site 4	Site 1-D	Site 2-D	Site 3-D	Site 4-D
Site 1	100.00	46.51	47.06	31.25	44.90	35.29	41.03	44.44
Site 2	46.51	100.00	25.81	27.59	34.78	12.90	33.33	23.81
Site 3	47.06	25.81	100.00	30.00	32.43	63.64	29.63	24.24
Site 4	31.25	27.59	30.00	100.00	22.86	40.00	56.00	45.16
Site 1-D	44.90	34.78	32.43	22.86	100.00	32.43	23.81	29.17
Site 2-D	35.29	12.90	63.64	40.00	32.43	100.00	44.44	36.36
Site 3-D	41.03	33.33	29.63	56.00	23.81	44.44	100.00	47.37
Site 4-D	44.44	23.81	24.24	45.16	29.17	36.36	47.37	100.00

Table V-A.4. PITFALL TRAP SPECIES Percentage Dissimilarity Index. Site-by-site matrix of Percentage Dissimilarity association coefficients calculated from Appleton-Whittell Research Ranch insect community data.

SITES	Site 1	Site 2	Site 3	Site 4	Site 1-D	Site 2-D	Site 3-D	Site 4-D
Site 1	0.00	53.49	52.94	68.75	55.10	64.71	58.97	55.56
Site 2	53.49	0.00	74.19	72.41	65.22	87.10	66.67	76.19
Site 3	52.94	74.19	0.00	70.00	67.57	36.36	70.37	75.76
Site 4	68.75	72.41	70.00	0.00	77.14	60.00	44.00	54.84
Site 1-D	55.10	65.22	67.57	77.14	0.00	67.57	76.19	70.83
Site 2-D	64.71	87.10	36.36	60.00	67.57	0.00	55.56	63.64
Site 3-D	58.97	66.67	70.37	44.00	76.19	55.56	0.00	52.63
Site 4-D	55.56	76.19	75.76	54.84	70.83	63.64	52.63	0.00

The dissimilarity association matrix in Table V-A.4 was used in the ORD ordination analysis.

Ordination

Principal Coordinate Analysis (ORD)

Principal Coordinate Correlations

Correlations of the seventeen species with the Principal Coordinate Axes were obtained using Principal Component Analysis (PCA) (Table V-A.5). The strength of the association of a species with a Principal Coordinate is represented by the magnitude of the correlation (absolute value). In Tables V-A.6 through V-A.11 the species are sorted by the strength of their correlation with Principal Components 1 through 6. The species with the highest associations appear at the top of the tables, along with their Principal Component axis correlation.

Table V-A.5. PITFALL TRAP SPECIES Principal Component Correlations. The correlations of the 17 species with the 6 Principal Component axes obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Species	AXIS 1	AXIS 2	AXIS 3	AXIS 4	AXIS 5	AXIS 6
Hemiptera 1	-0.064	-0.275	-0.289	0.645	-0.246	0.267
Coleoptera 12	0.412	0.748	-0.234	0.016	-0.184	0.218
Homoptera 1	-0.845	0.292	-0.141	-0.043	-0.105	0.133
Orthoptera 1	-0.057	0.152	0.122	-0.159	-0.206	0.105
Hemiptera 5	-0.094	0.219	-0.149	0.274	0.407	-0.062
Lepidoptera 1	0.067	-0.134	-0.198	-0.099	-0.102	-0.046
Coleoptera 2	-0.220	-0.005	-0.116	-0.108	-0.091	0.162
Lepidoptera 2	0.039	-0.140	-0.531	-0.050	0.314	0.246
Diptera 3	-0.100	0.246	-0.018	0.027	0.089	0.064
Orthoptera 3	0.001	-0.139	0.272	0.045	0.212	0.433
Coleoptera 7	0.054	0.205	0.014	0.355	0.456	-0.123
Diptera 8	-0.147	0.049	-0.007	0.180	0.166	-0.596
Coleoptera 11	0.057	-0.157	-0.512	-0.284	0.161	0.000
Orthoptera 4	0.006	-0.112	0.199	0.083	0.179	0.277
Coleoptera 6	0.018	0.044	0.154	0.026	0.225	0.303
Diptera 6	0.060	-0.089	-0.260	-0.086	-0.106	-0.160
Orthoptera 9	0.067	-0.010	-0.041	0.447	-0.400	-0.058

Table V-A.6. PITFALL TRAP SPECIES Principal Component Correlations. The correlations of the 17 species with the Principal Component Axis 1 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Species	AXIS 1
Homoptera 1	-0.845
Coleoptera 12	0.412
Coleoptera 2	-0.220
Diptera 8	-0.147
Diptera 3	-0.100
Hemiptera 5	-0.094
Lepidoptera 1	0.067
Orthoptera 9	0.067
Hemiptera 1	-0.064
Diptera 6	0.060
Orthoptera 1	-0.057
Coleoptera 11	0.057
Coleoptera 7	0.054
Lepidoptera 2	0.039
Coleoptera 6	0.018
Orthoptera 4	0.006
Orthoptera 3	0.001

Table V-A.7. PITFALL TRAP SPECIES Principal Component Correlations. The correlations of the 17 species with the Principal Component Axis 2 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Species	AXIS 2
Coleoptera 12	0.748
Homoptera 1	0.292
Hemiptera 1	-0.275
Diptera 3	0.246
Hemiptera 5	0.219
Coleoptera 7	0.205
Coleoptera 11	-0.157
Orthoptera 1	0.152
Lepidoptera 2	-0.140
Orthoptera 3	-0.139
Lepidoptera 1	-0.134
Orthoptera 4	-0.112
Diptera 6	-0.089
Diptera 8	0.049
Coleoptera 6	0.044
Orthoptera 9	-0.010
Coleoptera 2	-0.005

Table V-A.8. PITFALL TRAP SPECIES Principal Component Correlations. The correlations of the 17 species with the Principal Component Axis 3 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Species	AXIS 3
Lepidoptera 2	-0.531
Coleoptera 11	-0.512
Hemiptera 1	-0.289
Orthoptera 3	0.272
Diptera 6	-0.260
Coleoptera 12	-0.234
Orthoptera 4	0.199
Lepidoptera 1	-0.198
Coleoptera 6	0.154
Hemiptera 5	-0.149
Homoptera 1	-0.141
Orthoptera 1	0.122
Coleoptera 2	-0.116
Orthoptera 9	-0.041
Diptera 3	-0.018
Coleoptera 7	0.014
Diptera 8	-0.007

Table V-A.9. PITFALL TRAP SPECIES Principal Component Correlations. The correlations of the 17 species with the Principal Component Axis 4 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Species	AXIS 4
Hemiptera 1	0.645
Orthoptera 9	0.447
Coleoptera 7	0.355
Coleoptera 11	-0.284
Hemiptera 5	0.274
Diptera 8	0.180
Orthoptera 1	-0.159
Coleoptera 2	-0.108
Lepidoptera 1	-0.099
Diptera 6	-0.086
Orthoptera 4	0.083
Lepidoptera 2	-0.050
Orthoptera 3	0.045
Homoptera 1	-0.043
Diptera 3	0.027
Coleoptera 6	0.026
Coleoptera 12	0.016

Table V-A.10. PITFALL TRAP SPECIES Principal Component Correlations. The correlations of the 17 species with the Principal Component Axis 5 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Species	AXIS 5
Coleoptera 7	0.456
Hemiptera 5	0.407
Orthoptera 9	-0.400
Lepidoptera 2	0.314
Hemiptera 1	-0.246
Coleoptera 6	0.225
Orthoptera 3	0.212
Orthoptera 1	-0.206
Coleoptera 12	-0.184
Orthoptera 4	0.179
Diptera 8	0.166
Coleoptera 11	0.161
Diptera 6	-0.106
Homoptera 1	-0.105
Lepidoptera 1	-0.102
Coleoptera 2	-0.091
Diptera 3	0.089

Table V-A.11. PITFALL TRAP SPECIES Principal Component Correlations. The correlations of the 17 species with the Principal Component Axis 6 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Species	AXIS 6
Diptera 8	-0.596
Orthoptera 3	0.433
Coleoptera 6	0.303
Orthoptera 4	0.277
Hemiptera 1	0.267
Lepidoptera 2	0.246
Coleoptera 12	0.218
Coleoptera 2	0.162
Diptera 6	-0.160
Homoptera 1	0.133
Coleoptera 7	-0.123
Orthoptera 1	0.105
Diptera 3	0.064
Hemiptera 5	-0.062
Orthoptera 9	-0.058
Lepidoptera 1	-0.046
Coleoptera 11	0.000

Percentage Variance

The importance of the Principal Coordinate axes is measured by the amount of total variance accounted for by those axes. By definition, the first axis accounts for the most variation, and the proportion of the total variance decreases with succeeding axes. It is important to report the amount of total variance accounted for in the axes that are discussed in a scientific paper.

The amount of total variance accounted for, in a way, alludes to the strength of the analysis, somewhat similar to an R^2 value in a regression analysis. For example, reporting that the first three axes account for 77.92 percent of the total variance is equivalent to saying the R^2 value of the analysis is 0.7792. It is up to the reader to determine whether enough of the variance was accounted for, and therefore estimate the strength of the conclusions.

Table V-A.12. PITFALL TRAP SPECIES Percentage Variance and Cumulative Variance for Principal Coordinate Axes. The percentage of the total variance and the cumulative variance for the Principal Coordinate Axes resulting from PCA analysis of the Appleton-Whittell Research Ranch insect community data.

Axes	1	2	3	4	5	6
EIGENVALUE	4838.85	4298.20	2383.22	1706.96	997.25	576.20
% VARIANCE	32.73	29.07	16.12	11.55	6.75	3.78
CUM. %	32.73	61.80	77.92	89.47	96.22	100.00

Site Principal Coordinate Axes Scores

Included in the results of ORD are the scores (position) of the sampling sites on the Principal Coordinate Axes. These scores are used to produce graphs (Figures V-A.1, V-A.2, and V-A.3), to explore the structure of the data, and to form hypotheses about group associations for the sampling sites.

Table V-A.13. PITFALL TRAP SPECIES Principal Coordinate Axes Scores. The scores (positions) of the sampling sites on the Principal Coordinate Axes obtained from ORD analysis of the Appleton-Whittell Research Ranch insect community data.

SITE	AXIS 1	AXIS 2	AXIS 3	AXIS 4	AXIS 5	AXIS 6
1	-0.286	-0.038	0.065	-0.561	-0.026	0.624
2	-0.576	0.309	-0.448	0.053	0.053	-0.445
3	0.046	-0.581	-0.348	-0.186	0.261	-0.083
4	0.358	0.326	-0.177	0.427	0.531	0.373
1-D	-0.424	-0.223	0.533	0.551	-0.128	0.106
2-D	0.396	-0.444	0.002	0.094	-0.213	-0.26
3-D	0.276	0.332	-0.193	0.012	-0.724	0.104
4-D	0.209	0.319	0.566	-0.39	0.246	-0.421

Principal Coordinate Axes Ordinations

Ordinations derived from ORD analysis of the Appleton-Whittell Research Ranch insect community data are plotted in three axes combinations. It is standard to report Axis 1 vs. Axis 2, Axis 1 vs. Axis 3, and Axis 2 vs. Axis 3. Other plots can be constructed using the information in Table V-A.13.

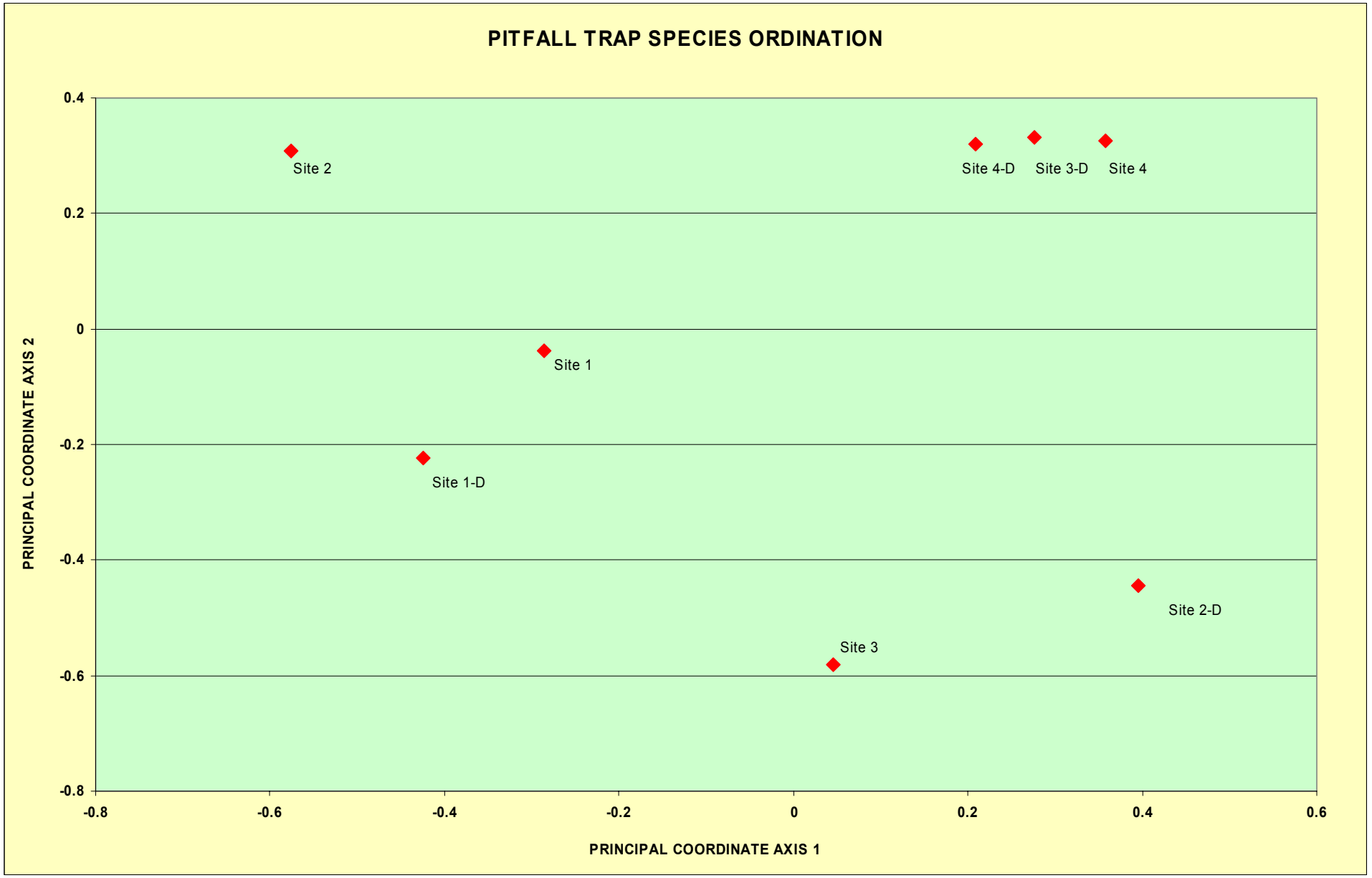

Figure V-A.1. PITFALL TRAP SPECIES Principal Coordinate Analysis Ordination, Axis 1 vs. Axis 2.

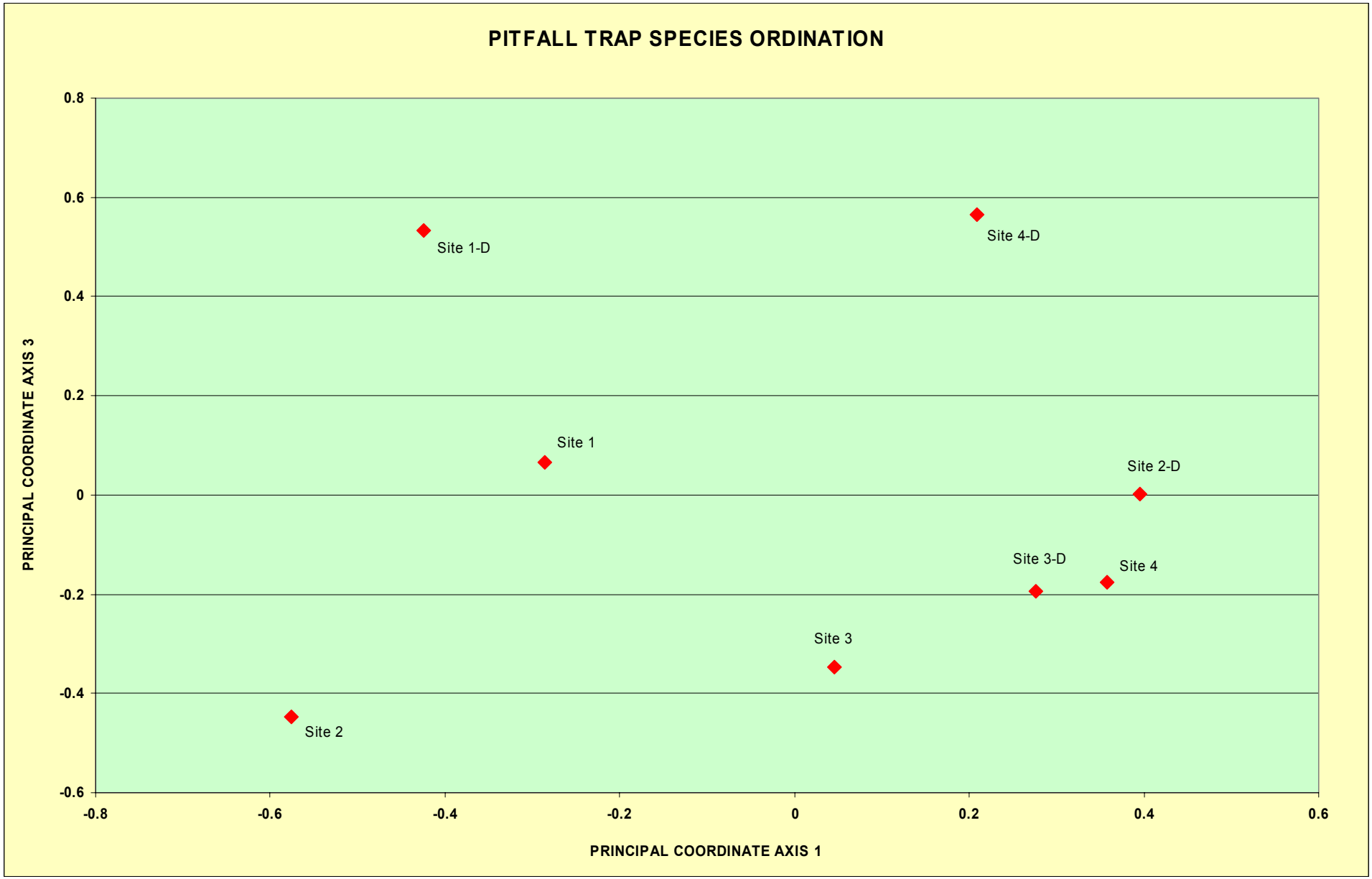

Figure V-A.2. PITFALL TRAP SPECIES Principal Coordinate Analysis Ordination, Axis 1 vs. Axis 3.

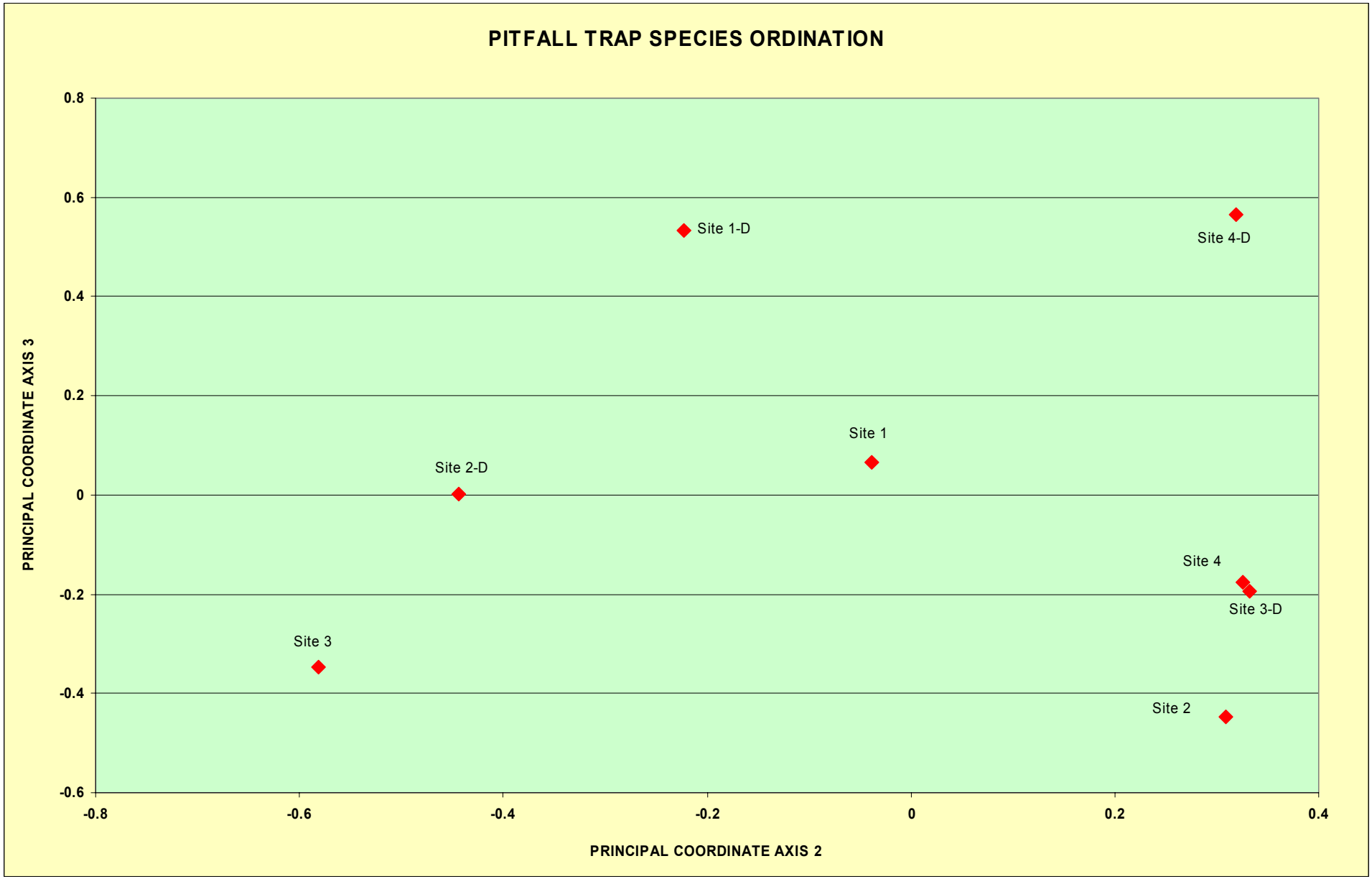

Figure V-A.3. PITFALL TRAP SPECIES Principal Coordinate Analysis Ordination, Axis 2 vs. Axis 3.

TWINSPAN

Groupings

Two-**W**ay **In**dicator **Sp**ecies **An**alysis (TWINSPAN) was used to form groups of the sampling sites based on species abundance rather than on dissimilarity indices as in Ordination. TWINSPAN provides another relatively unbiased method of forming groups.

The results of TWINSPAN are usually presented as a dendogram. Sites with similar community composition appear in groups. The differences between groups can be determined from the point of departure on the dendogram scale. The higher order the departure, the greater the group differences. This scale is not presented in this report because the biological basis of the groups was not clear. TWINSPAN resulted in the following groupings for the sampling sites (color-coded for viewing convenience).

Table V-A.14. PITFALL TRAP SPECIES TWINSPAN Groups. The groups of sampling sites resulting from TWINSPAN of the Appleton-Whittell Research Ranch insect community data.

Sampling Site	1st Order group	2nd Order Group
Site 3	0	0
Site 1-D	0	0
Site 2-D	0	0
Site 1	0	1
Site 2	0	1
Site 4	1	
Site 3-D	1	
Site 4-D	1	

Nonmetric Multidimensional Scaling (NMDS)

The vectors from the first six ORD axes were evaluated using NMDS. The results are presented as ordination plots of three axes configurations (Figures V-A.4, V-A.5, and V-A.6). These plots should be viewed to confirm ordination results obtained from ORD (Figures V-A.1, V-A.2, and V-A.3).

Table V-A.15. PITFALL TRAP SPECIES Nonmetric Multidimensional Scaling Axes Scores. The scores (positions) of the sampling sites on the rescaled axes obtained from NMDS analysis of the Appleton-Whittell Research Ranch insect community data.

SITE	AXIS 1	AXIS 2	AXIS 3	AXIS 4	AXIS 5	AXIS 6
1	-0.338	-0.046	0.051	-0.569	-0.021	0.633
2	-0.681	0.379	-0.489	0.065	0.064	-0.426
3	0.054	-0.652	-0.373	-0.189	0.268	-0.084
4	0.435	0.392	-0.214	0.410	0.558	0.373
1-D	-0.519	-0.287	0.578	0.561	-0.159	0.064
2-D	0.483	-0.535	0.039	0.103	-0.215	-0.235
3-D	0.316	0.391	-0.206	0.015	-0.742	0.097
4-D	0.250	0.358	0.614	-0.396	0.247	-0.421

After consultation with the client, it was decided that group configurations revealed by ORD, TWINSPAN, and NMDS had no clear biological meaning and therefore, there was no further analysis necessary.

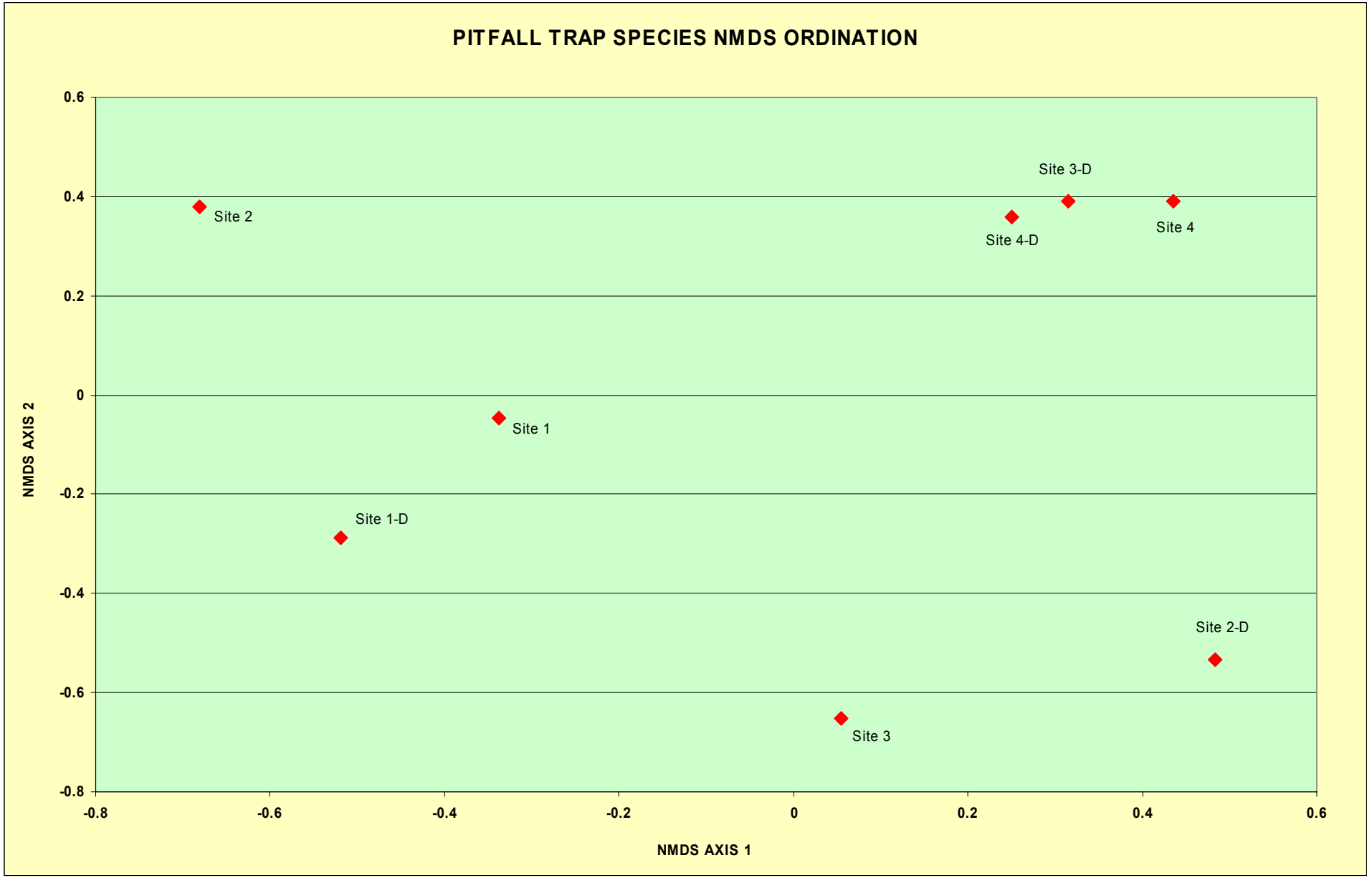

Figure V-A.4. PITFALL TRAP SPECIES NMDS Ordination Axis 1 vs. Axis 2.

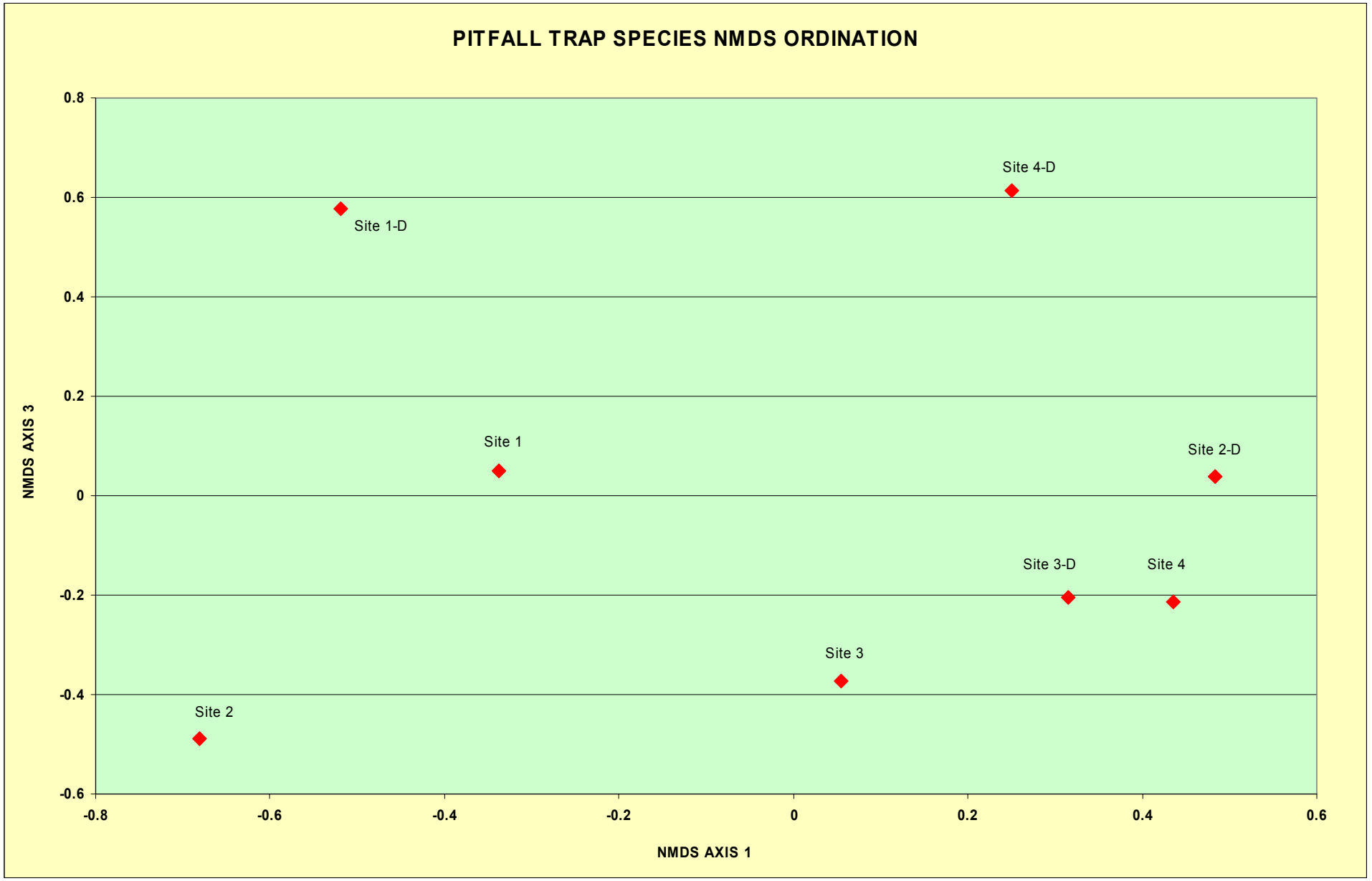

Figure V-A.5. PITFALL TRAP SPECIES NMDS Ordination Axis 1 vs. Axis 3.

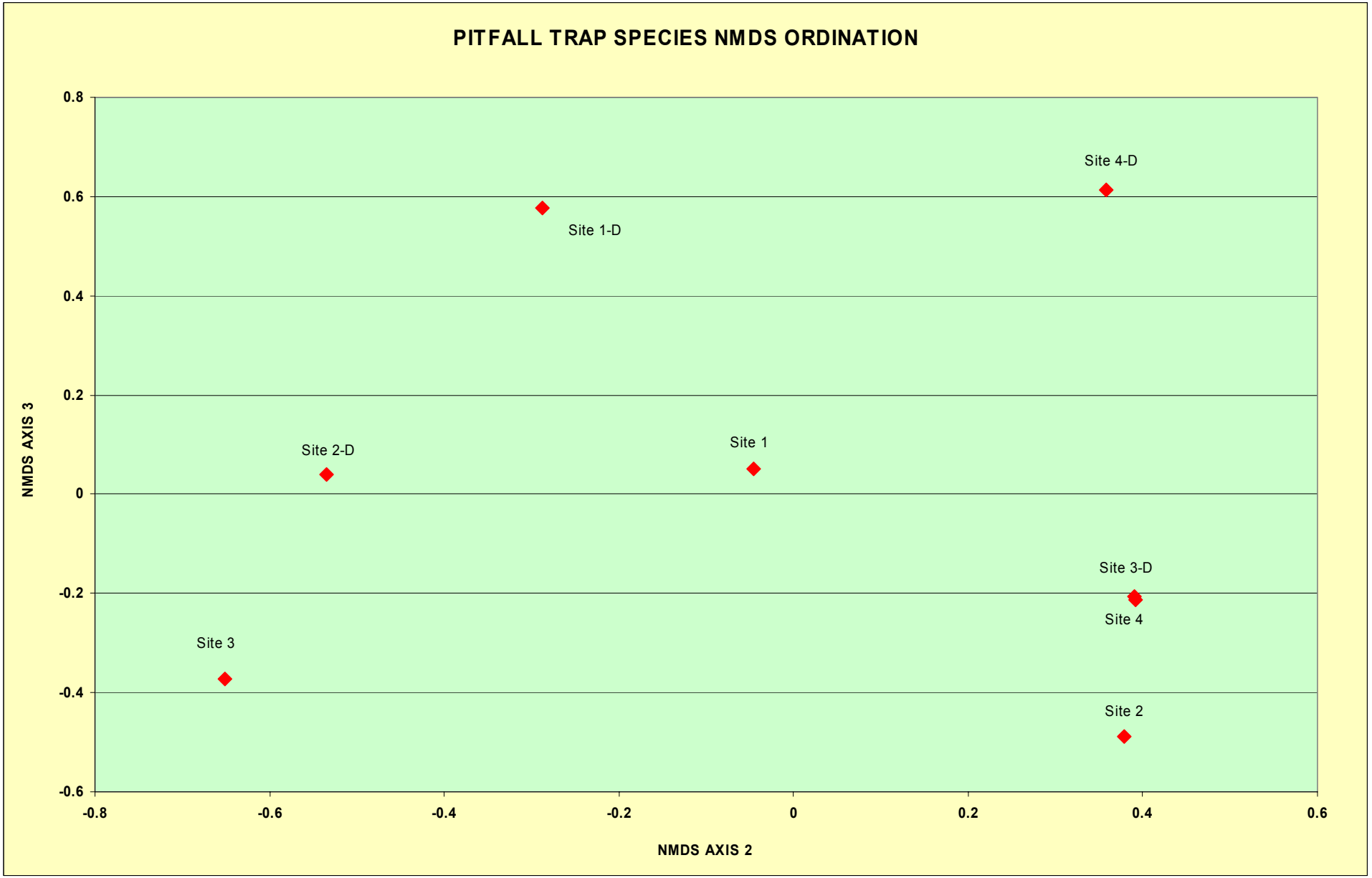

Figure V-A.6. PITFALL TRAP SPECIES NMDS Ordination Axis 2 vs. Axis 3.

B. SWEEP NET SPECIES

Species List

Table V-B.1. SWEEP NET Species List.
A list of the species in the SWEEP NET - Analytical Group 2, the total number of each species captures, and the proportion of the total number of individuals captured in pitfall traps.

Order	Species	Total	Proportion
Coleoptera	1	1	0.000
Coleoptera	2	1	0.000
Coleoptera	3	3	0.000
Coleoptera	4	11	0.002
Coleoptera	5	3	0.000
Coleoptera	6	3	0.000
Coleoptera	8	2	0.000
Coleoptera	10	1	0.000
Coleoptera	11	3	0.000
Coleoptera	12	1	0.000
Coleoptera	13	1	0.000
Coleoptera	14	1	0.000
Coleoptera	15	3	0.000
Coleoptera	16	2	0.000
Coleoptera	17	2	0.000
Coleoptera	18	1	0.000
Coleoptera	19	1	0.000
Coleoptera	20	4	0.001
Coleoptera	21	1	0.000
Coleoptera	21	1	0.000
Coleoptera	22	1	0.000
Coleoptera	23	3	0.000
Coleoptera	24	2	0.000
Coleoptera	25	4	0.001
Coleoptera	26	3	0.000
Coleoptera	26	5	0.001
Coleoptera	27	75	0.012
Coleoptera	28	1	0.000

Order	Species	Total	Proportion
Coleoptera	29	3	0.000
Coleoptera	30	29	0.005
Coleoptera	31	3	0.000
Coleoptera	32	1	0.000
Coleoptera	33	1	0.000
Coleoptera	34	1	0.000
Coleoptera	35	2	0.000
Coleoptera	36	1	0.000
Coleoptera	37	1	0.000
Coleoptera	38	1	0.000
Coleoptera	39	1	0.000
Coleoptera	40	2	0.000
Coleoptera	41	1	0.000
Coleoptera	42	1	0.000
Coleoptera	43	1	0.000
Coleoptera	44	507	0.083
Coleoptera	47	7	0.001
Coleoptera	48	5	0.001
Coleoptera	49	22	0.004
Coleoptera	50	13	0.002
Coleoptera	51	3	0.000
Coleoptera	52	3	0.000
Coleoptera	53	1	0.000
Coleoptera	54	55	0.009
Coleoptera	56	2	0.000
Coleoptera	57	21	0.003
Coleoptera	58	15	0.002
Diptera	1	1	0.000
Diptera	2	3	0.000
Diptera	3	33	0.005
Diptera	4	1	0.000
Diptera	5	5	0.001
Diptera	6	5	0.001
Diptera	7	1	0.000
Diptera	8	4	0.001
Diptera	9	1	0.000
Diptera	10	2	0.000
Diptera	11	1	0.000
Diptera	12	1	0.000
Diptera	13	25	0.004

Order	Species	Total	Proportion
Diptera	14	4	0.001
Diptera	15	3	0.000
Diptera	16	1	0.000
Diptera	17	1	0.000
Diptera	18	2	0.000
Diptera	19	9	0.001
Diptera	20	1	0.000
Diptera	21	1	0.000
Diptera	22	3	0.000
Diptera	23	1	0.000
Diptera	24	1	0.000
Diptera	25	1	0.000
Diptera	26	7	0.001
Diptera	27	4	0.001
Diptera	28	1	0.000
Diptera	29	3	0.000
Diptera	30	2	0.000
Diptera	31	3	0.000
Diptera	32	1	0.000
Diptera	33	1	0.000
Diptera	34	1	0.000
Diptera	35	21	0.003
Diptera	36	1	0.000
Diptera	37	1	0.000
Diptera	38	1	0.000
Diptera	39	1	0.000
Diptera	40	1	0.000
Diptera	41	6	0.001
Diptera	42	6	0.001
Diptera	43	2	0.000
Diptera	44	1	0.000
Diptera	45	1	0.000
Diptera	47	1	0.000
Diptera	48	1	0.000
Diptera	49	1	0.000
Diptera	50	1	0.000
Diptera	51	1	0.000
Diptera	52	3	0.000
Diptera	53	1	0.000
Hemiptera	1	1	0.000

Order	Species	Total	Proportion
Hemiptera	2	1	0.000
Hemiptera	3	9	0.001
Hemiptera	4	4	0.001
Hemiptera	9	7	0.001
Hemiptera	10	1	0.000
Hemiptera	11	1	0.000
Hemiptera	12	1	0.000
Hemiptera	14	1	0.000
Hemiptera	15	1034	0.170
Hemiptera	16	2	0.000
Hemiptera	17	3	0.000
Hemiptera	18	3	0.000
Hemiptera	19	2	0.000
Hemiptera	20	2	0.000
Hemiptera	21	4	0.001
Hemiptera	22	2	0.000
Hemiptera	24	3	0.000
Hemiptera	25	1	0.000
Hemiptera	26	1	0.000
Hemiptera	27	6	0.001
Hemiptera	27	1	0.000
Hemiptera	28	1	0.000
Hemiptera	29	1	0.000
Hemiptera	30	1	0.000
Hemiptera	31	4	0.001
Hemiptera	32	1	0.000
Hemiptera	33	1	0.000
Hemiptera	34	1	0.000
Hemiptera	35	1	0.000
Hemiptera	36	2	0.000
Hemiptera	37	1	0.000
Hemiptera	38	1	0.000
Homoptera	1	1062	0.175
Homoptera	2	13	0.002
Homoptera	3	2	0.000
Homoptera	4	1	0.000
Homoptera	5	5	0.001
Homoptera	6	1	0.000
Homoptera	7	7	0.001
Homoptera	8	4	0.001

Order	Species	Total	Proportion
Homoptera	9	3	0.000
Homoptera	10	1	0.000
Homoptera	11	31	0.005
Homoptera	12	4	0.001
Homoptera	13	11	0.002
Homoptera	14	2	0.000
Homoptera	15	2	0.000
Homoptera	16	2	0.000
Homoptera	17	1	0.000
Homoptera	18	4	0.001
Homoptera	19	268	0.044
Homoptera	21	1	0.000
Homoptera	22	1	0.000
Homoptera	23	1	0.000
Homoptera	24	200	0.033
Homoptera	25	845	0.139
Homoptera	26	159	0.026
Homoptera	27	13	0.002
Homoptera	28	371	0.061
Hymenoptera	1	1	0.000
Hymenoptera	2	3	0.000
Hymenoptera	3	1	0.000
Hymenoptera	4	2	0.000
Hymenoptera	5	2	0.000
Hymenoptera	6	1	0.000
Hymenoptera	7	3	0.000
Hymenoptera	8	5	0.001
Hymenoptera	9	1	0.000
Hymenoptera	10	1	0.000
Hymenoptera	11	1	0.000
Hymenoptera	12	1	0.000
Hymenoptera	13	2	0.000
Hymenoptera	14	2	0.000
Hymenoptera	15	2	0.000
Hymenoptera	16	3	0.000
Hymenoptera	17	1	0.000
Hymenoptera	18	3	0.000
Hymenoptera	19	2	0.000
Hymenoptera	20	1	0.000
Hymenoptera	21	1	0.000

Order	Species	Total	Proportion
Hymenoptera	22	1	0.000
Hymenoptera	23	1	0.000
Hymenoptera	24	1	0.000
Hymenoptera	25	1	0.000
Hymenoptera	26	1	0.000
Hymenoptera	27	1	0.000
Lepidoptera	1	3	0.000
Lepidoptera	2	3	0.000
Lepidoptera	3	1	0.000
Lepidoptera	6	1	0.000
Lepidoptera	7	2	0.000
Lepidoptera	8	4	0.001
Lepidoptera	9	1	0.000
Lepidoptera	10	1	0.000
Lepidoptera	11	1	0.000
Lepidoptera	12	2	0.000
Mantidae	1	5	0.001
Neuroptera	1	1	0.000
Neuroptera	2	2	0.000
Neuroptera	3	2	0.000
Neuroptera	4	1	0.000
Orthoptera	ag deo	42	0.007
Orthoptera	am co	13	0.002
Orthoptera	ar ps	2	0.000
Orthoptera	au fe	20	0.003
Orthoptera	bo fl	2	0.000
Orthoptera	co cr	33	0.005
Orthoptera	da va	86	0.014
Orthoptera	er si	99	0.016
Orthoptera	ha tr	3	0.000
Orthoptera	he ru	2	0.000
Orthoptera	he ve	53	0.009
Orthoptera	le ro	1	0.000
Orthoptera	me az	1	0.000
Orthoptera	me de	48	0.008
Orthoptera	me gl	6	0.001
Orthoptera	me la	5	0.001
Orthoptera	me me	9	0.001
Orthoptera	me re	1	0.000
Orthoptera	op ob	18	0.003

Order	Species	Total	Proportion
Orthoptera	pa wy	158	0.026
Orthoptera	ph ne	2	0.000
Orthoptera	po pa	14	0.002
Orthoptera	ps de	44	0.007
Orthoptera	ps te	36	0.006
Orthoptera	sp 1	6	0.001
Orthoptera	sp 15	113	0.019
Orthoptera	sp 4	1	0.000
Orthoptera	tr me	23	0.004
Orthoptera	tr pa	7	0.001
Phasmatidae	7	6	0.001

Table V-B.2. SWEEP NET Species List.
A list of the species from the SWEEP NET used for analysis in Analytical Group 2, the total number of each species captures, and the proportion of the total number of individuals captured in sweep nets.

Order	Species	Total	Proportion
Homoptera	1	1062	0.175
Hemiptera	15	1034	0.170
Homoptera	25	845	0.139
Coleoptera	44	507	0.083
Homoptera	28	371	0.061
Homoptera	19	268	0.044
Homoptera	24	200	0.033
Homoptera	26	159	0.026
Orthoptera	pa wy	158	0.026
Orthoptera	sp 15	113	0.019
Orthoptera	er si	99	0.016
Orthoptera	da va	86	0.014
Coleoptera	27	75	0.012
Coleoptera	54	55	0.009
Orthoptera	he ve	53	0.009
Orthoptera	me de	48	0.008
Orthoptera	ps de	44	0.007
Orthoptera	ag deo	42	0.007
Orthoptera	ps te	36	0.006
Diptera	3	33	0.005
Orthoptera	co cr	33	0.005
Homoptera	11	31	0.005
Coleoptera	30	29	0.005
Diptera	13	25	0.004
Orthoptera	tr me	23	0.004
Coleoptera	49	22	0.004
Coleoptera	57	21	0.003
Diptera	35	21	0.003
Orthoptera	au fe	20	0.003
Orthoptera	op ob	18	0.003
Coleoptera	58	15	0.002
Orthoptera	po pa	14	0.002
Coleoptera	50	13	0.002
Homoptera	2	13	0.002
Homoptera	27	13	0.002

Order	Species	Total	Proportion
Orthoptera	am co	13	0.002
Coleoptera	4	11	0.002
Homoptera	13	11	0.002
Diptera	19	9	0.001
Hemiptera	3	9	0.001
Orthoptera	me me	9	0.001

Similarity Indices

Percentage Similarity

Table V-B.3. SWEEP NET SPECIES Percentage Similarity Index. Site-by-site matrix of Percentage Similarity association coefficients calculated from Appleton-Whittell Research Ranch insect community data.

SITES	Site 1	Site 2	Site 3	Site 4	Site 1-D	Site 2-D	Site 3-D	Site 4-D
Site 1	100.00	66.32	47.85	58.44	43.07	53.37	61.11	31.42
Site 2	66.32	100.00	55.19	55.81	27.43	36.72	32.16	30.80
Site 3	47.85	55.19	100.00	54.88	13.62	23.15	20.93	20.93
Site 4	58.44	55.81	54.88	100.00	13.74	30.36	21.01	33.48
Site 1-D	43.07	27.43	13.62	13.74	100.00	52.46	46.37	38.72
Site 2-D	53.37	36.72	23.15	30.36	52.46	100.00	60.02	53.75
Site 3-D	61.11	32.16	20.93	21.01	46.37	60.02	100.00	37.46
Site 4-D	31.42	30.80	20.93	33.48	38.72	53.75	37.46	100.00

Table V-B.4. SWEEP NET SPECIES Percentage Dissimilarity Index. Site-by-site matrix of Percentage Dissimilarity association coefficients calculated from Appleton-Whittell Research Ranch insect community data.

SITES	Site 1	Site 2	Site 3	Site 4	Site 1-D	Site 2-D	Site 3-D	Site 4-D
Site 1	0.00	33.68	52.15	41.56	56.93	46.63	38.89	68.58
Site 2	33.68	0.00	44.81	44.19	72.57	63.28	67.84	69.20
Site 3	52.15	44.81	0.00	45.12	86.38	76.85	79.07	79.07
Site 4	41.56	44.19	45.12	0.00	86.26	69.64	78.99	66.52
Site 1-D	56.93	72.57	86.38	86.26	0.00	47.54	53.63	61.28
Site 2-D	46.63	63.28	76.85	69.64	47.54	0.00	39.98	46.25
Site 3-D	38.89	67.84	79.07	78.99	53.63	39.98	0.00	62.54
Site 4-D	68.58	69.20	79.07	66.52	61.28	46.25	62.54	0.00

The dissimilarity association matrix in Table V-B.4 was used in the ORD ordination analysis.

Ordination

Principal Coordinate Analysis (ORD)

Principal Coordinate Correlations

Correlations of the seventeen species with the Principal Coordinate Axes were obtained using Principal Component Analysis (PCA) (Table V-B.5). The strength of the association of a species with a Principal Coordinate is represented by the magnitude of the correlation (absolute value). In Tables V-B.6 through V-B.11 the species are sorted by the strength of their correlation with Principal Components 1 through 6. The species with the highest associations appear at the top of the tables, along with their Principal Component axis correlation.

Table V-B.5. SWEEP NET SPECIES Principal Component Correlations. The correlations of the 41 species with the 6 Principal Component axes obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Order	Species	AXIS 1	AXIS 2	AXIS 3	AXIS 4	AXIS 5	AXIS 6
Homoptera	1	-0.135	0.219	0.150	-0.163	-0.043	-0.047
Hemiptera	15	0.195	-0.027	-0.230	-0.104	-0.151	0.039
Homoptera	25	0.250	-0.024	-0.015	-0.040	0.221	0.043
Coleoptera	44	-0.041	0.249	0.090	-0.156	0.232	0.113
Homoptera	28	0.251	0.047	0.017	0.101	0.001	0.136
Homoptera	19	-0.079	-0.114	0.203	-0.225	-0.251	-0.083
Homoptera	24	0.038	-0.207	0.217	-0.153	0.078	-0.221
Homoptera	26	0.190	-0.008	0.181	-0.115	0.259	0.017
Orthoptera	pa wy	-0.030	0.194	-0.193	-0.235	0.174	0.016
Orthoptera	sp 15	0.211	0.079	0.198	-0.018	0.092	0.092
Orthoptera	er si	0.246	0.044	-0.140	-0.093	-0.059	-0.009
Orthoptera	da va	0.241	0.120	-0.014	-0.129	-0.002	-0.019
Coleoptera	27	-0.040	0.293	-0.029	-0.120	0.103	-0.017
Coleoptera	54	0.255	-0.072	-0.022	0.024	0.165	-0.002
Orthoptera	he ve	-0.013	0.100	-0.295	-0.250	-0.024	-0.042
Orthoptera	me de	0.077	0.006	-0.090	-0.312	-0.293	-0.083

Order	Species	AXIS 1	AXIS 2	AXIS 3	AXIS 4	AXIS 5	AXIS 6
Orthoptera	ps de	-0.047	0.187	0.098	0.158	-0.173	0.370
Orthoptera	ag deo	0.100	0.235	0.006	0.004	-0.291	-0.059
Orthoptera	ps te	-0.130	0.106	0.039	0.308	-0.121	-0.137
Orthoptera	co cr	-0.209	0.124	-0.046	-0.119	0.138	0.261
Diptera	3	-0.228	0.025	-0.036	-0.070	0.047	0.190
Homoptera	11	0.217	0.177	0.085	0.043	-0.015	-0.005
Coleoptera	30	0.141	0.199	0.169	0.133	-0.152	-0.029
Diptera	13	-0.056	-0.019	0.179	-0.371	0.101	-0.126
Orthoptera	tr me	-0.155	0.071	-0.070	0.082	0.185	-0.474
Coleoptera	49	0.021	0.289	0.001	0.007	-0.036	0.250
Diptera	35	-0.064	-0.185	0.087	-0.265	-0.233	0.114
Coleoptera	57	0.220	0.024	0.139	-0.059	0.247	0.020
Orthoptera	au fe	-0.070	0.305	0.032	-0.039	-0.015	-0.060
Orthoptera	op ob	0.265	-0.035	0.029	-0.054	0.089	0.033
Coleoptera	58	0.048	0.247	0.149	0.028	-0.233	-0.128
Orthoptera	po pa	0.221	0.137	-0.028	-0.056	-0.185	-0.088
Orthoptera	am co	0.220	-0.013	-0.154	-0.167	-0.063	-0.030
Homoptera	2	0.054	-0.095	0.300	-0.197	-0.055	-0.051
Homoptera	27	-0.135	0.082	-0.269	-0.097	0.140	-0.140
Coleoptera	50	-0.123	0.231	0.117	-0.145	0.012	0.205
Homoptera	13	-0.087	0.244	-0.054	-0.079	0.003	-0.356
Coleoptera	4	0.051	0.003	-0.342	-0.154	-0.084	0.045
Hemiptera	3	-0.112	-0.132	0.205	-0.198	-0.236	0.044
Orthoptera	me me	0.124	0.179	0.165	0.149	-0.046	-0.290
Diptera	19	0.120	-0.071	-0.272	0.098	-0.215	-0.005

Table V-B.6. SWEEP NET SPECIES Principal Component Correlations. The correlations of the 41 species with the Principal Component Axis 1 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Order	Species	AXIS 1
Orthoptera	op ob	0.265
Coleoptera	54	0.255
Homoptera	28	0.251
Homoptera	25	0.250
Orthoptera	er si	0.246
Orthoptera	da va	0.241
Diptera	3	-0.228
Orthoptera	po pa	0.221
Coleoptera	57	0.220
Orthoptera	am co	0.220
Homoptera	11	0.217
Orthoptera	sp 15	0.211
Orthoptera	co cr	-0.209
Hemiptera	15	0.195
Homoptera	26	0.190
Orthoptera	tr me	-0.155
Coleoptera	30	0.141
Homoptera	1	-0.135
Homoptera	27	-0.135
Orthoptera	ps te	-0.130
Orthoptera	me me	0.124
Coleoptera	50	-0.123
Diptera	19	0.120
Hemiptera	3	-0.112
Orthoptera	ag deo	0.100
Homoptera	13	-0.087
Homoptera	19	-0.079
Orthoptera	me de	0.077
Orthoptera	au fe	-0.070
Diptera	35	-0.064
Diptera	13	-0.056
Homoptera	2	0.054
Coleoptera	4	0.051
Coleoptera	58	0.048

Order	Species	AXIS 1
Orthoptera	ps de	-0.047
Coleoptera	44	-0.041
Coleoptera	27	-0.040
Homoptera	24	0.038
Orthoptera	pa wy	-0.030
Coleoptera	49	0.021
Orthoptera	he ve	-0.013

Table V-B.7. SWEEP NET SPECIES Principal Component Correlations. The correlations of the 41 species with the Principal Component Axis 2 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Order	Species	AXIS 2
Orthoptera	au fe	0.305
Coleoptera	27	0.293
Coleoptera	49	0.289
Coleoptera	44	0.249
Coleoptera	58	0.247
Homoptera	13	0.244
Orthoptera	ag deo	0.235
Coleoptera	50	0.231
Homoptera	1	0.219
Homoptera	24	-0.207
Coleoptera	30	0.199
Orthoptera	pa wy	0.194
Orthoptera	ps de	0.187
Diptera	35	-0.185
Orthoptera	me me	0.179
Homoptera	11	0.177
Orthoptera	po pa	0.137
Hemiptera	3	-0.132
Orthoptera	co cr	0.124
Orthoptera	da va	0.120
Homoptera	19	-0.114
Orthoptera	ps te	0.106
Orthoptera	he ve	0.100
Homoptera	2	-0.095
Homoptera	27	0.082
Orthoptera	sp 15	0.079
Coleoptera	54	-0.072
Orthoptera	tr me	0.071
Diptera	19	-0.071
Homoptera	28	0.047
Orthoptera	er si	0.044
Orthoptera	op ob	-0.035
Hemiptera	15	-0.027
Diptera	3	0.025

Order	Species	AXIS 2
Homoptera	25	-0.024
Coleoptera	57	0.024
Diptera	13	-0.019
Orthoptera	am co	-0.013
Homoptera	26	-0.008
Orthoptera	me de	0.006
Coleoptera	4	0.003

Table V-B.8. SWEEP NET SPECIES Principal Component Correlations. The correlations of the 41 species with the Principal Component Axis 3 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Order	Species	AXIS 3
Coleoptera	4	-0.342
Homoptera	2	0.300
Orthoptera	he ve	-0.295
Diptera	19	-0.272
Homoptera	27	-0.269
Hemiptera	15	-0.230
Homoptera	24	0.217
Hemiptera	3	0.205
Homoptera	19	0.203
Orthoptera	sp 15	0.198
Orthoptera	pa wy	-0.193
Homoptera	26	0.181
Diptera	13	0.179
Coleoptera	30	0.169
Orthoptera	me me	0.165
Orthoptera	am co	-0.154
Homoptera	1	0.150
Coleoptera	58	0.149
Orthoptera	er si	-0.140
Coleoptera	57	0.139
Coleoptera	50	0.117
Orthoptera	ps de	0.098
Coleoptera	44	0.090
Orthoptera	me de	-0.090
Diptera	35	0.087
Homoptera	11	0.085
Orthoptera	tr me	-0.070
Homoptera	13	-0.054
Orthoptera	co cr	-0.046
Orthoptera	ps te	0.039
Diptera	3	-0.036
Orthoptera	au fe	0.032
Coleoptera	27	-0.029
Orthoptera	op ob	0.029

Order	Species	AXIS 3
Orthoptera	po pa	-0.028
Coleoptera	54	-0.022
Homoptera	28	0.017
Homoptera	25	-0.015
Orthoptera	da va	-0.014
Orthoptera	ag deo	0.006
Coleoptera	49	0.001

Table V-B.9. SWEEP NET SPECIES Principal Component Correlations. The correlations of the 41 species with the Principal Component Axis 4 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Order	Species	AXIS 4
Diptera	13	-0.371
Orthoptera	me de	-0.312
Orthoptera	ps te	0.308
Diptera	35	-0.265
Orthoptera	he ve	-0.250
Orthoptera	pa wy	-0.235
Homoptera	19	-0.225
Hemiptera	3	-0.198
Homoptera	2	-0.197
Orthoptera	am co	-0.167
Homoptera	1	-0.163
Orthoptera	ps de	0.158
Coleoptera	44	-0.156
Coleoptera	4	-0.154
Homoptera	24	-0.153
Orthoptera	me me	0.149
Coleoptera	50	-0.145
Coleoptera	30	0.133
Orthoptera	da va	-0.129
Coleoptera	27	-0.120
Orthoptera	co cr	-0.119
Homoptera	26	-0.115
Hemiptera	15	-0.104
Homoptera	28	0.101
Homoptera	27	-0.097
Orthoptera	er si	-0.093
Orthoptera	tr me	0.082
Homoptera	13	-0.079
Diptera	3	-0.070
Coleoptera	57	-0.059
Orthoptera	po pa	-0.056
Orthoptera	op ob	-0.054
Homoptera	11	0.043
Homoptera	25	-0.040

Order	Species	AXIS 4
Orthoptera	au fe	-0.039
Coleoptera	58	0.028
Coleoptera	54	0.024
Orthoptera	sp 15	-0.018
Coleoptera	49	0.007
Orthoptera	ag deo	0.004
Diptera	19	0.001

Table V-B.10. SWEEP NET SPECIES Principal Component Correlations. The correlations of the 41 species with the Principal Component Axis 5 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Order	Species	AXIS 5
Orthoptera	me de	-0.293
Orthoptera	ag deo	-0.291
Homoptera	26	0.259
Homoptera	19	-0.251
Coleoptera	57	0.247
Hemiptera	3	-0.236
Diptera	35	-0.233
Coleoptera	58	-0.233
Coleoptera	44	0.232
Homoptera	25	0.221
Diptera	19	-0.215
Orthoptera	tr me	0.185
Orthoptera	po pa	-0.185
Orthoptera	pa wy	0.174
Orthoptera	ps de	-0.173
Coleoptera	54	0.165
Coleoptera	30	-0.152
Hemiptera	15	-0.151
Homoptera	27	0.140
Orthoptera	co cr	0.138
Orthoptera	ps te	-0.121
Coleoptera	27	0.103
Diptera	13	0.101
Orthoptera	sp 15	0.092
Orthoptera	op ob	0.089
Coleoptera	4	-0.084
Homoptera	24	0.078
Orthoptera	am co	-0.063
Orthoptera	er si	-0.059
Homoptera	2	-0.055
Diptera	3	0.047
Orthoptera	me me	-0.046
Homoptera	1	-0.043
Coleoptera	49	-0.036

Order	Species	AXIS 5
Orthoptera	he ve	-0.024
Homoptera	11	-0.015
Orthoptera	au fe	-0.015
Coleoptera	50	0.012
Homoptera	13	0.003
Orthoptera	da va	-0.002
Homoptera	28	0.001

Table V-B.11. SWEEP NET SPECIES Principal Component Correlations. The correlations of the 41 species with the Principal Component Axis 6 obtained from PCA analysis of Appleton-Whittell Research Ranch insect community data.

Order	Species	AXIS 6
Homoptera	1	-0.047
Hemiptera	15	0.039
Homoptera	25	0.043
Coleoptera	44	0.113
Homoptera	28	0.136
Homoptera	19	-0.083
Homoptera	24	-0.221
Homoptera	26	0.017
Orthoptera	pa wy	0.016
Orthoptera	sp 15	0.092
Orthoptera	er si	-0.009
Orthoptera	da va	-0.019
Coleoptera	27	-0.017
Coleoptera	54	-0.002
Orthoptera	he ve	-0.042
Orthoptera	me de	-0.083
Orthoptera	ps de	0.370
Orthoptera	ag deo	-0.059
Orthoptera	ps te	-0.137
Orthoptera	co cr	0.261
Diptera	3	0.190
Homoptera	11	-0.005
Coleoptera	30	-0.029
Diptera	13	-0.126
Orthoptera	tr me	-0.474
Coleoptera	49	0.250
Diptera	35	0.114
Coleoptera	57	0.020
Orthoptera	au fe	-0.060
Orthoptera	op ob	0.033
Coleoptera	58	-0.128
Orthoptera	po pa	-0.088
Orthoptera	am co	-0.030
Homoptera	2	-0.051

Order	Species	AXIS 6
Homoptera	27	-0.140
Coleoptera	50	0.205
Homoptera	13	-0.356
Coleoptera	4	0.045
Hemiptera	3	0.044
Orthoptera	me me	-0.290
Diptera	19	-0.005

Percentage Variance

The importance of the Principal Coordinate axes is measured by the amount of total variance accounted for by those axes. By definition, the first axis accounts for the most variation, and the proportion of the total variance decreases with succeeding axes. It is important to report the amount of total variance accounted for in the axes that are discussed in a scientific paper.

The amount of total variance accounted for, in a way, alludes to the strength of the analysis, somewhat similar to an R^2 value in a regression analysis. For example, reporting that the first three axes account for 84.78 percent of the total variance, equivalent to saying the R^2 value of the analysis is 0.8478. It is up to the reader to determine whether enough of the variance was accounted for, and therefore estimate the strength of the conclusions.

Table V-B.12. SWEEP NET SPECIES Percentage Variance and Cumulative Variance for Principal Coordinate Axes. The percentage of the total variance and the cumulative variance for the Principal Coordinate Axes resulting from PCA analysis of the Appleton-Whittell Research Ranch insect community data.

Axes	1	2	3	4	5	6
EIGENVALUE	7050.33	2761.40	1551.78	1066.88	724.53	545.87
% VARIANCE	52.60	20.60	11.58	7.96	5.41	1.86
CUM. %	52.60	73.20	84.78	92.73	98.14	100.00

Site Principal Coordinate Axes Scores

Included in the results of ORD are the scores (position) of the sampling sites on the Principal Coordinate Axes. These scores are used to produce graphs (Figures V-A.1, V-A.2, and V-A.3), to explore the structure of the data, and to form hypotheses about group associations for the sampling sites.

Table V-B.13. SWEEP NET SPECIES Principal Coordinate Axes Scores. The scores (positions) of the sampling sites on the Principal Coordinate Axes obtained from ORD analysis of the Appleton-Whittell Research Ranch insect community data.

SITE	AXIS 1	AXIS 2	AXIS 3	AXIS 4	AXIS 5	AXIS 6
1	0.09	0.395	-0.175	0.276	-0.171	0.102
2	0.304	0.132	0.199	0.319	0.772	-0.004
3	0.494	0.053	0.244	-0.729	-0.113	-0.142
4	0.439	-0.257	-0.21	0.401	-0.489	0.095
1-D	-0.448	0.151	0.721	0.131	-0.284	0.106
2-D	-0.314	-0.081	-0.237	0.032	0.012	-0.843
3-D	-0.332	0.375	-0.498	-0.313	0.087	0.38
4-D	-0.232	-0.767	-0.044	-0.117	0.186	0.306

Principal Coordinate Axes Ordinations

Ordinations derived from ORD analysis of the Appleton-Whittell Research Ranch insect community data are plotted in three axes combinations. It is standard to report Axis 1 vs. Axis 2, Axis 1 vs. Axis 3, and Axis 2 vs. Axis 3. Other plots can be constructed using the information in Table V-B.13.

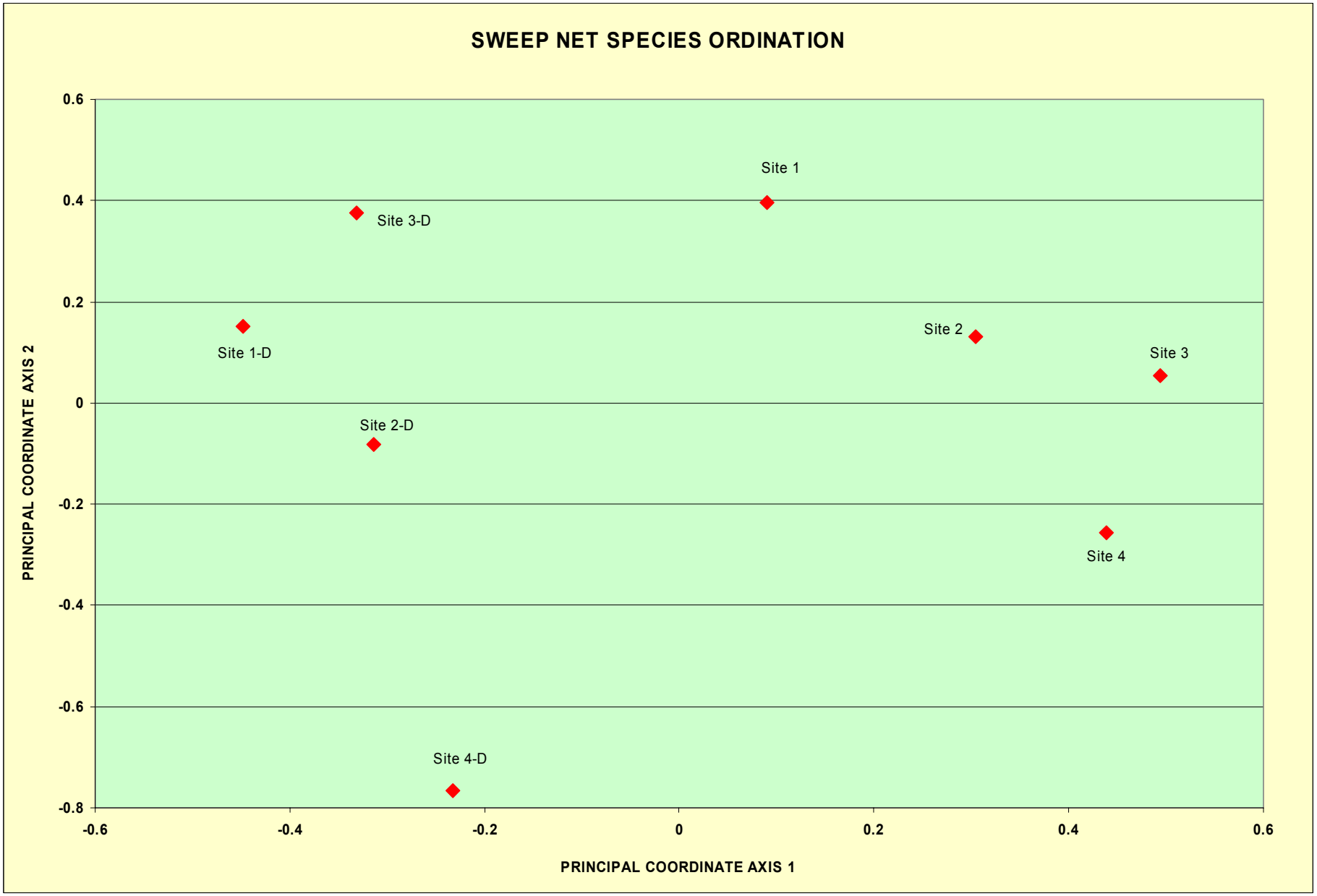

Figure V-B.1. SWEEP NET SPECIES Principal Coordinate Analysis Ordination, Axis 1 vs. Axis 2.

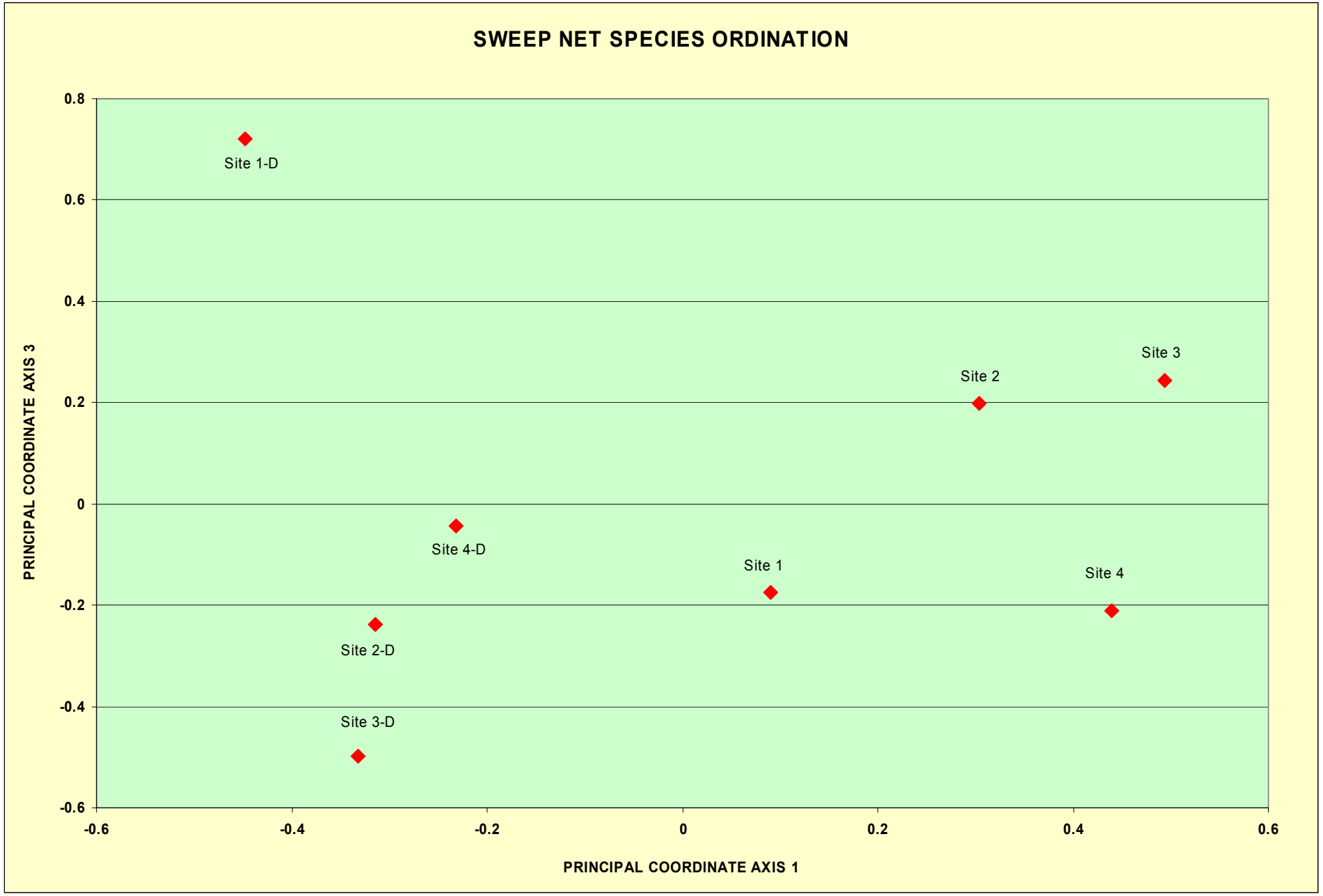

Figure V-B.2. SWEEP NET SPECIES Principal Coordinate Analysis Ordination, Axis 1 vs. Axis 3.

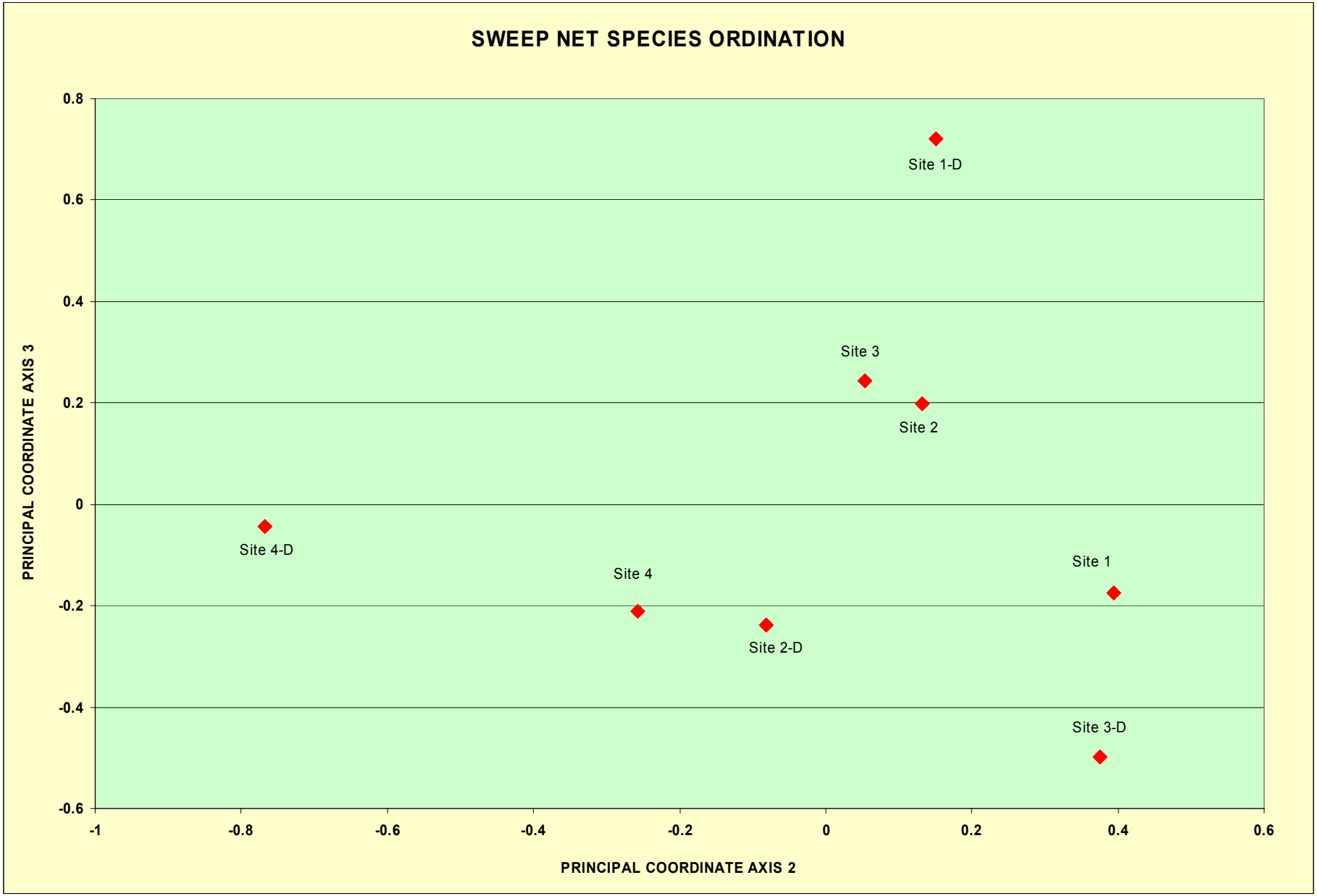

Figure V-B.3. PITFALL TRAP SPECIES Principal Coordinate Analysis Ordination, Axis 2 vs. Axis 3.

TWINSPAN

Groupings

Two-**W**ay **In**dicator **Sp**ecies **An**alysis (TWINSPAN) was used to form groups of the sampling sites based on species abundance rather than on dissimilarity indices as in Ordination. TWINSPAN provides another relatively unbiased method of forming groups.

The results of TWINSPAN are usually presented as a dendogram. Sites with similar community composition appear in groups. The differences between groups can be determined from the point of departure on the dendogram scale. The higher order the departure, the greater the group differences. This scale is not presented in this report because the magnitude of group differences were investigated using Multigroup Discriminant Analysis (MDA). TWINSPAN resulted in the following groupings for the sampling sites (color-coded for viewing convenience).

Table V-B.14. SWEEP NET SPECIES TWINSPAN Groups. The groups of sampling sites resulting from TWINSPAN of the Appleton-Whittell Research Ranch insect community data.

Sampling Site	1st Order group	2nd Order Group
Site0004	1	
Site0003	1	
Site0002	1	
Site003D	0	1
Site001D	0	1
Site0001	0	1
Site004D	0	0
Site002D	0	0

Nonmetric Multidimensional Scaling (NMDS)

The vectors from the first six ORD axes were evaluated using NMDS. The results are presented as ordination plots of three axes configurations (Figures V-B.4, V-B.5, and V-B.6). These plots should be viewed to confirm ordination results obtained from ORD (Figures V-B.1, V-B.2, and V-B.3).

Table V-B.15. SWEEP NET SPECIES Nonmetric Multidimensional Scaling Axes Scores. The scores (positions) of the sampling sites on the rescaled axes obtained from NMDS analysis of the Appleton-Whittell Research Ranch insect community data.

SITE	AXIS 1	AXIS 2	AXIS 3	AXIS 4	AXIS 5	AXIS 6
1	0.139	0.438	-0.166	0.279	-0.149	0.099
2	0.396	0.161	0.214	0.327	0.769	0.006
3	0.639	0.055	0.244	-0.758	-0.111	-0.160
4	0.568	-0.287	-0.212	0.393	-0.491	0.093
1-D	-0.589	0.169	0.747	0.161	-0.288	0.112
2-D	-0.422	-0.094	-0.251	0.038	-0.007	-0.838
3-D	-0.433	0.415	-0.525	-0.312	0.083	0.387
4-D	-0.298	-0.856	-0.051	-0.129	0.193	0.302

After consultation with the client, it was decided that group configurations revealed by ORD, TWINSPAN, and NMDS had biological meaningful and therefore, the first four Principal Coordinate (ORD) Axes were analyzed using Multigroup Discriminant Analysis.

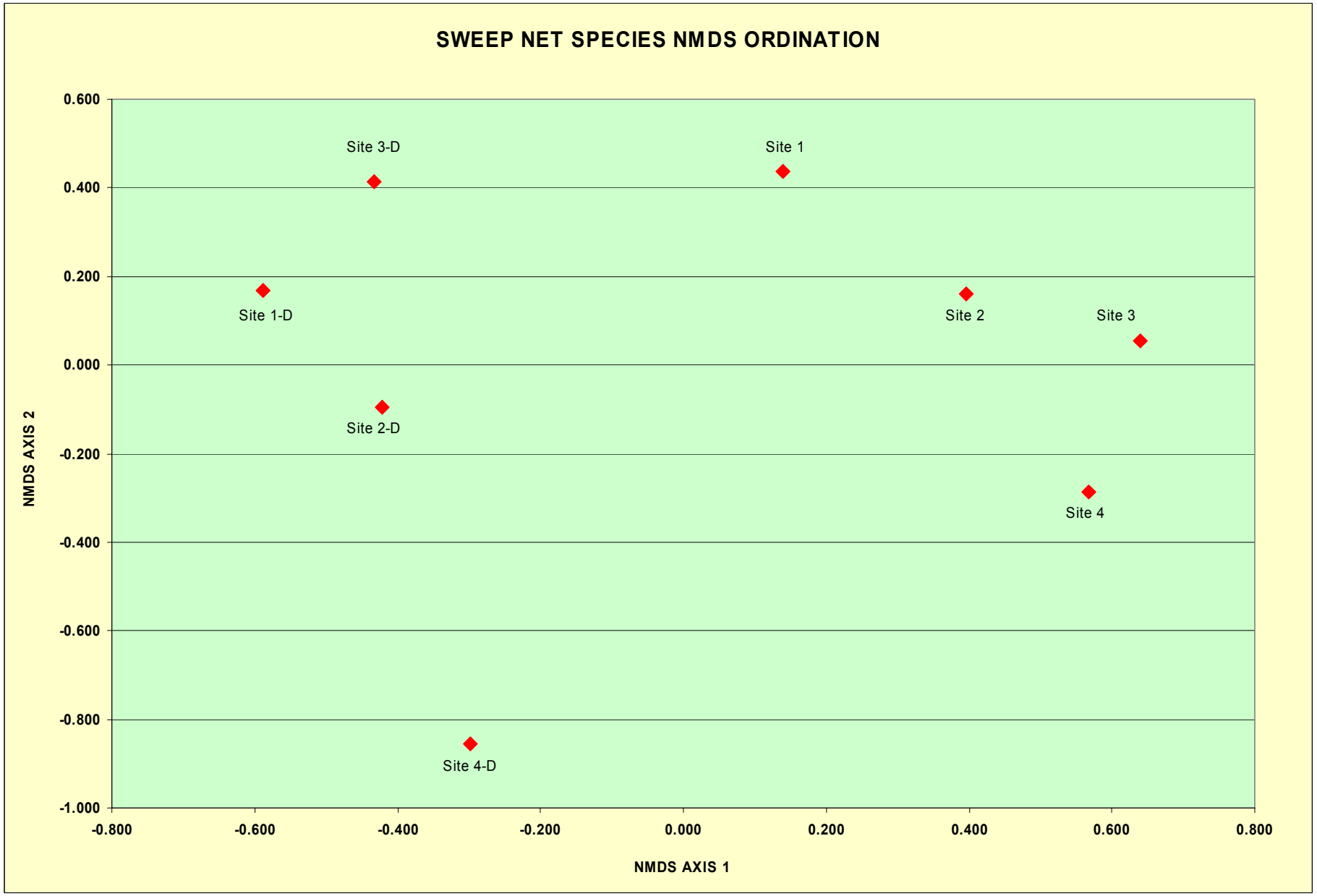

Figure V-B.4. SWEEP NET SPECIES NMDS Ordination Axis 1 vs. Axis 2.

Figure V-B.5. SWEEP NET SPECIES NMDS Ordination Axis 1 vs. Axis 3.

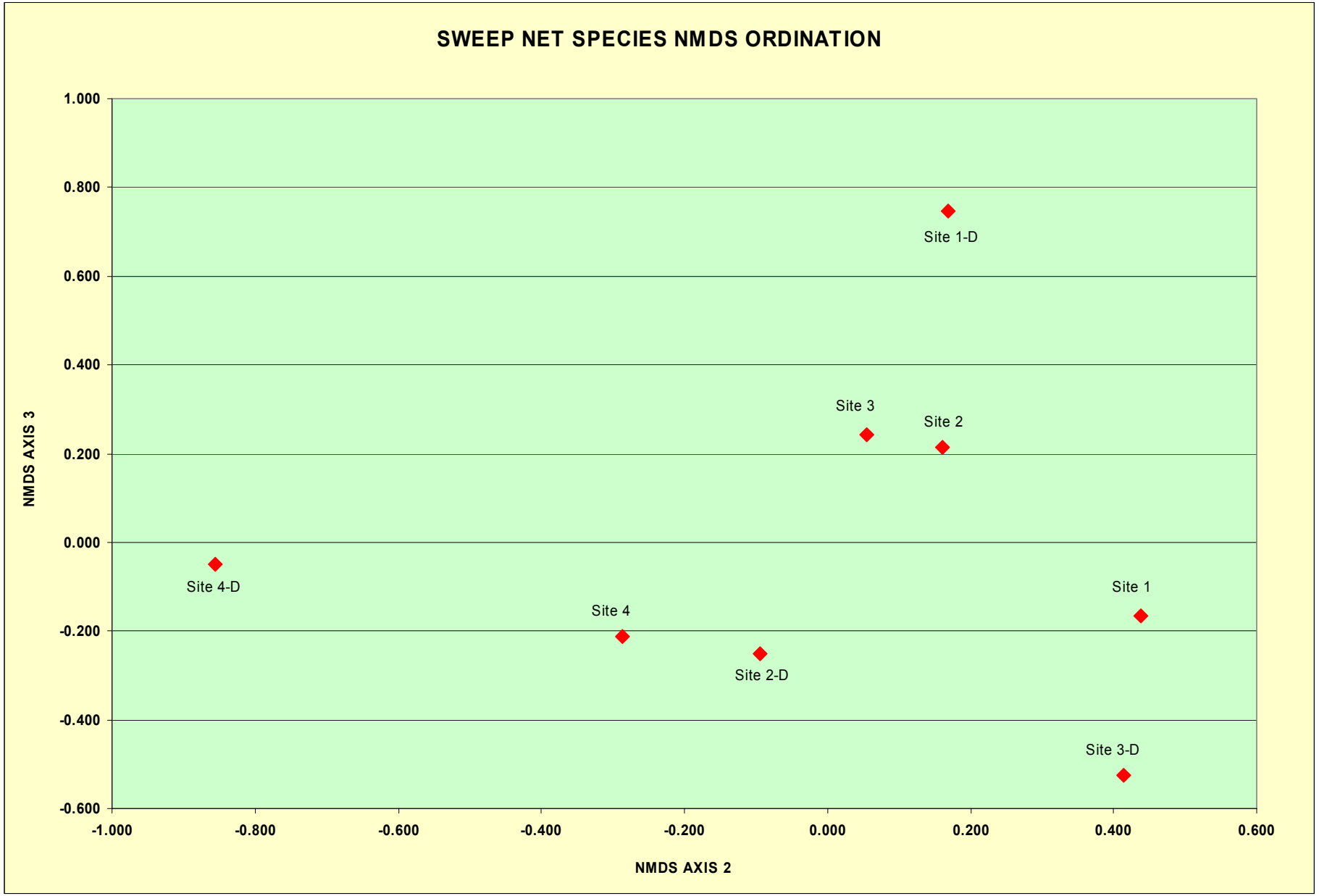

Figure V-B.6. SWEEP NET SPECIES NMDS Ordination Axis 2 vs. Axis 3.

Multigroup Discriminant Analysis (MDA)

The first four Principal Coordinate Axes were analyzed using Multigroup Discriminant Analysis (MDA). The purpose of MDA is to obtain information about the magnitude of the differences in a priori selected groups. Two separate MDA analyses were preformed. In the first analysis, 2 groups were evaluated. Group 1 consisted of Sampling Sites 1, 2, 3, and 4 (all non-grazed sites). Group 2 consisted of Sampling Sites 1D, 2D, 3D. and 4D (all grazed sites). In the second analysis 3 groups were evaluated. Group 1 consisted of Sampling Sites 1, 2, 3, and 4 (all non-grazed sites). Group 2 consisted of Sampling Sites 1D and 3D (all traditional range management grazed sites). Group 3 consisted of Sampling Sites 2D and 4D (all holistic range management grazed sites).

ANALYSIS 1

MANOVA

The analysis began with a univariate test of each of the variables (ORD axes). There was strong evidence of Group differences only on Axis 1. The test for overall discrimination between groups showed that there was strong evidence of group differences on the ORD axes
(Tables V-B.16 and V-B.17).

Table V-B.16. SWEEP NET SPECIES MDA MANOVA Table. Univariate testing for Group differences along each of the four Principal Coordinate axes.

Coordinate Axis	Among Mean Sq.	Within Mean Sq.	F-Ratio	Probability	Adjusted Probability
1	0.880	0.020	43.69	0.0000	0.00309
2	0.052	0.158	0.33	0.8791	0.97210
3	0.002	0.166	0.01	0.9676	0.99996
4	0.036	0.161	0.22	0.8421	0.98604

Table V-B.17. SWEEP NET SPECIES Discriminant Analysis Test Of Overall Discrimination (=Equality Of Centroids) Table. Test of overall discrimination between groups.

LAMBDA	F-RATIO	D.F. 1	D.F. 2	PROB.
0.0314937	23.064	4	3	0.01368

Geisser Classification

The integrity of the groups is measured by the fit of the sampling sites to their respective groups. In this analysis, all sites were classified into their a priori selected groups, i.e., 100% hits.

Distance Analysis

The distance between group centroids is measured by two metrics, Euclidean (Taxonomic) Distance and Generalized (Standard Deviation) Distance. The information is useful to determine the magnitude of the differences between the groups.

Euclidean Distance is used to assess the between group centroid differences in reference to the original variable coordinate axes. The Euclidean Distance between Groups 1 and 2 was estimated to be 0.696.

Generalized Distance (also known as Mahalanobius Distance) is the distance between centroids in discriminant space expressed in units of standard deviations. The Generalized Distance between Groups 1 and 2 was estimated to be 9.605.

95% Confidence Radii

The fit around each of the group centroids is measured by their 95% confidence radii (Table V-B.18). The smaller the number, the more similar each of the members of a group are to each other, relative to their similarity to members of the other groups. The confidence radii, like familiar confidence intervals expressed in regression and normal Gaussian statistical analysis, are highly influenced by sample size. It should be noted here that the sample sizes for each of the groups were small, and greatly influenced this MDA analysis.

Table V-B.18. SWEEP NET SPECIES Group 95% Confidence Radii. The 95% confidence radii for the two groups of sites analyzed using MDA.

GROUP	Confidence Radius
1	1.59
2	1.59

ANALYSIS 2

MANOVA

The analysis began with a univariate test of each of the variables (ORD axes). There was strong evidence of Group differences only on Axis 1. The test for overall discrimination between groups showed that there was suggestive evidence of group differences on the ORD axes
(Tables V-B.19 and V-B.20).

Table V-B.19. SWEEP NET SPECIES MDA MANOVA Table. Univariate testing for Group differences along each of the four Principal Coordinate axes.

Coordinate Axis	Among Mean Sq.	Within Mean Sq.	F-Ratio	Probability	Adjusted Probability
1	0.447	0.021	20.85	0.00464	0.01841
2	0.262	0.095	2.75	0.15634	0.49339
3	0.033	0.187	0.17	0.84483	0.99942
4	0.019	0.192	0.10	0.90712	0.99993

Table V-B.20. SWEEP NET SPECIES Discriminant Analysis Test Of Overall Discrimination (=Equality Of Centroids) Table. Test of overall discrimination between groups.

LAMBDA	F-RATIO	D.F. 1	D.F. 2	PROB.
0.0118136	4.100	8	4	0.09546

Geisser Classification

The integrity of the groups is measured by the fit of the sampling sites to their respective groups. In this analysis, all sites were classified into their a priori selected groups, i.e., 100% hits.

Distance Analysis

Euclidean Distance is used to assess the between group centroid differences in reference to the original variable coordinate axes.

Table V-B.21. SWEEP NET SPECIES Euclidean Distances between Groups.

GROUPS	No Grazing	Traditional	Holistic
No Grazing	0.000	0.767	0.810
Traditional	0.767	0.000	0.743
Holistic	0.810	0.743	0.000

Generalized Distance (also known as Mahalanobius Distance) is the distance between centroids in discriminant space expressed in units of standard deviations.

Table V-B.22. SWEEP NET SPECIES Generalized Distances between Groups.

GROUPS	No Grazing	Traditional	Holistic
No Grazing	0.000	8.950	10.434
Traditional	8.950	0.000	2.886
Holistic	10.434	2.886	0.000

95% Confidence Radii

The fit around each of the group centroids is measured by their 95% confidence radii (Table V-B.23). The smaller the number, the more similar each of the members of a group are to each other, relative to their similarity to members of the other groups. The confidence radii, like familiar confidence intervals expressed in regression and normal Gaussian statistical analysis, are highly influenced by sample size. It should be noted here that the sample sizes for each of the groups were small, and greatly influenced this MDA analysis.

Table V-B.23. SWEEP NET SPECIES Group 95% Confidence Radii. The 95% confidence radii for the two groups of sites analyzed using MDA.

GROUP	Confidence Radius
1	1.59
2	8.98
	8.98

VI. DISCUSSION

Not included in Chapter V. RESULTS were the results of testing assumptions and proper conditioning of the input data matrix for MDA. As discussed in IV. STATISTICAL PROCEDURES, the assumptions of MDA are random sampling, normality, independence of errors, equality of population dispersions (homoscedasticity), and additivity of treatment and error effects. The consequences of unsatisfied assumptions (proper conditioning of the input data matrix) can lead to several problems with interpretation of the results of MDA. Each assumption and the consequences of a lack of proper conditioning are addressed below.

Random sampling is required for any analytical procedure to ensure that the sample is representative of the population of interest. Because Pacific Analytics was not involved in the planning and design of this study, we rely on the client to make this determination. Scientists often use collecting techniques that introduce bias in their sampling. This can be especially true when collecting invertebrates. All trapping methods have bias. In scientific publications it is up to the author(s) to explain how the samples were collected and discuss trapping bias.

The influence of nonnormality of the data to be analyzed on statistical analysis can be relatively minor. The Central Limit Theorem asserts that averages based on large sample sizes have an approximately normal sampling distribution. Thus, the assumption of underlying normality need not be a serious issue, as long as sample sizes are large. In the case of the Appleton-Whittell Research Ranch insect community data,

the size of the groups formed from ORD was relatively small. Groups had only two to four members. Even when distributions follow normality, sample sizes this small are problematic. However, Burnaby (1966) and Olson (1977) found that nonnormality has only minor influence on the results of MDA (Pimentel 1993).

Dependence of errors and nonadditivity can cause inequality of group dispersions (heteroscedasticity). This can lead to serious problems when using standard statistical techniques such as t-tests and regression. When the pooled estimate of standard deviation does not accurately reflect the population parameter the t-ratio no longer has a t-distribution. The result is inaccurate estimates of the significance of the p-values obtained in such cases. For MDA, the lack homoscedasticity can lead to imprecise values for Generalized Distances and unreliable Geisser Classifications (Geisser 1977). However, heteroscedasticity does not invalidate the biological interpretation of the results (Pimentel 1993).

MDA is more appropriately applied to data in which sample sizes are equal or sample sizes are large. Problems that result from a lack of homoscedasticity are minimal when sample sizes are large, but there are no sure-cures for small sample sizes. When the results of several analytical procedures are similar, one may conclude that biological inferences are robust. In the case of the Appleton-Whittell Research Ranch insect community data, similar results were obtained from ORD, TWINSPAN, and NMDS, therefore inferences may be robust.

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