

Implications of Pollen Character Coding and Their Diagnostic Value In The Determination of Taxonomic Resemblance Among Some *Indigofera* Linn Species

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Abstract: Whereas phenetics emphasizes the use of maximum characters as practicable, decisions on how observations are translated to characters is of importance in systematics in order to partition objects in to non-overlapping groups. The acetolysed pollen of selected *Indigofera* Linn. species were viewed under Mg x100 in Leica light microscope. Pollen characteristics of the following *Indigofera* species deposited in Maseno University Herbarium have been studied: *I. paracapitata*, *I. asparagoides*, *I. ambelacensis*, *I. vohemarensis*, *I. sabargentea*, *I. circinella*, *I. zenkeri*, *I. arrecta*, and *I. vicinoides*. The highest taxonomic diversity (0.5) was observed when aperture character and amb were separately used in two character states. Shape class in 2 character state coding gives the least phenotypic diversity (0.149). *I. asparagoides* is of the highest mean dissimilarity (0.563) to other species in all the characters coded into two character states. *I. circinella* had 44.7% dissimilarity to the rest of the species when characters in three states were used, and was the most dissimilar to the rest of the species when all the pollen characters were used in both their 2 and 3 states. There was a 36.6% and 35.6% taxonomic diversity with pollen characters in their two and three character states respectively.

Keywords: *Indigofera*, Palynology, Character states, taxonomic resemblance, taxonomic diversity.

I. INTRODUCTION

Distinct taxa can be recognized because overall similarity between any two entities is a function of their individual similarities in each of the many characters in which they are being compared (Gurcharan, 2004). Decisions on translation of observations to characters are therefore of importance in systematics (Freudenstein, 2005). The distinction between character and character states was not introduced until mid 20C. It was with the rise of numerical approaches to taxonomy that the character and character state distinction became common (Freudenstein *et al*, 2003). Although continuous characters have been integrated in to analysis, no method for their treatment has received unanimous support. Some methods require a large number of character states to discretise continuous characters in order to keep the maximum level of information about taxa differences (Bardin *et al*, 2013). the value of the index increase and reach maximum when all phenotypic classes have equal frequencies (Yang *et al*, 1991). In the numerical study of the *Cytisus* (Leguminosae), Sneath and Sokal (1973) showed that a distortion in using a distance measure of relationship can be caused by changing in quantitative continuous character in to a qualitative binary one. Depending on the spread of values, qualitative multistate characters are very likely to be caused by more than one genetic factor and several two state characters can thus be more appropriate (Sneath and Sokal, 1973). phenetic approach necessitates a careful consideration of characters, their states,

coding, and scaling in their selection so there are no pieces of information (Dale, 1968). A character at minimum must partition the objects under study in to non-overlapping groups using a set of non overlapping descriptors known as character states ; character states should be independent i.e., any organism under a group of organisms being studied must fall in one of the character states. Characters don't have to be independent from each other. searching for at least 100 meaningful characters has been difficult to achieve in many plant groups, practicing taxonomists therefore seek more character information. This has lead to classifications with greater stability, predictiveness and information content (Sneath and Sokal, 1973; Stuessy, 2009). A potential taxonomic character has at least two character states (Sosa and Luna, 1998). Intermediate characters that show both states in a character are not very useful (McCarthy, 2006). Useful patterns of variation are exhibited by characters with significantly more variation among groups than within one of the groups being studied. Under any taxonomic study evaluation of each character state variation is important in the process of character selection (Sosa and Luna, 1998). A character is regarded primary when other characters depend on it and should have greater weight placed upon it in the assessment of resemblance in taxonomy (Williams, 1969). When characters are chosen and divided into states consistently, partitioning of the objects give much distinct clusters (Pierre and Rodgers, 1972). Characters with many states contribute more in determining the similarity than those with few states. The appropriate coding method dependence on the similarity coefficient to be computed (Stuessy, 2009). methods of coding continuous character can lead to the generation of well resolved phylogenetic trees that do not reflect phylogenetic phenomenon (Bardin *et al.*, 2013). Each taxon possesses a collection of characters of which each can be in one of the finite states; this facilities the description of taxa over a character states matrix (Mishra, 2001). Recoding characters in to binary requires assumptions about the determinants of the phenotypic differences in the character states. additive coding considers all increment among the group sequence in consort with the philosophy of additive binary coding. In gap coding, gaps along the continuum of a character are used to determine the classes for an ordered discrete multistate character. Comparative studies in the effect of these various techniques are however, urgently required (Stuessy, 2009). gap coding method is much reproducible, but sampling dependent; removing one taxon from the sample could alter the coding of the entire character (Schols *et al.*, 2004). Some systematists on the extreme suggesting procedures to partition continuous variation in to an arbitrary number of character states (Simon, 1983; Chappill, 1989).

Qualitative multistate characters frequently pose problems for character coding. Such problems can be solved by converting the multistate characters in to a series of binary characters as presence or absence data. Whatever the method, its implications on the assessment of phenetic relationships has to be determined in each particular case (Stuessy, 2009). Multistate characters in some types of analysis without having to reduce them to binary data. Although there are different methods available for scaling of characters to minimize the effects of character coding, (Sneath and Sokal, 1973), each case must be evaluated on its own merits. with the subjectivity of the investigator of conspicuous role (Stuessy, 2009). Some coding methods are difficult to reproduce and ignore a lot of information contained within the data (Schols *et al.*, 2004).The information contained in one character may be partial or complete redundancy of the information contained in another character. The independence of character shows that they contribute differently than complimentarily to a classification. The intrinsic structure of information a character provides refers to that part of information which has taxonomic value because it reflects the affinities and differences (Pierre and Rodgers 1972). Character varies in the properties they represent and their information content (McCarthy, 2006). Character quality is determined by the reliability of the notion that the similarity or difference embodied in a character actually reflects a biological fact. The quality of a character depends on the states it gives rise to, membership structures and reason for that membership (Williams, 1969). The quantity of information in a character is a measure of how difficult it is (on the average) to guess the state membership of randomly chosen object. As the number of states in a character increases, it becomes more difficult to make a choice. Different characters contain different quantities of information, The quantity of information increases with the number of character states. Characters with a highly skewed distribution within the states have low information quantity but this does not imply low in quality. The quality and quantity of information in a character could be important for development of diagnostic keys and evaluation of a classification. Characters vary in the classification value (Davis and Heywood, 1963).

In phenetic classification one can attempt to establish taxa either based on maximum similarity among OTUs at hand or on maximum predictive value (homogeneity of character states) Sokal (1985). Similarity between two OTU is generally estimated by means of similarity coefficient, which is a quantification of the resemblance between elements in a conventional 2x2 data matrix representing the character states of the two OTUs in question. Although coefficient of resemblance would be a more appropriate term, "similarity coefficient" is the commonest term. Resulting distance

analysis among characters help the discovery of the taxonomic structures of objects studied. congeneric species are often 50-60% similar to each other, the species level are always found around 75% of similarity, and subspecies around 85% of similarity. Although large disparities have been observed, this have been attributed to the group of objects studied and how well the information about the object is structured. Value of distance however, doesn't say everything about the type of correlation since it doesn't refer to the relative amount of information present in each of the characters compared (Pierre and Rodgers, 1972). This study investigated the implication of character coding in the taxonomic resemblance based on some pollen features of *Indigofera* species and the association between character state coding and character state membership distribution.

II. MATERIALS AND METHODS

Materials:

Pollen characteristics of the following *Indigofera* species deposited in Maseno University Herbarium have been studied:

I.paracapitata, *I.asparagoides*, *I.ambelacensis*, *I.vohemarensis*, *I.sabargentea*, *I.circinella*, *I.zenkeri*, *I.arrecta*, and *I.vicioides*. The major equipments used are: Nikon Type-102 Microscope, (Typ: W600 DINI 2877-KI, GERMANY Model).

Chemicals and reagents:

All chemicals and reagents were of analytical grade.

Acetolysis and Microscopy:

Acetolysis and microscopy according to according to Reitsima (1969) method. Light microscopy was carried out according to Perveen and Qaiser (1998) method.

Coding of pollen characteristics:

Pollen Characters were coded as in Table 1 below:

Table 1: Coding of pollen characteristics

Character	Character states	State 1/Code 1	State 2/Code 2	State 3/Code 3
Polar axis	2	<29.97µm	≥29.97 µm	-----
	3	23.63µm-<27.84 µm	≥27.84 µm-< 32.05 µm	≥32.05 µm
Equatorial axis	2	<26.25 µm	≥26.25 µm	
	3	<24.64 µm	≥24.64 µm-< 27.85 µm	≥28.75 µm
P/E ratio	2	<1.18	≥1.18	
	3	<1.147	≥1.147-<1.214	≥1.214
Aperture character	2	Colporate	Non-colporate	
	3	Colporate	Colpate	Porate
Shape class	2	Prolate	Non-plorate	
	3	Prolate	Plorate-spheroidal	Spheroidal-prolate
Amb	2	Circular	Angular	
	3	Circular	Angular- straight	Angular-convex

Statistical analysis:

Estimation of taxonomic resemblance was done using Simple Matching Coefficient (Sokal and Michener, 1958) with the basic assumption that character states carry equal information (symmetry) according to the following formula:

$$Dissimilarity = \frac{q + r}{t}$$

Similarity=1-Dissimilarity

Where q+r = Hamming distance.

p= Number of character states present in both taxa being compared.

q=Number of character states present in ith object and absent in jth object

r= Number of character states absent in ith object and present in jth object

s= Number of character states absent in both taxa being compared

t=p+q+r+s (Number of character states)

$$\text{Mean taxonomic dissimilarity} = \frac{\text{Sum of dissimilarities of comparisons}}{\text{Number of comparisons}}$$

$$\text{Agglomerative taxonomic dissimilarity} = \frac{\text{Sum of all dissimilarities based on all coding system used}}{\text{Sum of coding systems}}$$

III. RESULTS

Table 2:Coded pollen characteristics of the *Indigofera* species studied .

States Species	Polar axis		Equatorial Axis		P/E ratio		A.ctr		Shape class		Amb	
	2CS	3CS	2CS	3CS	2CS	3CS	2CS	3CS	2CS	3CS	2CS	3CS
<i>I.paracapitata</i>	1	2	1	1	1	2	2	2	2	2	2	3
<i>I.asparagoides</i>	2	3	2	3	1	2	1	1	2	2	2	3
<i>I.ambelacensis</i>	1	2	1	2	2	2	1	1	2	2	1	1
<i>I.vohemarensis</i>	1	1	1	1	1	1	1	1	2	2	2	2
<i>I.sabargentea</i>	1	1	1	1	1	1	1	1	2	2	2	3
<i>I.circinella</i>	1	1	1	1	2	3	2	2	1	1	2	3
<i>I.zenkeri</i>	1	1	1	2	1	1	2	3	2	2	2	2
<i>I.arrecta</i>	1	1	1	1	1	1	1	1	2	2	1	1
<i>I.viciooides</i>	1	1	1	1	1	1	1	1	2	2	1	1

KEY :2CS: Two character states coding; 3CS: Three character states coding; A.ctr:Aperture character.

From the table the distribution of the species into two character states in the 2-character state coding system ranged from (8:1/1:8; 2:7; 3:6/6:3). Polar axis, equatorial axis and shape class gave equal similarity coefficient (0.222). The P/E ratio had a distribution of 7:2 in character state 1 and 2 respectively. Aperture character and Amb had a distribution of (3:6 and 6:3). Shape class had a distribution of 1:8:0. The P/E ratio and the Amb had distribution of 5:3:1 and 3:2:4 respectively.

Table 3: Mean simple matching distance between tabled species and the rest of species.

States Species	Polar axis		Equatorial Axis		P/E ratio		A.ctr		Shape class		Amb	
	2CS	3CS	2CS	3CS	2CS	3CS	2CS	3CS	2CS	3CS	2CS	3CS
<i>I.paracapitata</i>	0.125	0.586	0.125	0.251	0.25	0.503	0.75	0.586	0.125	0.084	0.375	0.419
<i>I.asparagoides</i>	1.00	0.586	1.00	0.67	0.375	0.503	0.375	0.168	0.125	0.084	0.5	0.419
<i>I.ambelacensis</i>	0.125	0.586	0.125	0.586	0.625	0.503	0.375	0.251	0.125	0.084	0.5	0.503
<i>I.vohemarensis</i>	0.125	0.251	0.125	0.251	0.250	0.335	0.375	0.251	0.125	0.084	0.375	0.586
<i>I.sabargentea</i>	0.125	0.251	0.125	0.251	0.250	0.335	0.375	0.251	0.125	0.084	0.375	0.419
<i>I.circinella</i>	0.125	0.251	0.125	0.251	0.875	0.67	0.75	0.419	1.00	0.67	0.375	0.419
<i>I.zenkeri</i>	0.125	0.251	0.125	0.586	0.25	0.335	0.75	0.586	0.125	0.084	0.375	0.586
<i>I.arrecta</i>	0.125	0.251	0.125	0.251	0.25	0.335	0.375	0.251	0.125	0.084	0.75	0.53
<i>I.viciooides</i>	0.125	0.251	0.125	0.251	0.25	0.335	0.375	0.251	0.125	0.084	0.75	0.583
Mean taxonomic Dissimilarity	0.222	0.372	0.222	0.372	0.389	0.403	0.50	0.354	0.222	0.149	0.50	0.484

There was a similar ratio of distribution (1:8) of the Polar and equatorial axis in the 2 state character coding system, and 6:2:1 for the polar axis, equatorial axis in the 3 character state coding system giving a phenotypic diversity of 0.222 and 0.372 respectively. In a two character state coding system, the phenotypic diversity increases from 0.222, 0.389, 0.5 proportionately to 7, 5, 3 disparities in state membership. the trend is also observed In the 3 character state coding ranging from 0.149,0.372,0.354,0.403,0.484 with corresponding membership disparities ranging from 8,5,5,4,2 respectively.

Table 4. Mean taxonomic dissimilarity between tabled species in both the 2 and 3 character states of all the pollen characters.

	Character states		
	2CS (dissimilarity)	3CS (dissimilarity)	Mean dissimilarity
<i>I.paracapitata</i>	0.292	0.405	0.349
<i>I.asparagoides</i>	0.563	0.405	0.484
<i>I.ambelacensis</i>	0.313	0.419	0.366
<i>I.vohemarensis</i>	0.229	0.293	0.261
<i>I.sabargentea</i>	0.229	0.265	0.247
<i>I.circinella</i>	0.542	0.447	0.495
<i>I.zenkeri</i>	0.292	0.404	0.348
<i>I.arrecta</i>	0.292	0.284	0.288
<i>I.vicioides</i>	0.542	0.284	0.413
Mean taxonomic dissimilarity	0.366	0.356	0.361

From the table, the 2 character state coding system gives highest mean dissimilarity (all pollen characters) of 0.366, slightly higher than 0.356 in a 3 character state coding system.

Table 5. Agglomerative taxonomic dissimilarity matrix (2 character states).

	1	2	3	4	5	6	7	8	9
<i>I.paracapitata</i>	0								
<i>I.asparagoides</i>	0.500	0							
<i>I.ambelacensis</i>	0.500	0.667	0						
<i>I.vohemarensis</i>	0.167	0.333	0.333	0					
<i>I.sabargentea</i>	0.167	0.333	0.333	0.000	0				
<i>I.circinella</i>	0.333	0.833	0.500	0.500	0.500	0			
<i>I.zenkeri</i>	0.000	0.500	0.500	0.167	0.167	0.333	0		
<i>I.arrecta</i>	0.333	0.500	0.167	0.167	0.167	0.667	0.333	0	
<i>I.vicioides</i>	0.333	0.500	0.167	0.167	0.167	0.667	0.333	0	0

1: *I.paracapitata*; 2: *I.asparagoides*; 3: *I.ambelacensis*; 4: *I.vohemarensis*; 5: *I.sabargentea*; 6: *I.circinella*; 7: *I.zenkeri*; 8: *I.arrecta*; 9: *I.vicioides*

From the table above, there was 100% similarity between the pollen characteristics of *I.zenkeri* and *I.paracapitata* as well as between *I.sabargentea* and *I.vohemarensis*.

Table 6: Agglomerative dissimilarity matrix (3 character states).

	1	2	3	4	5	6	7	8	9
<i>I.paracapitata</i>	0								
<i>I.asparagoides</i>	0.334	0							
<i>I.ambelacensis</i>	0.334	0.334	0						
<i>I.vohemarensis</i>	0.445	0.445	0.445	0					
<i>I.sabargentea</i>	0.334	0.334	0.334	0.334	0				
<i>I.circinella</i>	0.334	0.334	0.334	0.334	0.334	0			
<i>I.zenkeri</i>	0.556	0.556	0.556	0.556	0.334	0.556	0		
<i>I.arrecta</i>	0.445	0.445	0.445	0.445	0.111	0.445	0.334	0	
<i>I.vicioides</i>	0.445	0.445	0.445	0.445	0.111	0.445	0.334	0.00	0

I.zenkeri and *I.paracapitata*; *I.zenkeri* and *I.asparagoides*; *I.zenkeri* and *I.ambelacensis* show the highest (0.556) agglomerative dissimilarity in a 3 character state coding system.

Table 7. Agglomerative dissimilarity matrix, both the 2 and 3 character states.

	1	2	3	4	5	6	7	8	9
<i>I.paracapitata</i>	0								
<i>I.asparagoides</i>	0.417	0							
<i>I.ambelacensis</i>	0.417	0.500	0						
<i>I.vohemarensis</i>	0.306	0.389	0.389	0					
<i>I.sabargentea</i>	0.250	0.333	0.389	0.056	0				
<i>I.circinella</i>	0.333	0.639	0.584	0.472	0.417	0			
<i>I.zenkeri</i>	0.278	0.528	0.472	0.195	0.250	0.445	0		
<i>I.arrecta</i>	0.389	0.472	0.250	0.139	0.139	0.556	0.333	0	
<i>I.vicioides</i>	0.389	0.472	0.250	0.139	0.139	0.556	0.333	0	0

Zero dissimilarity is observed between *I.vicioides* and *I.arrecta*; A dissimilarity of 0.333 is observed between *I.vicioides* and *I.zenkeri*, and also between *I.zenkeri* and *I.arrecta*. *I.vicioides* and *I.arrecta* have the same dissimilarity with the rest of the species.

IV. DISCUSSION

Although the taxa in the study herein fell in at least one of the characters states, in the aperture character 3 character state coding no species was represented. Based on the phylogenetic concept of homology, the two and three character state coding system qualifies the pollen features in this treatment as potential taxonomic characters with at least two character states and are capable of showing discrete patterns within the taxa studied as earlier suggested by (Sosa and Luna, 1998), Character state should vary between taxa (McCarthy, 2006) and each character representing a taxon was represented in one of the finite states capable of giving forth to a character state matrix. The pollen characters were also mutually exclusive among the *Indigofera* taxa studied (Freudenstein, 2006). Because the quantity of information in a character increases with the number of character states (Pierre and Rodgers, 1972), the 3 character state coding system was generally expected to provide a higher quantity of information (Davis and Heywood, 1963). The distribution of the species into two character states in the 2-character state coding system ranged from (8:1/1:8; 2:7; 3:6/6:3). Polar axis, equatorial axis and shape class had the same distribution of species (1:8, 1:8, 8:1) respectively and gave equal similarity coefficient (0.222) The P/E ratio had a distribution of 7:2 in character state 1 and 2 respectively. The P/E ratio, the Polar axis and equatorial axis were originally quantitative characters converted to qualitative data. Aperture character and Amb had a distribution of (3:6 and 6:3). Although the characters were discrete in the sense of distribution of species within each of the character states, there was significant variation in the distribution. The most even distribution was observed in the aperture character and the Amb while the most skewed distribution was observed in polar axis, equatorial axis and the shape class. In the 3 character state coding system, the polar axis, equatorial axis and the aperture character had a 6:2:1 distribution of the nine *Indigofera* species studied in character states 1, 2 and 3. Shape class had a distribution of 1:8:0, since none of the species expressed the prolate spheroidal character that is represented in character state 3 of the aperture character. The P/E ratio and the Amb had distribution of 5:3:1 and 3:2:4 respectively. In the 3 character state coding system, shape class had the least even distribution of species in to character states with Amb having the most even distribution.

There seem to be an association between the taxonomic resemblance and the evenness of distribution of species in the character states of the character in question. Similar ratio of distribution (1:8) of the Polar and equatorial axis in the 2 state character coding system, and 6:2:1 for the polar axis, equatorial axis in the 3 character state coding system giving a phenotypic diversity of 0.222 and 0.372 respectively. The phenotypic diversity tends to increase with more even distribution of the species into various character states. The evenness of distribution herein is estimated from the magnitude of disparity in the state membership between character states with the largest and smallest number of species in a character state coding system. In a two character state coding system, the phenotypic diversity increases from 0.222, 0.389, 0.5 proportionately to 7, 5, 3 disparities in state membership. the trend is also observed In the 3 character state coding ranging from 0.149,0.372,0.354,0.403,0.484 with corresponding membership disparities ranging from 8,5,5,4,2

respectively (Table 3). The general trend is an inverse relationship between evenness (species membership difference between the largest and the smallest membership in the character states) and the calculated taxonomic resemblance. Although this general trend seem to apply, the same difference between the largest and smallest character state population (5) gives a phenotypic diversity of 0.389, in a 2 character state coding system for P/E ratio, while in polar and equatorial axis a phenotypic diversity of 0.372 is given in a 3 character state coding system. This implies the possible interaction between the number of character states and the distribution of species with the character states of a coding system. The shape class has the highest difference of (8) in a 3 character coding classification system and also has the least phenotypic diversity of 0.149; Polar axis, equatorial axis and the shape class have the highest difference of 7(2 character coding system) and had the least taxonomic resemblance of 0.222. Amb in the two and three character state coding system have the highest taxonomic resemblance of 0.5 and 0.484 in the two and three character state coding systems respectively (Table 3). The observations on the distribution of taxa in the character states is in consort with Yang *et al* (1991) that value of the taxonomic resemblance index reaches maximum when all phenotypic classes, here represented as character states have equal frequencies with conclusions based on average diversity of comparisons. The more evenly distributed character states would therefore be of value in the development of diagnostic keys for the *Indigofera* taxa studied as earlier suggested by David and Heywood, (1963). In consideration of these facts therefore, the pollen characters of the *Indigofera* species would be conferred with varied classificatory value irrespective of any other quality difference that may exist. High level of skewness would portend high overlapping nature of the descriptors (character states) designed during this phenetic treatment resulting in a decimated independence which is a necessary property of the character states.

The 2 character state coding system gives highest mean dissimilarity (all pollen characters) of 0.366, slightly higher than 0.356 in a 3 character state coding system this mean value could have been contributed by the relatively high dissimilarity values (0.5) of the Amb and aperture character. This might have implications on the choice of character state coding system during a classification or phenetic studies of the *Indigofera* species. *I.asparagoides* has the highest mean dissimilarity (0.563) towards all the possible comparisons with other species in the study (all the pollen characters used in a two character state coding system). This could be attributed to its distinctness based on its polar axis and equatorial axis; it's the only species with character state 2 ($\geq 29.97\mu\text{m}$ and $\geq 26.25\mu\text{m}$) in the polar and equatorial axis respectively (Table 4). It is the species with largest polar and equatorial axis ($36.31\mu\text{m}$ and $31.06\mu\text{m}$ respectively). Although the polar and the equatorial axis could not be with the highest ability to distinguish the members of the genus in this study, it has the ability to segregate *I.asparagoides* from the rest of the taxa under study. *I.circinella* has the highest mean dissimilarity (0.447) in using all the pollen characters in a 3 character state coding system. Although slightly less than the mean dissimilarity of *I.asparagoides* towards the rest of the species in a three character state coding system, the dissimilarity could be attributable to its distinct presence in character state 3 ($\geq 1.214\mu\text{m}$, polar axis) and its prolate shape class. Both the species have mean dissimilarity above 0.5 (two character state coding system) and 0.405 (three character state coding system) table 5. *I.asparagoides* and *I.circinella* also show high distinction from the other species in the same characters that record high dissimilarities. Equal mean dissimilarities among species were observed (*I. zenkeri* and *I.arrecta*-0.292; *I. vohemarensis* and *I.sabargentea*-0.229) in the 2 character state coding system, this is attributable to their similar pollen features. The same trend was observed in the three character state coding system.

I. vohemaensis and *I.subargentea* are the least distinct from the rest of the species in 2CS based on the mean dissimilarity. The agglomerative dissimilarity index provides mean dissimilarities between each pair of the species compared based on all the pollen characteristics in the character state coding systems. There was zero dissimilarity (100% similarity) between the pollen characteristics of *I.zenkeri* and *I.paracapitata*. These species have the same pollen characteristics. The same pair of species show the highest (0.556) agglomerative dissimilarity in a 3 character state coding system. *I.subargentea* and *I.vohemarensis* have maximum similarity of pollen characteristics in a 2 character state coding system. This however changes drastically with a 3 character states coding system where the dissimilarity rises to 0.334. Although the mean dissimilarity table shows the average dissimilarities in a 2, 3 and 2 and 3 character state coding system, it isn't able to point out the dissimilarity between a pair of species. The two approaches are bound to give varied results, however it is at the discretion of the user to extract the type of information required. Zero dissimilarity is observed between *I.viciooides* and *I.arrecta*; A dissimilarity of 0.333 is observed between *I.viciooides* and *I.zenkeri*, and also between *I.zenkeri* and *I.arrecta*. *I.viciooides* and *I.arrecta* have the same dissimilarity with the rest of the species. This trend implies that the species with zero dissimilarity between or amongst themselves would have equal dissimilarities with each of the species under comparison.

Although multistate characters pose unscrupulous problems for character coding (Stuessy, 2009), the approach here involved the conversion of the characters into a series of binary characters in the assessment of taxonomic resemblance of the taxa. Classification based on as many as possible observed features is the basis of phenetics (McCarthy, 2006). The use of similarity to compare the degrees of resemblance among taxa; the overall similarity of organism was of interest in this study as has been addressed by the past works by Spring (2012), Stuessy (2009), Sokal (1985). Although there are various techniques available for measuring of resemblance in numerical taxonomy, here the coefficient of association according to (Sokal, 1985) in 2x2 convenient data arrangement has been used. The parametric resemblance between any two OTUs in this study was expressed as a percentage of unmatching character (dissimilarity) in this manner the resemblance could be expressed as a single proportion.

V. CONCLUSION

This study finds that increasing the number of character states of the pollen features has neither a significant nor direct implication of the estimation of taxonomic resemblance among the *Indigofera*.

It has also been observed that the level of taxonomic dissimilarities in pollen characters of the *Indigofera* species increases with evenness of character state membership distribution.

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