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***Research Article** (Open Access)*

SET DIAGRAM KEY: AN ALTERNATIVE WAY OF PRESENTING SINGLE- ACCESS DIAGNOSTIC TOOLS FOR PLANT IDENTIFICATION

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ABSTRACT
Identification is one of the major activities in plant taxonomy and a *sine qua non* to making informed decisions on health care, food production, sustainable housing, forest resources utilisation and biodiversity conservation. It is usually carried out by means of diagnostic keys, the most widely used being the dichotomous type. Opinions of users of keys point to structural and functionality attributes of the dichotomous key as being charged with inadequacies, including tedious construction and boring navigation. Plant identification is therefore viewed by many as intractable mission, leading to declining interest in plant taxonomy. This paper with the aim of making the practice of plant taxonomy more attractive to upcoming students of biology, has designed, illustrated, and proposed the 'set diagram key format' as a template upon which reliable plant diagnostic tools can be based, with highlights of its features, construction procedures and application. The status of the proposed key format is discussed amidst the challenges noted in the dichotomous key format, with the conclusion that the set diagram key has the potential to re-energise the dwindling interest in taxonomy.

Keywords: *Automated Plant Identification; Computerised Key; Diagnostic Key; Dichotomous Key; Multi-Access Key; Plant Identification; Single-Access Key; Taxonomic Key*

INTRODUCTION
Basically, there are two complementary problems in taxonomy: firstly, given a set of objects (e.g. plants), examine their characteristics in order to find a classification i.e. group the objects into subsets (or taxa), and assign names to the subsets; and secondly, given a classification and an object, identify that object. In other words, given a list of the characteristics of named subsets which are known to exist, and an additional object, decide which subset the object belongs i.e. recognise it, or find its name (Pankhurst, 1970). Emanating from these focal problems is the usual definition of taxonomy as the science of classification (Cain, 2020) and identification (Olorode and Illoh, 2014) even though, as it can be deduced from the above submission, nomenclature and description are also involved (Simpson, 2010). In addition to these four, Enghoff and Seberg (2006) have listed three other activities in taxonomy: comparing of taxa, undertaking studies on their genetic variation and defining them in the ecosystem. Up to 1.4 million species of plants, animals and microorganisms share the planet earth with man (Asthana and Asthana, 2012). Since humans are dependent on this biological wealth for their existence, a system to retrieve, utilise, communicate and accumulate information about these organisms is necessary, and taxonomy provides this platform. The concept and practice of taxonomy originated in biology (Raven *et al.*, 1971) but its application has cut across many fields of human endeavour with a realisation that classification simplifies and organises our everyday lives. Kendig and Witteveen (2020) have therefore aptly described taxonomy as information science because the practice of acquiring, storing, labeling, organising, retrieving, mobilising, and integrating data about the natural world has always been an enabling aspect of scientific work.
Biologists categorise living things into taxa (singular, taxon) to reflect their current knowledge of the evolutionary relationships among the organisms. A 'taxon', or 'taxonomic group' is therefore a formal

category of living things recognised by having certain characteristics in common which are taken as evidence of genetic relationship, and is sufficiently different from other such groups of the same rank to be treated separately from them (Rickett, 1958; Radford *et al.*, 1974). In taxonomic groupings, there is the relationship of inclusion between levels and of complementarity within levels so that each taxon (except the highest), such as a species belongs to one and only one taxon of the next higher rank, such as a genus, implying each individual belongs to exactly one species (and has one name) in any particular taxonomic treatment of its group (Price, 1967). The current rates of species lost to extinction (IUCN, 2017) necessitate collective efforts to protect and conserve biodiversity. Species conservation, however, requires species identification skills. In order to facilitate identification or recognition of unknown organisms, taxonomists frequently prepare organized written descriptions or lists of the characteristics of named similar taxa such as species or genera *etc.* These lists are otherwise known as diagnostic or identification keys, which come in different formats or styles as presented in taxonomic publications such as Hopkins and Stanfield (1966), Lowe and Stanfield (1974), Payne *et al.*, (1974), Payne and Preece (1980), Jones *et al.*, (1998), and Javatpoint (2018), each with its merits and demerits.

Taxonomic key formats fall into two main categories namely single- access and multiple access types. In all single-access keys, there is only one point of entry, and a fixed path to be followed as determined by the author of the key (Hagedorn *et al.*, 2010). In order to enhance their usability, such keys are made to start with characters that are reliable, convenient and generally available throughout most of the year, but in reality, these conditions are not often achievable for all the taxa in a key. Random-access or multiple-access key is the identification tool which helps to overcome this challenge in that it lets the user make character choices in the key according to the state of the plant specimen being identified and the prevailing circumstances such as seasonal variations, and field situations (Bock and Norris, 2016).

Dichotomous key is the most frequently used single- access identification key format (Sinh *et al.*, 2017), and had been a clever means of organising taxonomic information before the age of computers (Godfray *et al.*, 2007). Its use is known to have contributed to increasing the quality and durability of knowledge of plant classification acquired in comparison to traditional teaching techniques (Andic *et al.*, 2019) and an established method for teaching plant identification skills (Stagg and Donkin, 2013). However, certain features tend to diminish its functionality, including: being tedious to construct (Lobanov, 2003), having fixed point of entry and daunting path of navigation (Jacquemart *et al.*, 2016), the problem of 'unanswerable couplet' (Hagedorn *et al.*, 2010), the associated 'momentary distractions' that can cause a user to forget his or her position in a key (Walter and Winterton, 2007), being unusable for confirmation of suspected identity, as well as being non- readily amenable to automation (Yin *et al.*, 2016). These challenges can sometimes be frustrating to novice taxonomy students, and appear to be the reasons for perpetual shrink in the number of those interested in botany (The Conservation, 2020). Therefore, invention of new key formats with more tolerable features are a necessity with a view to ameliorating the declining interest in plant taxonomy, and so, the objective of this paper is to propose a new taxonomic key format equipped with features and functionality attributes to circumvent some of the enumerated challenges.

MATERIALS AND METHODS

Addressing the weaknesses of extant single-access key formats using heuristic approach

Taking the taxonomists' diagnostic key as an important tool in the process of identification, the first step towards actualising the aim of this study was to examine the frequently used single-access diagnostic key formats and styles *vis-a-vis* the challenges associated with their features, construction and application (Walter and Winterton, 2007). This exercise focused mainly, but not solely on the dichotomous key giving the fact that it is the most frequently used key format (Tofilski, 2018). In order to address some of the identified inadequacies, consideration was also given to selection criteria for construction of efficient diagnostic keys (Payne, 1981 and 1988). Information obtained from these two steps were heuristically integrated into a thought to develop an alternative single-access key format herein referred to as set

Table 1: comparison chart of anatomical features in transverse sections of the barks of 13 herbal materials collected from Ogbomoso, Nigeria

	Character	***ENAC***	***ALBO***	***PANI***	***THCA***	***UVAC***	***SALA***	***PTOS***	***ZAZA***	***CAHA***	***ARRI***	***OKAU***	***MAIN***	***KHSE***
1	Rays	Present	Present	Present	Present	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent
2	Type of ray cells	RE, contiguous with parenchyma cells	Mainly SQ, sometimes TE	Uniseriate, more or less SQ	Multiseriate, TE cells	TE cells, wedge-shape rays	Multiseriate, RE cells.	NA	NA	NA	NA	NA	NA	NA
3	Phellodermsecondary cortex	Present	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Present
4	Thickness of secondary cortex (µm)	<200	>500	>500	NA	NA	NA	NA	NA	NA	NA	NA	NA	<200
5	Sclereids or stone cells	Present	Present	Absent	Present	Absent	Absent	Present	Absent	Absent	Absent	Present	Present	Present
6	Type and frequency of sclereids	Macro 1-3%	Macro, Brachy, about 16%	NA	Macro, about 7%	NA	NA	Macro, about 22%	NA	NA	NA	Macro, Brachy, greater than 70%	Macro, Brachy, about 22%	Macro, Brach, about 20%
7	Resin ducts	Absent	Absent	Absent	Present	Absent	Absent	Present	Present	Absent	Absent	Present	Present	Absent
8	Density of cork cells/mm^2	About 700	< 400	< 400	About 400	< 400	< 400	< 400	< 400	< 300	< 300	About 520	About 700	About 700

9	Cork cambium	Present	Absent	Absent	Absent	Absent	Absent	Absent	Present	Absent	Absent	Absent	Absent	Absent
10	Axial paren-chyma	Rad, 1 or 2 rows	Copious, in groups	Solitary and groups of 2-6	Narrow tangential bands with fibres	Tangential bands with fibres	Copious, widely distributed	Copious, in large aggregates	Copious, widely distributed	Scanty, small groups	Tangential bands with sieve tubes	Solitary and groups of 2-3	Groups of varying number	Groups of varying number
11	Fibres	Groups of short and long tangential bands	Diffuse aggregates	Diffuse, solitary units, small groups	Groups of short and long tangential bands	Groups of short and long tangential bands	Diffuse aggregates of small groups	Diffuse, solitary units, small groups	Diffuse aggregates	Diffuse aggregates of small groups	Scanty, solitary units	Diffuse aggregates of small groups	Diffuse aggregates	Diffuse aggregates
12	Sieve tubes	Short bands, 2 or more contiguous tubes	Solitary units or in pairs	Copious, in large groups	Solitary units, and groups 2-3 tubes	Scanty, solitary units	Solitary units, and groups 2-4	Solitary units, and groups 2-4	Small groups 3-4 tubes	Copious,irregular arrangement	Copious, tangential tiers or irregular	Scanty, solitary, pairs, small groups	Solitary units, pairs, small groups	Solitary units, pairs, small groups

ALBO = Alstonia boonei (stem); *ARRI= Aristolochia ringens* (root); *CAHA = Calliandra haematocephala* (root); *ENCH = Enantia chlorantha* (stem); *KHSE = Khaya senegalensis* (stem)*; MAIN = Mangifera indica* (stem); *OKAU = Okoubaka aubrevellei* (stem); *PANI = Parquetina nigrescens* (root)*; PTOS = Pterocarpus osun* (stem)*; SALA = Sarcocephalus latifolius* (root)*; THCA = Theobroma cacao* (stem)*; UVCH= Uvaria chamae* (root)*; ZAZA= Zanthoxylum zanthoxyloides* (root)..RE, radially –elongated; SQ, square; TE, tangentially- elongated; *NA*, not applicable.
Source: 2019 unpublished data compiled at the medicinal plants research laboratory, Ladoke Akintola University of Technology, Ogbomoso, Nigeria.

diagram key with far reaching desirable qualities in terms of design/features, construction procedure, navigation efficiency and possibility of automation.

Data procurement for the purpose of illustration

Wood bark anatomical data on thirteen medicinal herbs marketed as plant roots, root barks and stem barks in Ogbomoso township, south western Nigeria were sourced for the purpose of illustration from the 2019 compilation of unpublished results at the medicinal plants research laboratory in the Department of Pure and Applied Biology, Ladoke Akintola University of Technology, Ogbomoso, Nigeria. The data were collected in accordance with the standard procedures: tissue sectioning/ maceration (Lin *et al.*, 1995), staining (Mota *et al*., 2017), mounting and microscopic observations (Liu *et al.*, 2020).The terminology and descriptions of observed features followed those of the International Association of Wood Anatomists (IAWA Committee, 1989). Fourteen diagnostic characters/character combinations, consisting of ten qualitative and four quantitative features were compiled into a comparison chart for the 13 plant species (Table 1), involving only transverse sections and tissue macerations of the barks. Prepared specimens were stained in 1% alcoholic safranin, mounted in Canada balsam and examined using Olympus biological microscope CH20i Model with binocular facility. Quantitative characters were considered diagnostic of the species only if the means of the replicated values were statistically significant at $\alpha = 5$ following One- Way Analysis of Variance, and Duncan multiple range classification of the means (Landau and Everitt, 2004).

Conceptualisation of procedures for construction and application of the set diagram key

Given a number of taxa with certain observable characters, and adopting a heuristic approach to solving the problem at hand, conceptualisation of the structure as well as the procedure for constructing a set diagram key was initiated by first classifying the taxa into few subsets and each subset independently classified in recursive manner into smaller subsets until the entire group is resolved into the individual taxa (Pankhurst, 1970). This exercise was carried out from both the lumpers'(emphasizing similarities) and splitters' (emphasizing differences) classificatory points of view (Forth, 2015) as found appropriate and practicable. As a further step to achieving the objectives of the study, the algorithm so thought out, including the procedure for navigating the new key format was systematically executed, and is here, being proposed.

Design and statement of the features of the set diagram key

Structurally, a set diagram identification key was conceived as consisting of two parts: the first part, which is the main body of the key as a number of circles interlocked diagrammatically according to defined rules, each circle representing a taxon (or a set of diagnostic characters), which may either be a taxonomic category such as variety, or species, or sub-genus, or genus, etc., or a non-taxonomic category of some sort (e.g. Harmon and Elliott, 2018). The circles, not drawn to scale, are arranged in multiples of three or lesser number, interlock with one another, or connected by means of lines or other notation (also not drawn to scale), to indicate characters, represented as numbers 1, 2, 3, *etc*., shared by taxa, and those not shared among them. The second part of the key is a list of the unit characters or character combinations pertaining to the plant taxa in the key, which are assigned numerical values 1, 2, 3, etc, as appropriately indicated inside or outside of the circles.

Procedure for constructing a set diagram key

The notation, essential rules and the activities involved in constructing a set diagram key were conceived as follows:

The name of each taxon represents, or is defined by a 'set of plant features'; these are the elements comprising the diagnostic characters, which distinguish the taxon from the other taxa in the key;

i. The diagnostic characters, denoted by numerals 1, 2, 3, *etc*. are inserted as the case may be in the inside , or outside of the circle representing each taxon;

ii. The basic rules of the mathematical set theory and algebra relating to notation (AMSI, 2011) are applicable in the construction and labeling of set diagram key, but additional guidelines also apply as follows:

a. As much as possible, the circles/taxa should primarily appear in clusters of three's or two's, which are drawn to intersect in such a manner as to indicate characters shared by the taxa. However, one or more circles may not intersect with any other, and thus, independent of them, but each of such circles, here referred to as single-taxon cluster, should form part of the key network by being connected with at least one line or by means of other notation;

b. Secondary clusters of taxa are made practicable by means of the universal set notation, of a square/rectangle drawn round two or more primary clusters, or by connecting primary clusters as appropriate using lines with nodes. A node is here, defined as a small square connected by two or more lines to indicate that at least a relationship exists between or among the locations so connected to it (see Figure 1). An empty node indicates that the connected locations share exactly the same set of characters, a node with one or more numeric values indicate only the characters so shared, while a line connecting two points without a node simply depicts connection without necessarily indicating a relationship between the two points; only to ensure that no portion of a key is left 'floating' (See Figure 2);

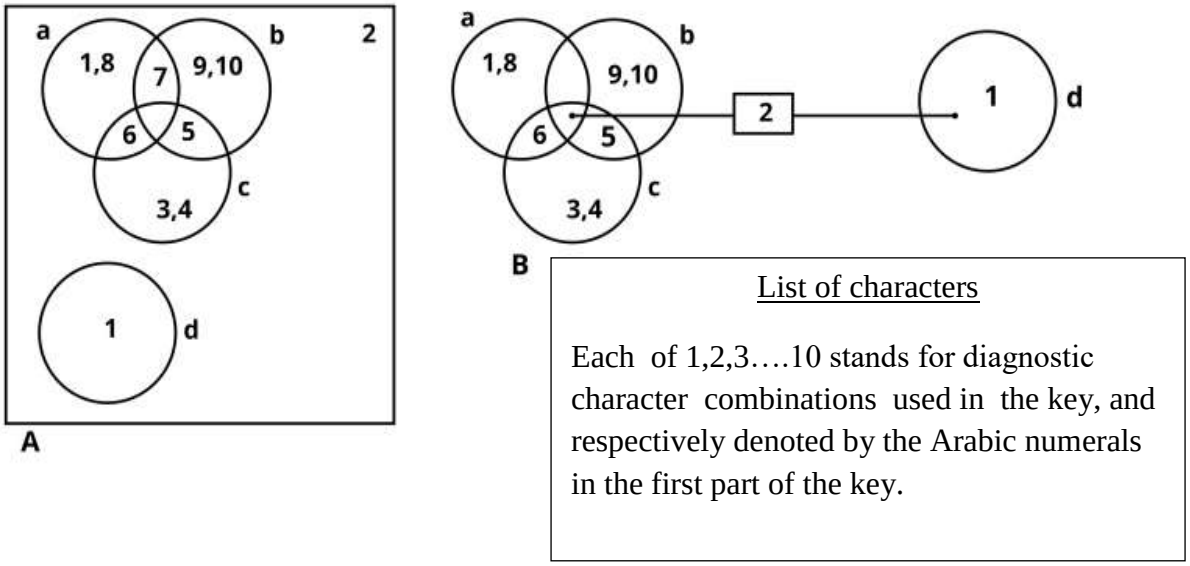
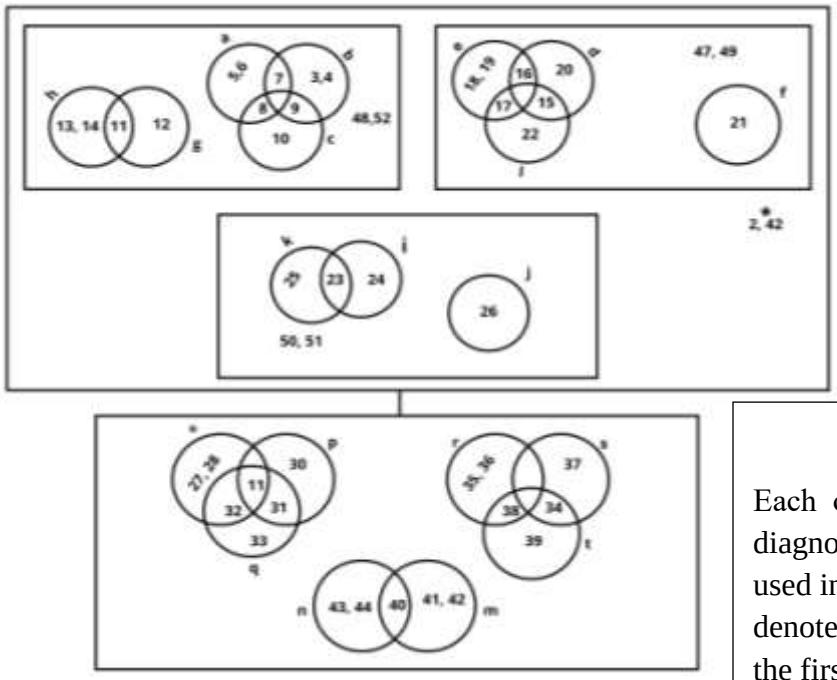


Figure 1: A hypothetical set diagram key for four taxa a, b, c, and d. The ten diagnostic character combinations used are denoted by 1, 2, 3, …10. A and B are two alternative forms of presenting the key; the universal set in 'A' is a cluster at secondary level of classification.

c. For the purpose of constructing a set diagram key, a universal set is simply defined and conceived as a higher (but not necessarily taxonomic) category of plant classification diagrammatically created to enclose one or more clusters of taxa of lower category, and to that extent, it differs in conception from the point of view stipulated in the mathematical set theory. As such, the diagnostic characters defining a taxon or circle within a universal set are not merely a subset of the universal set; rather, each taxon as it were, shares all the features of its universal set. The relationship between the sets (essentially, the taxa) and the universal set should therefore be viewed from the point of view of biological classification, displaying lower (complementary) categories within one higher (inclusive) category (see Figure 2 and Price, 1967);

d. If a key involves many plant taxa, the writer of the key may adopt the use of universal sets in tiers/ layers, in which the first tier of universal set directly encloses the (primary) clusters of taxa as one secondary cluster (see Figure 1A); the second tier, distinguishable by means of an asterisk, or other forms

of identifier encloses a maximum of three secondary clusters of the first tier to form a tertiary cluster (Figure 2); and the third tier, distinguishable by means of two asterisks, or other forms of identifier encloses a maximum of three tertiary clusters of the second tier to form a quaternary cluster, and so on and so forth;



List of characters

Each of 1,2,3….52 stands for diagnostic character combinations used in the key, and respectively denoted by the Arabic numerals in the first part of the key.

Figure 2: A hypothetical set diagram key for 20 taxa 'a, b, c….t' using 52 character combinations denoted by 1, 2, 3, …52. The universal set with asterisk is a cluster at tertiary level of classification.

e. Two types of diagnostic characters (primary and secondary) were conceived, and are being proposed for the key format. The primary characters are the consequential or significant features of the plants, which the user should note for recognition of a taxon or a cluster of taxa. Such characters are simply denoted by numerals to indicate characters applicable to the respective taxa. The secondary characters, which are inserted in parentheses in the body of the key are inconsequential in that, although they are, or may be diagnostic of a taxon or a cluster of taxa, the characters need not be observable for taxa recognition to occur. When a character, primary or secondary is assigned a negative sign, such feature is confirmed absent in the taxon/taxa concerned, and may be so useful for diagnostic purpose;

iii. The basic requirement in constructing a set diagram key is a comparison chart or table of character comparison with the taxa in columns and diagnostic characters in rows as shown in Table 1 , and the procedure involves a number of steps as follows:

a. Following the lumper's technique of classification, examine the comparison chart and either adopt a bottom-up approach and well defined shared diagnostic features to directly partition the taxa (or columns) into small clusters preferably, of three's but if impossible, then of two's and one's; or as an alternative, adopt a top down approach to fragment the taxa/columns into larger clusters, if possible, of multiples of three taxa. In order to facilitate this step, the taxa may have to be swapped column for column so that the taxa with similar features can form recognisable clusters;

b. If bottom-up approach has been adopted, re-examine the table for the possibility of regrouping the small clusters into larger/higher categories of few clusters each; and if top down approach has been adopted, consider the possibility of further compartmentalising the large groups into smaller clusters preferably of three taxa each, but of 2 or 1, if so appropriate or possible;

c. Following the splitter's technique of classification, and based on the distinguishing features observable in the comparison chart, repeatedly partition each of the small clusters obtained in sub-step 'b' above into smaller subsets until each cluster has been resolved into its various taxa, stating clearly those features that separate one taxon from another;

d. Depict the outcome of sub-steps 'a to c' above as set diagrams with regards to the adopted diagnostic characters in the table; each taxon is represented by a circle, and is so labeled, and each cluster of taxa by appropriate cluster of interlocking circles, while larger groups of few manageable clusters of taxa are represented as universal sets. It is advised that a universal set (otherwise called secondary cluster) should ordinarily not enclose more than ten (primary) sets/taxa, and if found necessary and practicable, higher categories of universal set namely, tertiary and quaternary clusters are drawn to ordinarily also enclose a maximum of three universal sets of their respective lower categories;

e. Provide a list of all the diagnostic characters used in creating the set diagrams, and then, insert the serial number of each character at the appropriate location(s) in the diagram indicating characters, which appear as numbers 1, 2, 3, *etc.*, shared by the taxa and those not shared among them. Additionally, make use of lines, with nodes to connect all the appropriate locations in the set diagrams which share certain characters, or without nodes for the purpose of making the diagram a single nexus;

f. If for the purpose of illustration one carefully examines Table 1 and uses the top down approach to constructing a set diagram key, one discovers that too large mutually-exclusive groups are discernible as follows:

First: *Enantia chlorantha* (*ENAC*), *Alstonia boonei* (*ALBO*), *Parquetina* nigrescens (*PANI*), *Theobroma cacao* (*THCA*), *Uvaria chamae* (*UVAC*), and *Sarcocephalus latifolius* (*SALA*), in all of which rays are observable in the inner barks; and

Second: *Pterocarpus osun* (*PTOS*), *Zanthoxylum zanthoxyloides* (*ZAZA*), *Calliandra haematocephala* (*CAHA*), *Arristolochia ringens* (*ARRI*), *Okoubaka aubrevillei* (*OKAU*) *Mangifera indica* (*MAIN*), and *Khaya senegalensis* (*KHSE*), all of which do not have rays in their inner barks.

g. A further scrutiny of the taxa in the first group in 'sub-step f' in line with the guidelines for construction of set diagram keys earlier enumerated reveals two clusters of three taxa each, that is *ENAC, ALBO* and *PANI* as the first, all the three species having phelloderm or secondary cortex, while *THCA, UVAC* and *SALA* constitute the second cluster in which secondary cortex is absent. Similarly, for the second group, there are three recognisable clusters i.e. *PTOS* as the first cluster, being the only taxon in the group in which only one type of sclereids/ stone cells i.e. macrosclereids are observable in the inner bark; *ZAZA, CAHA* and *ARRI* as the second cluster, the three of which have no sclereids; while *OKAU, MAIN* and *KHSE* constitute the third cluster which share a number of features: density of cork cells in the outer bark is at least 500/mm^2, both macro and brachy-sclereids are observable in their inner barks, and sieve tubes occur as solitary units along with those in pairs and small groups. Lastly, and from the splitter's point of view, each taxon in all these clusters are distinguishable within their cluster using the characters listed in the table;

h. As an alternative to 'sub-step f' above, one may choose to classify the taxa in Table 1 into three large non-mutually exclusive groups as follows:

First: Enantia chlorantha (*ENAC*), *Parquetina nigrescens* (*PANI*), *Theobroma cacao* (*THCA*), *Uvaria chamae* (*UVAC*) and *Sarcocephallus latifolius* (*SALA*) in which rays are present in the inner bark;

Second: Enantia chlorantha (*ENAC*), *Alstonia boonei* (*ALBO*), *Pterocarpus osun* (*PTOS*), *Theobroma cacao* (*THCA*), *Okoubaka aubrevillei* (*OKAU*), *Mangifera indica* (*MAIN*) and *Khaya senegalensis* (*KHSE*) in which sclereids/stone cells are found in the inner bark;

Third: Alstonia boonei (*ALBO*), *Parquetina nigrescens* (*PANI*), *Theobroma cacao* (*THCA*), *Uvaria chamae* (*UVAC*), *Sarcocephallus latifolius* (*SALA*), *Pterocarpus osun* (*PTOS*), *Arristolochia ringens* (*ARRI*), *Calliandra haematocephala* (*CAHA*) and *Zanthoxylum zanthoxyloides* (*ZAZA*) in which the mean density of cork cells per mm^2 area of the outer bark is relatively low, being maximum of 400/mm^2.

i. Following the procedure in 'sub-step g' above, each of the three large groups in 'h' is classified into recognisable sub-groups on the basis of the characters shared by the taxa, further classification by means of distinguishing characters will then lead to the resolution of the clusters into individual taxa;

j. In line with the provisions for construction of the set diagram key highlighted in 'steps i-iii' above, each recognisable subgroups from 'step iv(f)' and 'iv(h)' is represented with appropriate number of interlocking circles. By directly observing the list of characters in table 1, the characters shared by pairs and groups of taxa; and those diagnostic of each taxon are indicated inside or outside the circles in each case as appropriate. While significant and readily scored characters are represented by numerals, the additional (inconsequential, but diagnostic) features are enclosed in parentheses (see Figures 3 and 4);

k. All the characters used in 'step iv(j)' are listed as part of the identification key.

Application of the set diagram key

Application of a set diagram key was conceptualised as user's tasks to be performed following a number of steps as follows:

i. Enter the key through any universal set of clusters of taxa, commencing from the outermost set/highest level of cluster (see Figures 2A, 3 and 4) and proceeding inwards if the universal sets are in tiers. Evaluate the plant specimen for identification based on the diagnostic features listed in the universal set under consideration, if the diagnostic features listed in the set are not in agreement with those in the plant specimen, then the exercise is considered aborted or terminated at that point, so drop the universal set, including those of lower categories in it and proceed to select another (universal) set for navigation; but if the feature(s) in a universal set are in agreement with the observation on the plant specimen, proceed by navigating the universal sets of the next lower category within it one at a time and repeat the exercise of character matching until the process is either aborted or is pursuable until a universal set of the lowest category in the group has been navigated; then, select one primary cluster of taxa enclosed within this set at a time for navigation to determine the identity of an unknown plant specimen included in the key. Commencing from the centre, navigate the primary cluster in centrifugal progression (i.e. proceeding outwards, away from the centre), evaluating the plant specimen and selecting fewer and fewer taxa as probable/likely identities of the plant as the exercise proceeds. At this point, it is advisable for user to try out all the available alternative routes (maximum of three, as it were) before a final decision is made, and in event that an intersection between two or more circles is encountered empty/without a character label, the decision should be made as if a character that is in agreement with the plant specimen being identified had been encountered; if however the procedure is aborted or identification of the specimen is not possible due to confirmed disagreement between the listed and observable diagnostic features in the plant, proceed to the next primary cluster, and then the next, until identification is either made possible (when only one taxon in the key can be associated with the unknown plant), or until all the clusters have been navigated with or without success;

ii. If the entry condition in "i" above does not apply to the key, i.e. if there are no universal sets to be used as entry points, enter the key through any node connecting two or more (primary) clusters of taxa (see Figure 1B); evaluate the plant specimen for identification based on the diagnostic features listed in the node. If the diagnostic features listed in the node are not in agreement with those in the plant specimen, proceed to select another node for navigation but if the feature(s) apply to the plant, then select one cluster connected to the node at a time for navigation to determine the identity of an unknown plant specimen included in the key. Again, starting from the centre, navigate the primary cluster in centrifugal progression as described in "i" above, substituting nodes for universal sets, until identification is made possible or otherwise;

iii. If the entry condition in "ii" does not also apply to the key, i.e. there are no nodes to be used as entry points, then enter directly through the centre into any of the primary clusters of taxa available in the key; navigate the cluster in centrifugal progression, evaluating the plant specimen and systematically selecting taxa as probable identities of the unknown plant as the exercise proceeds; if the procedure is aborted or identification of the specimen is not possible due to disagreement between the listed and

observable diagnostic features in the plant specimen, proceed to the next cluster, and then the next, until identification is either made possible, or until all the clusters have been navigated with or without success.

Illustrative execution of the propositions

The proposed techniques for making and navigating a set diagram key developed from this study were executed using the wood bark anatomical data in Table1, the outcomes of which are two single-entry diagnostic keys usable for identifying 13 medicinal herbs marketed in Ogbomoso, Nigeria.

RESULTS

Figures 3 and 4 are the results obtained following execution of the proposed procedures for constructing and using the set diagram key. While Figure 3 is a product of initial classification of the 13 plant species used into two mutually exclusive groups, figure 4 is a result of such exercise into three non- mutually exclusive groups.

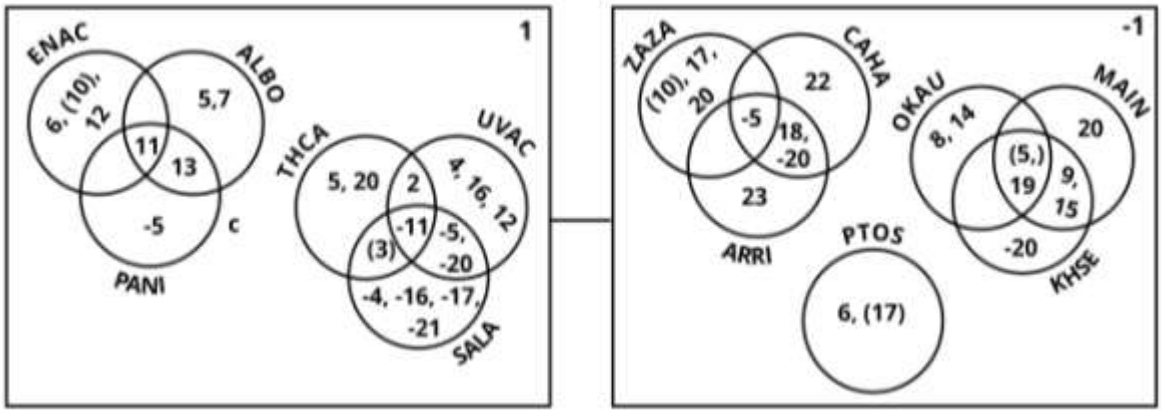


Figure 3: Type I set diagram identification key for diagnosing thirteen medicinal herbs in Ogbomoso, Nigeria based on wood bark anatomy. *ALBO* = *Alstonia boonei* (stem); *ARRI*= *Aristolochia ringens* (root); *CAHA* = *Calliandra haematocephala* (root); *ENCH* = *Enantia chlorantha* (stem); *KHSE* = *Khaya senegalensis* (stem); *MAIN* = *Mangifera indica* (stem); *OKAU* = *Okoubaka aubrevellei* (stem); *PANI* = *Parquetina nigrescens* (root); *PTOS* = *Pterocarpus osun* (stem); *SALA* = *Sarcocephalus latifolius* (root); *THCA* = *Theobroma cacao* (stem); *UVCH*= *Uvaria chamae* (root); *ZAZA*= *Zanthoxylum zanthoxyloides* (root).

List of characters/Character combinations

1. Rays are observable in the inner bark
2. Ray cells are tangentially elongated, and the rays may be wedge-shaped; sometimes, not wedge-shaped
3. Rays are multiseriate
4. Rays are exclusively wedge-shaped
5. Sclereids are found in the inner bark
6. Only one type of sclereids/stone cells is found (i.e. macrosclereids)
7. Both macro- and brachy- sclereids are observable in the inner bark
8. Sclereids are of high frequency of occurrence (>70%) relative to other fundamental tissues of the inner bark (i.e. fibres, axial parenchyma and sieve tubes)
9. Sclereids are of low frequency of occurrence (about 20%) relative to other fundamental tissues of the inner bark (i.e. fibres, axial parenchyma and sieve tubes)
10. Cork cambium is present
11. Phelloderm/secondary cortex, present
12. Thickness of secondary cortex < 200µm; character 15
13. Thickness of secondary cortex >500µm; density of cork cells <400/mm^2; cork cambium, absent

14. Density of cork cells, about 520/mm^2
15. Density of cork cells, about 700/mm^2
16. Sieve tubes occur in solitary units
17. Sieve tubes occur in small groups; usually of 2 or 3 – 4 units per group
18. Sieve tubes occur in large numbers (copious) and are irregular in arrangement; sometimes in tangential tiers
19. Characters 7; 14;16;17
20. Resin ducts found in the inner bark
21. Axial parenchyma cells form tangential bands with fibres
22. Fibres in TS occur as diffuse aggregates of small groups
23. Fibres in TS are scanty, being in solitary units

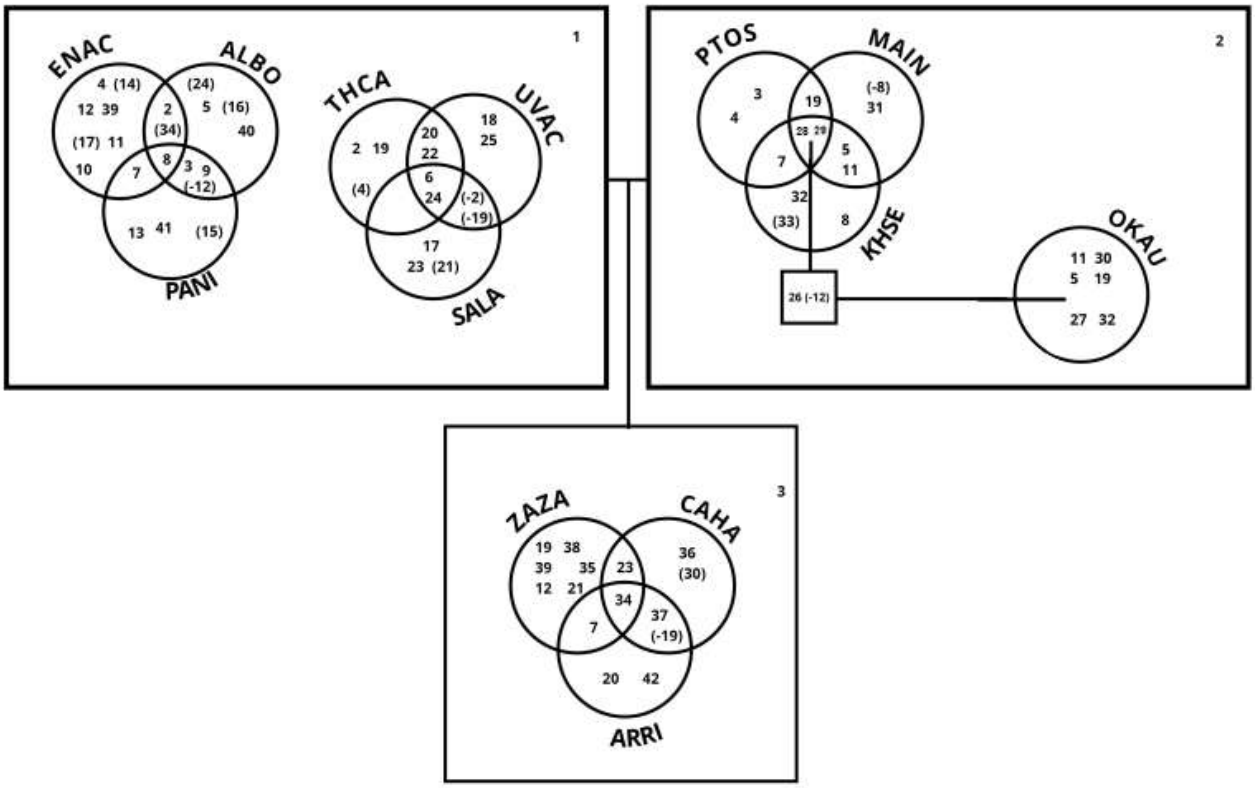


Figure 4: Type II set diagram identification key for diagnosing thirteen medicinal herbs in Ogbomoso, Nigeria based on wood bark anatomy. *ALBO* = *Alstonia boonei* (stem); *ARRI= Aristolochia ringens* (root); *CAHA = Calliandra haematocephala* (root); *ENCH = Enantia chlorantha* (stem); *KHSE = Khaya senegalensis* (stem); *MAIN = Mangifera indica* (stem); *OKAU = Okoubaka aubrevellei* (stem); *PANI = Parquetina nigrescens* (root); *PTOS = Pterocarpus osun* (stem); *SALA = Sarcocephalus latifolius* (root); *THCA = Theobroma cacao* (stem); *UVCH= Uvaria chamae* (root); *ZAZA= Zanthoxylum zanthoxyloides* (root).

List of Characters/Character Combinations

1. Rays are present in the inner bark
2. Sclereids/ stone cells are observable in the inner bark
3. Mean density of cork cells in the outer bark, relatively low, maximum of 400/mm^2; sometimes less than 200/mm^2
4. Only macro-sclereids are found ; brachy-sclereids are absent in the bark
5. Both macro- and brachy- sclereids are present
6. Multi-seriate rays (i.e. rays of more than two contiguous rows of cells in their thickness) are present in the inner bark
7. Uni-seriate rays are found in the inner bark
8. Phelloderm/secondary cortex is observable in the bark
9. Mean thickness of phelloderm/secondary cortex, greater than 500µm
10. Mean thickness of phelloderm/secondary cortex, less than 200µm
11. Mean density of cork cells, about 700/mm^2 or at least, greater than 500/mm^2
12. Cork cambium, present
13. Rays, entirely of uni-seriate type
14. Bi-seriate and tri-seriate rays are found along with uni-seriate rays
15. Ray cells in TS are more or less square in shape
16. Ray cells in Ts, predominantly square-shaped; sometimes tangentially/laterally elongated
17. Ray cells in TS, radially procumbent/elongated
18. Rays, wedge-shaped
19. Resin ducts, present in the inner bark
20. Axial parenchyma cells occur as narrow or wide tangential/lateral bands, alternating with those of fibres or sieve tubes
21. 21. Axial parenchyma cells are abundant (or copious) and widely distributed among other tissues of the inner bark
22. 22. Fibres occur as groups of short (square) and long (rectangle) tangential/lateral bands
23. 23. Fibres, diffuse aggregates of small groups of cells
24. 24. Solitary sieve tubes are observable in the inner bark
25. 25. Sieve tubes occur as solitary units only
26. 26. Sieve tubes occur both as solitary units and in small groups, usually of 2-4 tubes
27. 27. Mean percent of sclereids by volume of inner bark (relative to other fundamental tissues i.e fibres, axial parenchyma cells and sieve tubes), greater than 70
28. 28. Mean percent of sclereids by volume of inner bark (relative to other fundamental tissues i.e fibres, axial parenchyma cells and sieve tubes), about 20
29. 29. Axial parenchyma cells are abundant (or copious), occurring in large groups or aggregates of varying number
30. 30. Axial parenchyma occur as solitary units and small groups of 2 to 3 cells
31. Sclereids in the inner bark are more frequently of macro-type and less frequently brachy-sclereids; fissures (i.e. large or empty spaces) in-between the fundamental tissues of the inner bark (namely, fibres, axial parenchyma and sieve tubes; and sclereids if applicable) are present but not conspicuous
32. 32. Sclereids in the inner bark are more frequently of brachy-type and less frequently macro-sclereids; the latter, arranged in large groups of rectangle or square-shapes; fissures (i.e. large or empty spaces) in-between the fundamental tissues of the inner bark (namely, fibres, axial parenchyma and sieve tubes; and sclereids if applicable) are present and conspicuous

33. Cells of phelloderm in TS are isodiametric or oblong in shape, and thin-walled with few inter-cellular spaces
34. Fissures (i.e. large or empty spaces) in-between the fundamental tissues of the inner bark (namely, fibres, axial parenchyma and sieve tubes; and sclereids if applicable) are conspicuously absent
35. Fissures (i.e. large or empty spaces) in-between the fundamental tissues of the inner bark (namely, fibres, axial parenchyma and sieve tubes; and sclereids if applicable) are absent but few inter-cellular spaces occur among the abundant/copious axial parenchyma cells
36. . Fissures (i.e. large or empty spaces) in-between the fundamental tissues of the inner bark (namely, fibres, axial parenchyma and sieve tubes; and sclereids if applicable) are absent but few inter-cellular spaces occur among the abundant/copious sieve tubes
37. Mean density of cork cells in the outer bark, less than 300/mm^2
38. Mean density of cork cells in the outer bark, about 400/mm^2
39. Cells of phelloderm in TS are rectangle- shaped, and thin-walled with few inter-cellular spaces
40. Cells of phelloderm in TS are isodiametric/rounded in shape, and thin-walled with few inter-cellular spaces
41. Cells of phelloderm in TS are predominantly oblong in shape, thin-walled with few inter-cellular spaces; fissures (i.e. large or empty spaces) in-between the fundamental tissues of the inner bark (namely, fibres, axial parenchyma and sieve tubes; and sclereids if applicable) are present but not conspicuous
42. Fibres, scanty in the inner bark, occurring in solitary units of cells

DISCUSSION

The central position of classification in taxonomy

There are four main components in taxonomy, namely: classification, identification, description and nomenclature (Simpson, 2010). In practice, it is not clear which of these activities should come first, and to be followed by which one because a critical review of the concepts seems to restate the 'riddle of egg and fowl, which came first' (Australian Academy of Science, 2018). However there is evidence to believe that the last three are subsumed in the first, i.e. classification. In preparing a diagnostic key for identification, Morse (1971) advises a writer to divide (or classify) the initial group of taxa by a character couplet into two sub-groups, each of which should be independently divided into further sub-groups, and so forth, until every taxon has been distinguished from all others. Consenting to this piece of advice, Hagedorn *et al.,* (2010) regarded keys as 'divide and conquer' search algorithms that reduce the result set recursively until the remainder is small enough to be solved by direct comparison. Further to classifying the initial group of taxa, a suggestion by Radford *et al.,* (1974) is to "identify all groups to be included in the key and prepare a description of each taxon". From these submissions, two facts are discernible: firstly, is the fact that although identification is a separate activity in taxonomy, in practice, it involves the other three major components earlier enumerated; and secondly, that all conceivable activities in taxonomy including writing and using a key are rooted in classification. There is therefore little wonder that taxonomy has been defined by many (e.g. Walker, 1988; Lawrence, 2005; Judd *et al.,* 2007; and Kirk, 2008) as the science of classification. In this study, the central position of classification in developing diagnostic keys has been brought to bear.

Implication of the constraints on the process of species identification

Identification of living organisms is basic to understanding biodiversity and ecology (Randler, 2008) and is a prerequisite for judicious use of bio-resources (Dubey *et al.,* 2011). Concerted efforts to protect and conserve biodiversity are necessary, given the spate of species loss to extinction in recent time (IUCN, 2017), but species conservation requires species identification skills that are not possessed by many individuals involved in conservation activities. Additionally, non-biology specialists interested in bio-resources development and exploitation often desire correct identification of their plant or animal specimens, but are constrained by lack the technical know-how. There is also the general belief that the construction and use of identification keys require intensive training and experience, which only few

individuals do have (Waldchen *et al.,* 2018). Arising partly from this perception, students' and researchers' interests in taxonomy have steadily declined (Drew, 2011). Another constraint on species identification relates to the structure and functionality of the tools for executing the process, i.e. taxonomic keys. Some of these have been enumerated above as demerits associated with dichotomous and other extant single-access keys. So, in health care, food production, forest resources management and criminal justice, to mention but a few of human endeavours, we are compelled to contend with plant misidentification and misrepresentation with associated public health (Upton and Romm, 2010), social (Gonzalez *et al.*, 2017), environmental (Arora, 2018), legal (Dukes, 2006), and economic (Noble Research Institute, 2001) burdens. The essence of this paper therefore, is to make a contribution towards ameliorating this gap.

Justification of the set diagram key as alternative to dichotomous key

Dichotomous key is the most widely used single-access identification tool (Sinh *et al.,* 2017) but it seems that its weaknesses demoralisingly outweigh its strengths. It is therefore necessary to highlight some challenges associated with its structure and functionality, and compare with those of the set diagram key being proposed. In both of these key formats, the sequence and structure of identification steps are fixed by the author, and there is only one point of entry, so that there is a single path to be followed by the user. All single- access keys have this structural defect, which is accompanied by the problem of 'unanswerable couplet' i.e. a user may get stuck and identification will be impossible if a choice cannot be decided at any point (Hagedorn *et al.,* 2010). Additionally, a user of single-access keys will often be confronted with the problem of 'dead ends', and 'momentary distractions' that can cause him to forget his position in a key (Walter and Winterton, 2007). These situations can arise when a character cannot be observed or adequately scored (e.g. when the feature is in its developmental stage or is season-based, and hence not visible in the specimen) or because the options are not stated clearly enough in the key. While the dichotomous key is well-known for these challenges, such difficulties can be more tolerable with the application of the set diagram key since it is much easier to retrace one's steps in case a wrong choice has been made. In fact, a user is free to exit if necessary, and re-enter the key at other points without losing focus.

The construction and navigation of dichotomous keys are believed to be daunting tasks for many students (Jacquemart *et al.,* 2016), and that the key format is difficult to automate, if at all amenable to conventional programming techniques (Yin *et al.,* 2016). In contrast, both of these processes in the set diagram key have clear-cut algorithms, which can be followed by key makers and users with relative ease. These algorithms can also be coded using the desired programming languages, and so automation of these activities should not be an intractable problem.

Confirmation of plant identity is what a key user sometimes desires, especially if a particular name has been suspected of a specimen. An ideal tool for identification should equally be usable for identity confirmation, and one might question the functionality of such tool if it cannot effectively and efficiently assist in doing so. While both the paper-based and computerised dichotomous keys (Tofilski, 2018) are not readily usable for confirmation of suspected identity of a plant, this exercise is manually practicable and electronically achievable using the newly created single access key format in this study. Suppose that an unknown plant specimen, one of the taxa included in a key is suspected by a user as its identity, the procedure to confirm is first locate the position of the suspected taxon in a key and then work on the key along the established route of identifying the taxon, paying particular attention to only those statements/questions regarding the suspected taxon name, and ensuring that all such (not most) statements are in agreement with the observable features of the specimen under consideration.

As an illustration, if a user in applying the key in Figure 3 suspects the identity of a plant to be *Alstonia boonei*, confirmation is done by first locating the universal set/secondary cluster (i.e. on the left hand side) in which the suspected name has been keyed out as a taxon, and then the specimen is evaluated based on those characters namely: 1, 11, 13, 5 and 7 respectively pointing to the name. Similarly if the same taxon is suspected using the key in Figure 4, the specimen is evaluated based on

either characters 1, 8, 2, 34, 5, 40, 16, and 24 or 1, 8, 3, 9, 12, 5, 40, 16, and 24 respectively. So, if given a set diagram key, with the assurance that a suspected taxon is included in that key, plant identity confirmation can be carried out efficiently without the user having to pass through the regular identification process. By and large plant identity confirmation can be explored as a means of assessing leaners' extent of familiarity with the vegetation around them. They will not only find the exercise pleasing and refreshing, but also inspiring, much like a game.

Promotion of interest in plant taxonomy

There is evidence to believe that learners' declining interest in plant taxonomy (Drew, 2011) is largely due to the way the subject is taught (Stagg and Donkin, 2013). Among the panacea earlier recommended by Tilling (1987) to promte learners' interest in botany include provision of appealing plant identification resources, making botany relevant to people's lives, and correct use of new teaching aids. It is gratifying to have the newly developed set diagram key as answers to these calls. So also, the challenge of tedious construction and boring navigation of dichotomous keys that have been sources of discouragement to beginners in taxonomy are surmountable with the advent of the set diagram key.

Putting the new key format in perspective, taxonomic key construction and use for identification or identity confirmation should turn out to be favourite pastime for specialists and novices alike. At the primary, secondary and tertiary levels of botanical knowledge impartation, these exercises should turn out to be fun, with full participation of learners. As an illustration, children can be provided with six plant specimens with which they are familiar; asked to list some botanical features of the plants; guided to draw three interlocking circles in two places to represent the plants on the basis of the closeness of the features; and asked to indicate with appropriate serial numbers, those features in the list shared among all the three in each case, and between pairs of circles in each group, as well as those features peculiar to, or diagnostic of each circle/plant. Choosing one of the plant specimens for a test, and entering the just constructed key from the centre of the two groups of interlocked circles, one at a time, the children are guided to navigate the device centrifugally to achieve identification.

CONCLUSIONS AND RECOMMENDATIONS

From this study, the set diagram key, a new single-access taxonomic key format has been designed, illustrated and proposed for use in plant taxonomy. With the use of the key format, the trio activities of key construction, plant identification, and plant identity confirmation are made possible and practicable through robust algorithms. A scrutiny of these algorithms will show that they are in conformity with the principal features of a good/executable computer algorithm, being deterministic, general, finite, and with capacity to act on at least one input to produce at least one output. Therefore, it is believed that the alternative key format should be programmable. Relying on its structural and functionality attributes, the set diagram key format is recommended as a useful template upon which reliable plant diagnostic tools can be based. Also emerging from this study are two wood bark anatomy- based diagnostic keys usable for authenticating 13 medicinal herbs marketed as plant roots and stem barks in Ogbomoso, Nigeria.

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