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ORIGINAL PAPER

Homeopathy and systematics: a systematic analysis of the therapeutic effects of the plant species used in homeopathy

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The therapeutic effects of the plant species used in homeopathy have never been subjected to systematic analysis. A survey of the various *Materiae Medicae* shows that over 800 plant species are the source of medicines in homeopathy. As these medicines are considered related to one another with respect to their therapeutic effects for treating similar symptoms, the aim is to classify and map them using the concept of homology. This involves placing the discipline of homeopathy into a comparative framework using these plant medicines as taxa, therapeutic effects as characters, and contemporary cladistic techniques to analyse these relationships. The results are compared using cladograms based on different data sets used in biology (e.g. morphological characters and DNA sequences) to test whether similar cladistic patterns exist among these medicines. By classifying the therapeutic actions, genuine homologies can be distinguished from homoplasies. As this is a comparative study it has been necessary first to update the existing nomenclature of the plant species in the homeopathic literature in line with the current *International Code of Botanical Nomenclature*. *Homeopathy* (2008) 97, 122–128.

keywords: cladistics; homology; homoplasy; cladograms; nomenclature

Introduction

The plant species used in homeopathy have never been subjected to systematic analysis. A survey of the various *Materiae Medicae* shows that over 800 plant species[1,2] are the source of medicines in homeopathy and that their therapeutic actions are interrelated.[3] Convergent similarities between effects of plants from diverse families, genera or groups, together with relationships of remedies according to their chemical constituents have also been observed. The aim here is to test whether these plant medicines fall into a hierarchical system that has some predictive value and this work was carried out as part of a Ph.D. thesis.[4] For systematic comparison the plant medicines have been treated as taxa, the therapeutic effects as characters, and cladistic methods used to evaluate relationships. To ascertain whether the results indicate any general pattern of relationships, cladograms were prepared and compared with those cladograms[5] based on DNA sequences and morphological data sets.

The data for analyses were derived from the homeopathic repertory.[3] This repertory is arranged on the basis of overall similarity of therapeutic effects. No distinction is made between similarity due to true relationships, usually from common ancestry (homology), and superficial similarity due to convergence (homoplasy). Cladistics determines the difference between homology and homoplasy by congruence and incongruence as discovered by parsimony, which is simplicity of explanation minimising ad hoc hypotheses. Homology is not "evidence" for common ancestry. This can only be inferred based on extra sources of information other than the characters used to determine a cladogram.[6]

In homeopathy, various attempts have been made to group remedies and hence establish their relationships, but this work is far from complete with most remedies yet to have their clinical relationships described. Currently, no clear explanations or criteria[7–10] are given as to how these relationships were arrived at and it is therefore

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necessary to establish some criteria for the classification of these remedies.

Systematic biology is the study of relationships between organisms and encompasses taxonomy, which includes identification[11] and nomenclature,[12] as well as systematics, which includes phylogeny and classification.[13] By discovering, describing and studying the diversity of and relationships between organisms, the aim of taxonomy and systematics, is to produce classifications that are robust and informative.

For this study, cladistic methods provide the criteria for the grouping of medicines (remedies), to determine which of these are most closely related to one another by observing the distribution of their therapeutic actions. Cladistics can be described as a discovery procedure of evaluating characters (homologies) and taxa.[14] It encompasses a suite of methods and aims to discover, groups of organisms that have evolved from a common ancestor (i.e. monophyletic groups) through the relational concept of homology, and uses parsimony as the criterion of choice between competing hypotheses of relationship. It groups taxa hierarchically into nested sets and conventionally represents these relationships as a cladogram. These subsets represent monophyletic groups or sister-groups and only these are accepted as the most valid for cladistic results. By observing the distribution of characters among a group of organisms, cladistics attempts to determine which organisms are most closely related to one another. The pattern of relationships supported by the largest subset of 'special shared similarities'(synapomorphies) is then adopted as the working hypothesis to infer historical relationships.[6] The key to understanding these relationships comes from studying a wide range of characters and, in botany, those most often used are morphological features and DNA sequences. Although cladistics was developed within the disciplinary domain of biological systematics, it is not restricted to it. It can be applied to any field in which any kind of empirical historical reconstruction, comparable to homology, is recognised as it deals with the evaluation and interpretation of homologies.[15]

As this is a comparative study, approximately 1,700 plant names with synonyms were revised and brought in line[1,2] with the current *Botanical Code of Nomenclature*.[16] These revisions were necessary because the plant medicines used in homeopathy have accumulated over a long period of time, and the homeopathic *Materiae Medicae* have not adhered to a consistent nomenclatural standard. As a result, confusion over the correct identity of some of the plants has occurred, with some known by a variety of epithets. A few plant remedies (16 of 802) remain obscure.[1]

Material and methods

A relational database using an object-oriented approach was developed for the conversion, interpretation and modelling of homeopathic data.[4] In an object-oriented approach, both the data and methods are encapsulated in the object,[17] with the relational database becoming the storage mechanism. Encapsulation is an information-hiding technique that combines data and the set of operations that can be used to manipulate it, to form an object. It provides a form of data independence, by preventing an application becoming so interdependent that a small change has enormous ripple effects.

The homeopathic data, in electronic format, were supplied as 42 text files from *The Complete Repertory*.[3] The data set included not just the plant medicines but medicines from all sources used in homeopathy and their associated therapeutic effects. These therapeutic effects, written as descriptive phrases, are known as 'rubrics' and are arranged into 'chapters' to coincide with the category system used in the *Materiae Medicae*.

Interpretation of the data files

Each of the 42 text files are 'chapters' in *The Complete Repertory*© and each represents an anatomical part or function of the body, with a few exceptions, such as sensations, e.g. 'Vertigo' or 'Head pain'. The records within each file are the therapeutic effects described in the rubric text string, and the list of names in the header describes column headings and corresponds to abbreviated medicine names. The rubric descriptions correspond to the attributes of the 1,633 medicines listed in the header as treating the described therapeutic effects. The majority of attributes are presence/absence values, with absences dominating the matrix. Absences are denoted by the hyphen character '-', and presence as numerical grades (1, 2, 3, or 4), which correspond to the type face of the abbreviated medicine names in the repertory. Grade 1 is in plain type, grade 2 italics, grade 3 bold type and grade 4 bold type underlined. Each grade refers to successive degrees of verification, which potentially indicate reliability, of the therapeutic effects (see Table 1).

Five objects are recognised in the object-oriented model. Two represent real-world physical objects, including the medicines used and the parts of the body treated. A third object describes the therapeutic effects, some of which are measurable and others not. The fourth object refers to literature reports which link the material to its therapeutic effects and is measurable. However, there is no literature object included that can be used to build a trace to source and so this information is not directly measurable. A fifth object defines the category of the materials used as medicines, whether of plant, animal, mineral or other source.

Table 1 Each presence value in the data set has a numerical grade ranging from 1 to 4, signifying the degree of verification of therapeutic effects

Grades	*Degree of verification of therapeutic effects*
1	Therapeutic effects recorded from 'provings', toxicology or animal experimentation
2	Therapeutic effects frequently confirmed by 'provings' with some clinical verification
3	Therapeutic effects confirmed by repeated clinical verification
4	Therapeutic effects confirmed by re-provings and clinical verification compiled by Pierre Schmidt (Kent, 1897, 1924) and those from the Guiding Symptoms (Hering, 1879–1891).

Profile of the plant medicines

Filters were used in the relational database to select just the plant medicines (taxa) and their associated therapeutic effects (characters), for the construction of the data matrices. Only 49% of the total data were associated with plant medicines and these are represented by 802 taxa. Of these, 16 taxa were excluded as they remain obscure.[1] Table 2 gives a summary of this profile.

The data were supplied with just the abbreviated medicine names, with corresponding full names supplied as a separate list. The nomenclature database linking all of the abbreviated names to the revised full names was linked to one of the tables in the object-oriented model.

Selection of the medicines (taxa), therapeutic effects (characters) and the outgroup

Filters were implemented to select just the angiosperms (flowering plants) plant medicines (739) and their associated characters (therapeutic effects). Fungi, lichens, algae and gymnosperms were excluded.

The frequency with which the grades (1–4) occur in the whole data set for the plant medicines adds up to 414,247 states. The frequency of attributes with grade 1 (plain type) is 312,931 and for grades 2, 3 & 4 (italics, bold type and bold type underlined, respectively) is 101,316. The total number of attribute values for the 739 angiosperms is 376,856. By applying a filter the frequency of attributes for grade 1 is 285,086 and those for grades 2, 3 & 4 is 91,770 in total.

The outgroup used for analysis was *Tsuga canadensis*, a gymnosperm. In cladistic analysis a taxon outside the group of interest is used to determine the root and thus the polarities of the characters used to compute it.

Coding of the therapeutic effects (characters)

"Coding" in systematics is a method of assigning numerical states to characters. The characters (therapeutic effects) are the rubrics of the angiosperms and the outgroup (*Tsuga canadensis*). The purpose of coding is to convert observed information into data that can be classified and stored in a suitable format for numerical analysis. The method used was presence/absence (i.e. binary coding) whereby every character was assigned a "1" for presence or "0" for absence. All states are assumed to be independent. As the data are largely subjective, this method was preferred so that no more assumptions were built into the data set. Other methods of coding[6] involve making prior assumptions about the relatedness or similarity of characters, through transformation from one character state to another.

Table 2 Analysis of the data for the plant medicines

Original list of taxa	802
Taxa available for analysis	786
Therapeutic effects associated with the taxa available for analysis	88,769
Total data set	414,247
Plant families represented by 786 taxa	178
Families with more than two taxa that can be used for analysis	72

Construction of data matrices

The format used for storing the coded data sets was two-dimensional matrices. Three matrices were built by using the user interface of the relational database and this involved 9 stages of successive filtering. The user interface allowed for a range of selections to be made for the building of the data matrices by families, any or all parts of the body and any grade (1–4; typefaces) for the therapeutic effects.

An assortment of tests on the final data selection were carried out to determine that the matrices were built in the form that was required for cladistic analysis using WINCLADA version 0.9.99m24.[18] WINCLADA is an interactive program that is effectively the front and back ends of the calculating engine. Tests were also made at this stage on the lengths of strings and character set used as input to WINCLADA.

Although only the angiosperms have been selected for analysis the data set is still very large by any computing standard. To more easily examine the contents of any given matrix the 0's and 1's were pre-sorted so that the shared attributes (synapomorphies) were arranged to the left and to the bottom of the rectangular matrix. The details of the matrices are given in Table 3.

By using this successive filtering approach, the execution speeds were increased by 3 orders of magnitude when compared with any method attempting to apply all of the filters in a single analysis.

Cladistic methods and analysis

The different methods of cladistic analysis are given in Kitching *et al.*[6] Of these the parsimony-based method was chosen for this study as it is the most appropriate for analysing large data sets. Analysing large data sets creates optimisation problems (i.e. the process of finding the best solution to some problem, where "best" accords to some pre-stated criteria).[19] In cladistics this is the fitting of characters to cladograms, according to a pre-stated criterion, which in this case is the shortest (parsimonious) number of steps on the cladogram. Furthermore the process of finding the optimal solution grows exponentially as the size of the problem increases.[6] Parsimony analysis of large data sets is also well known to present a computationally complex problem,[20] and finding the most parsimonious trees is computationally very expensive or NP-complete (i.e. a non-deterministic polynomial). This simply means that one abandons all hope of finding an efficient algorithm for the exact solution of the given problem.[21,22]

Cladistic analysis of the angiosperm remedy data set

For this analysis the Parsimony Ratchet, an iterative search strategy[23] was implemented through the

Table 3 Details of the matrices for the angiosperms (flowering plants)

Matrix	*Grades*	*Number of characters*	*Number of taxa*	*Parts of the body*
1	1	35,134	739	All
2	2, 3 and 4	12,333	433	All
3	3 and 4	3190	218	All

WINCLADA software programme package, using NONA version 2.0 for Windows as the calculating engine.[24] For a complete description of the steps involved in implementing the analysis see Nixon.[23]

Analysis of matrices 1, 2 and 3

The 'outgroup' used for rooting the cladograms in all of the analyses was *Tsuga canadensis*. When analysing matrix 1, the shortest cladograms were not found even after 96 hours of run time. Consequently it was decided that the search be abandoned. For analysing matrix 2, the analysis was carried out by following the steps described by Nixon,[23] and took approximately 32 hours to complete. Five multiple ratchet runs of such replications were performed and each took around the same number of hours to complete. The time taken to analyse matrix 3 to find the shortest cladogram was around 2 hours for each of the 200 iterations and 5 ratchet runs were performed. Eventually, 11 separate analyses were carried out for the 3 matrices.

Results

A summary of the results is presented in Table 4, only the analysis of matrix 1 (grade1) failed to return a cladogram.

The cladograms generated from matrix 3 (grades 3 & 4 only) did not have enough remedies representing either families or genera to make meaningful comparisons with trees derived using morphological characters or DNA sequences. Therefore only cladograms generated from matrix 2 (grades 2, 3 & 4) were evaluated.

Evaluation of the cladograms for matrix 2

Only one cladogram for each replication was created. Since the topologies of the clades in all replications were identical, only one cladogram was selected to represent the data and evaluate the different character optimisations on the topology.[4]

This homeopathic remedies cladogram was not congruent with trees derived from other data sets. However, the pattern of relationships of the taxa was interesting because some of the critical clades were forming groups that related to parts of the body. One such clade, given as Figure 1, relates to the cardiovascular system and this was evaluated.

The reason for choosing this clade is that, according to World Health Organisation estimates, 16.6 million people around the globe die of cardiovascular disease (CVD) annually, and in the United Kingdom it is currently the leading cause of death.[25] Treatment of CVD is not clear-cut as many complex etiological factors contribute to the functioning and regulation of this system. In homeopathy, many remedies are used for treating symptoms of the cardiovascular system and of these remedies, some are seen to have a more significant effect on the heart than others. What is interesting is that the taxa seen to exert significant effects on the heart group as two sub-sets in the cladogram topology, highlighted in Figure 1, while the others have an overall effect on the cardiovascular system.

As the therapeutic effects of plants are generally attributed to their chemical constituents, it should follow that the grouping of the taxa illustrated in Figure 1 would be corroborated by studying the distribution of their chemical diversity. Recorded chemical analysis of plants indicates cardiac glycosides as potent constituents that affect the heart and blood vessels. The cardio-active glycosides primarily to affect the cardiovascular, neurological, and gastrointestinal systems and, most significantly, the cardiac system. They are potent inotropics (affecting the contraction of the heart muscle) and cardiotonics (increasing the force of cardiac contractions) and diuretics.[26]

In biomedicine, the therapeutic efficacy is confined principally to a small group of drugs that affects the function of the heart directly, and this includes the cardiac glycosides.[27] These glycosides are found distributed in a dozen plant families.[28–30] Some of the main genera in these families containing cardiac glycosides include those from the clade in Figure 1. These are *Adonis vernalis* (Ranunculaceae); *Convallaria majalis* (Convallariaceae); *Strophanthus kombe* (Apocynaceae) and *Digitalis purpurea* (Scrophulariaceae). These are four of the taxa of the sub-sets in Figure 1.

Evaluation of the highlighted sub-groups 1 and 2

Those taxa (of the sub-groups highlighted in Figure 1) known to have cardiac glycosides are *S. kombe*, *C. majalis*, *A. vernalis*, and *D. purpurea*.[29] However it is also reported that, although the cardioactive properties of *C. majalis*,

Table 4 Results for each of the 11 analyses undertaken for the angiosperm remedy data set for matrices 1, 2 and 3

No of replications	*Matrix*	*No. of taxa*	*Total no. of characters*	*Approximate run time in hours*	*No. of cladograms*
1	1	739	35,134	–	–
2	2	433	12,333	33	1
3	2	433	12,333	32	1
4	2	433	12,333	32	1
5	2	433	12,333	32	1
6	2	433	12,333	32	1
7	3	218	3190	3	1
8	3	218	3190	2	6
9	3	218	3190	2	6
10	3	218	3190	2	1
11	3	218	3190	2	1

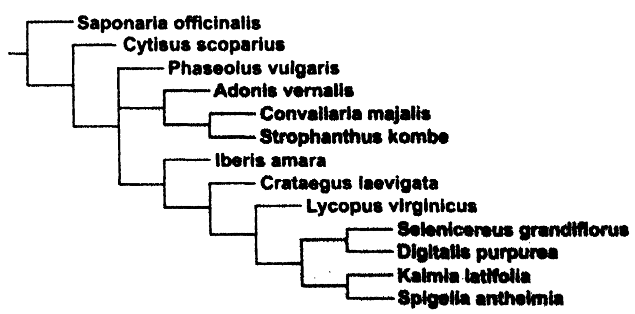

Figure 1 A clade seen to have a significant effect on the cardiovascular system.

A. vernalis, and *S. kombe* are similar to those of *D. purpurea*,[29-31] they act similarly to those of *S. kombe*,[29] and those of *C. majalis* and *S. kombe* are much less cumulative in their side effects. This appears to corroborate the grouping of the three taxa thus: (*A. vernalis* (*C. majalis*, *S. kombe*)).

For the second sub-group ((*S. grandiflorus*, *D. purpurea*) (*K. latifolia*, *S. anthelmia*)) (Figure 1), only the pharmacological properties of *D. purpurea* are well defined and it is the most widely used of the cardiac glycosides in biomedicine. Although cardiac glycosides have not been recorded for *S. grandiflorus*, *K. latifolia* and *S. anthelmia*, the presence of cardioactive constituents has been reported[32-36] but their effects have not been much studied. Hordenine (cactine) is documented to have effects similar to *Digitalis* and it is used in Europe for treating irregular heartbeat, angina pectoris and cardiac neuralgia. This compound has a spasmolytic effect on the coronary arteries.[26]

Spiganthine, the main cardioactive principle of *S. anthelmia*, according to Achenbach *et al.*,[34] causes a delay in the development of the contraction of the heart muscle. Mancini[37] reports cytotoxic principles from the sap of *K. latifolia*, and the US Food and Drug Administration Center[38] reports toxic effects for *Kalmia* similar to those of *Digitalis* with observed responses affecting the skeletal and heart muscles and the central nervous system. The chemistry, therefore, of some of the taxa of this sub-group has not been fully investigated.

Evaluation of the remaining taxa of this clade

Saponaria officinalis (Caryophyllaceae) contains saponins, haemolytic glycosides which are non-toxic when taken orally. Historically, saponins have been used as a diuretic[26,30] and diuretics are essential in the treatment of heart failure. Recent chemical studies of *S. officinalis* include the isolation of new triterpenoid saponins and sapogenins[39] and saporin, a plant toxin that disrupts protein synthesis in rats.[40] Saponins are currently also being studied for their cholesterol-lowering effects as these compounds can bind with cholesterol and thus reduce intestinal absorption. A good review of the saponins is given by Lacaille-Dubois & Wagner.[41]

Cytisus scoparius (Fabaceae). According to Bruneton,[30] this is rich in active substances belonging to various chemical classes. They include Sparteine, which has a wide range of action and is mildly ganglioplegic in that it shields the myocardium by decreasing the frequency and amplitude of its contractions. Another constituent, Scoparium is mildly diuretic.[26] Although cardiac glycosides are reported in the family Fabaceae, their presence is limited to very few taxa which, according to Evans,[29] do not include *C. scoparius* nor *P. vulgaris*.

Phaseolus vulgaris (Fabaceae). Much work continues to be carried out on the cholesterol-lowering effect of the beans on animals[42,43] to determine if the hypocholesterolemic effects would reduce the risk of *CVDs* in humans. Lectins, present in this taxon, have the ability to agglutinate red blood cells[28] and *P. vulgaris* is an important food plant.

Iberis amara (Brassicaceae) has been shown to have amines, cucurbitacines, flavonoglycosides, and mustard oil glycosides[44] which have marked effects on the gastrointestinal tract. Evans[29] reports cardiac glycosides in other genera of this family but their presence in this species has also been recorded.

Crataegus laevigata (Rosaceae). The historical use of *Crataegus* species to treat cardiovascular disorders is well documented. Bruneton[30] cites them as having an effect on the myocardium and attributes this effect to the synergy involving several components of the drug. Rigelsky *et al.*[45] report their use in controlled and uncontrolled clinical trials for class II congestive heart failure and postulate their effects to flavonoids with suggestions of beneficial effects on blood lipids. Clinical studies carried out by Fong & Bauman[46] have shown that standardized extracts show promising results for their use as adjunctive agents for the treatment of left ventricular dysfunction. Other trials consistently demonstrated their ability to improve exercise tolerance and symptoms of mild to moderate heart failure.

Lycopus virginicus (Lamiaceae). The potential of using this taxon for the treatment of hyperthyroidism is reported by Auf'mkolk *et al.*[47] and Harvey.[48] Its historic usage in treating palpitations of the heart is listed also and Harvey[48] cites one study in which the extract of *Lycopus* inhibited iodine metabolism and thyroxine release in the thyroid in humans. There are no reported references to clinical trials for its treatment for cardiovascular disorders.

Discussion

The cladogram resulting from the analysis showed that the patterns of relationships did not correspond to those derived using other data sets. Wilkins[49] claimed that "interesting data is what fails to be predicted by the default hypothesis, forcing revision and refinement of the hypothesis". According to Kitching *et al.*,[6] a cladogram is just a set of nested groups or clades that summarises a pattern of character distribution. The pattern of character distributions of the homeopathic species cladogram was realised. As there was no burden of making inferences implying ancestry, the results of the homeopathic species cladogram were looked at afresh and allowed for a different hypothesis. As the characters used for analysis are therapeutic effects it would make more sense that these effects would group taxa in relation to parts of the body. So by observing the pattern of distribution of the therapeutic effects one could, hypothesise that other taxa forming subsets could have similar constituents.

Reported chemical constituents for the remedies in the clade (Figure 1) indicated that most shared chemical compounds. They had various therapeutic effects on the cardiovascular system. Of these compounds, the cardiac glycosides have a more significant effect on the heart, while the other constituents have a wider spectrum of influence on the whole cardiovascular system. Some of the taxa used in homeopathy have a broad spectrum of action but are not used in biomedicine. These include taxa that have dietary or culinary uses and are also seen to have medicinal properties and *vice versa*; *P. vulgaris* (Figure 1) is one such example. Many food plants fall into this category and a lack of pharmaceutical application does not necessarily imply that these remedies are devoid of biological activity.

Systematics has always been an important tool in pharmacognostical practice and research. Its predictive value lies in the observation that related families often contain similar types of compounds and that an understanding of the systematic position of a medicinal plant species allows deductions to be made about the (biologically active) secondary natural products from the species.[50]

In the prospecting of potential medicines in biomedicine much is made of the contribution of ethnobotanical leads and traditional medicine to pharmaceutical development.[51–53] But the focus is mainly on the identification of a single active principle. Even the validation of traditional patterns of plant use is re-cast in the light of this reductionist explanatory model and is the current standard in use. Bodeker & Hughes[54] state that this reductionist approach, however relevant, might miss the synergistic effects of multiple components because of our focus on ever smaller units of analysis. They support this argument by using doshas (underlying organising principles), described in Ayurvedic theory, as an example.

At present, the evaluation of any system tends to be based upon the standards of western scientific medicine (biomedicine), viewed by anthropologists as the ethno-medicine of industrialised countries. Biomedicine is often assumed to be rational and systematic, based on empirical evidence and inductive or deductive logic. Its systematic classification of diseases is formally codified in the International Classification of Diseases, now in its tenth revision and known as ICD-10. However, the overall rationale for the ICD-10 classification is not explicit and a wide variety of criteria used in the classification, with decisions on definitions being influenced by political, judgemental and scientific factors.[55]

An interesting result of this study is that the holistic model employed in homeopathy could have the potential to explain synergism in traditional medicine, and that of reductionism in biomedicine. According to Etkin & Johns[56] "more complex phenomena are apprehended only at a lower level of resolution and so tend to be perceived through more holistic abstractions". This is in keeping with traditional concepts of health and disease, with food and medicine seen as two interconnected aspects of human culture. By further investigating the subsets of clades, this method could also be used as a predictive tool for the identification of single active constituents that have significant effects on specific parts of the body.

The method of analysing therapeutic actions using cladistic methods described in this paper makes the study of the whole process of sickness and illness less superficial, as the main focus is on understanding the whole and parts of the whole as correlative categories.

Conclusion

As this was a multidisciplinary project, it was important to convert and model data into a useful database. This database can now be completely queried and is analysable with systematic techniques. It provides the starting point against which many analyses and "what if" scenarios can be tested. The use of cladistics as a method of systematic analysis beyond the discipline for which it was originally devised was also tested. The aim was to establish whether the plant medicines used in homeopathy fall into a predictive, hierarchical system comparable to other data sets. What appeared initially as irreconcilable disagreement, turned out to present an interesting pattern. This pattern is quite unlike the generally accepted systematic pattern based on morphological characters or DNA sequences, but is nonetheless of considerable value.

What this analysis has brought sharply into focus is that to understand and explain the complexity of human illness and sickness, it is necessary to move beyond the mechanistic world view of contemporary science and take into account the holistic and integrated aspects of biological complexity. This depends on the questions that are asked and it is notable that analysing data using cladistic analysis, the holistic model to which homeopathy subscribes has the potential to offer an explanatory framework to both accommodate and validate assumptions of complexity and synergism in the plant medicines and reductionism in biomedicine.

This analysis is just the starting point for further research and analyses to be undertaken and hypotheses to be tested. The standardised checklist of the plant names used in homeopathy should not only prevent the wrong plants from being used in the preparation of the remedies but also allow for the exchange of information for all concerned with plant remedies in homeopathy.

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References

1 Bharatan V, Humphries CJ, Barnett JR. *Plants names in homeopathy: an annotated checklist of currently accepted names in common use*. London: The Natural History Museum, 2002, p. 149.
2 Bharatan V, Humphries CJ. Plants names in homeopathy: an annotated checklist of currently accepted names in common use. *Homeopathy* 2002; **91**(3): 156–161.
3 Van Zandvoort R. *The complete repertory: mind – generalities*. The Netherlands: Institute for Research in Homeopathic Information and Symptomatology, 2000, p. 570.
4 Bharatan V. Homeopathy and systematics. Ph.D. thesis, University of Reading, 2003, p. 163 + CD.
5 Chase MW, Soltis DE, Olmstead RG, *et al*. Phylogenetics of seed plants: an analysis of nucleotide sequences from the plastid gene *rbc*L. *Ann Mo Bot Gard* 1993; **80**: 528–580.

6 Kitching IJ, Forey PL, Humphries CJ, *et al*. *Cladistics: the theory and practice*. 2nd edn. Oxford: Oxford University Press, 1998, p. 248.
7 Boericke W. *Homoeopathic materia medica with repertory*. London: Homoeopathic Book Service, 1987, p. 1042.
8 Miller RG. *Relationship of remedies*. London: Homoeopathic Publishing Co, 1933, p. 32.
9 Clarke JH. A dictionary of practical Materia Medica, 3 Vols. New Delhi: 1978.
10 Wright-Hubbard E. A brief study course in homeopathy, St Louis: 1977, p. 102.
11 Judd WS, Campbell CS, Kellogg EA, *et al*. *Plant systematics: a phylogenetic approach*. Sunderland, MA: Sinauer Associates, 1999, p. 464.
12 Jeffrey C. Biological nomenclature. In: Special Topics in Biology. 3rd edn. London: Edward Arnold, 1989, p. 86.
13 Davis PH, Heywood VH. *Principles of angiosperm taxonomy*. Edinburgh and London: Oliver and Boyd, 1973, p. 558.
14 Nelson G, Patterson C. Cladistics, sociology and success: a comment on Donoghue's critique of David Hull. *Biol Philos* 1993; **8**: 441-443.
15 Paterson C. Cladistics. *Biologist* 1980; **27**: 234–239.
16 McNeill J, Barrie FR, Burdet HM, *et al*. *International Code of Botanical Nomenclature (Vienna Code): adopted by the Seventeenth International Botanical Congress, Vienna, July 2005*. Ruggell, Liechtenstein: Gantner Verlag, 2006, p. 568.
17 Goldberg A, Robson D. *Smalltalk-80: the language and its implementation*. Reading, MA: Addison-Wesley, 1983, p. 736.
18 Nixon KC. *Winclada (Beta) ver. 0.9.9*. Ithaca NY: Nixon, 1999.
19 Illingworth V (ed). Dictionary of Computing. 4th edn. Oxford: Oxford University Press, 1997.
20 Goloboff PA. Analyzing large data sets in reasonable times: solutions for composite optima. *Cladistics* 1999; **15**: 415–428.
21 Day WHE. Computationally difficult parsimony problems in phylogenetic systematics. *J Theor Biol* 1983; **103**: 429–438.
22 Graham RL, Foulds LR. Unlikelihood that minimal phylogenies for a realistic biological study can be constructed in reasonable computational time. *Math Biosci* 1982; **60**: 133–142.
23 Nixon KC. The Parsimony Ratchet, a new method for rapid parsimony analysis. *Cladistics* 1999; **15**: 407–414.
24 Goloboff PA. *NONA (NO NAME), version 2.0 (for Windows)*. Tucumán, Argentina. Program and manual available at: <http://www.cladistics.com>; 1999.
25 Petersen S, Ranger M, Wolstenholme J. *Coronary heart disease statistics: heart failure supplement*. London: BHF, 2002.
26 Reynolds JEF (ed). Martindale: the Extra Pharmacopoeia. 29th edn. London: The Pharmaceutical Press, 1989, p. 1896.
27 Grossmann M. Effects of cardiac glycosides on 24-h ambulatory blood pressure in healthy volunteers and patients with heart failure. *Eur J Clin Invest* 2001; **31**(Suppl. 2): 26–30.
28 Hollman A. Plants and cardiac glycosides. *Br Heart J* 1985; **54**: 258–261.
29 Evans WC. *Trease and Evans' pharmacognosy*. 15th edn. London and Philadelphia: Bailliere Tindall, 2002, p. 583.
30 Bruneton J. *Pharmacognosy: phytochemistry, medicinal plants*. 2nd edn. Paris: Lavoisier Publishing, 1999, p. 1136.
31 Hipsz M, Kowalski J, Strzelecka H. Cardenolide glycosides of *Convallaria majalis*. II. Assay of convallatoxin and locundioside. *Acta Pol Pharm* 1975; **32**(6): 695–701.
32 Petershofer-Halbmayer H, Kubelka O, Jrentsch J, *et al*. Isolation of Hordenine ("Cactine") from *Selenicereus grandiflorus* (L.) Britt. & Rose and *Selenicereus pteranthus* (Link & Otto) Britt. & Rose. *Sci Pharm* 1982; **50**: 29–34.
33 Wagner H, Seegert K, Gupta MP, *et al*. Cardiotonic active principles from *Spigelia anthelmia*. *Planta Med* 1986; **5**: 378–381.
34 Achenbach H, Hubner H, Vierling W, *et al*. Spiganthine, the cardioactive principle of *Spigelia anthelmia*. *J Nat Prod* 1995; **58**(7): 1092–1096.
35 Hubner H, Vierling W, Brandt W, *et al*. Minor constituents of *Spigelia anthelmia* and their cardiac activities. *Phytochemistry* 2001; **57**(2): 285–296.
36 Knight AP, Walter RG. Plants affecting the cardiovascular system. In: Knight AP, Walter RG (eds). A Guide to Plant Poisoning of Animals in North America. Jackson, WY: Teton NewMedia, 2002.
37 Mancini SD, Edwards JM. Cytotoxic principles from the sap of *Kalmia latifolia*. *J Nat Prod* 1979; **42**(5): 483–488.
38 U S Food & Drug Administration Center for Food Safety & Applied Nutrition. *Kalmia* poisoning from food borne pathogenic microorganisms and natural toxins, <http://caltest.nbc.upenn.edu/poison/plants/ppmount.htm>; 1992 (accessed August 03).
39 Koike K, Jia Z, Nikaido TJ. New triterpenoid saponins and sapogenins from *Saponaria officinalis*. *J Nat Prod* 1999; **62**(12): 1655–1659.
40 Angner RT, Kelly RM, Wiley RG, *et al*. Preferential destruction of cerebellar Purkinje cells by OX7-saporin. *Neurotoxicology* 2000; **21**(3): 395–403.
41 Lacaille-Dubois MA, Wagner H. Saponins – a review of the biological and pharmacological activities of saponins. *Phytomedicine* 1996; **2**: 363–386.
42 Shutler SM, Bircher GM, Tredger JA, *et al*. The effect of daily baked bean (*Phaseolus vulgaris*) Consumption on the plasma lipid levels of young, normo-cholesterolaemic men. *Br J Nutr* 1989; **61**(2): 257–265.
43 La Rosa JC, Hunninghake D, Bush D. The cholesterol facts: a summary of the evidence relating dietary fats, serum cholesterol, and coronary heart disease. *Circulation* 1990; **81**: 1721–1733.
44 Saller R, Reichling J. Drugs with *Iberis amara* as a modern phytotherapy to treat chronic functional disorders of the gastrointestinal tract. *Forsch Komplementarmed Klass Naturheilkd* 2002, Dec9;(Suppl. 1): V–VI.
45 Rigelsky JM, Sweet BV. Hawthorn: pharmacology and therapeutic uses. *Am J Health Syst Pharm* 2002; **59**(5): 417–422.
46 Fong HH, Bauman JLJ. Hawthorn. *Cardiovasc Nurs* 2002; **16**(4): 1–8.
47 Auf'mkolk M, Kohrle J, Gumbinger H, *et al*. Antihormonal effects of plant extracts: iodothyronine deiodinase of rat liver is inhibited by extracts and secondary metabolites of plants. *Horm Metab Res* 1984; **16**(4): 188–192.
48 Harvey R. *Lycopus europaeus* L. and *Lycopus virginicus* L.: a review of scientific research. *Br J Phytother* 1995/96; **4**(2): 55–65.
49 Wilkins J, The vicious circle and the virtuous spiral: the need for a null hypothesis, version of Tuesday, 28 July 1998, <http://www.users.bigpond.com/thewilkins/papers/nullhyp.html> (accessed August 2003).
50 Stahlhut R, Park G, Petersen R, *et al*. The occurrence of the anti-cancer diterpene taxol in *Podocarpus gracilior* Pilger (Podocarpaceae). *Biochem Syst Ecol* 1999; **27**(6): 613–622.
51 Balick MJ. Ethnobotany, drug development and biodiversity conservation – exploring the linkages. In: Prance GT, Chadwick DJ, Marsh J (eds). Ethnobotany and the Search for New Drugs, Ciba Foundation Symposium Series 185. Chichester: John Wiley, 1994, p. 4–24.
52 Cox PA. The ethnobotanical approach to drug discovery: strengths and limitations. In: Prance GT, Chadwick DJ, Marsh J (eds). Ethnobotany and the Search for New Drugs, Ciba Foundation Symposium Series 185. Chichester: John Wiley, 1994, p. 25–41.
53 Prance GT. Conclusions. In: Prance GT, Chadwick DJ, Marsh J (eds). Ethnobotany and the Search for New Drugs, Ciba Foundation Symposium Series 185. Chichester: John Wiley, 1994, p. 266–268.
54 Bodeker G, Hughes MA. Wound healing, traditional treatments and research policy. In: Prendergast HDV, Etkin NL, Harris DR (eds). Plants for Food and Medicine. Kew: Royal Botanic Gardens, 1998, p. 345–359.
55 Hahn R. *Sickness and healing – an anthropological perspective*. Yale University Press, 1996, p. 336.
56 Etkin NL, Johns T. "Pharmafoods" and "Nutraceuticals": paradigm shifts in biotherapeutics. In: Prendergast HDV, Etkin NL, Harris DR (eds). Plants for Food and Medicine. Kew: Royal Botanic Gardens, 1998, p. 3–16.