

‘The Realm of Hard Evidence’: Novelty, Persuasion and Collaboration in Botanical Cladistics

*Jim Endersby**

In 1998 a new classification of flowering plants generated headlines in the non-specialist press in Britain. By interviewing those involved with, or critical of, the new classification, this essay examines the participants’ motives and strategies for creating and maintaining a research group. It argues that the classification was produced by an informal alliance whose members collaborated despite their disagreements. This collaboration was possible because standardised methods and common theoretical assumptions served as ‘boundary objects’. The group also created a novel form of collective publication that helped to unite them. Both the collaboration and the publishing strategy were partly motivated by the need to give taxonomy a degree of ‘big science’ credibility that it had previously lacked: creating an international team allowed more comprehensive results; and collective publication served to emphasise both the novelty of the work and its claims to objectivity. Creating a group identity also served to exclude practitioners of alternative forms of taxonomy. Finally, the need to obtain funding for continuing work both created the need to collaborate and influenced the way the classification was presented to the public. © 2001 Elsevier Science Ltd. All rights reserved.

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1. Introduction: ‘A Rose is Still a Rose’

On 23rd November 1998, the *Independent* newspaper announced that ‘A rose is still a rose, but everything else in botany is turned on its head’. The story, by the paper’s environment correspondent Michael McCarthy, concerned a new classification of the angiosperms (flowering plants) done by an international team of plant systematists, led by Mark Chase (Kew Gardens), Peter F. Stevens (then at Harvard University), and Kåre Bremer (Uppsala University). According to McCar-

* Department of the History and Philosophy of Science, Cambridge University, Free School Lane, Cambridge CB2 3RH, U.K.

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thy's article, the new classification 'will cause a botanical revolution', because 'the exploding science of genetics has made possible a complete—and now accurate—reclassification of all the families of flowering plants', which 'represents for the first time an evolutionary tree of plants which is certain to be accurate'. Chase, who was interviewed by McCarthy for the story, said of the new classification: 'I think you would have to say it is a breakthrough' (quoted in McCarthy, 1998a).

McCarthy's article created considerable interest and over the next few weeks radio and TV programme-makers, and many newspapers and magazines, picked up the story.¹ The popular magazine *Garden News* reported (under the headline 'DNA shake-up: botany world is rocked by genetic revelations') that 'scientists using DNA techniques have discovered the true picture of how all the world's plants are related', and quoted Chase as saying that the new work took taxonomy 'out of the realm of opinion and into the realm of hard evidence. It cannot be disputed.' (quoted in Warters, 1998). The non-specialist media rarely gives botany this degree of coverage, and for taxonomy to get front page newspaper headlines is unprecedented. Their interest was partly aroused by the classification's claim to be revolutionary because it was accurate, but also because this accuracy was based on the use of DNA and computers—two 'sexy' topics for the popular press.² However, these are not the most interesting aspects of the way the story was told.

This essay examines aspects of the new classification by interviewing some of the scientists involved³—as well as one or two of their critics—with the initial aim of discovering how and why the media presented it as they did. However, the interviews also shed light on the process of collaboration between the scientists involved, and in particular, on their motives and strategies for creating and maintaining a research group. The technical paper that created all this interest, 'An ordinal classification for the families of flowering plants' (APG, 1998), was produced by an informal alliance whose members disagree with each other over various issues, but were nevertheless able to collaborate. As will be shown, this collaboration was made possible by the creation of 'boundary objects', standardised methods and common theoretical assumptions. The decision to publish as a collective also helped to unite the collaborators. However, I hope to show how the group's collaboration and their publishing strategy were also motivated by the need to give taxonomy a degree of 'big science' credibility that it had previously lacked.

¹The details of the different reports are not discussed here because most of them are copied substantially from the *Independent's* story, making them rather similar in their general tone and approach.

²However, in the case of the Swedish media, their initial interest was aroused by nationalism—the *Independent's* story reported that 'Linnaeus was out of date': the Swedes reported this as 'a British botanical revolution' ('*Den brittiska botaniska revolutionen*') that had overthrown the taxonomic system of Sweden's greatest ever scientist. It took Kåre Bremer and his Swedish colleagues some effort to overcome this misconception (Jacobsson, 1998).

³Christopher Quinn, one of the authors of the APG paper, taught me systematics at the University of New South Wales (UNSW), and I introduced myself to the people I interviewed as his student. The candour of some of the interview responses I quote in this essay may reflect the interviewee's perception of me as—in some loose sense—an 'insider'.

The international team allowed more comprehensive results than its members could have achieved individually, but collective publication also served to emphasise both the novelty of the work and its claims to be objective. Creating a group identity that excluded practitioners of alternative forms of taxonomy was a further aspect of this latter strategy. Finally, the need to obtain funding for continuing work both created the need to collaborate and influenced the way the classification was presented to the public.

2. Background: Cladistics

The scientists involved in this project are practitioners of a form of systematics called cladistics. A brief explanation of cladistics and definitions of some of its technical terms are necessary to follow aspects of the story which follows. A necessarily sketchy outline of the history of plant classification is also useful to understand some of the issues raised.

Traditionally, plant taxonomy has been based on morphology, the physical appearance of plants, which was assessed visually. Plants were classified according to their overall similarity: those which closely resembled one another were grouped together, those that were dissimilar were placed into different taxa. (Taxa is the plural of taxon, the generic term for any sort of taxonomic group, such as a species or genus.)

The morphological approach pre-dates Darwinism, but as evolutionary ideas gained increasing acceptance during the latter half of the nineteenth century, the view that taxonomic patterns might reflect those of genealogy became increasingly widespread. Species that resemble one another were assumed to be related, with the degree of resemblance being presumed proportional to the degree of relatedness. However, the correlation between genealogical and taxonomic patterns can be described either in purely descriptive terms (that accurate taxonomy inevitably converges on evolutionary history), or as a prescription for how taxonomy *ought* to be done. This latter view has led to various programs for creating an explicitly evolutionary taxonomy. At the same time, concerns over the lack of rigorous taxonomic methodology (and the resultant lack of consensus between taxonomists) led to proposals for reforming taxonomic procedures. Cladistics is a proposal that aims to do both—to create a rigorous, objective methodology for reconstructing phylogenies upon which classifications can be based. This outline of taxonomic history is simplified to the point of caricature, but broadly reflects the opinion of the cladists themselves, as will become apparent (Hull, 1988; Campbell, 1993; Stevens, 1994).

Cladistics can be traced to a number of biologists and has methodological and other debts to earlier taxonomic schools (most noticeably phenetics, or numerical taxonomy). However, the German entomologist Willi Hennig is usually cited as the founder of cladistics. Hennig tried to assess phylogeny (evolutionary lineage) by looking for an explanation of the distribution of characters in living species.

The intention is to find the branching order of species, the order in which they separated from their ancestral precursors.

The method Hennig adopted was to identify characters that retained their original 'primitive' forms (which cladists refer to as 'plesiomorphic'), as opposed to those which had the recent, derived ones ('apomorphic'). He then generated hypothetical phylogenies (represented as branching diagrams called 'cladograms') that matched the observed distribution of characters (this is now done with computers, but these are not essential). Finally, the assumption of parsimony was used to decide which was the most likely pattern; the hypothetical phylogeny with the fewest character reversals (shifts from the plesiomorphic to the apomorphic state, and then back again) was taken to be the most likely.⁴ Each change in a character state is called a 'step' and the phylogeny with the fewest steps is the 'shortest tree'. In modern cladistics, this process is carried out using many different characters from many different taxa simultaneously, so that the shortest tree that emerges reflects the most parsimonious explanation of all the data, for all the characters, for all the taxa analysed.

Normally a cladistic analysis produces several, equally short, trees and the computer program combines these into a single 'consensus cladogram' that shows only the branches ('clades') present in all trees. The result is then evaluated in two ways: 'decay analysis' and 'bootstrap' or 'jackknife' tests.

Decay analysis evaluates the assumption of parsimony by relaxing it and seeing whether the clades still appear. For example, if the shortest trees that were combined into the consensus cladogram contained 100 steps, one would call up all the trees with 101 steps and see whether the consensus cladogram that they produce showed the same clades as the 100-step one. Then the 102-step trees are analysed, and so on. The number of additional steps that a given clade survives is its decay rating and higher numbers represent well supported clades.

Bootstrap and jackknife are procedures for assessing the extent to which the cladogram depends on the specific characters used in the data. Many characters of organisms are linked; for example, a plant that is adapted to withstand a desert environment will have a number of correlated features because they are all adaptations to a single environment and are often interdependent. Other desert plants will have many of the same features for the same reason, a situation known as convergent evolution. Similarities caused by convergent evolution are traditionally called 'analogies', but cladists prefer the term 'homoplasies'. Those due to common descent are called 'homologies', and cladistic analysis (like any taxonomic analysis) should be based on the latter, not the former. Bootstrap and jackknife check simultaneously for homoplasy and for sampling errors by randomly removing some of the data

⁴It is important to note that this practice is regarded by cladists as simply a methodological assumption, often known as Occam's Razor, that is common to all sciences—that of using the simplest explanation available; most cladists do *not* regard it as embodying any assumption about the actual nature of evolution, least of all the assumption that evolution is in fact parsimonious.

from the sample and re-analysing the remainder. The main difference between them is that a bootstrap analysis generates new ‘dummy’ data based on the remaining real data to ensure that the total number of character states remains constant, whereas jackknife analysis does not. Cladograms are then produced with bootstrap or jackknife values for each clade, showing the percentage of the test trees that included the clade—as with decay analyses, higher values mean better support.

Many aspects of cladistics are criticised by taxonomists of other schools, and there are also differences of opinion between cladists as to which methodology is best. However, the highly simplified account given here should be enough to make sense of the story that follows.

One final issue needs to be discussed: even among cladists, there is considerable disagreement about how one derives a taxonomy (a classification) from a phylogeny (an evolutionary history). Taxonomies are hierarchical, in that they consist of an ascending series of taxa, each more inclusive than the last (such as species, genus, family, order and so forth), and each taxon has to be distinguished from other taxa. For example, the kingdom *Plantae* is subdivided into divisions (the equivalent of phyla for animals), which are in turn sub-divided into classes, orders, families, genera and species. There are established naming conventions that specify what each taxon is called. This hierarchical structure facilitates the storage and retrieval of information, but also the successful prediction of the properties of plants based on their affinities. For example, edible corn is called *Zea mays*, which identifies it as a unique species (*mays*) of the genus *Zea*. *Zea* is part of the family Poaceae, the grasses, and thus has features in common with other grasses, such as the possession of hollow stems. In turn Poaceae are members of the order Poales, which is in turn part of the class Monocotyledones, all of which have seedlings with a single cotyledon (seed leaf). So, if a botanist discovered a new species of corn and placed it in *Zea*, every botanist would automatically know that it had hollow stems and a single cotyledon (Raven, Evert *et al.*, 1992, pp. 171–85).

However, the difficulty that cladistics creates is that there is no obvious way in which to create such a hierarchical taxonomy (and thus naming system) from a phylogeny. There are, for practical purposes, a finite number of levels in a taxonomic hierarchy but an indefinite number of ancestors in a phylogeny.⁵ The problem is that cladists insist on the principle of monophyly. A clade is by definition a monophyletic group, that is, one that includes all the descendants of one, but only one, ancestor.⁶ Monophyly distinguishes ‘good’ taxa from ‘bad’ ones: the latter either include only some of the descendants of their ancestor (paraphyletic

⁵In fact the International Code of Botanical Nomenclature does not set a limit on the number of levels in the taxonomic hierarchy; however in practice botanists restrict them to a manageable and fairly widely standardised number.

⁶When an earlier draft of this paper was circulated to interviewees for comment, several of them disagreed with the definition of monophyly that I had given. The one included here is, as far as possible, a consensus position; but the fact that none of the cladists was entirely happy with it tends to reinforce the main argument of the paper.

groups) or include the descendants of more than one ancestor (polyphyletic groups). The concept of monophyly means that clades of the same taxonomic rank cannot be nested within one another; a monophyletic group must be on a different level from its ancestor. In Figure 1, the species A and B are each other's closest relatives and form a clade. If we name them as a genus, then the clade that includes them and C, which is also monophyletic, must be a rank higher than genus; in which case, A, B, C and D form an even higher ranked taxon, and so on. Even allowing for the fact that it is not necessary to name every clade, there is clearly a potential problem of running out of taxonomic levels well before one runs out of ancestors; either the principle of monophyly or the traditional taxonomic hierarchy must be sacrificed. Cladists solve this problem in various ways: Hennig, for example, insisted that the ancestral species ceases to exist when a speciation event occurs (however there seems to be no consensus among contemporary cladists as to exactly what he meant by this); alternatively, a few cladists have proposed a radically new naming scheme. The details of these and other solutions lie outside the scope of this essay, but the issue remains somewhat contentious among some cladists, as will become apparent.

3. The Angiosperm Phylogeny Group

The new classification was not published under the individual author's names, but under the collective identity 'the Angiosperm Phylogeny Group'—it carries the footnote 'Recommended citation, abbreviated as 'APG, 1998'.' (APG, 1998, p. 531) There are no precedents for this style of publication in any of the major

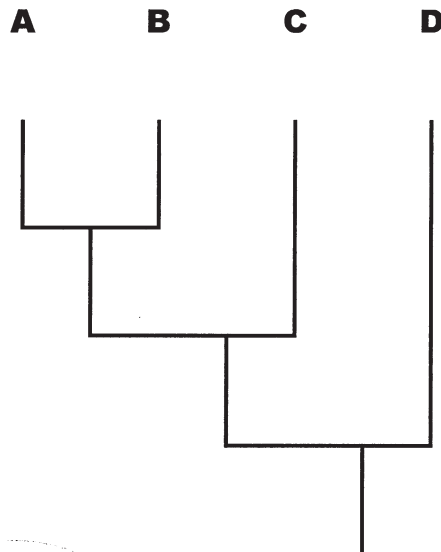


Fig. 1. A hypothetical cladogram.

taxonomic journals, and its use gives the paper the faint air of a manifesto. Chase explained that this:

... was done for two main reasons. One was we didn't want it to be cited as 'somebody *et al*', because it did represent the work of so many different people in different places. And secondly we wished to stress the fact that this *wasn't* a system of classification done by an expert—that is somebody like a Cronquist, or a Takhtajan, or Thorne . . . We wanted to explicitly say that botanists had gone beyond the need for authorities in this way; that really the authority came from the production of the data and the analyses we were doing . . . This was one way of signalling that, to publish it under a group name. (Chase, 1999)

Shifting authority from an individual expert to 'the data and the analyses' created intra-subjective consensus between the scientists who worked on the scheme, and is thus part of the claimed objectivity of the new approach. However, publication under the group name is also a rhetorical device that draws attention to this objectivity.

As previously mentioned, the scientists involved in this project are cladists, and thus aim to create a taxonomy based on a rigorous, objective methodology for assessing phylogeny. For the purposes of the present essay there are three things about cladistics that are central: it has a specialised language; it is computer-based; and it claims to be more objective than the systems of taxonomy it is intended to replace.

The objectivity of the new analysis is the main basis for its claim to be novel. The APG paper notes that previous angiosperm classifications have 'been rudely shattered as new kinds of data and new methods of analyzing conventional data have become firmly established'. It also notes that 'classifications such as those by Cronquist (1981) and Takhtajan (1980), although still in frequent use, have become outdated' (APG, 1998, p. 532).

However, while Chase sees the APG name as allowing the members of the group to efface themselves and their subjective opinions, by shifting authority to objective realm of 'the data' and 'the methods', the group's other members do not entirely share his view. The other two main authors, Bremer and Stevens, were asked if they shared this view. Bremer responded, via email, that:

Yes and no. Hitherto classifications have to a large extent been idiosyncratic schemes presented by individuals . . . The APG-system is different and more 'objective' in several ways. (Bremer, 1999)

He added that 'there is, however, still an element of subjectivity, or tradition, involved, viz. with respect to which groups should be named' (Bremer, 1999). So, while Bremer also rejects the 'idiosyncratic' schemes of their predecessors, his insertion of inverted commas around 'objective' serves to emphasise the 'element of subjectivity' involved in creating a taxonomy from a phylogeny—something Chase chose not to accentuate.

Stevens was asked the same question as Bremer, and after making a similar point about the objective, methodological basis for the consensus, added that:

The classification based on the tree represents a collaborative agreement of a somewhat different sort. That is because the orders are almost purely and simply conveniences, and in a number of cases there is no real reason whatsoever to prefer one delimitation of a group over another. However . . . the community has to come to a consensus as to the limits of groups—and that is what the work of the APG really represents. (Stevens, 1999)

This is similar to Bremer's statement—consensus over phylogeny does not lead automatically to consensus over taxonomy. The notion that 'the orders are almost purely and simply conveniences' seems very remote from the idea that the classification represents, in McCarthy's words, an 'evolutionary tree of plants which is certain to be accurate'.

These differences of emphasis may seem relatively minor, but Stevens also commented that:

The human mind simply cannot cope with the analyses of the immense dataset that the literature represents. Rather, I think of the evolving pre-computer classification as perhaps similar to a very slowly running computer analysis. (Stevens, 1999)

This implies that the cladistic methodology, and the use of computers to handle the large data sets involved, are not radical breaks from earlier work but continuations of it. Such comments reveal a range of opinions behind the APG's 'united front', but the group still needed to co-operate, partly to acquire global data sets (the APG taxonomists work in different countries and on many different groups of plants). The ways in which this collaboration occurred in the absence of complete consensus become clearer when the group's relations with taxonomists outside the APG are considered.

4. Beyond the APG

Professor Chris Humphries is head of the Higher Plants Division in the Department of Botany at the Natural History Museum, London. He is one of a group called pattern cladists (or 'transformed' cladists), who have some significant methodological differences with other cladists. The precise disagreements between the cladistic schools are not relevant to this essay, but they centre on the issue of deriving a taxonomy from a phylogeny. During the interview, Humphries gave a brief history of cladistics that stressed the diversity of views among cladists:

. . . you've got three major groups. And then there were the old guys: the pheneticists and the evolutionary systematists hanging about as well, creating a hell of a ferment . . . Then the rise of molecular stuff brought all these people in who weren't biologists at all and as a result there's been this terrific explosion. (Humphries, 1999)

He also regards some of the 'mainstream' cladists as insufficiently interested in the issue of whether the observed distribution of characters is the result of homology or homoplasy:

Pattern cladists and people who are interested in organisms tend to take a view like this [i.e. his own]; whereas people who've come at it through molecular stuff tend

to take a view rather like . . . Farris⁷ and others, who think you can get a tree out of any old matrix. Once you decide on your characters, you just get your specimens and score them off—which is a form of phenetics in a way. (Humphries, 1999)

The ‘matrix’ referred to is the table of initial data that is to be analysed. His last sentence, which describes the mainstream cladists as engaging in ‘a form of phenetics’ is noteworthy because cladistics was largely created in opposition to phenetics in a series of highly charged debates and disputes (see Hull, 1988; chapter 5); no cladist would take kindly to being described as doing any form of phenetics.

Humphries returned to the issue of the divisions within cladistics at a later stage in the interview:

You’ve got the parsimony guys—Farris and others—who are really Hennigians, but they’re not like the German Hennigians and they’re not like the Hennigians of the Sixties—so you’ve got a bit of a mix there. And then you’ve got people like me, pattern cladists, who tend to come at it like this [draws a phylogenetic tree of cladists, with three branches]. So there’s at least three groups, but in here [indicates the ‘parsimony guys’ on his drawing] you’ve got an immense proliferation . . .

I’m interested in the whole philosophical debate, because the politics in this is just *unreal*. (Humphries, 1999)

However, it is important to note that while Humphries has some ‘philosophical’ differences with Chase and other members of the APG group, these are relatively minor compared with their common ground. It was therefore surprising to find Humphries quoted in the magazine *Amateur Gardening* as saying that the APG’s work ‘has been overhyped. It’s not a total rewrite, but a modification’ (Anon., 1998). However, when asked about this comment during the interview, he said that it was prompted by what he regarded as McCarthy’s misrepresentation of the APG’s work:

I had . . . a phone conversation with *Amateur Gardening*, who were up in arms. And they got on the blower to me and published something from me saying that I thought it was all overhyped. What I was trying to say was ‘taxonomy’s been changing all along’. In systematics you’ve got a tension always [draws a scale], with identification at one end and systematisation at the other end. (Humphries, 1999)

Humphries’ desire to distance himself from any suggestion of ‘hype’ is not surprising because, despite their minor differences, Humphries and Chase are themselves collaborators; they published a paper together a few months before the APG paper appeared (Källersjö, Farris *et al.*, 1998). Steve Farris, with whom Humphries also disagrees on some issues, was another author of the same paper, as was Bremer—whom Humphries referred to during the interview as a ‘firm friend’.

In view of their methodological differences, it might perhaps be thought surprising to find professional collaboration and friendships between Humphries and the other cladists. However, there is a clue as to how this collaboration works in the

⁷(James) Steve Farris wrote the jackknife program—*Jac*—that was used by several of the APG’s members to evaluate their analyses.

fact that the paper that Humphries collaborated on used the same gene (*rbcL*) and some of the same software (i.e. Steve Farris' *Jac*) as the APG's paper. The cladistic methodology seems to allow collaboration even among those with 'political' or 'philosophical' differences. For example, although Humphries refers to other cladists as 'parsimony guys', he acknowledges that the parsimony assumption is one they all share:

I don't think there's any [cladistic] methodology these days that doesn't apply the parsimony criterion. My view is that normal science is about parsimony. You don't make a more elaborate hypothesis if a simple one explains the data—and I think that's the way you should defend it. Nobody knows whether evolution is parsimonious or not, because . . . nobody will *ever* know what the true tree is—it will always be a hypothesis. So, parsimony gives you the best explanation of the data. (Humphries, 1999)

It seems that the DNA, the computer software and certain theoretical assumptions (notably the parsimony criterion and monophyly) serve as 'boundary objects', in the sense defined by Star and Griesemer: entities that are 'adaptable to different viewpoints and robust enough to maintain identity across them' (Star and Griesemer, 1989, p. 388). Star and Griesemer argue that boundary objects allow collaboration in the absence of complete consensus because they are stable enough to move from one participant to another, yet can change their meanings in the process. In the current case, a DNA sequence can be produced by a pattern cladist (like Humphries), but then be fed into a computer being run by a mainstream cladist (like Chase). As long as the analysis produces parsimonious trees showing monophyletic clades, the participants can agree to differ about other areas of their theoretical commitments.

However, Star and Griesemer analysed collaboration between scientists and non-scientists during the creation of a natural history museum, while the current essay looks only at relationships between scientists, so there are both similarities and differences between this case and theirs. On the one hand, there are various disagreements between the people involved that are overcome using what Star and Griesemer call 'standardised forms': common methods and objects of study—in this case, DNA sequences and cladistic software. On the other, the distance between the participants is smaller than in the scientists/non-scientists case, and as a result the boundary objects are less subject to re-interpretation as they move between participants. Instead, the boundary objects appear to serve the secondary purpose of taking some of the 'heat' out of disputes over interpretation—disagreements over other people's cladistic theories clearly don't prevent friendships, whereas if taxonomy is based on individual subjective expertise, criticism can only be taken personally.

Peter Galison's work on relationships between theoreticians and experimenters within particle physics provides another way of looking at collaboration in the absence of complete consensus. He developed the idea of a 'trading zone', by analogy with the geographical spaces where different cultures can meet and exchange goods without sharing beliefs or values: 'What is crucial is that in the local context of the trading zone, *despite* the differences in classification, signifi-

cance, and standards of demonstration, the two groups can collaborate' (Galison, 1997, p. 803). For Galison, the material culture of the particle physics communities he studied produced trade goods—such as the images created by the experimenters. When these goods were exchanged with the theorists they shifted their meaning, thus allowing the two communities to collaborate. A key aspect of this was a shared, simplified language containing only terms common to the two communities, which have to be stripped of some of their theoretical or experimental contexts to become part of a 'pidgin', thus allowing the material artefacts to be traded. In the process, certain material practices—such as that of interpreting cloud chamber photos—become what Galison calls 'wordless creoles', mature natural languages that have developed from the pidgin:

This suggests that the process of 'black-boxing' can be seen as the precise material analogue of the more linguistic forms of pidginization; just as terms like 'electron' can acquire a decontextualised meaning, so *items* like a local oscillator, a charged coupled device, and a computer memory can function as binding elements between subcultures when stripped from their original contexts and co-ordinated with new ones. (Galison, 1997, p. 836)

There are some clear similarities between Galison's examples and the present case; for example, the DNA sequences and computer programs form 'binding elements' between the sub-cultures of mainstream and pattern cladists. The overlap of experimental and theoretical concerns is also apparent in cladistics. David Bloor discussed the nature of scientific co-operation using as an example the development of models of the electron. He noted that, regardless of how individual scientists conceived electrons, something is only a model once a community of scientists uses it as such. Shared models enable communication and allow co-operation (Bloor, 1995, p. 12). The fact that the present case looks at co-operation between scientists means that their boundary objects tend to be more esoteric ones—like Bloor's electrons. This is a further difference from Star and Griesemer's case, since their actors were concerned with relatively un-theorised objects, such as natural history specimens. Comparison with Bloor's example of the way that shared models allow collaboration accentuates the degree to which the theoretical assumptions of the cladists, such as the parsimony assumption, are intimately bound up with their objects of study, such as the DNA. Nevertheless, a shared commitment to methods and models need not entail a shared theory; in practice the models help overcome the theoretical distance between the scientists. Ian Hacking makes a similar point, that the collaborators on a project need not share a common core of beliefs (Hacking, 1983, p. 264).

Standardised methods—whether one calls them boundary objects or binding elements—and their attendant common theoretical assumptions are essential to the internal cohesion of a collective like the APG, because it is a loose group without formal links. However, such methods also allow collaboration with 'outsiders' like Humphries. Chase stresses such collaboration as the key to new approach:

We've eliminated . . . this peculiar expert who thinks he can taxonomise the world . . . We don't actually need those people to synthesise the data together; we can do this collectively, co-operating, collaborating. (Chase, 1999)

This is clearly a shift from old-fashioned 'small science' to the 'big science' of international teams and multi-authored papers; in fact, at one point in the interview Chase explicitly compared the APG's work to the Human Genome Project. The rewards of such collective efforts are higher status and, as is discussed below, better funding. These rewards partially help to explain the need to overcome differences and establish collaborative efforts. Publishing under a collective name is part of the process of creating cohesion within the group, but—as we shall see—it is also part of a strategy by which to underscore the novelty of the APG's classification and methods by excluding an earlier generation of non-cladists.

5. Creating Outsiders

S. Max Walters is the former head (now retired) of the Cambridge University Botanic Garden and the author of numerous taxonomic papers and books, including co-editing *Flora Europaea* (Tutin, Heywood *et al.*, 1964–80). His view of taxonomy is strikingly different from those of the cladists, in that he regards historical issues as having played a large role in determining the existing families of flowering plants. His hostility to cladistics was very marked during the interview, but he commented that:

It's not unreasonable to see how it happened, because it's an attempt to objectify what is presented by many evolutionary taxonomists as being self-evident. I have that amount of sympathy with it, that I can see why it happened, but I have no sympathy at all with the *game* . . . I find it rather distressing. (Walters, 1999)

Walters' comment that he can 'see why [cladistics] happened' refers to comments he had made earlier, about the emergence of phenetics, or mathematical taxonomy.⁸ In response to his observations about the accidents of history within taxonomy, it was suggested that these might be reasons for reforming it:

That's what numerical taxonomy in the fifties and sixties was doing . . . [Attempting] to objectify taxonomy, to say 'could we get rid of this burden of history . . .'.

The impact of numerical taxonomy was to make people think about what they were actually doing. The really worrying thing about taxonomy is that it's a game played by a few people in a few institutions according to rules which, very often, are unstated. To some extent, the numerical taxonomic attack, the mathematical attack, was a breath of fresh air really. (Walters, 1999)

This comment closely parallels Chase's remarks about the way the APG's work has eliminated the need for 'peculiar experts'. However, Walters believes that the necessary reform—phenetics—has already happened, whereas Chase sees cladistics

⁸See Briggs and Walters (1984).

as the essential change. Despite their differences, phenetics and cladistics share a good deal, including the use of computer-based methods to remove subjectivity from taxonomy. Obviously, there are also important differences between them, but to an outsider—such as a member of a funding body—the similarities might be more striking. It is therefore important for the APG's purposes that the differences between the old and new approaches be emphasised, perhaps even exaggerated, in order to reinforce the new classification's claims to be innovative.

Walters takes the pragmatic view that the stability of plant nomenclature is essential and that cladistics threatens to disrupt it, but his opposition to cladistics is motivated by several factors: his commitment to phenetics; his sense of history and of what constitutes a scientific question; and his perception of the pragmatic need for stable nomenclature. However, a further reason is apparent in his comments on Chris Humphries:

Chris has this little coven of cladists which sits in a local pub. If you really want to see how ideas thrive in rather superheated atmospheres then talk to him. Quite interesting. I went to talk to them three or four years ago. There are bright people involved . . . one or two of whom were asking very pertinent questions, I thought, but I got the impression there was a pressure to conform. And they thought they were an elite body . . . always a *dangerous* assumption in science. (Walters, 1999)

Later in the interview he was asked whether the cladists' language and methods created a distance between them and traditional taxonomists:

Well it's a coven sort of thing. It's inbred. And it produces a jargon and a self-satisfaction. I think that's true. It's happened before. Cytogenetics was similar, went to people's heads. The idea that seems to be so widespread now amongst DNA men that *finally* they've got the tool that will answer all these questions. (Walters, 1999)

Walters' perception of the cladists as a clique who regard themselves as superior to older taxonomists gives the impression that he regards cladistics as 'taking over'. He also argued that cladists are only concerned with results and ignore important conceptual issues:

Most of the cladists don't make a start; I don't think they're interested in the logical, philosophical problems. They just bash on with the system. [Take] Kåre Bremer's setup in Uppsala—which I haven't actually seen, but I hear about second-hand—his line is just give out to a lot of tame research students exercises to do, and that's it. They find results. Is that science? It's a game, it's a game you can play if you've got money. It's very unfortunate that change in Uppsala. (Walters, 1999)⁹

Walters also described Uppsala's current approach as 'sterile' and 'very sad'. Both his arguments and sense of distress over the changes illustrate how the cladists'

⁹Bremer commented that: 'Walters' characterisation of cladistics and our work in Uppsala as a game is in my opinion applicable to any scientific school or methodology and the research departments adopting them. If you disagree with it, you can of course, as Walters does, ridicule it as a game with rules and players' (personal communication via email, 8/9/99).

common methodology and terminology serves not only to provide a basis for cooperation between themselves, but also to exclude non-cladists like Walters.

A new language and methodology may serve to create incommensurability between a new paradigm and its predecessor. Mario Biagioli has argued that the lack of dialogue between Galileo and his Aristotelian opponents was deliberately created by Galileo to exclude the previous generation of natural philosophers from his new science (Biagioli, 1990, pp. 183–85). It might be argued that Biagioli uses the term ‘incommensurability’ in too loose a sense, and that perhaps ‘pseudo-incommensurability’ might be more accurate; nevertheless a similar process seems to be at work in the case of botanical cladistics. The decision of Chase and his collaborators to publish as the ‘Angiosperm Phylogeny Group’ represents, among other things, a rhetorical strategy that excludes non-cladists; the ‘APG’ name, and the associated rhetoric of rendering traditional taxonomic expertise redundant, symbolise precisely the changes that distress people like Walters.¹⁰

My analysis of these rhetorical strategies should not be taken as implying that any member of the APG has any personal hostility to their opponents (apart from the fact that I have no way of knowing how they feel about each other, the issue is not relevant to my argument). I assume that Chase’s justification for publishing as the APG should be taken entirely at face value, but that it nevertheless serves as a rhetorical device that creates incommensurability between the ‘new’ cladistic paradigm and older ones, including phenetics. The press coverage called the new classification a ‘revolution’, and when asked explicitly about the way the story had been presented, none of the APG members disassociated themselves from this emphasis.¹¹

As Biagioli noted, one of the main reasons why Galileo set out to create incommensurability between himself and the Aristotelians was to establish a new professional identity for himself and win patronage (Biagioli, 1990, pp. 188–91). In the current case, similar concerns are at work; access to funding is a key concern for all those involved.

6. In Search of Patronage

The press coverage of the APG’s work focuses on the practical implications of more accurate taxonomy, such as finding economically valuable or medicinal plants. Chase was quoted in the *Independent* as saying ‘its importance is economic as well as scientific’ (McCarthy, 1998a), and the feature article in the same issue makes a similar

¹⁰This should not be taken as implying that Chase or his collaborators *intend* to exclude older taxonomists; in fact, Chase explicitly denied any such intention when commenting on a draft of this paper, arguing that cladistics ‘incorporates traditional taxonomic practices; it merely discards the need for intuitive authorities—it “democratises” systematics’. However, his statement does not change the fact that taxonomists who have spent decades becoming ‘intuitive authorities’ feel excluded.

¹¹However, when I circulated a draft of this essay to the people I interviewed, Peter Stevens commented ‘Well, I should have!’—the fact that he places less emphasis on this point than Chase does, and that Bremer expressed no view on this issue, tends to substantiate my overall thesis.

observation (McCarthy, 1998b). Bremer used the same argument in the Swedish press coverage (Winge, 1998), and Chase emphasised it during the interview. In explaining the need for continued funding of his work, he mentioned genetic engineering:

If we want to improve breeding, all this talk about transforming plants . . . all this sort of stuff is based on an accurate assessment of what the characters are, how they're constituted, what their evolutionary history has been . . . All those kinds of questions are absolutely necessary and the work at that level is just *immense*. (Chase, 1999)

During the interview with Walters, he was asked whether such practical benefits would be enough to persuade him to accept the new classification:

It might. But you would immediately suspect that the PR boys had been 'at it', just looking for cases to strengthen the next application for money. The game is so impure at that sort of level and it's getting worse. I hate to be so cynical about it, but it does look worse than it was when I came into it. (Walters, 1999)

This reinforces his earlier point about Uppsala, that cladistics was 'a game you can play if you've got money'. Humphries also highlighted the importance of funding issues when explaining why he thought the mainstream cladists are currently the dominant group:

At the moment this approach is winning because of the big investment in molecular stuff—to get a sequence out costs a few grand. What does Chase get? I think it's about thirty sequences a week—something like that. He has a system set up there so he can really drag them out fast. (Humphries, 1999)

His picture of Kew as a 'DNA factory' is surprisingly similar to Walters' characterisation about Uppsala—another suggestive example of similarity between their supposedly incommensurable views.

According to Chase, both Walters and Humphries are mistaken in their assumption that cladistics is expensive. He points out that although a DNA sequencer costs approximately £100,000, this is cheap compared with scanning electron microscopes or magnetic resonance imaging equipment. More importantly, once installed the equipment allows a sequence to be obtained for about £6. Nevertheless, he did acknowledge the influence of funding issues when it comes to presenting systematics to the public:

This is [something] Chris Quinn's been pretty upset with, because most of the Australian plant taxonomists in the last two years haven't had any funding from their Australian Research Council. And the comment has come out that [systematics] is sort of like stamp collecting: 'you're just collecting DNA sequences, that may have been cool five years ago, but it's not cool now—what are you going to do next that's more interesting? We're not going to fund any more molecular systematics because that was something we did five years ago, and after all things do move on. Do something more relevant'.

We've been trying to convince them that this isn't 'done', by any stretch of the imagination, and that this isn't something that's going to be replaced by something better. This *is* the thing that we need to do and we have to do it thoroughly. (Chase, 1999)

The specific question that prompted this comment was whether there was a danger in allowing the APG's work to be described as 'a complete—and now accurate—reclassification' and as 'certain to be accurate'. Might funding bodies interpret this as meaning that plant taxonomy is 'complete' and so doesn't need any more money? There appears to be a tension between the need to present the work as innovative and comprehensive, but simultaneously as unfinished and in need of further resources. Chase commented that:

This isn't just the latest thing, this is sort of the ultimate thing. At least as far as we can see it is. And I don't think anyone has ever been in that situation before with any of the previous techniques that came along, because we were using those as a way of getting at the genetic information, which was our ultimate goal. (Chase, 1999)

This tension suggests one further reason for the way in which the APG's work has been presented. Despite the press talk of 'botanical revolutions' and 'genetic revelations', cladistics is not particularly 'new', having been around for several decades. However, it has only had a major impact on *botanical* systematics relatively recently, particularly because the large-scale simultaneous analysis of numerous DNA sequences (which forms the basis of the APG's work) has only been possible since the advent of relatively cheap DNA sequencers and more sophisticated computer programs—both of which have occurred in the last ten years. As previously noted, cladistics does not rely on computers, but large-scale analyses like the APG's would be virtually impossible without them. Chase notes that:

When we did the '93 paper [i.e. Chase, Soltis *et al.*, 1993] it was barely possible to do the analysis on that number of taxa. In fact the main program that people use is [David] Swofford's *PAUP* [Phylogeny Analysis Using Parsimony] and when we first loaded this matrix of 500 sequences in, back in late '91, the program just crashed.

According to Chase, 'when we loaded it, it said it had an "integer overflow problem". I had no idea what that meant, but Swofford knew', and Swofford was called in to do 'a little bit of fussing' with the program, after which the analysis could be run. So, as Chase comments, 'the '93 analysis was done exactly at the moment when it was first possible to do it' (Chase, 1999). This example serves to reinforce Galison's comment about 'black-boxing'; as Chase acknowledges, he does not know much about the internal workings of the software but puts his trust in it, as do the other cladists, which allows the software to bind them together. Of course, Chase and the others know how cladistics itself works and can (and do) analyse small sets of data without computers; but an increasing degree of trust in the software is entailed as the analysis gets more complex. Yet it is worth noting that the software in question is relatively straightforward, often created by systematists who are self-taught computer programmers ('hackers', in computer parlance) and that it runs on standard personal computers (PCs). The precise stage of development of a particular program, like *PAUP* or *Jac*, determines what kinds of analyses can be done at a particular time. This 'hacker culture' seems a long way from the kind of big science represented by the Human Genome Project, and another aspect of

the rhetorical strategy of the APG and their allies is that the popular press coverage includes vague references to ‘more powerful computers’, not the details of the rather modest computing resources involved.

In the interview Chase maintained that the use of PCs makes cladistics a more democratic taxonomy than that practised by the experts: ‘the fact that this is a much more interactive way of doing analysis is a real benefit and makes it something that everybody can do, you don’t have to have access to big computers’ (Chase, 1999). This claim is slightly contradicted by the cost of the DNA sequencer, but Chase notes that Kew can and does make its resources available to a wide range of researchers who need to use it. Nevertheless, perhaps Chase’s claim about democracy is also an attempt to make a virtue out of necessity: arguing for the ‘democratic’ nature of the work stresses its novelty and thus its claims to continued funding.

7. Conclusion

For the popular press the exciting aspect of the new classification was the move to ‘the realm of hard evidence’—the accuracy of the APG’s work and its use of DNA and computers. However, the decision to publish under the name ‘Angiosperm Phylogeny Group’ is perhaps more interesting. The DNA and the computers served their role as boundary objects, allowing collaboration in the absence of complete agreement, but that collaboration is part of a larger strategy of transforming the ‘small science’ of traditional, expert taxonomy into a new ‘big science’, a ‘botanical revolution’. The tactic was to present cladistics (which is not really new) as a ‘new paradigm’, but at the same time as a well established science that requires continued funding. The APG name, and the specialised methods and language of cladistics, helped to create and sustain the central collaborative group without excluding a looser circle of allies among other cladists. At the same time it served to emphasise—perhaps to over-emphasise—the break with tradition; apart from the novelty of publishing collectively, the strategy serves to exclude the practitioners of earlier methods. For some of the paper’s authors at least, money was one aspect of the motivation for the way they presented the APG’s work: obtaining ongoing funding for systematic botany has been difficult in recent years, and Chase and his collaborators seem to share the hope that their new ‘big’ taxonomy will prove to be both sufficiently novel, but at the same time sufficiently stable, to attract continuing funding for the research. In pursuing this goal, their rhetorical strategies included dismissing previous approaches as ‘rudely shattered’ and ‘outdated’. None of this implies that the new work is not every bit as innovative and important as it is claimed to be—I am not remotely competent to judge—but it does highlight the multiple persuasive purposes that scientific methods and techniques can serve.

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