

Why names change: the new thinking in taxonomy

A paper published recently by Kevin Thiele from the Western Australian Herbarium and Austin Mast from the University of Florida has created controversy among native plant and wildflower enthusiasts. Mast and Thiele have recommended that the two well-established genera *Banksia* and *Dryandra* should be merged into one genus (which under the International Code of Botanical Nomenclature must be the older genus, *Banksia*). To effect the merge, all *Dryandra* species have been renamed as species of *Banksia*.

Not surprisingly, this move has caused a stir in the community. An implicit question is clearly this — why on earth would anyone do such a clearly nonsensical thing as to sink *Dryandra* into *Banksia*, when they are such obviously good genera?

In this article the *Banksia-Dryandra* issue will be approached in several stages, firstly with an explanation for some of the reasons why taxonomists ‘keep changing the names’, followed by a short history and philosophy of classification, and finally with a discussion of the reasons behind the *Dryandra* change itself. Along the way, an explanation will be given of the differences between classical taxonomy, which has resulted in many of the names in current use, and an emerging ‘new’ taxonomy that in some cases is creating a great deal of change.

Why names change

There are several main reasons why taxonomists from time to time need, or choose, to change the name of an organism such as a plant.

Firstly, the naming of plants is covered by a set of rules — the International Code of Botanical Nomenclature — which sets out how to correctly name plants and how to resolve cases where two or more names have been used for one species. It sometimes happens that applying the rules requires us to change a name.

For example, if a species named by one botanist turns out to have been previously legitimately named by an earlier botanist, then the Code stipulates that (except under certain conditions) the earlier name must replace the later name. This is a sensible rule when you think about it, as it gives due recognition to the first person who named a particular species, which is only fair.

Secondly, and more importantly for the purpose of this article, names may change because our knowledge grows. For example, at one stage most of the world’s grasses were placed in a single genus, *Poa*. As more and more grasses became

known, it became clear that this was simply silly — imagine if all the world's c. 9000 species of grass, from bamboos to spinifex, were called *Poa*! It wouldn't be a very useful taxonomy.

Interestingly, the fact that names often need to change when our knowledge grows is actually a problem caused by our very system of naming, a system formalized by Linnaeus, the father of taxonomy, whose tercentenary was celebrated in 2007. In the Linnaean binomial naming system which we use today, every species is given a double-barreled name (such as *Poa annua*), much like names of people (e.g. John Smith) and of many things (e.g. apple pie). This was a brilliant innovation. Not only does it make it relatively easy to create a unique name for every species, but it also encodes handy relationship information in the name. That is, encoded in the name *Poa annua* is the fact that the species in question belongs in the genus *Poa*. This makes it easy to remember where a species *fits* as well as what it *is*.

But here's the nub of a problem — if the name encodes where a species fits, then what do you do if you decide that it fits better somewhere else. This issue will be discussed later, as it lies at the heart of the *Banksia-Dryandra* issue. As an aside, it's likely that Linnaeus himself would have been mortified to be told that his binomial system causes problems, largely because he would have regarded that once a species was named and placed into a genus by Linnaeus then it would never need to be renamed into another genus by anyone else!

So, names sometimes need to change when our knowledge — our understanding of the relationships of species — grows. Taxonomy and systematics, like any science, evolves. Who would tell dream of telling physicists that their new understanding of the Universe is too complicated so we should stick with Newton. It doesn't make sense. Similarly, taxonomy grows and changes, and because names are the core of taxonomy, it would be a tragedy if they were to stay the same and not reflect new knowledge and understanding.

Why taxonomies change

So why do taxonomists sometimes change their minds about the relationships of species? To understand this requires an understanding of the philosophy and practice of taxonomy and systematics.

What taxonomists and systematists attempt to do is no less than to understand and describe, in great detail, the patterning of all life. This enterprise began well before Linnaeus, when early Greek philosophers such as Theophrastus (370–285 BC) began classifying plants.

Taxonomy began with the obvious observation that some species naturally group with others. Any schoolchild can tell you that a mouse and a rat 'go together', and both are clearly very different from a cow. Similarly, *Dryandra nivea* and *D.*

brownii clearly fit together, and both are obviously different in many ways from *Banksia coccinea*.

For the vast majority of our history, from Theophrastus through Linnaeus and right up to the mid 20th Century, taxonomies were constructed by simply putting together things that clearly ‘go together’. In the early days, the thinking was very simplistic — for example, before Linnaeus all ‘trees’ were classified together, separate from all ‘shrubs’ and ‘herbs’. Linnaeus introduced a more sophisticated method, grouping plants based on the numbers of stamens and pistils. The French botanist Antoine Laurent de Jussieu used a more sophisticated approach still, arguing for what we would now call a ‘whole-of-evidence’ approach — assess *all* the characteristics (of leaves, flowers, fruits etc), then group like with like according to overall similarities and differences.

But there’s an interesting difficulty with the approaches described so far. Plants are complex organisms, with many characteristics. Suppose one taxonomist believes, from observation of certain characteristics, that species A and B naturally ‘fit’ together into one genus, and species C and D naturally form a second genus. Suppose a second taxonomist believes, from observation of perhaps other characteristics, that it works better to put A and C into one genus and B and D into another. How could we choose which was the better taxonomy? We would have to either decide which arrangement worked better for us, or choose to believe the more respectable and important taxonomist. Both are very subjective and unsatisfactory judgments.

Without a clear underpinning idea for *why* some things ‘go’ with others, the question of which classification is better is probably meaningless anyway. It’s like asking which is better, a taxonomy that groups cups with bowls and plates with saucers, versus another that groups cups with saucers and plates with bowls. There is no reason to suppose that either is better than the other; both are equally valid (and equally meaningless).

Taxonomy of organisms, fortunately, is different from taxonomies of crockery or stamps, because it does have an underpinning framework, provided by Charles Darwin when, in the *Origin of Species*, he introduced the concept of evolution by descent with modification.

Darwin convinced scientists that all living organisms were part of a single ‘family tree’ of life (a phylogeny). This is a grand idea and one of the most important unifying concepts in biology. It explains beautifully, amongst other things, *why* mice and rats are similar (because they share many features inherited from a recent common ancestor), and cows are fairly different (because the common ancestor of rats, mice and cows is more distant). Because most of us simply accept evolution as self-evident now, it’s sometimes hard to grasp the revolution that Darwin brought to our thinking about nature.

Taxonomists, after Darwin, gradually accepted the idea that the purpose of a classification is not simply to group superficially like with like, but to classify organisms in a way that reflects their evolutionary relationships in some fashion. With this acceptance came the notion that some classifications are indeed superior to others — because organisms evolved, and because there appears to be only one tree of life, a classification that more closely reflects the patterns of evolution is better than one that doesn't. The former became known as a “natural” classification, the latter as an “artificial” one.

For many years until the middle of the 20th Century, taxonomists accepted the idea that classification should reflect evolution, but really had no idea how to put it into practice. There was a vague hope that grouping organisms according to overall likeness would result in a classification that reflected in some way the tree of life. But with no way of testing the fit, if two taxonomists came up with different classifications, you still pretty much believed whichever you preferred. Darwin had provided taxonomists with an underpinning framework, but no way of applying that framework to the problem of taxonomy.

A breakthrough came in the 1950s when a German entomologist, Willi Hennig, developed a method for mathematically *calculating* the most likely family tree or phylogeny from the patterns of characteristics in a group of organisms. Hennig's method, now called *phylogenetics* (and other similar methods developed in the last few decades), allows taxonomists to find a way through the vast array of similarities and differences that occur in any group of organisms, and to work out a best fit with the tree of life.

It's outside the scope of the present article to explain cladistic methods and related analysis techniques in detail. The most important point is that these methods, at least in theory, are rigorous, repeatable and produce classifications that can be tested, rather than vague and untestable ideas as has been the case in the past. It was these methods that were used to try to understand that branch of the tree of life that contains the banksias and dryandras.

The evolution of *Banksia* and *Dryandra*

To understand the significance of the results that Mast and Thiele obtained, consider Figure 1 which represents what most taxonomists would have drawn twenty years ago if they'd tried drawing a family tree of banksias and dryandras. They would almost certainly have imagined two branches on the tree of life, one comprising all the *Banksia* species and one comprising all the *Dryandra* species.

By contrast, when Mast and Thiele used phylogenetic methods to investigate the same question, they got the surprising, and very interesting, result shown in Figure 2. Their studies suggested that *Dryandra* is a branch that springs *out of* the

greater *Banksia* branch, instead of being a sister branch. That is, dryandras are modified and specialized banksias.

Look at Figures 1 and 2 again in terms of ancestors and descendants (shown by arrows on the figures). If Mast and Thiele are correct, then *Dryandra* comprises all the descendants of the ancestral *Dryandra* species (the one that first evolved from a *Banksia*). In modern taxonomy, such a group is called *monophyletic*.

But *Banksia*, as traditionally understood, comprises only some of the descendants of the ancestral *Banksia* (that is, only those that haven't subsequently evolved into dryandras). Such a group is called *paraphyletic*. Viewed in this way, the two traditional genera are not equivalent — one is a monophyletic group and the other is a paraphyletic one.

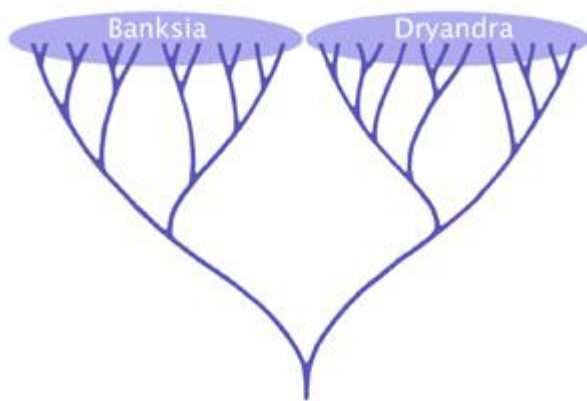


Figure 1. The traditional understanding of the evolutionary relationship between *Banksia* and *Dryandra*. Each “twig” on the evolutionary tree represents a species.

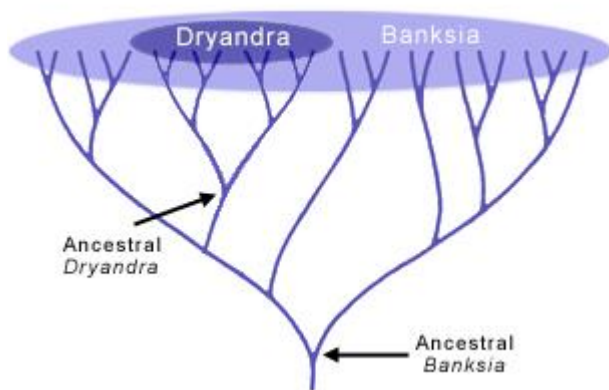


Figure 2. The new understanding of the relationship between *Banksia* and *Dryandra*, with the dryandra branch as an evolutionarily specialised offshoot of a *Banksia* tree.

This difference (between what we now call monophyletic and paraphyletic groups), was of great interest to Greek philosophers at the time of Plato, who pointed out to the Greeks a problem in the way they thought of themselves and of others. Many Greeks regarded that there were two classes of people, Greeks and Barbarians. Plato pointed out that these two classes are different in kind. ‘Greeks’ is a true class, because it comprises all people of Greek descent. But ‘Barbarians’ is not a class at all, as it comprises the class of all people minus the class of Greeks. It’s a grouping that can only be defined by what it’s not rather than what it is.

Plato’s problem with a group like ‘Barbarians’ is that some members of the group are more closely related to members outside the group than they are to other members inside the group — some ‘Barbarians’ are more closely related to the Greeks than they are to other ‘Barbarians’. This makes nonsense of the ‘Barbarian’ group.

A little reflection shows that this is exactly the same as the situation with *Banksia* and *Dryandra*. Because dryandras evolved from inside *Banksia*, some banksias (such as the ones on the left side in Figure 2) are more closely related to dryandras than they are to other banksias (e.g. the ones on the right side). To most modern taxonomists a genus should include *all* species that are inter-related through common ancestry rather than only some, and this makes the old *Banksia* an untenable group.

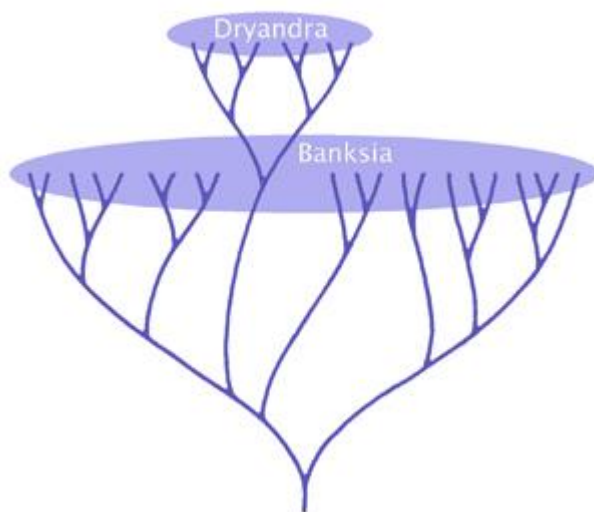


Figure 3. Another way of looking at the relationship between *Banksia* and *Dryandra*.

Banksia-Dryandra is an almost perfect example of what is becoming a common issue in modern taxonomy. Many of the groups that were established under the old, purely intuitive taxonomy are being found to be paraphyletic when studied more carefully. Examples abound at all taxonomic levels. The family Epacridaceae is

merely a specialized, mainly Australian offshoot of the larger cosmopolitan family Ericaceae, the two families having exactly the same relationship as *Banksia* and *Dryandra*. Most taxonomists are now using the family name Ericaceae. The change from *Eucalyptus* to *Corymbia* for the bloodwoods was caused by a similar situation (in this case the solution to the paraphyly problem was to split *Corymbia* from *Eucalyptus*). Recently, *Acacia* has been discovered to comprise separate groups spread over many parts of the tree of life. It has been split into several genera (luckily for us, the name has been saved for the Australian group). New research is suggesting that the genus *Hakea* may be nested inside *Grevillea* in much the same way as *Dryandra* within *Banksia*. That is, the problem of paraphyly is a common one.

Returning to Figures 1 (the old way of imagining *Banksia* and *Dryandra*) and Figure 2 (the new understanding), it's interesting to ask: why did we think that banksias and dryandras were so separate in the first place? Figure 3 is another way of drawing the new understanding. In this figure, *Dryandra* still emerges from within *Banksia*, but since evolving it's very much gone its own way and has diverged a lot in morphology. It's like a wild branch that, once evolved from *Banksia*, goes off on its own. This is why we've always thought of *Banksia* and *Dryandra* as two quite separate genera. The many changes that have occurred on the *Dryandra* branch since it evolved from its *Banksia* ancestor have resulted in a very different appearance in the two genera, even though in an evolutionary sense they are not so different at all.

What to do with *Dryandra*?

The discussion above has sought to explain what is now believed to be the true pattern of relationships of the species in the *Banksia-Dryandra* branch of the tree of life, derived from phylogenetic analyses. To reflect the new knowledge, botanists have chosen to put *Dryandra* in its rightful place, as a specialized offshoot within the *Banksia* branch. Unfortunately, the rules of the Code and the new, widely accepted tenet in taxonomy that only monophyletic branches in the tree of life should be named, requires that either *Dryandra* be merged into *Banksia*, or *Banksia* be split into several monophyletic genera. Mast and Thiele decided that the former option was preferable as it provides the simplest change and maintains an instantly recognizable genus rather than several genera that would be difficult to recognise as distinct.

Many people will question, and criticize, this change. There are three possible criticisms — firstly, that the cladistic methods used in the analyses are flawed, secondly, that the information used for the analyses is incorrect or inadequate, and finally that even if the answer is correct, *Dryandra* and *Banksia* should still not have been merged, but instead should be retained despite our new understanding of their relationships.

The first two criticisms can be dealt with quickly. If either the cladistic method is fundamentally flawed — that is, it cannot reconstruct the branching pattern of the tree of life — or the data used are inadequate, then it would be expected that different and contradictory answers would be obtained if the same type of analysis was run using two or more different and independent data sets. This is the “garbage in/garbage out” scenario, and throughout science it’s a good indicator that something’s wrong with either theory or practice.

In fact, the opposite was found. Mast analysed several independent genes, and Thiele analysed morphological and anatomical characters. All analyses pointed to the same answer (at least in broad outline). The fact that more or less the same answer was obtained from independent data sets gives confidence that the analysis, both in terms of data and method, is giving an answer that must mean *something*. It can’t be discounted easily as simply nonsense or an error.

Interestingly, this is an important difference between modern taxonomy based on phylogenetic analysis and the old intuitive taxonomy — using phylogenetics allows a rigorous test of the answers by comparing them with other results and checking for congruence. No such test is possible using the old ways.

The third criticism — that despite new knowledge of the relationships in *Banksia-Dryandra* the *status quo* should be maintained — is also hard to maintain. No science should work like this, rejecting new understanding simply because we’re comfortable with the old. As explained above, this would result in two genera that are quite different in kind, and in the anomalous situation of some *Banksia* species being more closely related to *Dryandra* species than they are to other *Banksia* species, something that Plato himself would object to. It’s also likely that if we were to keep the two genera, then generations of newcomers would make the old mistake of thinking that they are related in the way of Figure 1, and this is now known to be false.

Such mistaken thinking may then hold back future interesting research. For example, the difference in distribution of banksias and dryandras can be very neatly explained now that we understand their true relationships. Dryandras are restricted to south-west Western Australia, while banksias occur more widely around southern, eastern and northern Australia and into the islands to our north. Our new understanding helps explain this — the dryandra branch evolved from its *Banksia* ancestor relatively recently, after the drying of the continent isolated the south-west from the remainder, and they never escaped from this south-west origin.

Similarly, realizing that dryandras are specialized members of *Banksia* raises the interesting question: what happened when the first dryandra evolved from its *Banksia* ancestor, and why? Dryandras are highly successful — there are more species in the dryandra branch than in the rest of *Banksia*, and the dryandras appear

to have colonized different habitats. Wondering how they did this makes the group more fascinating even than it was before.

For an overview of the reasons for the name changes in *Dryandra* and *Banksia*, please see the accompanying short article: [Why dryandras have changed their name](#).

References

- Mast, A.R. & Thiele, K. (2007). [The transfer of *Dryandra* R.Br. to *Banksia* L.f. \(Proteaceae\)](#), *Australian Systematic Botany* 20: 63–71.
- M^cNiell, J., Barrie, F.R., Burdet, H.M., Demoulin, V., Hawksworth, D.L., Marhold, K., Nicolson, D.H., Prado, J., Silva, P.C., Skog, J.E., Wiersema, J.H. and Turland, N.J. (2006). [International Code of Botanical Nomenclature \(Vienna Code\)](#). *Regnum Vegetabile* 146. A.R.G. Gartner Verlag KG. ISBN 0080-0694.

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