

Evolution, Adaptive Radiation and Vireya Rhododendrons

Part I

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“... evolution consists of an infinitude of trivial, unconscious events . . . ” (Pollan, 2001)

Species are one of the basic means by which botanical science organizes its view of the plant world. But with the advent of genetic analysis the interpretation of the species concept has moved from field observations and dried specimens in the herbarium to the clinical atmosphere of scientific laboratories. Here the hard science of chemistry, complex instruments and precise measurements take place and new details of living organisms can be discovered. Recently new discoveries regarding vireyas based on genetic analysis have been published and we will try to convey these findings.

In traditional taxonomy (study of classification), from the pioneering work of Linnaeus in the early 18th century to recent times, botanists have had to rely on observations of physical characteristics (“morphology” or study of shape or configuration) of plants, supplemented with evidence from anatomy, cytology and other areas. Both microscopic and large-scale structures are compared to characterize species. Vireya species are distinguished by flower colors, leaf arrangement (pseudowhorks, spirals) and the size, and shape of flowers and leaves, and other parts. Like all rhododendrons, vireyas also have several distinct types of complex hairs called “scales” (multicellular hairs) which may be found on many parts of the plant and distinguish species.

But species are not only organized by their individual visual characteristics.

Species are also grouped together into relationships beginning with subsections, then gathered into sections, subgenera, genera, families and so on. Most importantly, ever since Darwin developed the concept of evolution, it has been understood that these relationships should reflect a species’ evolution from its ancestors to the present. Remember the many species of finches Darwin found in the Galapagos Islands? All were related back to individuals called common ancestors. This is called phylogenesis, the development and diversification of species through evolution. Genes, a familiar term to many now, are those parts of DNA that determine the physical characteristics of all organisms. Therefore, today the scientific study of phylogenesis is based on genetic analysis. As Lyn Craven stated: “Modern taxonomic classification is based upon the findings of rigorous genetic investigations” (Craven, pers. comm.) and that “formal classification should always be based upon evolutionary relationships, as far as these are known” (Craven et al. 2008).

The subject of genetic analysis is, no surprise, the gene. Genes are sections of the long, helical-shaped double strands of chromosomal DNA in the cell nucleus. Genes are like a long array of poppit beads on each chromosome. The “beads” are named for simplicity A, T, G and C [the four nucleotide bases of a DNA strand—adenine, cytosine, guanine, thymine]. Each DNA chromosome strand is formed because one side of each bead acts like a socket and the other side acts like a plug. Between the two DNA strands, the A beads are paired only with T beads, and G beads with C beads. These are termed the “base pairs” and these bonds join two strands together. The sequence of genes in DNA provides the overall blueprint for any organism. The identity of these base pairs in any location within a gene may

change over time as the result of mutation. This variation between species defines a major physical basis of evolution.

For each plant variety, the sequence of base pairs within a gene can then be compared with the sequence of base pairs in the same gene in any suspected related species. Then a phylogenetic tree, a branching structure diagram, may be constructed of related species. The mathematics of building a phylogenetic tree minimizes the total number of base pair changes required to join the sequences of all species considered in a single tree. In this tree, species that share the same inner branch are related and the lengths of outer branches indicate degrees of difference from their common ancestor. This results in a diagram that progressively shows increasing differences between ends of the branches, as shown in Fig. 1.

Using genetic analysis, the modern scientific goal is to assemble “monophyletic” groups of organisms called “clades” that have evolved from a common ancestor and that include all its living descendents. For instance, all reptiles have a common ancestor. But in recent years it has been established that birds are descended from reptiles. So reptiles can only be called a monophyletic clade if birds are included.

This change in approach is exemplified by several genetic analyses of vireyas that have begun to illuminate the genetic relationships between vireya species. These results have required a reconsideration of how vireya species are organized in subsections and sections. In addition, teasing out genetic relationships has also allowed new insights in how vireyas traveled from the Asian Mainland throughout the Malaysian region (Malay Peninsula east through New Guinea), Philippines and further.

In an important paper with new and fascinating results, major speciation was shown to accompany the dispersal

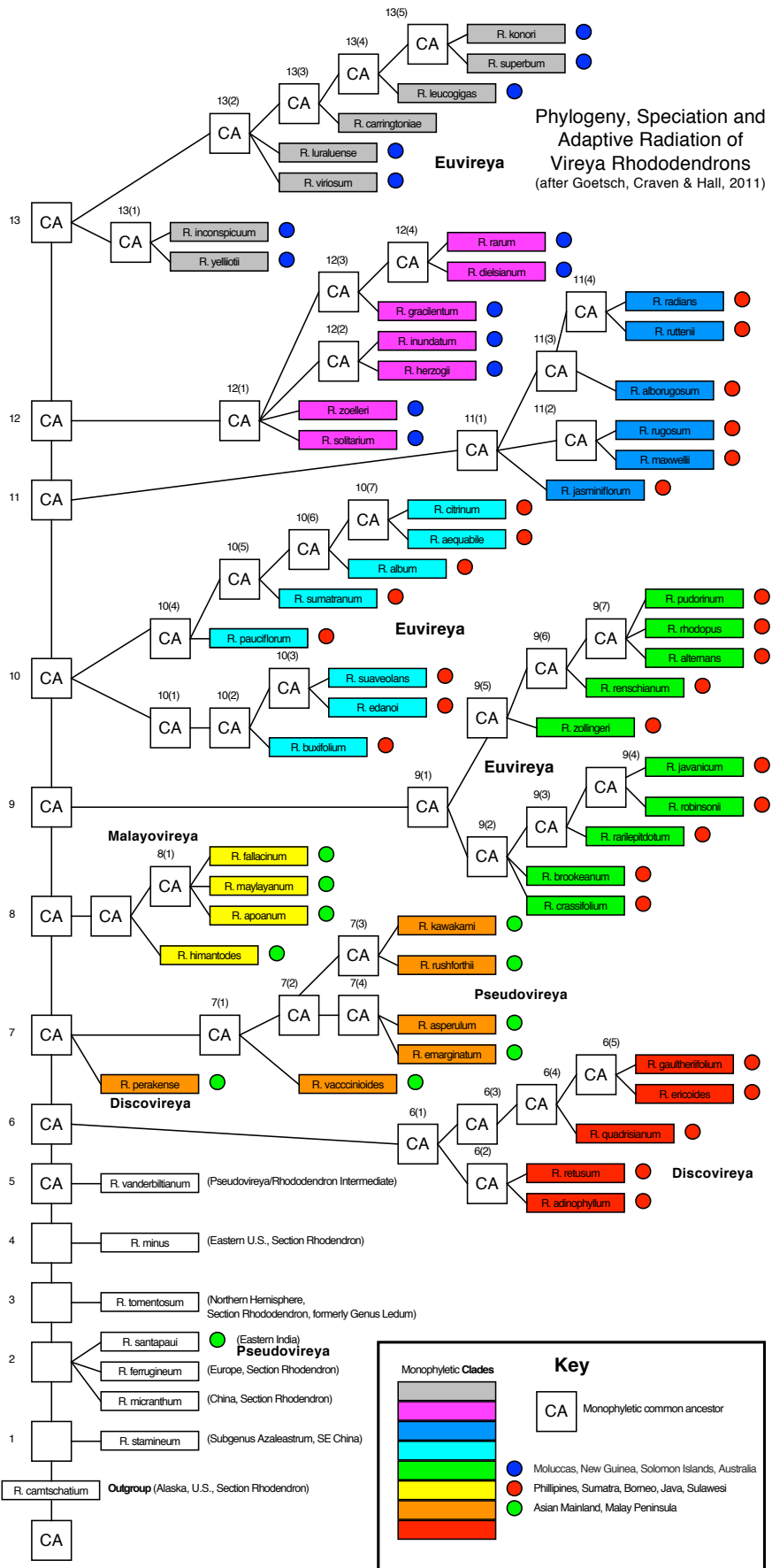


Figure 1.

of vireya rhododendrons (Goetsch et al. 2011). There were three goals in their study: determining the monophyletic groups that comprise vireyas, correlating monophyletic groups and the geographical distribution of vireya species, and finally, comparing determinations of phylogenetic relationships of vireyas with previous morphological-based taxonomic classifications.

To accomplish this, they performed complex and detailed genetic analyses of three nuclear genes as they occur in 113 vireya species. Species were obtained from the Rhododendron Species Foundation and Botanical Garden, WA; Craven's collection in Australia; and contributions from the Royal Botanic Garden, Edinburgh, and from two New Zealand collectors, David Binney and Richard Currie.

The details of their molecular analysis in the laboratory are numerous and beyond the scope of this article. Briefly, DNA was extracted from young growth of the various species and then cleaned and purified. Specific regions of the DNA of each species were then "amplified" from the tiny amounts available from the cells in order to provide sufficient material for analysis. Special marker chemicals, "DNA primers," are able to bracket relatively active (more variable) regions of DNA, and an enzyme, DNA polymerase, is directed by the markers to amplify regions between the markers. Using automated machines, this amplified material is then sequenced to determine the order of the base pairs in these particular regions. Then the corresponding regions from various species are visually "aligned" on a desktop computer

to show the base differences between the species. Then, from these alignments, a computer program constructs a branching phylogenetic tree that reflects the relative similarity or differences in sequence between the various species. As noted earlier, relatively fewer differences between two species place them closer together on the tree and greater differences place them further away on the branches. Very similar sequences are grouped together into clades. In the majority of relationships in the study, very high levels of statistical confidence in the inherited sequences were found and in many cases, almost complete certainty.

One of their exciting results is that a monophyletic clade has been discovered for all vireya species (except one, *R. santapau*; see Fig. 1). This means perhaps only one common ancestor existed for nearly all the vireya species tested! Further, their results indicate that much of the organization of vireyas suggested by Drs. Sleumer (1966) and Argent (2006) needs to be revised into much broader groups of subsections and sections because much closer genetic relations were discovered between many species. Within vireyas, three of the seven distinct clades they discovered correspond to the existing *Pseudovireya*, *Discovireya* and *Malayovireya* subsections of the earlier classifications. But subsections *Albovireya*, *Phaeovireya* and *Euvireya* from these existing classifications were determined to be polyphyletic (mixed into several distinct clades). Since the classification of species must rest on discrete evolutionary relationships, the two former subsections of *Albovireya* and *Phaeovireya* could not thus be supported as separate entities. Four

of the clades found were therefore folded into the remaining *Euvireya* subsection. Finally, their research showed that vireyas (which for technical purposes is now named section *Schistanthe* (Craven et al. 2011) are genetically subsumed within the subgenus *Rhododendron* (within the species *Rhododendron*) and that Argent's (2006) elevation of *Vireya* to subgenus level was not supported by their genetic analysis.

In a subsequent article (Part II), I will summarise other fascinating findings of the Goetsch et al. (2011) study, including significant genetic support for the eastward geographic dispersal of vireyas from mainland Asia all the way to Papua New Guinea and Australia.

References

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LED Lights

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Recently, a friend sent me a tip for emergency lights during a power outage. If you have solar lights around your garden, during a power outage bring a few indoors to light the rooms. Our member Chris Aldred tried this experiment. She brought in a solar light at 8:30 p.m. after a relatively cloudy day and placed it in a

vase in her darkened kitchen. It lit up the room all night and was still working fine at 7:30 a.m. the next morning. Although the early versions of solar lights did not have much longevity, the newer lights, with LED technology and improved battery life, work much longer. Give them a try sometime!