CLOSURE OF BCRI, RYDALMERE AND RELOCATION OF HERBARIUM DAR

On 10 October, the NSW State Government announced the closure of the Biological and Chemical Research Institute, Rydalmere, as part of a number of measures to cut $28 million from the Department's operating budget over the next four years. This is in effect a 20 per cent cut which will apparently be achieved through volutary redundancy, natural attrition and efficiency gains. All staff located at Rydalmere (139 consolidated fund staff) will be relocated at up to 14 centres throughout the State. Many of these centres have been identified as 'key centres' of research which in some cases will be Cooperative Research Centres closely linked with regional Universities.

The Plant Pathology Herbarium (DAR) and the Entomology Insect and Mite Collections are to be relocated to the Agricultural Research and Veterinary Centre at Orange, on the central tablelands, about 270 km west of Sydney. The Department has given a verbal commitment to provide suitable and protected housing for both collections at Orange. A proposal for capital works funding for the collections is currently being sought in the next State budget due in May 1996. It is therefore unlikely that the Herbarium will be relocated before late 1996 although the Institute is to be closed in Feburary 1997.

It appears that the statutory protection of the Herbarium, its status in the National reference Collections of Plant Pathogens and the recent construction using Commonwealth funds (three years ago!!!) of a brand new building for the Herbarium at Rydalmere have assisted in its survival. The replacement of Herbarium staff who do not relocate is a question that has to date not been answered.

Michael Priest

POSSIBLE WORK OPPORTUNITY

There is a possibility of eight months full time work on a project to database fungal collections, and analyse distribution patterns and conservation status. If the position becomes available it would be based at the National Herbarium of Victoria in Melbourne, and commence early in 1996. Good typing and research skills would be required. Interested persons should contact Dr Tom May, by 31 Dec 1995, at the National Herbarium of Victoria, Birdwood Ave, South Yarra, Victoria 3141. PH: (03) 9252 2319, FAX: (03) 9252 2350.

REPORT ON OVERSEAS TRAVEL, 4–20 NOV. 1995

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In November 1995, I travelled to Geneva, Switzerland to examine type specimens of species described by A. P. de Candolle, attended a workshop on *Alternaria* taxonomy held at Penn State University, U.S.A., and visited the USDA National Fungus Collection at Beltsville. The trip was funded by the Erysiphales of Australia project, funded by ABRS.

The visit to the cryptogamic herbarium at Geneva was to study the Erysiphales (powdery mildew fungi) described by A. P. de Candolle. Previously published descriptions of most of these species have only described the morphology of the teleomorphs, while our interest is in the morphology of the anamorphs, because these fungi do not produce their teleomorphs in Australia. In particular I wanted to study the type of *Erysiphe cichoracearum* DC. because I had no real idea of the precise morphology of that species, and because I was able to discern differences between specimens that could be referred to that species, on different hosts. Braun's (1987, Monograph of Erysiphales) illustration of the fungus shows a rather variable anamorph and my objective was to define the precise anamorph morphology of *E. cichoracearum* in the strict sense. However, examination of the type showed that the fungus is indeed as variable as shown in Braun's monograph, so that it might not be easy to separate different host forms as I had supposed.

The *Alternaria* workshop at Penn State University was led by Emory Simmons, and organised by Mary Palm (USDA National Fungus Collection) and Rodney Roberts (USDA Fruit Research Station). Emory Simmons is arguably the only person with a real understanding of the taxonomy of *Alternaria*, and this was an excellent

opportunity to benefit from his experience. Over 80 isolates of over 60 species were available for examination over the 5 days of the workshop. The isolates were grouped into themes, and our examination was guided by Dr Simmons' commentary. Most of us came away from the workshop exhausted, and having confirmed that *Alternaria* is as difficult as we thought it was. The difference now is that we know how difficult it is. We now know that much of what we have been calling *A. alternata* is not that species. We know also that cultural conditions are critical in determining the morphology of the fungus. During the workshop it was discovered that the slightly higher humidity in the workshop lab, had caused several changes in the cultures, when compared with conditions in Simmons' own lab. Critical characters such as conidiophore branching patterns and conidial ornamentation were affected to such an extent that isolates no longer conformed to their descriptions.

I also visited the National Fungus collections at Beltsville, and had useful discussions with Mary Palm, Amy Rossman, Gary Samuels and David Farr.

CLADISTIC ANALYSIS IN THE MACROFUNGI USING MORPHOLOGICAL CHARACTERS

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Studies of the Australian taxa of the Hygrophoraceae suggested that cladistic analysis might be useful when applied to morphological data. Puttock (1992) applied cladistic analysis to morphological characters found in the Australian Gardenieae and obtained apparently useful results, so the application of similar analysis to fungal data seemed to have good possibilities. The 57 taxa established for the Australian Hygrophoraceae and 51 associated morphological characters were used to set up the required data matrices and both PAUP 3.1 (Swofford 1993) and HENNIG86 (Farris 1988) employed for their processing. Although the experience has been interesting (if occasionally very frustrating), the results can only be said to have limited value—at least thus far.

To underscore one of the main problems, fungal taxa are extremely variable...this is probably the understatement of the year. Arnolds (1985) wrote: 'It is inherent to nature that some species are more variable than others, in other words that there is variation in variability'. The results of this study of the Hygrophoraceae concur absolutely. The extreme homoplasy created by fungal characters appearing and disappearing in both related and unrelated taxa creates a very fluid situation which is most definitely not conducive to producing data that is readily processed by cladistics programs.

One of the stated aims of cladistic analysis is the attempt to reduce the intuitive nature of phenetic taxonomy (Steussy 1990). An essential part of such analysis is the allocation of primitive and derived states for the various characters. In the fungi, this is extremely difficult or impossible when using macro/micro-characters for without a fossil record, primitive states can only be set by opinion...but then that is what traditional, phenetic systematics is so often all about. The selection of the outgroup taxon to best mirror the primitive states is also a matter of opinion. Finally, just to give the opinion knife a little twist, which morphological characters are useful for a cladistic analysis and which are not, and should any of them be weighted? This is not in any way intended to decry the value of cladistic analysis. On the contrary, such analyses are already shedding extremely valuable light on the derivation of fungal taxa and their geographical distributions. The problems raised do, however, point out to the cladist intending to use morphological characters some of the difficulties involved when they are applied to the macrofungi.

A recently published procedure for analysing the value of phylogenetic data is the 'phylogenetic signal to random noise' test proposed by Hillis (1991). This involves using PAUP to set up a frequency distribution plot of at least 1000 randomly produced trees. (PAUP has this facility built in.) Tree numbers greater than 1000 will probably give better results. Hillis postulated that a purely random set of data with no phylogenetic signal would produce a normal distribution of generated tree lengths and consequently there would be no skew. This would also mean large numbers of equal length, minimum parsimony trees. PAUP's measure of skew (g_1) would then give $g_1 = 0$. If a data matrix did contain a phylogenetic signal, then there would be a definite skew, g_1 would have a larger absolute value and there would be fewer minimum parsimony trees. Hillis' proposal seems to have been confirmed by Hopple & Vilgalys (1994) using DNA mapping, where a strong left skew (g_1