The 5SDNA Units of *Acacia* species[1]

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The Angiosperm 5SDNA consists of the 5SRNA gene, which is approximately 120bp long, and a non-transcribed spacer region, which is 200-700bp long (Sastri *et al.* 1992). These 5SDNA units are present in multiple copies and arranged in tandem arrays. In most angiosperms studied the 5SDNA units are located at multiple chromosomal sites (Appels and Honeycutt 1986). Arrays at one locus appear to evolve in unison and there is little exchange between units at different loci (Appels *et al.* 1992).

The analysis of variation within and between species using 5SDNA is facilitated by varying levels of conservation of different parts of the DNA. The gene region is relatively highly conserved, presumably reflecting its function as a component of the ribosome (Appels and Honeycutt, 1986). The non-transcribed spacer region is less variable, although moderately conserved in the 3' upstream and 5' downstream regions, close to the gene (Scoles *et al.* 1988).

5SDNA sequences were collated from seven species of *Acacia* encompassing the three subgenera of the genus. Where sequences showed less within-species than between-species variation, a consensus sequence was developed. The sequences were analysed using phenetic and cladistic methods. 5SDNA sequences from *A. bidwillii* and *A. boliviana* are located at several positions on the resulting cladogram (Figure 1). Using the information available from the detailed studies of the *Triticeae* 5SDNA sequence data (Appels *et al.* 1992, Baum and Appels 1992) it has been hypothesised that there are three lineages of 5S DNA in *Acacia*. These have been labelled on the cladogram as 5SDna-1 (represented by ABid101 and ABid040), 5SDna-2 (represented by *A. melanoxylon, A. pycnantha, A. ulicifolia*, ABol120, Abid17, and *A. albida*) and 5SDna-3 (represented by ABid017, ABol013, AS071 and AS021).

The genes coding for 5SRNA rarely occupy only a single chromosomal location (Sastri *et al. 1992)* and in the *Triticeae* it has been possible to demonstrate two major lineages each confined to a chromosomal locus, because of the availability of wheat substitution lines containing single chromosomes from other *Triticum ssp* (Reddy and Appels 1989).

The primary separation in both the cladogram and the phenogram can be interpreted as to be the result of different 5SDNA lineages. At least three lineages are distinguished in the present analysis, based on the separation of *A. bidwillii* 5SDNA sequences into three groups.

The three putative lineages are not represented from every species studied within the limits of the 5SDNA clones sequenced. *5SDNA-2* however, is present in clones from all but *A. senegal.* This lineage shows that the Australian species of subgenus *Phyllodineae* (*A. ulicifolia, A. pycnantha* and *A. melanoxylon)* grouped together as a unit separated from the other subgenera of *Acacia (Aculeiferum* and *Acacia)* which are very similar for this character. *Acacia albida*

[1] This paper is an expanded abstract of the talk delivered to the 7th IGSM Meeting by J. Playford titled: "5SDNA Evolution in *Acacia*".

(Faidherbia albida) is quite separate from the other *Acacia.* This indicates some potential for 5SDNA for phylogenetic analysis.

It is interesting to note that the existence of 5SDNA lineages, as argued here, implies that the *5SDNA-2* lineage must have evolved (or been amplified) before the breakup of Gondwana, because it is present in species endemic to Africa (*A. albida),* Australia (*A. bidwillii, A. melanoxylon, A. pycnantha, A. ulicifolia)* and South America (*A. boliviana).* Further work is required to see if other chromosomal lineages are common to these subgenera and whether they evolved major lineages after the breakup of Gondwana.

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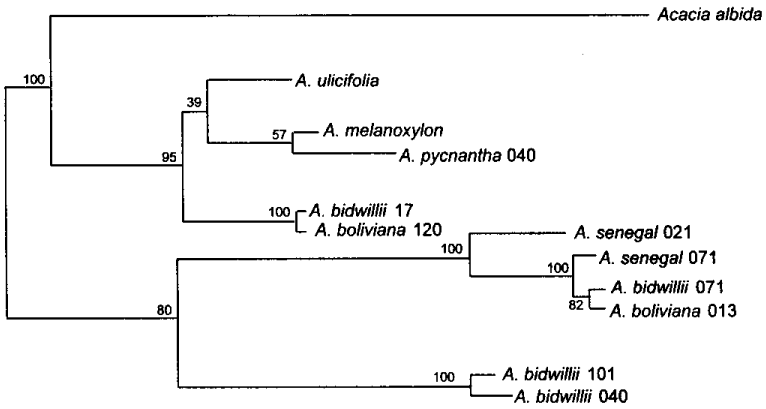

Figure 1. Cladogram produced by sequence alignment of 5S DNA sequences from *Acacia*.