



Phyloclimatic Modelling Can Estimate Ancestral Areas

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Abstract - Ancestral area selection is traditionally based on geographic patterns analyzed alongside phylogenetic data. The approach assumes consistent climate and will only select areas from within present day distributions. The combination of observed distribution and inferred climate preferences have been used to determine the potential distribution of species in the past, present and future. The heritability of environmental niches, based on climate preferences, has been demonstrated, and ancestral niches have been reconstructed using phylogenetic techniques. These techniques can be combined to estimate ancestral areas. Ancestral area selection via environmental preference differs from traditional methods, as areas which are outside the current observed distribution can be selected if they are environmentally suitable.



Drosera rosulata (photo A. Culham)

South Western Australia is a global biodiversity hotspot. Many plant groups are thought to have diversified in the mediterranean type climate of this region.

One third of Sundew (*Drosera*) species are found in this winter-wet biome.

Drosera subgen. *Ergaleium* are known as the Tuberous Sundews, they spend summer droughts reduced to tubers.

Where did the tuberous sundews grow 8 million years ago?

Dispersal Vicariance Analysis (DIVA) can reconstruct ancestral areas on a phylogeny (Ronquist, 1997).

Figure 1 shows a chronogram of Tuberous Sundews (*Drosera* subgen *Ergaleium*) from Yesson & Culham (2006).

The first stage of DIVA is to partition the present distribution into areas A-D (present-day distribution is shown as red points on the inset map). This is a subjective process.

Area A is selected as the ancestral area of the tuberous sundews.

Was the climate of millions of years ago suitable for this group?

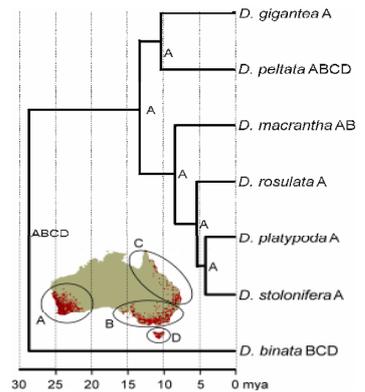


Figure 1 – DIVA reconstruction of ancestral areas

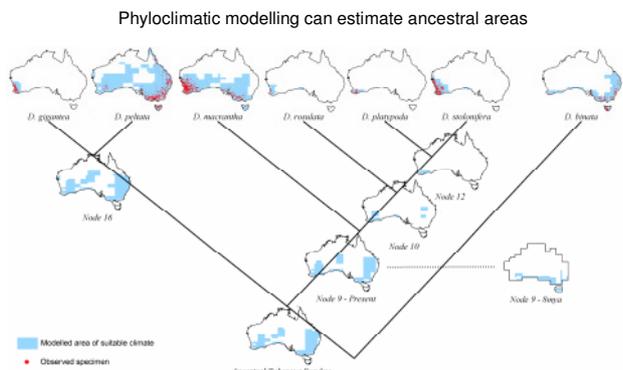
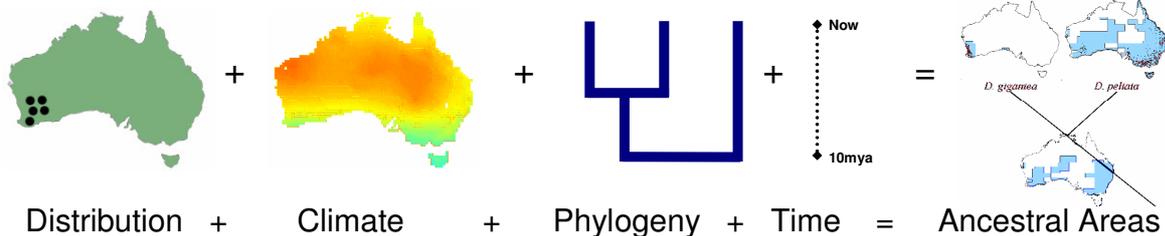


Figure 2 – Phyloclimatic reconstruction of ancestral areas (from Yesson & Culham, 2006)

Figure 2 shows a phyloclimatic ancestral area reconstruction for *Drosera* Subgen. *Ergaleium*.

Extant species (top) have distributions modelled using present day distribution data and present day climate.

Each climate variable has been optimised on the phylogeny to produce ancestral climate preferences. We can combine these preferences creates an ancestral model of climate preference.

These models can be used to select areas with a suitable environment by examining present day climate data. The same models can be used to select palaeo-historic areas by examining palaeo-climate reconstructions.

The ancestor of the clade *D. macrantha* – *D. Stolonifera* (fig. 2, node 9) is approximately 8 million years old. A reconstruction of the climate at this time reveals Southern Australia and Tasmania would have been climatically suitable for this ancestral lineage.

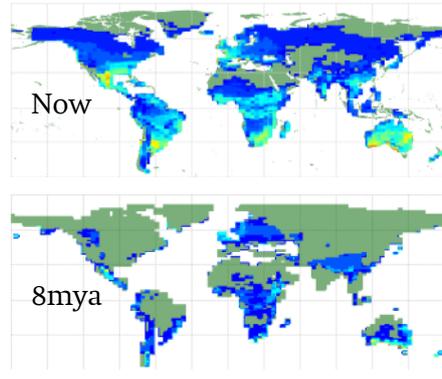


Figure 3 – Hotspots of *Drosera* diversity, for the present-day & 8mya

Phyloclimatic modelling at a global scale can be used to produce hotspots maps of *Drosera* diversity for both the present day, and the past.. (Red indicates most species, dark blue the least).

Fig. 3 demonstrates that 8 million years ago Southern Australia (lightest areas) could have been the main centre of *Drosera* diversity just as South Western Australia is today.

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