

Summary

During the course of this thesis, AFLP technique was successfully applied to the Aizoaceae taxa. This study involved a substantial component of laboratory work including generating and analysing AFLP data, the operation of an ABI377 automated DNA sequencer, and use of GeneScan and Genotyper software (Applied Biosystems).

The initial motivation for this study was to reconstruct relationships between species of the genus *Carpobrotus*. However, it soon became clear that this would be impossible via the use of DNA sequence data. This was due to the inability to find DNA regions with sufficient variable characters for phylogenetic reconstruction.

Therefore applying the AFLP fingerprinting technique to the question of species-level relationships in *Carpobrotus* resulted in individuals of the same species not forming distinct groups. This has subsequently led to the conclusion that gene flow is common across species boundaries in *Carpobrotus* as a result of hybridisation. An alternative explanation for the pattern observed may be that current species delimitations in this group are not well defined. These results also concord well with isozyme studies carried out for *Carpobrotus* taxa in the Mediterranean Basin. Increased sampling of species other than *C. acinaciformis* and *C. edulis* would allow further investigation into the genetic delimitation and affinities of *Carpobrotus*, and shed light on the extent of gene flow between these other taxa.

In the biotechnological age the use of molecular techniques has the potential to greatly improve the bio-prospecting process. This has particular relevance to plants with medicinal properties, such as *Carpobrotus*, whereby targeted selection of genotypes with well-characterised medicinal properties may increase efficiency. Genetic and phylogenetic information can also help to identify closely related species and genera that may share similar metabolic pathways and properties. These issues are quickly coming to the forefront in the new South Africa, with the opening up of traditional knowledge systems, and subsequent integration and contact with the biotechnology community.