CHAPTER 9: FUTURE RESEARCH

The end purpose of systematics is to produce a classification which reflects the evolutionary history of a group and this process requires that a phylogeny has to be determined. This phylogeny can then be used to assemble a classification (Judd *et al*., 2008).

A phylogeny is produced in four steps. Firstly, the characters which will be used for the construction of the phylogenetic tree are observed and recorded. These characters are obtained from morphology, anatomy, palynology and DNA sequencing data, after which a character × taxon matrix is constructed. This is followed by choosing an appropriate outgroup before the final analyses can be done and the phylogeny inferred (Simpson, 2006; Judd *et al*., 2008).

Judd *et al*. (2008) states that one can gain confidence in a phylogenetic hypothesis by comparing phylogenies obtained from different sets of characters; that is, phylogenies based on morphology, nuclear DNA sequences, chloroplast DNA sequences and combined morphological and DNA characters. If these different phylogenies show similar groupings, it is more likely to reflect the true order of evolutionary events.

Hence, the end purpose of this study was to identify a range of characters that will allow for the production of a workable classification for the southern African *Boerhavia* and *Commicarpus*, and to make a first attempt to understand their evolutionary history in southern Africa.

As the southern African *Boerhavia* and *Commicarpus* species had not previously been studied nor characters recorded, the morphology, anatomy and palynology of the two genera was investigate, firstly to describe or define the taxa (that needed to be studied phylogenetically) and to identify the characters that could be used for the phylogenetic analyses. This was done in chapters 4 to 6. A preliminary phylogenetic investigation was done in chapter 7 with the use of sequences obtained from the ITS nuclear region and the *ndh*F chloroplast region.

The morphological data can now be translated into a character × taxon matrix for future phylogenetic analyses. The choice of characters for use will be based on the criteria used by Hernández-Ledesma *et al*. (2010), who did a cladistic analysis on the genus *Anulocaulis* (Nyctaginaceae). Analysis will be done with Nona (Goloboff, 1996) via Winclada (Nixon, 1999).

As explained in Chapter 7 (p. 167), to produce a meaningful phylogenetic hypothesis based on molecular data, more genes and specimens need to be analyzed and final analysis will be done with the same methodology. The combined morphological and molecular matrices will be analysed with Nona (Goloboff, 1996) via Winclada (Nixon, 1999).

The trees will be rooted by an outgroup. According to the study of Douglas and Manos (2007) and Hernández-Ledesma *et al*. (2010), as well as the analyses done in Chapter 7, *Mirabilis* will be used as an outgroup as it shares a common ancestor with *Boerhavia* and *Commicarpus*.

The final phylogenetic trees can then be interpreted with the biogeographical data to make a first attempt to understand the evolutionary history of *Boerhavia* and *Commicarpus* in southern Africa and translated into a workable classification which will not only reflect the evolutionary history of the group, but also the morphology.