CHAPTER 5

GENERAL CONCLUSIONS

Central to the systematics of the Eriophyoidea is the need for alpha taxonomic descriptions of new species to address the huge short fall in our knowledge on their extant diversity and to obtain new information from the unknown taxon diversity for improving our understanding of and hypotheses on the phylogeny of the group. The description of new species and other taxa justifiably forms the bulk of systematic studies on the Eriophyoidea. During the present study it became increasingly clear that improvement in the systematics of the group should not be to the detriment of documenting the diversity, which is largely still unknown, but should be complimentary to it.

The descriptions of new taxa are relatively standardized and adhering to a certain quality and format, but particular shortcomings are persistent. These inadequacies include lack of detail in the description of minute morphology, over-simplified and schematic descriptive drawings, inaccurate and vaguely defined morphometric data, lack of needed improvement in the standardization, definition and delimitation of characters and character states, and additionally some descriptions include wrong and ambiguous data to the point where they become inadequate. The need for accurate and complete descriptions, and documenting of descriptive data, is exacerbated for these fragile mites, of which slide-mounted type material is not permanent and in time will be destroyed and lost to further study.

While capturing published descriptive data and attempting to structure it for a relational database including species sampled across the diversity of the Eriophyoidea, and eventually defining and scoring a data matrix for phylogenetic analyses during the present study, the shortcomings of the published descriptive data came to the forefront. It became clear that alpha taxonomic descriptions should be improved, particularly in detail, accuracy, standardization and definition of terminology. The definition and demarcation of characters and character states must be improved and when a species is described, it should be described rather in terms of hypothesizing primary homologies than merely describing a new taxon in a mechanical manner using repetitive formats and patterns. This may sound contradictory, but improving description does not necessarily entail diverging from a standardized format entirely, but rather to improve within the framework, and still keep the descriptions complete and comparable. From the experience of the present study it is strongly proposed that the best way to do this would be to set up and master an electronic protocol and procedures where the descriptions can rather be done as structured data, from which natural language descriptions can be generated. It will be ideal, to develop such a structured definition of characters and character states collaboratively between practicing eriophyoid systematists. If such a descriptive structure could be collaboratively populated and primary descriptive data captured by each person describing a new taxon, the data would be available, without much extra work and to the detriment of describing new taxa, for developing interactive keys, monographs, catalogues and undertaking phylogenetic studies. It is by no means suggested that the autonomy and recognition of the research and data of each person, so necessary for building a career and securing funding, should be compromised, but rather that already published information be available in the same format and structure for larger collaborative studies on a worldwide scale. Unfortunately, there seems to still be technical difficulties and lack of general holistic software programs that can facilitate such an approach, but hopefully these will improve with time.

Eriophyoid mites are morphologically so simplified that there are relatively few additional characteristics from slide-mounted specimens, apart from those already utilized in taxonomy, to use for classifying and delimiting taxa and for inclusion in data matrices for phylogenetic analyses. This was somewhat confirmed by the present study. This restriction can be alleviated by adding molecular data, but it is crucial that morphological data should also be increased and improved. One way to increase comparative morphological data would be to study the morphology of these minute organisms in more detail and accuracy. The increased resolution of scanning electron microscopy (SEM) above light microscopy can serve to this end. Up to now SEM studies and images have contributed to our understanding of eriophyoid morphology, improvement of descriptions, and in a few cases added supplementary descriptive information. Generally, SEM studies remain infrequently and sporadically used in eriophyoid systematics, though, and when used, it is merely used to support descriptions from slide-mounted specimens, and not for additional morphological information. SEM studies are also not focused on specific body areas or structures, and the present study demonstrated with a comparative study of the gnathosoma between only a few species, that useful additional characters can be found in this way.

Not only can SEM studies contribute additional morphological information, but in the present study it was found that descriptive data from slide-mounted specimens may be seriously flawed by artefacts apart from the inability to study some structures sufficiently with light microscopy. To improve the accuracy of descriptions and lessen artefacts, it is not sufficient to do any SEM study, but the best available SEM techniques should be incorporated to study the specimens in as real and natural way as possible to avoid introducing yet another set of artefacts. Incorporating SEM studies will not just contribute to data for phylogenetic studies, but will improve the descriptions and thus the taxonomy. It is also importance to improve slide-mounting of specimens, apart from incorporating new techniques like SEM as this will improve the quality of the descriptions for use in practical identification and classification.

The classificatory framework within which taxa are described, delimited, diagnosed, identified and classified is very important. The advantages of a natural classification, built with monophyletic groups, above an artificial classification are well-known and accepted. Before the present study it was generally proposed that the classification of the Eriophyoidea is largely artificial. Although a few preliminary small scale studies were undertaken to test the monophyly of suprageneric groupings of the present eriophyoid classification, the present study is the first attempt at a comprehensive phylogenetic study, incorporating a sample and analysis attaining a holistic exploratory study of the phylogeny of the Eriophyoidea. Although almost no unambiguous conclusions about the relationships between suprageneric eriophyoid taxa, and the monophyly of the groups in the present classification, it contributed a large amount of useful hypotheses in this regard, and tested previous hypotheses. Some of the results can be incorporated into the present classification and will improve it for practical taxonomic uses and base it on potentially more natural groupings than it is at the moment. It also showed areas in which research on phylogeny is particularly needed. With the summary above, incorporating phylogenetic studies as part of the everyday practical taxonomy will be to the advantage of improving the systematics theoretically and practically. It will also improve the scientific quality of eriophyoid systematics by incorporating empirical analyses.

The study set out to appraise some aspects of eriophyoid systematics. The families, subfamilies and tribes of the Eriophyoidea in the present classification, with the exception of the Diptilomiopidae, are shown not to be monophyletic. The present study did not prove this conclusively, but also did not find the groupings to be monophyletic, to the degree that it is proposed that some changes should be made to the presently accepted classification. Additionally, useful alternative hypotheses about relationships between taxa could be proposed, and it was again found that the characters currently used in eriophyoid taxonomy are highly homoplasious, but this could be probably attributed to high natural levels of homoplasy in the group. It was found that slide-mounted specimens contain artefacts and that these are incorporated in eriophyoid descriptions and classification, to a lesser or greater degree, depending on the quality of slide-mounting. Additional morphological data, more than what was expected, were found by studying specimens using SEM. The definition and delimitation of characters and character states were found to be insufficient and problematic when structuring descriptive data for taxa across the Eriophyoidea and for use as primary homologies in phylogenetic analyses. With the correct and carefully constructed protocol for capturing primary descriptive data from the start, it should be possible to incorporate phylogenetic studies as part of alpha taxonomic endeavours and should be strongly advocated.

Finally, there is a need, for new technologies to be incorporated more extensively in the systematics of the Eriophyoidea. This may in some respects be a daunting task in practice, though, and the author will attempt to follow the conclusions found in this study, but there may be restrictions, such as infrastructure and funding, in attempting it. The quality and usefulness of systematic study of the Eriophyoidea by the author has already been improved as a result of the present study.