

## CONCLUSIONS AND FUTURE WORK

This work highlights the need for concerted efforts towards documenting and describing, as yet unknown biodiversity - particularly those small sized organisms which are so easily overlooked. Several of the 17 new species of psyllid collected and described during this project are rare and their habitats are increasingly threatened. In other instances, psyllids previously recorded from sites - such as *Arytainilla delarbrei* in the Moroccan Middle Atlas - were no longer found in these locations. In the case of *A. delarbrei*, there has been severe overgrazing of the host plants in Morocco. Informed conservation using data on species numbers and distributions is critical to the preservation of biodiversity, which in this case implies knowledge of insects, host plants and host habitats.

Molecular techniques provide a valuable contribution, together with morphological and biological data, to the overall picture of speciation processes and genetic divergence. In particular, there is sometimes a surprising discrepancy between morphological and genetic divergence which emphasises the importance of a combined approach to biodiversity assessments. I would argue therefore, that a comprehensive approach, such as that taken in this study, is the best way forward for evolutionary studies.

Further work towards a broader phylogeny of the psyllids, including Southern African, American and Asian members of the Arytaininae, as well as a larger sampling of the sister subfamily Psyllinae, would help to clarify delimitations between the subfamilies, and to clarify the placement of outlying species/groups. In addition, using selected nuclear genes would provide a comparison to the mitochondrial genes used in this study. As for the host plant phylogeny, further sampling of legume species in, or allied to, the genus *Genista*, in particular, the two continental members of *Teline* section *Chronanthus*, would contribute to an understanding of the genesis of the two *Teline* groups.

Techniques for dating speciation events using molecular phylogenies are developing rapidly and these will be crucial to future analysis of coevolutionary histories of associated organisms. A broader sampling strategy for both legume and psyllid groups, combined with additional DNA data from mitochondrial and/or nuclear genes may result in more robust phylogenies which would facilitate a more accurate comparison of cladogenic patterns.