Japoshvili, G.O. (Department of Invertebrate Animals, Institute of Zoology, Tbilisi, Georgia).

An annotated list of the Encyrtidae (Hymenoptera: Chalcidoidea) of Tbilisi (Georgia).

A list of 42 species of Encyrtidae recorded in the city of Tbilisi to date is given. The species belong to 23 genera, the most numerous of which are *Microterys* (7species), *Blastothrix* and *Psyllaephagus* (4 species each), *Trichomasthus* and *Metaphycus* (3 species each). 22 species are recorded for the first time: *Microterys sylvius* (Dalman), *M. hortulanus* Erdvs, *M. clauseni* Compere, *M. ferrugineus* (Nees), *M. duplicatus* (Nees), *Metablastothrix truncatipennis* (Ferriere), *Blastothrix longipennis* Howard, *B.* sp. aff. *nikolskajae* Sugonjaev, *Psyllaephagus bachardenicus* Myartseva, *P. tokgaevi* Myartseva, *P.* sp. aff. *rubriscutellatus* Myartseva, *Discodes coccophagus* (Ratzeburg), *Cerapterocerus mirabilis* Westwood, *Cheiloneurus claviger* (Thomson), *Zaomma lambinus* (Walker), *Mahencyrtus coccidiphagus* (Mercet), *Encyrtus lecaniorum* Mayr, *Anthemus funicularis* (Bakkendorf), and a genus aff. *Bureshiella* Hoffer. One new species of *Psyllaephagus* is also proposed.

Laurenne, N.M[1], [2]D. Carmean, [1]J. Muona and [3]D.L.J. Quicke ([1]Zoological Museum/Entomology Division, University of Helsinki, Finland; [2]Biological Sciences, Simon Fraser University, Burnaby, British Columbia, Canada; [3]Unit of Parasitoid Systematics, CABI Bioscience UK Centre (Ascot), Department of Biology, Imperial College at Silwood Park, Ascot, Berkshire, UK).

A preliminary molecular phylogeny of the basal apocritan families based upon the D2 expansion region of 28S rDNA.

The D2 expansion region of the nuclear genome 28 S nuclear rDNA have been used to date primarily for the reconstruction of genus-subfamily level relationships within the Hymenoptera. The utility of this, c. 500 bp, gene fragment for higher level phylogeny has been limited partly by the lack of available sequence data and partly by alignment difficulties. Using an alignment procedure that is intimately connected with tree construction (POY: Wheeler, 1998) we have investigated the utility of this gene region for resolving superfamily and family level relationships among the Apocrita and a number of "symphytan" outgroups. This preliminary study involving c. 30 taxa representing 15 superfamilies, indicate that the gene region in question has considerable phylogenetic utility at this level.

Lewis[1], G.A., [2]A.D. Austin and [2]P.C. Dangerfield ([1]Department of Zoology and [2]Department of Applied and Molecular Ecology, The University of Adelaide, Adelaide, South Australia, Australia).

Collecting protocols for assessing ant diversity in Australian mallee vegetation.

Ants are a common target group in many ecological and biodiversity studies in Australia. However, little attempt has been made to standardise collecting protocols or assess the performance of various collecting techniques. Pitfall traps are most commonly used to sample ant populations, but their design in terms of diameter, rim and preservative used differs substantially among studies. Here we compare the performance of pitfall traps of four different diameters with other collecting techniques used for arthropods (i.e. Malaise and