



Fig. 5: Minor workers, lateral views and fronts of heads, in clades U, D, A, E and their collection sites.

ed to the *C. maculatus* group with a similar set of characters, are not monophyletic, but appear in an unresolved cluster together with the Australian *C. maculatus* group specimens, an African taxon that does not belong to the *C. maculatus* group viz *C. baynei* ARNOLD, 1922 and two Australian taxa of which one is considered to be a *C. maculatus* group member viz *C. tricoloratus*, while the other viz *C. terebrans* LOWNE, 1865 is not considered a *C. maculatus* group member. Pairwise sequence divergence among the unresolved clades at the base of the phylogram ranges from 12.1 - 18.4 %. Pairwise sequence divergence among the Australian clades assigned to the *C. maculatus* group ranges from 7.4 - 10.5 %.

In order to better resolve the relationships among the Australian groups we added partial sequences of a 457 bp

product of the CytB gene to a subset of the Australian *C. maculatus* group-specimens ($n = 17$, Tab. 1). Phylogenetic reconstructions of the CO1 and CytB combined dataset were performed using Bayesian and parsimony methods. Although the majority of the clades remained intact the additional sequences did not result in a better resolution. Clade U consistently appeared as the sister group of the remaining clades with high support (posterior probability 0.99). Clade T, which appeared in the CO1-only analysis (Fig. 3) as the sister clade of the remaining specimens with the exclusion of clade U, appeared at the tip of tree in the combined analysis, but had low support. The pairwise sequence divergence among specimens of clades T and PQRS is large (6.0 - 7.8 %). The position in the tree of the remaining clades is unresolved.