



Fig. 3: Phylogenetic relationships presented as a Bayesian consensus tree of Australian and African *Camponotus* species, based on sequence data derived from the cytochrome c oxidase (CO1) gene. Posterior probabilities are shown above the branches and parsimony bootstrap values (10000 replicates) below the branches. Clades **P** = yellow *C. novaehollandiae* from Western Australia, **Q** = brownish, originally thought to be near *C. novaehollandiae* from Queensland, **R** = yellow *C. novaehollandiae* from Queensland, **S** = brownish, originally thought to be near *C. novaehollandiae* from Queensland, **T** = brown, *C. crozieri* sp.n. from Queensland and Western Australia, **U** = *C. humilior* st.n. from eastern Australia, **D** = *Camponotus* sp. D from Africa, **A** = *Camponotus* sp. A from Africa, **E** = *Camponotus* sp. E from Africa, **X** = *C. tricoloratus* from Queensland, **G** = *C. terebrans* from South Australia, **H** = *C. baynei* from Africa, and **J** = *C. fulvopilosus* from Africa.