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A phylogenetic study of the freshwater crayfish genus *Cherax* Erichson and related genera using sequences from mitochondrial and nuclear genes

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Cherax is the most widely distributed genus within the southern hemisphere freshwater crayfish family, Parastacidae. Currently more than 40 species of *Cherax* are recognised in Australia and New Guinea and some species are important in economically and ecologically. The recent molecular phylogenetic studies of Australian *Cherax* species and related genera were done by using a single gene region and with a limited taxon sampling.

Therefore, this study designed to examine systematics relationships between *Cherax* and the closely related genera *Geocharax*, *Gramastacus*, *Engaeus* and *Tenuibranchiurus* using multiple gene regions and more comprehensive taxon sampling. This study used up to 1440 nucleotides from three different gene regions (16S, 12S and 28S rRNA) and 23 species to investigate phylogenetic relationships within a statistical framework. The results indicate that *Cherax* species are divided among three lineages on the basis of geography: a widespread clade from central and southeastern Australia, a clade containing the northern Australian and New Guinean species and a southwestern Australian clade. It also provided support for the monophyly of the genus *Cherax* and revealed a sister group relationships with a lineage made up of the genera *Geocharax*, *Gramastacus*, *Engaeus* and *Tenuibranchiurus*. Within the '*Engaeus* group' a sister group relationship between *Geocharax* and *Gramastacus* is supported, which is sister to all the *Engaeus* samples with exception of *E. lyelli*. This latter species is placed in a basal position in relation to all other samples in the '*Engaeus* group' clade. The monophyly of each of *Geocharax* and *Gramastacus* was also supported; however the monophyly of *Engaeus* was less certain. Results also indicate that combining gene regions in a single matrix generally resulted in increased resolution and support for major lineages relative to those obtained from single gene analyses.

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