



Speciation in the Australian *Amitermes* Group: First insights from molecular genomics

Author(s): Bastian Heimbürger, Bastian Heimbürger , Stefanie Agne , Paul Schmidt , Sun Diqui , Tamara Hartke

Institution(s): JF Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany ; JF Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany ; JF Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany ; JF Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany ; JF Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany ; JF Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany ; JF Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany

The Australian *Amitermes* group (Blattodea: Termitidae) is the most species-rich and diverse group of termites in Australia. The success of this group, diverging during a time of rapid climate change on the continent, can help us understand how termites have adapted to their environment and may continue to do so under future climate-change scenarios. We began by sampling from the species-rich area of Western Australia near the proposed origin of *Drepanotermes*, one of the major genera of the Australian *Amitermes* Group, to reconstruct the diversification of this group after its colonization of Australia. The information from mitochondrial genome sequencing and selected nuclear genes recovered a monophyletic *Drepanotermes* split into a clade of species with extensive and another with restricted geographic ranges. All *Amitermes* we have sequenced to date are basal to *Drepanotermes* and separate into a number of clades without clear geographical, morphological or nesting trait divisions. Our preliminary estimate of the divergence of *Drepanotermes* from *Amitermes* at 20 ± 5 Mya is probably not accurate; we expect future analysis will recover the split between the Australian *Amitermes* Group and the rest of the globally distributed *Amitermes* to have occurred around this time, with the *Drepanotermes*-*Amitermes* division being more recent, in congruence with other taxa that arrived in Australia after its collision with the Southeast Asian plate. This initial dataset suggests intriguing stories of multiple introductions, waves of diversification, undescribed diversity, and incomplete lineage sorting and/or introgression during divergence, which will be revealed as we collect more complete data from additional Australian *Amitermes* Group taxa.