*Molecular data processing*

We used mitochondrial genomes to reconstruct termites’ calibrated phylogenetic trees with a focus on species and lineages with reviewed data on tandem runs [1], while also encompassing all recognized extant families and subfamilies *sensu* Hellemans *et al*. [2], Most mitochondrial genomes used in this study have been previously published [3,4,13–22,5,23,6–12] (Table SX1).

We sequenced six additional samples from species with data on tandem runs (Table SX1). Specimens were collected in Japan and preserved in absolute ethanol stored at -20°C until DNA extraction. DNA was extracted using the DNeasy Blood & Tissue extraction kit (Qiagen). Libraries were prepared using the NEBNext® Ultra™ II FS DNA Library Preparation Kit (New England Biolabs) and the Unique Dual Indexing Kit (New England Biolabs), with reagent volumes reduced to one-fifteenth of recommended volumes. Libraries were pooled in equimolar concentration and paired-end sequenced on the Novaseq platform at a read length of 150 bp.

Raw reads were trimmed from adapters and low-quality bases using fastp *v*0.20.1 [24]. Trimmed reads were assembled using metaSPAdes *v*3.13 [25], and mitochondrial scaffolds were identified and annotated using MitoFinder *v*1.4 [26]. The six mitogenomes produced herein were deposited in GenBank under accessions XXX-XXX.

*Phylogenetic reconstructions*

Annotated mitochondrial features were separately aligned. For the 13 mitochondrial protein-coding genes, we translated DNA sequences into the corresponding amino acid sequences using the transeq function from EMBOSS *v*6.6.0 [27] and aligned protein sequences with MAFFT *v*7.305 [28]. Protein alignments were back-translated into codon alignments using PAL2NAL *v*14 [29]. The two rRNA and 22 tRNA mitochondrial genes were aligned as DNA sequences. All alignments were concatenated in a supermatrix using FASconCAT-G\_v1.04.pl [30]. The mitochondrial supermatrix was separated into five distinct partitions: combined rRNAs, combined tRNAs, and combined first, second, and third codon positions of protein-coding genes.

Time-calibrated phylogenetic trees (with and without the third codon positions partition) were reconstructed using BEAST v2.6.2 [31]. Trees and clock models were set as linked, while site models were kept unlinked. A GTR+G model of nucleotide substitution was selected for all partitions. The trees were given a Yule speciation process as prior. An uncorrelated lognormal relaxed clock was used to model rate variation among branches [32]. We used 12 fossils as minimum age constraints (Table SX2). Fossil calibrations were implemented as exponential priors on node time with a 97.5% soft maximum bound [33]. Minimum age constraints and soft maximum bounds were obtained from PaleoBioDB (<https://paleobiodb.org>; last accessed: 25/02/12). Additionally, we constrained the (i) monophyly of Macrotermitinae + Sphaerotermitinae and non-Macrotermitinae non-Sphaerotermitinae Termitidae, (ii) the sistership of Stylotermitidae to all extant Neoisoptera, to match the topology retrieved by genome-scale reconstructions [2,11,34]. Markov Chain Monte Carlo analyses were run for a total of 500 million generations. Trees and parameters were sampled every 50,000 steps. We visually inspected the trace file with Tracer v1.7 [35] and accordingly used a burn-in of 20%. Maximum clade credibility trees with median heights were obtained using TreeAnnotator (Supplementary Data 2 and 3).

*Ancestral state reconstruction*

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