

1 Complete mitochondrial genome of the drywood termite *Cryptotermes havilandi*  
2 (Isoptera: Kalotermitidae)

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## 15 16 **ABSTRACT**

17 We report the first complete mitochondrial genome of an important pest of timber,  
18 the drywood termite *Cryptotermes havilandi*. The gene content and synteny of the  
19 mitochondrial genome of *C. havilandi* is identical to that of other termite species  
20 reported to date. It is composed 13 protein-coding genes, two ribosomal RNA genes,  
21 and 22 transfer RNA genes. Our phylogenetic tree, that includes the mitochondrial  
22 genomes of 14 species of Kalotermitidae, including *C. havilandi*, resolves the  
23 phylogenetic position of *C. havilandi* within Kalotermitidae.

## 24 25 26 **Main text**

27 *Cryptotermes havilandi* Sjöstedt, 1900 (Isoptera: Kalotermitidae) is an important pest  
28 of structural lumber and sheltered wood (Su and Scheffrahn 2000). Although it is now  
29 distributed across the tropical and subtropical regions, *C. havilandi* originated from  
30 Africa, and has been introduced outside its native range largely by the intermediary of  
31 human transportation (Evans 2011, Evans et al. 2013). It is now invasive in various  
32 Caribbean islands, Guiana, Surinam, Brazil, Madagascar, the Comores, and India  
33 (Evans et al. 2013). Despite its economic importance, the mitochondrial genome of *C.*  
34 *hakilandi* has not been sequenced yet. Here, we provide the first complete  
35 mitochondrial genome sequence of a *C. havilandi* extracted from the sample CAM101  
36 collected on 7<sup>th</sup> of April 2015 in an abandoned wooden house in northern Cameroon,  
37 Africa (N04°42'25" E009°43'08"), by the authors. The sample CAM101 is available in  
38 Petr Stiblik (stiblik@fld.czu.cz) collection at Czech University of Life Sciences, Prague,  
39 Czech Republic in both states, as an 80% ethanol voucher sample and in RNAlater  
40 preservative.

41 We sequenced *C. havilandi* (Genbank: MW208858) mitochondrial genome using  
42 Illumina HiSeq2000. The genome was assembled using the clc suite of programs as  
43 described by Bourguignon et al. (2015). The total length of the complete mitochondrial  
44 genome of *C. havilandi* is 15,559bp. As in other mitochondrial genomes of termites  
45 previously sequenced (Cameron and Whiting 2007, Cameron et al. 2012, Bourguignon  
46 et al. 2015, 2016, 2017, Wu et al. 2018, Wang et al. 2019), the mitochondrial genome  
47 of *C. havilandi* is composed of 13 protein-coding genes (following the order: *nad2*,

48 *cox1*, *cox2*, *atp8*, *atp6*, *cox3*, *nad3*, *nad5*, *nad4*, *nad4l*, *nad6*, *cytb*, and *nad1*), two  
49 ribosomal RNA genes (*rnl* and *rns*) and 22 transfer RNA genes (following the order: *Ile*,  
50 *Gln*, *Met*, *Trp*, *Cys*, *Tyr*, *Leu*<sup>(UUR)</sup>, *Lys*, *Asp*, *Gly*, *Ala*, *Arg*, *Asn*, *Ser*<sup>(AGN)</sup>, *Glu*, *Phe*, *His*, *Thr*,  
51 *Pro*, *Ser*<sup>(UCN)</sup>, *Leu*<sup>(CUN)</sup>, and *Val*). The GC-content is 34%. Our results confirm that termite  
52 mitochondrial genomes are stable in gene content and preserved their synteny.

53 To shed light on the phylogenetic position of *C. havilandi* within the Kalotermitidae,  
54 we reconstructed a phylogenetic tree that included all mitochondrial genomes of  
55 Kalotermitidae sequenced to date, including the mitochondrial genome of *C. havilandi*,  
56 and three outgroups: *Zootermopsis angusticolis* (Isoptera: Archotermopsidae),  
57 *Porotermes adamsoni* (Isoptera: Termopsidae) and *Coptotermes sepangensis*  
58 (Isoptera: Rhinotermitidae) (Figure 1). All genes were aligned separately using MAFFT  
59 v. 7.3 (Katoh and Standley 2013), concatenated, and the phylogenetic tree was  
60 reconstructed using MrBayes v. 3.2.1 (Ronquist et al. 2012). The parameters of the  
61 phylogenetic analysis were set as described by Bourguignon et al. (2017). Overall, our  
62 phylogenetic tree confirms the monophyly of *Cryptotermes*, within which *C. havilandi*  
63 is nested.

64 The genus *Cryptotermes* includes several invasive species that cause major economic  
65 losses in the world (Evans et al. 2013). Surprisingly, very few studies have used  
66 molecular markers to study the population genetics of *Cryptotermes* species. In this  
67 paper, we provide the mitochondrial genome of one of the most important termite  
68 pest. The new mitochondrial genome presented here will help to understand how the  
69 major termite pests have been introduced around the world.

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#### 71 **Disclosure Statement**

72 The authors report no conflict of interests.

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#### 74 **Author contribution**

75 PS and JS conceived the study, carried out bioinformatics analyses and wrote the  
76 paper. PA facilitated the fieldwork in Cameroon.

77

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84

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87

#### 88 **Data availability statement**

89 The data that support the findings of this study are available in GenBank at  
90 <https://www.ncbi.nlm.nih.gov>. The mitochondrial genome of *Cryptotermes havilandi*  
91 has been deposited in GenBank under the accession number: MW208858

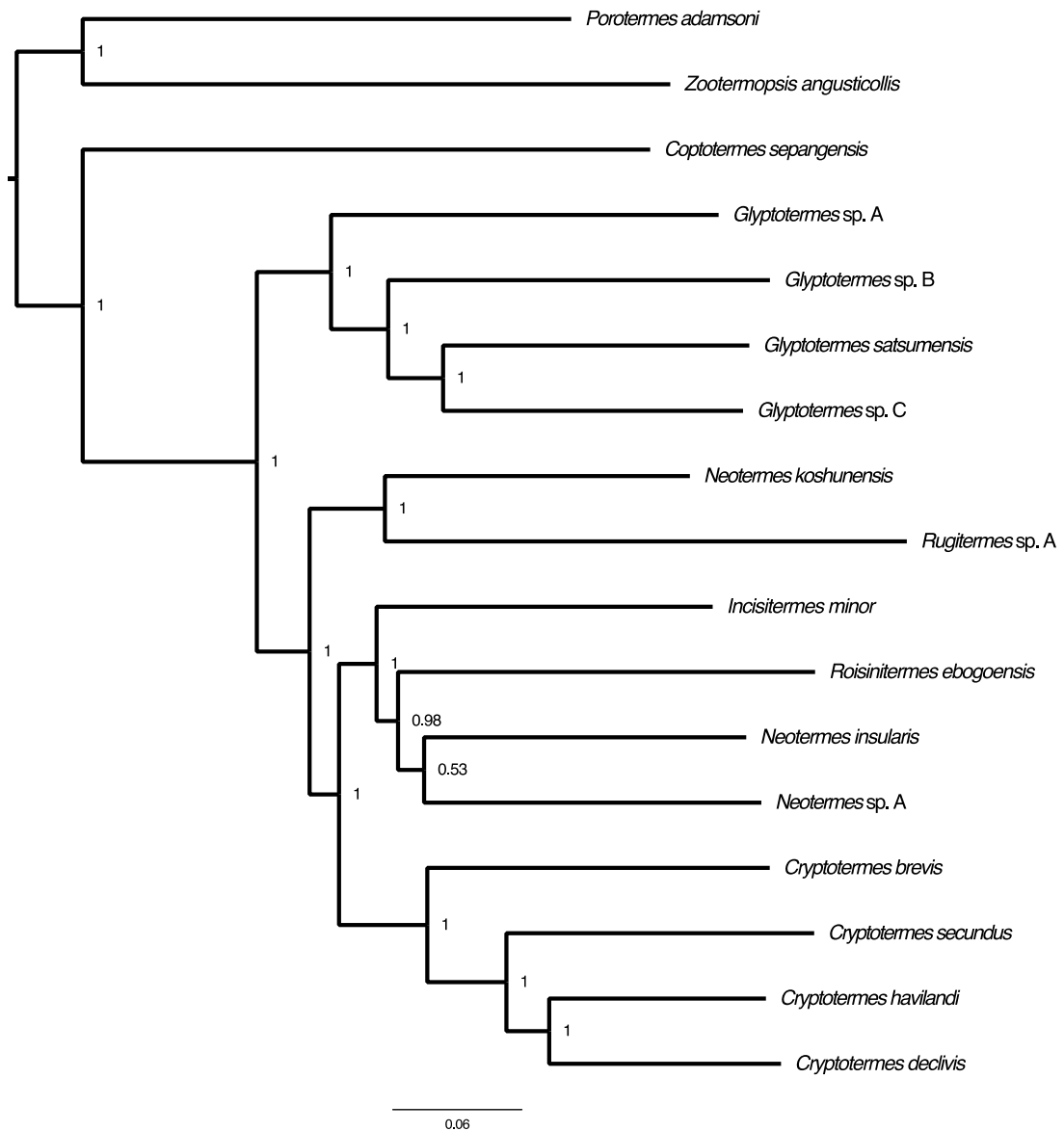
92 Data are also accessible at:

93 <https://mfr.osf.io/render?url=https%3A%2F%2Fosf.io%2F4ykip%2Fdownload>

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95 **References**

- 96 Bourguignon T, Lo N, Cameron SL, Šobotník J, Hayashi Y, Shigenobu S, Watanabe D,  
97 Roisin Y, Miura T, A ET. 2015. The evolutionary history of termites as inferred from 66  
98 mitochondrial genomes. *Mol Biol Evol* 32:406–421.
- 99 Bourguignon T, Lo N, Šobotník J, Sillam-Dussès D, Roisin Y, Evans TA. 2016. Oceanic  
100 dispersal, vicariance and human introduction shaped the modern distribution of the  
101 termites *Reticulitermes*, *Heterotermes* and *Coptotermes*. *Proc R Soc B-Biological Sci*  
102 283:20160179.
- 103 Bourguignon T, Lo N, Šobotník J, Ho SYW, Iqbal N, Coissac E, Lee M, Jendryka MM,  
104 Sillam-Dussès D, Křížková B, Roisin Y, Evans TA. 2017. Mitochondrial phylogenomics  
105 resolves the global spread of higher termites, ecosystem engineers of the tropics. *Mol*  
106 *Biol Evol* 34:589–597.
- 107 Cameron SL, Whiting MF. 2007. Mitochondrial genomic comparisons of the  
108 subterranean termites from the genus *Reticulitermes* (Insecta: Isoptera:  
109 Rhinotermitidae). *Genome* 202:188–202.
- 110 Cameron SL, Lo N, Bourguignon T, Svenson GJ, Evans TA. 2012. A mitochondrial  
111 genome phylogeny of termites (Blattodea: Termitoidae): robust support for  
112 interfamilial relationships and molecular synapomorphies define major clades. *Mol*  
113 *Phylogenet Evol* 65:163–173.
- 114 Evans TA. 2011. Invasive termites, p. 519–562. *In* Bignell, DE, Roisin, Y, Lo, N (eds.),  
115 *Biology of termites: A modern synthesis*. Springer, Dordrecht Heidelberg London New  
116 York.
- 117 Evans TA, Forschler BT, Grace JK. 2013. Biology of invasive termites: a worldwide  
118 review. *Annu Rev Entomol* 58:455–474.
- 119 Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7:  
120 improvements in performance and usability. *Mol Biol Evol* 30:772–780.
- 121 Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L,  
122 Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic  
123 inference and model choice across a large model space. *Syst Biol* 61:539–542.
- 124 Su NY, Scheffrahn R. 2000. Termites as pests of buildings, p. 437–453. *In* Abe, T, Bignell,  
125 DE, Higashi, M (eds.), *Termites: Evolution, Sociality, Symbioses, Ecology*. Kluwer  
126 Academic Publishers, Dordrecht, The Netherlands.
- 127 Wu LW, Bourguignon T, Šobotník J, Wen P, Liang WR, Li HF. 2018. Phylogenetic  
128 position of the enigmatic termite family Stylotermitidae (Insecta: Blattodea). *Invertebr*  
129 *Syst* 32:1111–1117.



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**Figure 1.** Bayesian phylogenetic tree of all species of Kalotermitidae sequenced to date. Numbers in nodes state for posterior probabilities and the scale indicates 6% genetic variation for its length.