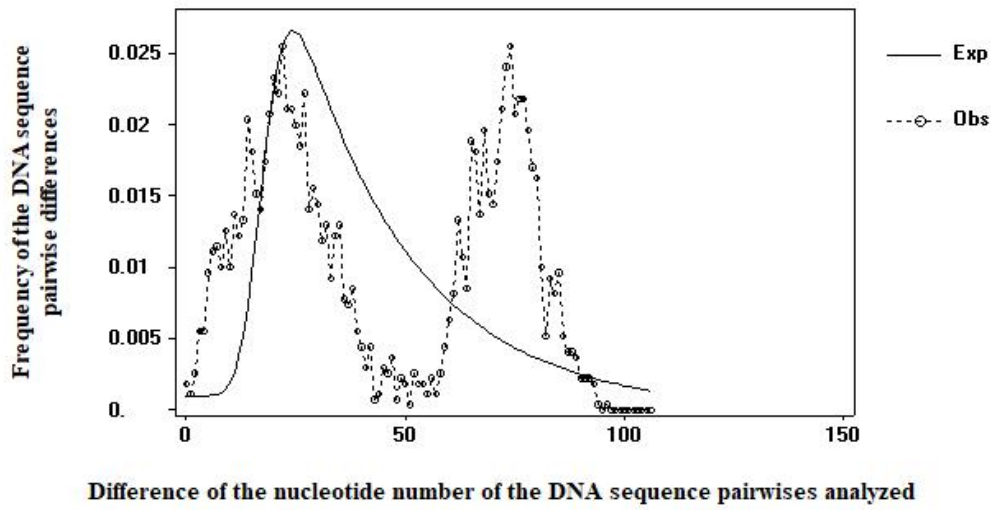
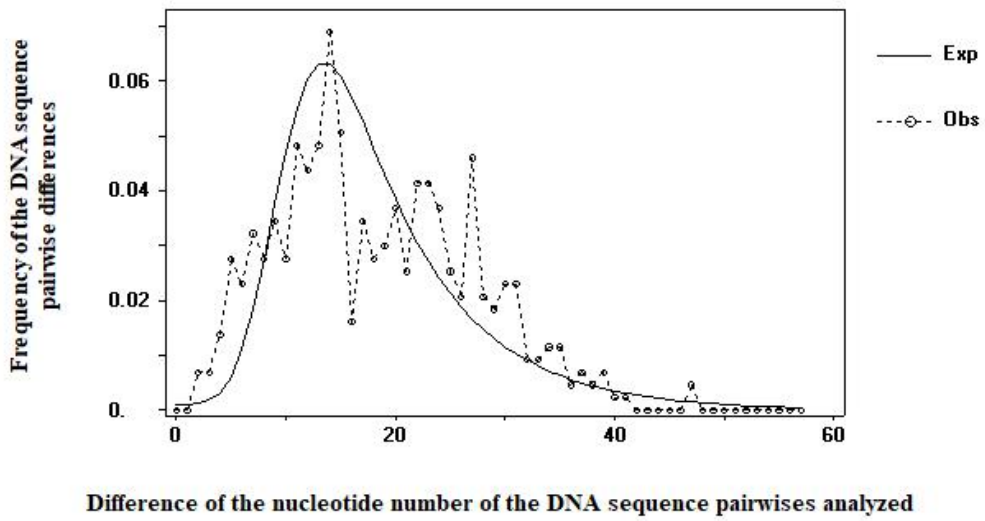


Supplementary Materials

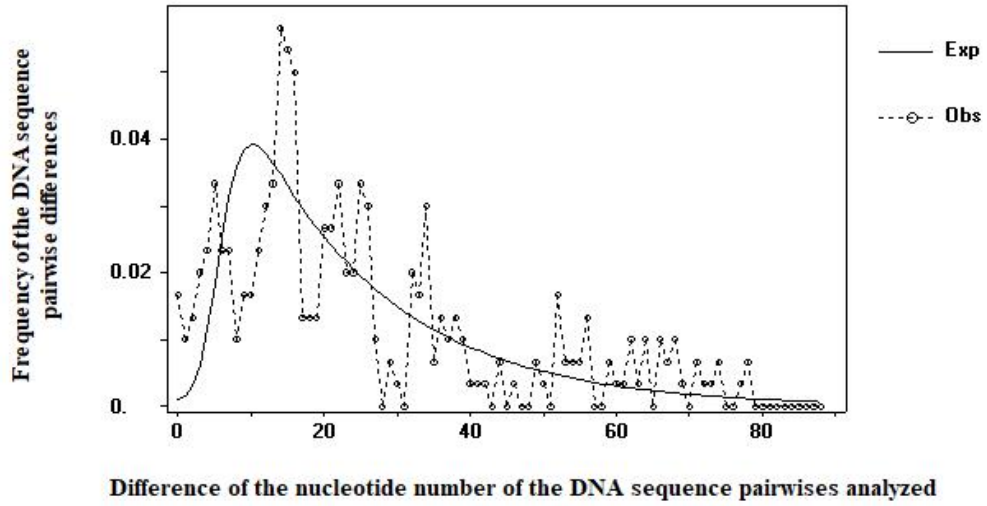
(A)



(B)

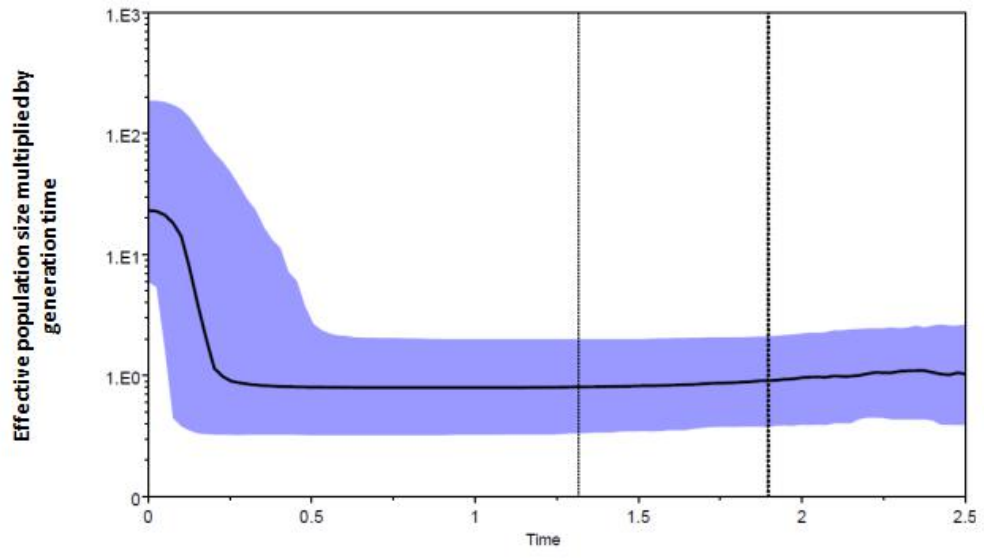


(C)

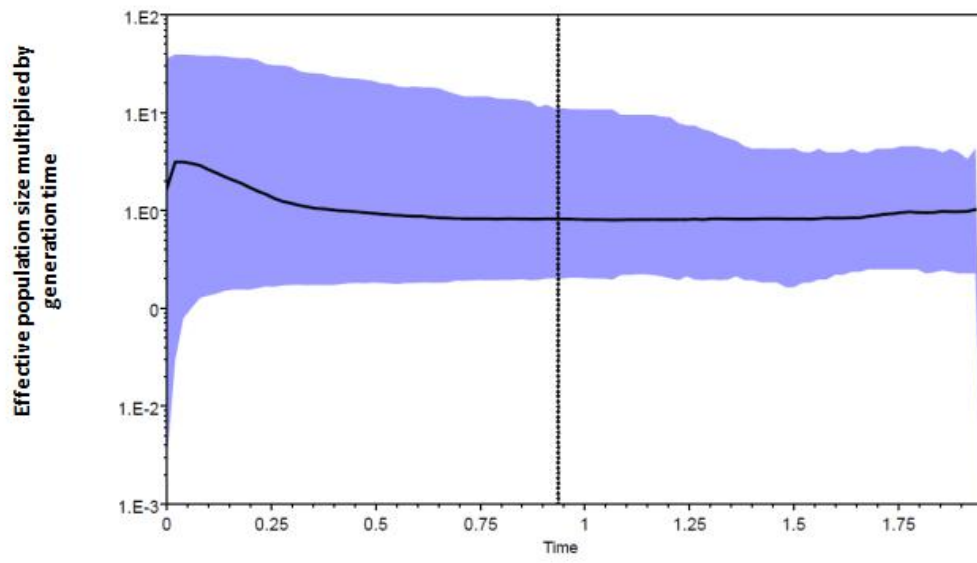


Supplementary Figure S1 Mismatch distributions (pairwise sequence differences) of entire mitogenomes of *Tamandua* sp. Overall sample (A); haplogroup THI (B); haplogroup THIII (C).

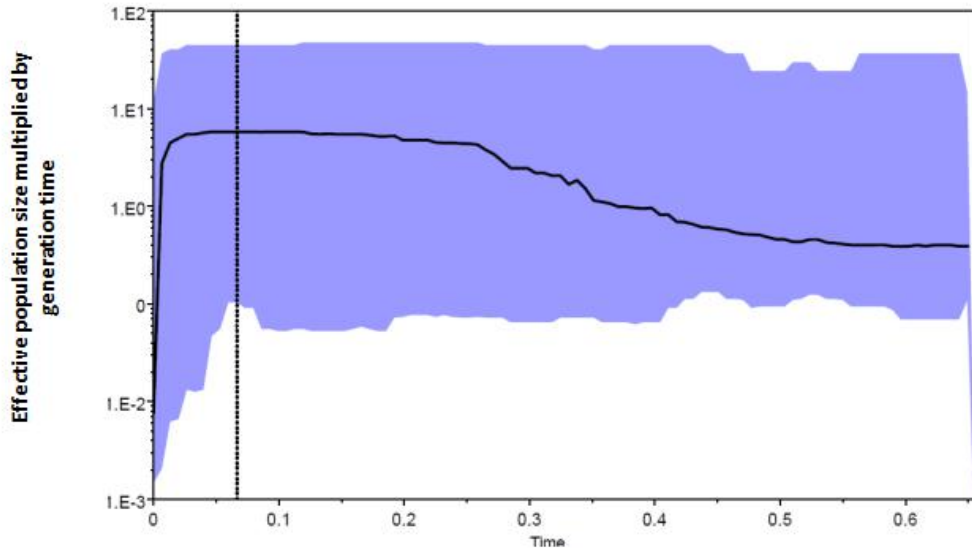
(A)



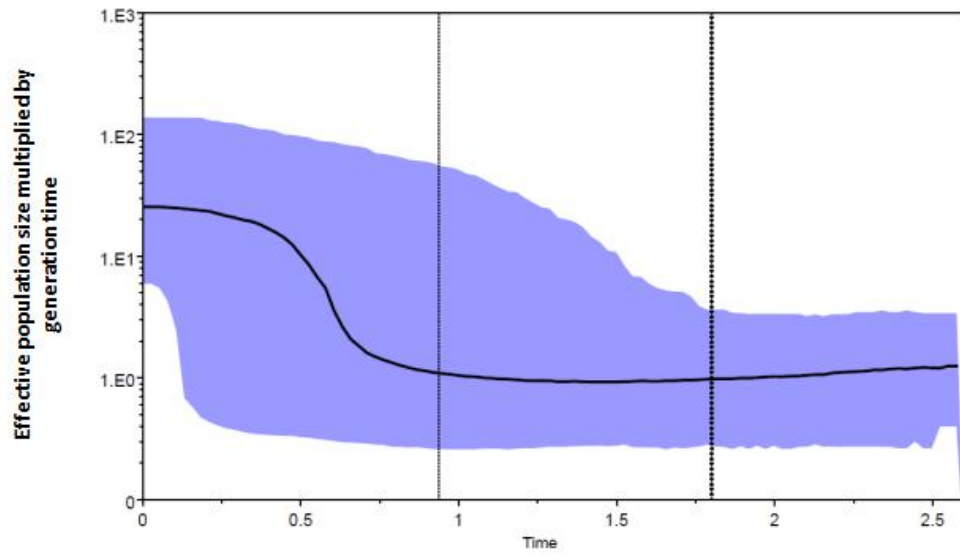
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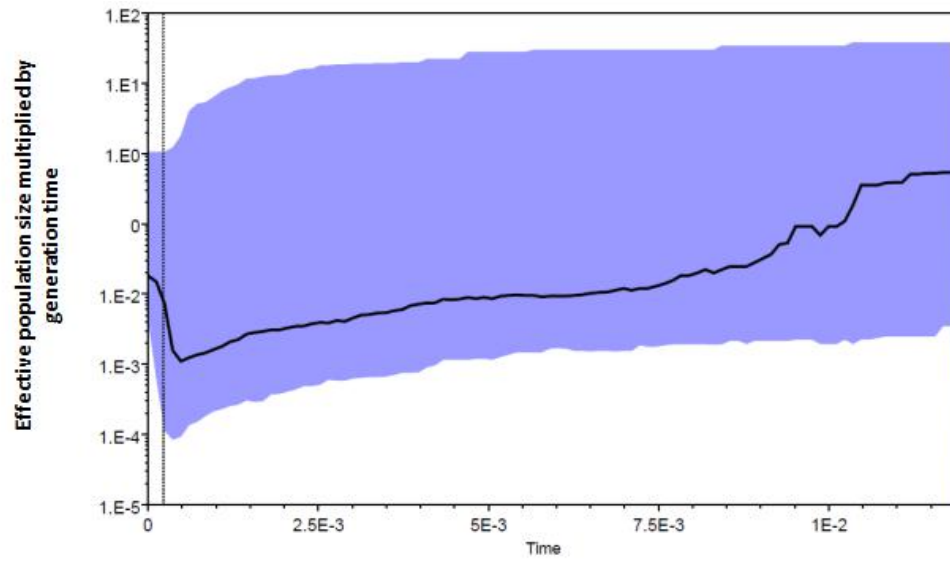
(C)



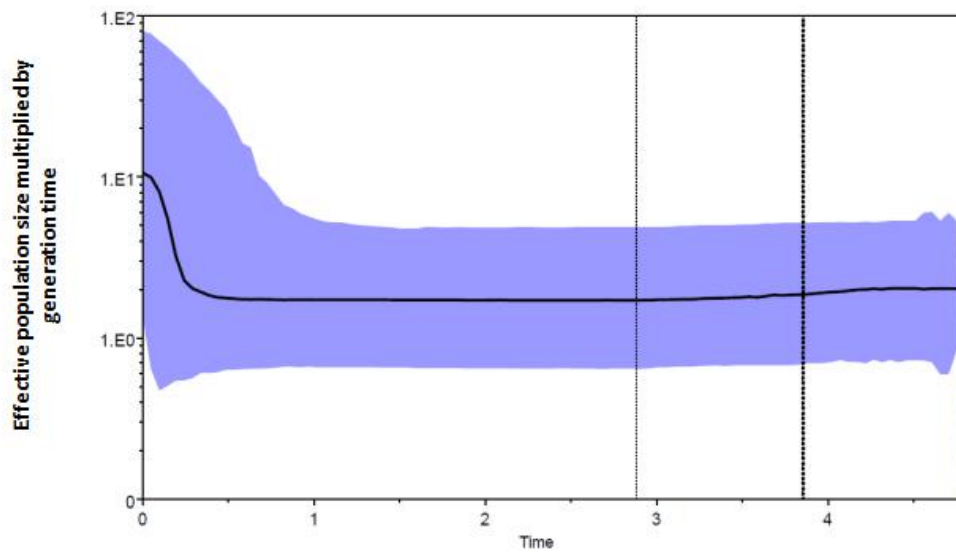
(D)



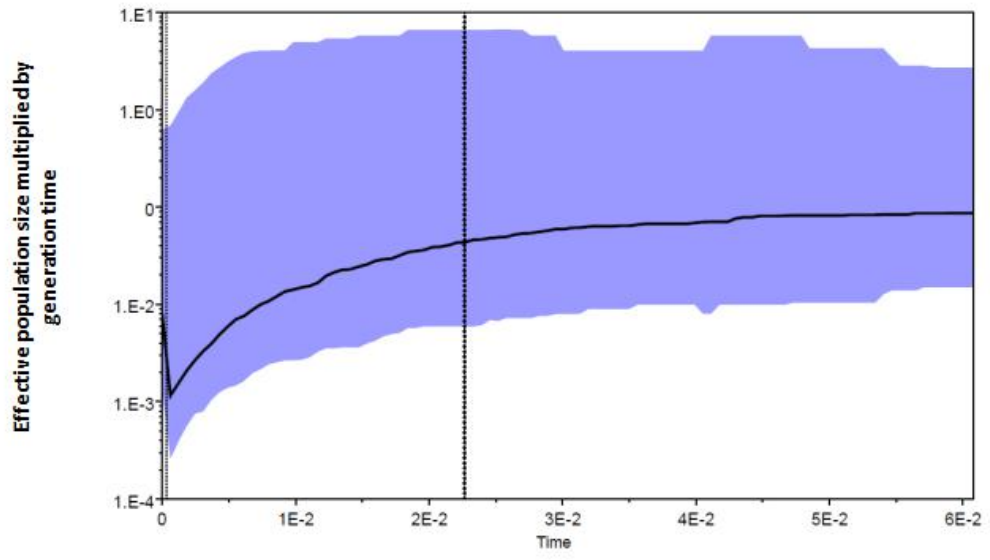
(E)



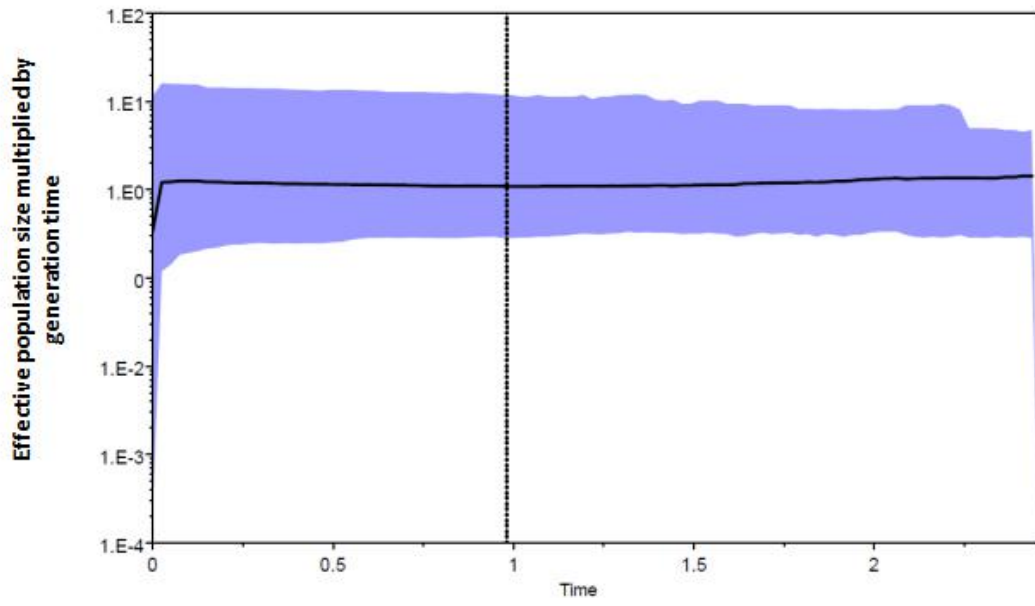
(F)



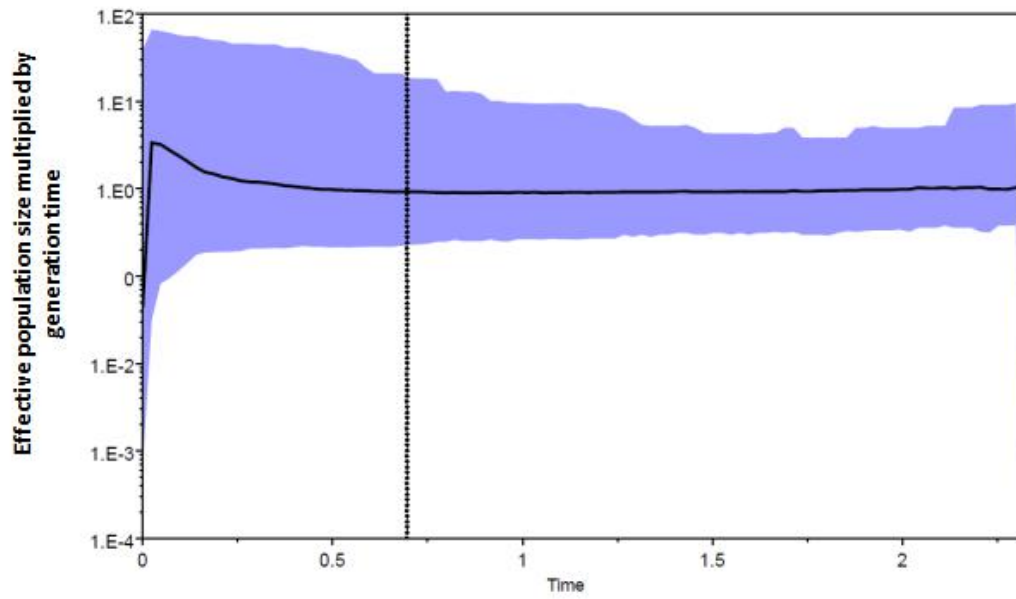
(G)



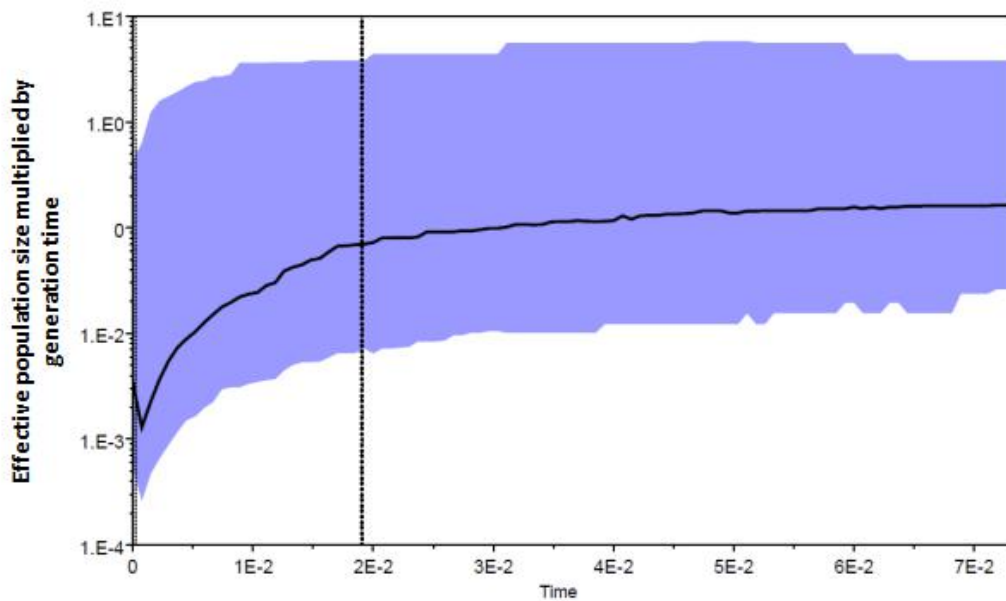
(H)



(I)



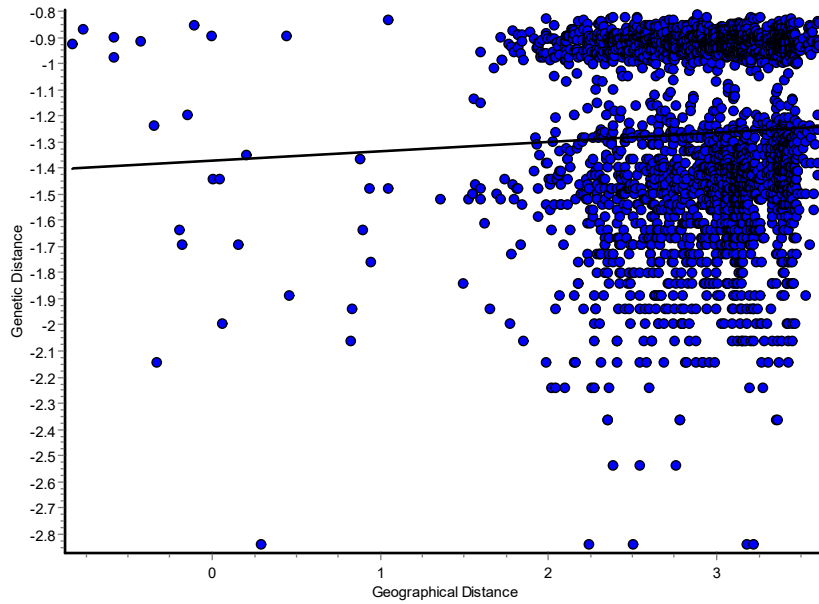
(J)



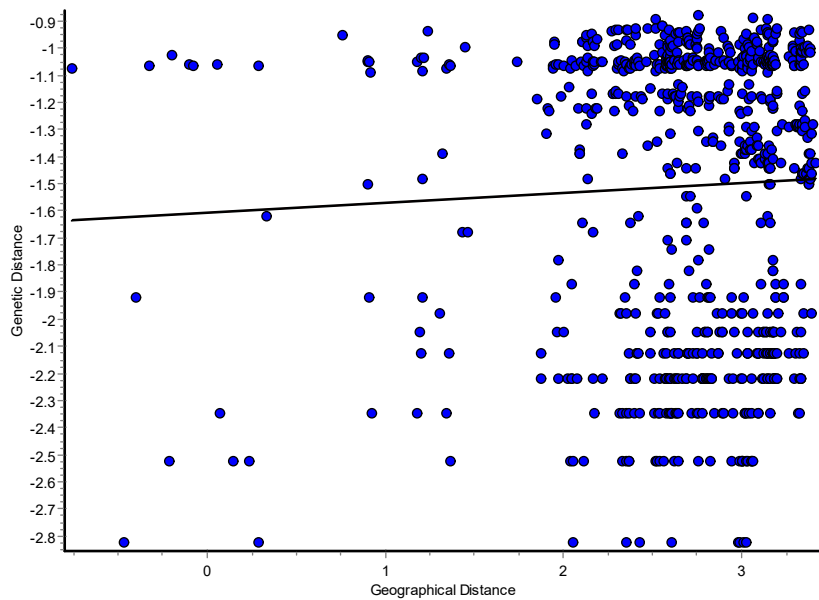
Supplementary Figure S2 Bayesian skyline plot analysis (BSP) to determine possible demographic changes across natural history of *Tamandua* sp. and *Myrmecophaga tridactyla*. X-axis, time in millions of years; Y-axis, log effective population size of females. Overall *Tamandua* sp. samples (A); *Tamandua* haplogroup THI (B); *Tamandua* haplogroup THII (C); *Tamandua* haplogroup THIII (D);

Recent amplification of THIII (E); Overall *Myrmecophaga tridactyla* samples (F); Recent amplification of overall *Myrmecophaga tridactyla* samples (G); *Myrmecophaga* haplogroup MHI (H); *Myrmecophaga* haplogroup MHII (I); Recent amplification of MHII (J).

(A)

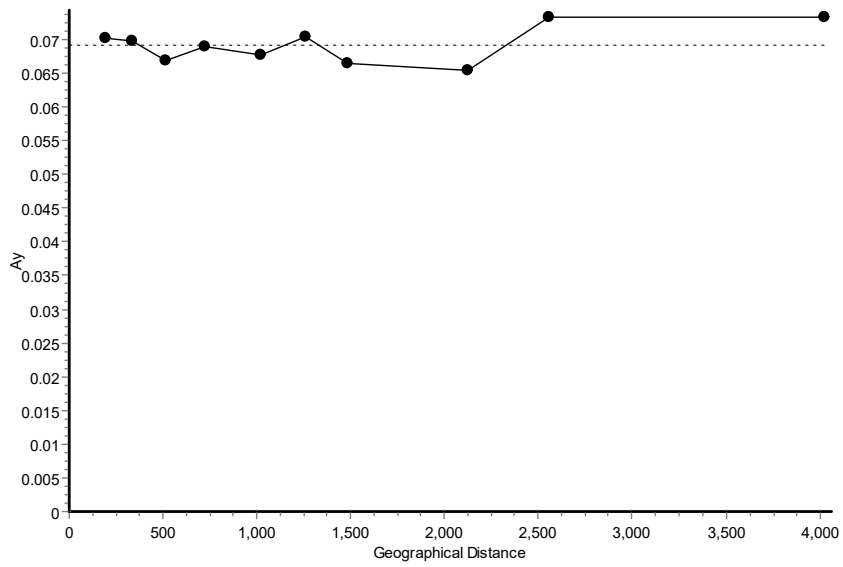


(B)

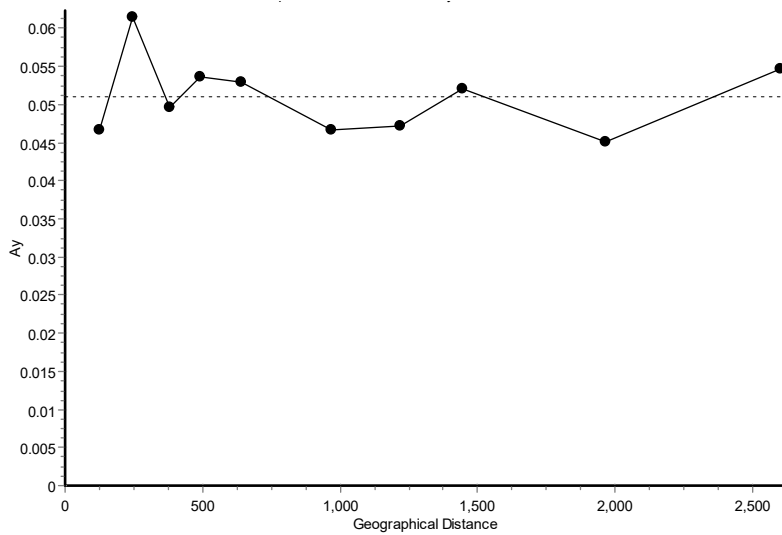


Supplementary Figure S3 Mantel test between geographic and genetic distances for entire mitogenomes of 74 *Tamandua* sp. and 41 *Myrmecophaga tridactyla* specimens. *Tamandua* sp. (A) and *Myrmecophaga tridactyla* (B).

(A)



(B)



Supplementary Figure S4 Spatial autocorrelation analyses for *Tamandua* sp. mitogenomes sequenced with 10 distance classes (DC) (A) and *Myrmecophaga tridactyla* mitogenomes sequenced with 10 distance classes (DC) (B).