

Development of Microsatellite Primers

Prior to this study, there were no available microsatellite primers for bat flies of the family Streblidae. We used Roche 454 pyrosequencing to develop 9 polymorphic microsatellite markers for *T. frequens*. DNA was extracted from 7 *T. frequens* using the ZR Tissue and Insect MicroPrep kit (Zymo Research, Irvine, California) and eluted using 20uL of sdH₂O. Extractions were combined into two pools. Sequencing and library preparation was done at the University of Florida Interdisciplinary Center for Biotechnology Research (ICBR). Libraries were constructed using the "Rapid Library Preparation" reagents contained in the Roche Applied Science kits. The protocol used was a slight modification of the method described by the kit manufacturer (Rapid Library Preparation Manual, GS FLX Titanium Series, Oct. 2009; Rev. Jan. 2010). The library was barcoded using the Library Prep Kit Rapid Library MID Adaptors kit (Roche, Cat # 05619211001). However, each species was run on a separate 1/8 picotiter plate region. Briefly, 500 ng of high MW genomic DNA was fragmented in an S2 Covaris instrument to sizes in the 500-800 bp range. Fragment ends were repaired, and ligated to Rapid Library Adaptors. Small fragments and excess adaptors were removed by a procedure using AMPure beads. The final library was quantitated in the QUBIT fluorometer (Invitrogen) and the BioAnalyzer (Agilent). A suitable amount of the library was diluted in TE/0.05% Tween-20 to 10⁸ copies per microliter. Further dilutions were prepared to 10⁶ copies per microliter for emPCR titrations set in the 1-4 library copies per bead range (2.4x10⁶ beads/reaction). The conditions and procedures for emPCR and bead enrichment were exactly as described in the Roche protocols. A total of 340,000 enriched sequencing beads were loaded on a 1/8 region of a picotiter plate for sequencing on the 454 GS FLX instrument. Raw image signals were processed offline using the

GS Run Browser v.2.0, providing Standard Flowgram Format (SFF) files that contain sequence trace data for the reads. In addition to SFF files, ICBR provided base called reads with associated per-base quality scores as FASTA files.

We used the Galaxy instance (Giardine *et al.* 2005; Goecks *et al.* 2010; Blankenberg *et al.* 2010a) on the University of Florida HiperGator (Research Computing, University of Florida) to quality filter 454 sequences. FASTA and QUAL files were combined to make a single FASTQ block using Galaxy (Blankenberg *et al.* 2010b). Reads were quality filtered using a cutoff threshold where 50% of the per-base quality score of a read had \geq Phred score of 30 (FASTX Toolkit). FastQC implemented in Galaxy was used to check per base and per sequence quality scores of 454 sequencing reads. Barcodes were removed from the 5' end of sequences using CutAdapt v.1.1a in Galaxy and reads shorter than 15bp were discarded. Modified FASTQ files were converted to FASTA (Gordon and Hannon 2010) and exported from Galaxy. QDD v.3.1 was used to eliminate sequences shorter than 80bp and those that do not contain microsatellites (Meglécz *et al.* 2010; Meglécz *et al.* 2014). QDD also conducts an “all against all” BLAST search to identify unique reads. In insects, flanking regions of microsatellites can be similar to each other, forming microsatellite families (Meglécz *et al.* 2007). Due to their similarity, primers developed using these similar regions will lead to non-specific amplification of multiple microsatellites (Meglécz *et al.* 2007). QDD prepares a FASTA file that only contains singletons and consensus sequences that did not group with other reads in the “all against all” BLAST search. Default values in QDD were used to define consensus sequences and grouped sequences. We used a perl script written by Castoe *et al.* (2009) and edited by Dr. Matthew Gitzendanner to run Primer3 (Untergasser *et al.* 2012). The script extracts reads that contain di-, tri-, and tetranucleotide repeats that have at least 6 tandem repeats. The script then submits batches of

reads to the program Primer3 for primer design (Untergasser *et al.* 2012). Our criteria for primer design follow that described in Castoe *et al.* (2009). In addition to these parameters, we also enforced a minimum distance of 50bp between the end of the primer and the beginning of the microsatellite repeat to ensure good amplification. Our study does not require many microsatellite loci, but studies seeking to develop more than 10-20 microsatellite loci might consider a smaller area of exclusion surrounding the microsatellite repeat. Reads recommended for microsatellite amplification were visually checked in Geneious™ v.6.1.7 (Kearse *et al.* 2012) to ensure that there were no monomer repeats longer than 5 bases, that the targeted microsatellite was a perfect repeat, and that there were no other microsatellites in the portion amplified by proposed primer pairs. Following these criteria, we identified 45 candidate primer pairs. We use a nested PCR approach for microsatellite amplification and added universal CAG or M13 tags to the 5' end of the forward primer (Table S2) that correspond with universal tags on FAM, VIC, NED, and PET dyes (see Ascunce *et al.* 2013). We screened 3 bat flies for all primer pairs for successful PCR amplification using PCR conditions described below and annealing temperatures ranging from 55-60°C based on melting temperature of primers. Primers that did not amplify in at least two of the three bat flies were discarded. We used a temperature gradient to identify the best annealing temperature for the remaining primers and then screened these primer pairs for variability using an additional three bat flies so that a total of 6 bat flies had been amplified for each remaining primer pair and that these bat flies were collected from localities separated by the NPC. We multi-plexed PCR products that were tagged with different dyes, using 1.5uL of PCR products with FAM and VIC dyes and 3uL PCR products with NED and PET dyes. We then diluted multi-plexed PCR products up to 50uL with sdH₂O and sent them to the University of Florida ICBR for visualization on an ABI3730xl DNA Analyzer. Raw peak data was manually

scored in Geneious™ using the microsatellite plugin (Kearse *et al.* 2012). Primer pairs that amplified fewer than three alleles were discarded, leaving 9 viable primer pairs (Table S2).

Verification of Population Structure following Removal of Potential Null Alleles

Direct tests of Hardy-Weinberg Equilibrium (HWE) indicated that some loci in some populations deviated from expectations. This is not surprising considering populations of *E. sezekorni* and *T. frequens* are small on the Little and Great Bahama Banks and that there is low gene flow from external sources. However, homozygote excess may also be indicative of the presence of null alleles, where mutations have occurred in primer sites that prevent the amplification of the locus and falsely appear as homozygotes (van Oosterhout *et al.* 2004). In order to verify the patterns of population structure evidenced by microsatellites, we used MICROCHECKER to detect homozygote excess and identify potential null alleles. Following sequential Bonferroni correction (Rice 1989), two alleles in TRFR40 and TRFR43 were recoded as missing data and three loci (TRFR4, 13, and 37) were removed from the dataset. For *E. sezekorni*, we removed three loci (ES38, 43, and 46). We re-ran estimates of F_{ST} , G''_{ST} , and D_{EST} on the purged datasets and found high population structure between islands of the Great and Little Bahama Bank and no significant structure within banks of islands in *T. frequens* (Table S3 and S4). In *E. sezekroni*, we found low, but significant, population structure across the NPC (Table S3 and S4). As results following purging of potential null alleles are the same as the complete dataset, we use the complete dataset for analyses to prevent inappropriately removing homozygotes.

Ascunce MS, Toups MA, Kassu G, Fane J, Scholl K, Reed DL (2013). Nuclear genetic diversity in human lice (*Pediculus humanus*) reveals continental differences and high inbreeding among worldwide populations. *PLoS One* **8**: e57619.

Blankenberg D, Gordon A, Von Kuster G, Coraor N, Taylor J, Nekrutenko A, *et al.* (2010). Manipulation of FASTQ data with Galaxy. *Bioinformatics* **26**: 1783–1785.

Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, *et al.* (2010). Galaxy: a web-based genome analysis tool for experimentalists. *Curr Protoc Mol Biol* **Chapter 19**: Unit 19.10.1–21.

Castoe TA, Poole AW, Gu W, Jason de Koning AP, Daza JM, Smith EN, *et al.* (2010). Rapid identification of thousands of copperhead snake (*Agkistrodon contortrix*) microsatellite loci from modest amounts of 454 shotgun genome sequence. *Mol Ecol Resour* **10**: 341–347.

Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, Shah P, *et al.* (2005). Galaxy: a platform for interactive large-scale genome analysis. *Genome Res* **15**: 1451–1455.

Goecks J, Nekrutenko A, Taylor J, Galaxy Team (2010). Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome Biol* **11**: R86.

Gordon A, Hannon GJ (2010). Fastx-toolkit. *FASTQ/A short-reads preprocessing tools (unpublished)* http://hannonlab.cshl.edu/fastx_toolkit **5**.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, *et al.* (2012). Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28**: 1647–1649.

Megléc E, Costedoat C, Dubut V, Gilles A, Malausa T, Pech N, *et al.* (2010). QDD: a user-friendly program to select microsatellite markers and design primers from large sequencing projects. *Bioinformatics* **26**: 403–404.

Megléc E, Pech N, Gilles A, Dubut V, Hingamp P, Trilles A, *et al.* (2014). QDD version 3.1: a user-friendly computer program for microsatellite selection and primer design revisited: experimental validation of variables determining genotyping success rate. *Mol Ecol Resour* **14**: 1302–1313.

Rice WR (1989). Analyzing Tables of Statistical Tests. *Evolution* **43**: 223–225.

Untergasser A, Cutcutache I, Koressaar T, Ye J, Faircloth BC, Remm M, *et al.* (2012). Primer3—new capabilities and interfaces. *Nucleic Acids Res* **40**: e115–e115.

Table S1 - List of all samples used in this publication organized by island and Field ID. Some bat flies were collected from the same bat, so the bat information is repeated, but the bat fly information (Extraction ID, sex, specimen type) are unique. For bats that had remaining tissue after the study, we deposited this tissue at the Florida Museum and the FLMNH catalogue number is indicated.

Field ID	Bat Fly Extraction ID	Bat Microsat.	Bat Fly Microsat.	Bat Fly COII	Bat Fly Sex	Bat Fly Specimen Type	FLMNH Catalogue Number	Genus	Species	Bat Sex	Island	Date Collected
ASC 289	23	Y	Y			whole	32911	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 290	5	Y	Y			3 legs	32912	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 291	3		Y	MK924034		punctured	32913	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 292	72		Y	MK924005		whole	32914	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/3/13
ASC 293	8	Y	Y			whole	32915	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 293	73	Y	Y	MK924006	male	whole	32915	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 293	74	Y	Y	MK924007	male	whole	32915	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 293	75	Y	Y	MK924008	female	whole	32915	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 297	Y						32919	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 298	Y						32920	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/3/13
ASC 299	Y						32921	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/3/13
ASC 301	168		Y		female	head and thorax	32923	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/3/13
ASC 302	9	Y	Y			whole	32924	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 303	Y						32925	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 304	2	Y	Y			punctured female	32926	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 304	42	Y	Y	MK924035	male	whole	32926	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 305	29		Y		female	whole	32927	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 308	169		Y		female	head and thorax	32930	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 309	1		Y			whole female	32931	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 309	30		Y	MK924036	female	whole	32931	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 310	170		Y		female	head and thorax	32932	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/3/13
ASC 311	77	Y	Y	MK924010	male	whole	32933	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 312	171		Y		female	head and thorax	32934	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 312	172		Y		female	head and thorax	32934	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 313	78		Y		female	whole	32935	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 314	Y						32936	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 315	173	Y	Y		female	punctured	32937	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 316	174	Y	Y		male	punctured	32938	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 317	56	Y	Y	MK923993	male	whole	32939	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 317	57	Y	Y	MK923994	female	whole	32939	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 318	175	Y	Y		male	punctured	32940	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 319	176	Y	Y		male	punctured	32941	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 320	177	Y	Y		male	punctured	32942	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 321	178	Y	Y		female	head and thorax	32943	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 322	Y						32944	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13

Field ID	Bat Fly Extraction ID	Bat Microsat.	Bat Fly Microsat.	Bat Fly COII	Bat Fly Sex	Bat Fly Specimen Type	FLMNH Catalogue Number	Genus	Species	Bat Sex	Island	Date Collected
ASC 323		Y					32945	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 324	79	Y	Y		male	whole	32946	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 324	80	Y	Y	MK924011	female	whole	32946	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 324	81	Y	Y	MK924012	female	whole	32946	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 325	82	Y	Y		male	whole	32947	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 325	83	Y	Y		female	whole	32947	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 326	84	Y	Y		male	whole	32948	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 326	85	Y	Y		male	whole	32948	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 327	179	Y	Y		female	head and thorax	32949	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 328	86	Y	Y	MK924013	male	whole	32950	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 328	87	Y	Y	MK924014	male	whole	32950	<i>Erophylla</i>	<i>sezekorni</i>	Female	Abaco	3/4/13
ASC 329	180	Y	Y		male	punctured	32951	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
ASC 330		Y					32952	<i>Erophylla</i>	<i>sezekorni</i>	Male	Abaco	3/4/13
BF1	31		Y		male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/3/13
BF2	182		Y		male	punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	NA
BF3	32		Y		male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/3/13
BF4	183		Y		female	punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	NA
BF5	33		Y		male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF5	58		Y		female	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF5	59		Y		male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF5	60		Y		male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF6	4		Y	MK924037		punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/3/13
BF6	76		Y	MK924009	male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/3/13
BF7	34		Y		female	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF7	44		Y		male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF7	88		Y		female	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF7	89		Y		male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	3/4/13
BF8	184		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Abaco	NA
BF10	90		Y		female	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Eleuthera	5/1/13
BF10	91		Y		female	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Eleuthera	5/1/13
KAS 1		Y					32392	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 2	111	Y	Y		male	punctured	32393	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 3	114	Y	Y		female	head and thorax	32394	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 4	118	Y	Y		male	punctured	32395	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 5		Y					32396	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 6	191	Y	Y		unknown	abdomen ruptured	32397	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 7		Y					32398	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 8	115	Y	Y		female	head and thorax	32399	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 8	116	Y	Y		female	punctured	32399	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13

Field ID	Bat Fly Extraction ID	Bat Microsat.	Bat Fly Microsat.	Bat Fly COII	Bat Fly Sex	Bat Fly Specimen Type	FLMNH Catalogue Number	Genus	Species	Bat Sex	Island	Date Collected
KAS 9	123	Y	Y	MK924021	female	punctured	32400	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 9	124	Y	Y	MK924022	male	punctured	32400	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 9	125	Y	Y	MK924023	male	punctured	32400	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 9	126	Y	Y	MK924024	male	punctured	32400	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 9	127	Y	Y	MK924025	female	punctured	32400	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 9	128	Y	Y	MK924026	female	punctured	32400	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 10	188	Y	Y		unknown	abdomen ruptured	32401	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 11	112	Y	Y		male	punctured	32402	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 13	120	Y	Y		female	head and thorax	32404	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 13	121	Y	Y		male	punctured	32404	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 13	122	Y	Y		male	punctured	32404	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 14	119		Y		male	punctured	32405	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 15		Y					32406	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 16	110	Y	Y	MK924020	female	head and thorax	32407	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 17		Y					32408	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 18		Y					32409	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 19	117	Y	Y		female	head and thorax	32410	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 20	192	Y	Y				32411	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	4/30/13
KAS 21		Y					32412	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	4/30/13
KAS 23		Y					32414	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	5/1/13
KAS 24		Y					32415	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 25		Y					32416	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 26		Y					32417	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 27		Y					32418	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 28		Y					32419	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 29		Y					32420	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 31	93	Y	Y	MK924015	male	whole	32422	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 32	94	Y	Y	MK924016	female	whole	32423	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 32	95	Y	Y	MK924017	female	whole	32423	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 33		Y					32424	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 34		Y					32425	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	5/1/13
KAS 35		Y					32426	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 37	96	Y	Y	MK924018	female	punctured	32428	<i>Erophylla</i>	<i>sezekorni</i>	Female	Eleuthera	5/1/13
KAS 38		Y					32429	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 39	97	Y	Y	MK924019	female	head and thorax	32430	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 40	193	Y	Y				32431	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
KAS 41		Y					32432	<i>Erophylla</i>	<i>sezekorni</i>	Male	Eleuthera	5/1/13
BF18	129		Y	MK924027	female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF19	130		Y	MK924028	female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13

Field ID	Bat Fly Extraction ID	Bat Microsat.	Bat Fly Microsat.	Bat Fly COII	Bat Fly Sex	Bat Fly Specimen Type	FLMNH Catalogue Number	Genus	Species	Bat Sex	Island	Date Collected
BF20	131		Y	MK924029	female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF21	132		Y	MK924030	female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF22	133		Y	MK924031	female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF23	134		Y	MK924032	female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF24	135		Y	MK924033	female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF24	136		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF25	137		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF26	138		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF27	139		Y		male	punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF28	61		Y	MK923995	male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/9/13
BF29	63		Y	MK923997	male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/9/13
BF30	140		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF31	185		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
BF32	62		Y	MK923996	male	whole	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Grand Bahama	7/10/13
KAS 101		Y					33031	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/9/13
KAS 102		Y					33032	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 103		Y					33033	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 104		Y					33034	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 105		Y					33035	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 106		Y					33036	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 107		Y					33037	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 108		Y					33038	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 109		Y					33039	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 110		Y					33040	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 111		Y					33041	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 112		Y					33042	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 113		Y					33043	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 114		Y					33044	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 115		Y					33045	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 116		Y					33046	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 117		Y					33047	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 118		Y					33048	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 119		Y					33049	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/9/13
KAS 122	14	Y	Y			3 legs	33053	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/10/13
KAS 124		Y					33055	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 125		Y					33056	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/10/13
KAS 126		Y					33057	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 127		Y					33058	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 128		Y					33059	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13

Field ID	Bat Fly Extraction ID	Bat Microsat.	Bat Fly Microsat.	Bat Fly COII	Bat Fly Sex	Bat Fly Specimen Type	FLMNH Catalogue Number	Genus	Species	Bat Sex	Island	Date Collected
KAS 129	12	Y	Y			3 legs	33060	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/10/13
KAS 130		Y					33061	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 131		Y					33062	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 132	186	Y	Y			turgid fer punctured	33063	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 133		Y					33064	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 134	13	Y	Y			3 legs	33065	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 135		Y					33066	<i>Erophylla</i>	<i>sezekorni</i>	Male	Grand Bahama	7/10/13
KAS 137		Y					33068	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/10/13
KAS 138	187		Y		female	head and thorax	33069	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/10/13
KAS 140		Y					33071	<i>Erophylla</i>	<i>sezekorni</i>	Female	Grand Bahama	7/10/13
BF13	144		Y		female	punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Long Island	7/14/13
BF13	145		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Long Island	7/14/13
BF15	146		Y		male	punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Long Island	7/15/13
BF15	147		Y		female	punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Long Island	7/15/13
BF16	148		Y		female	punctured	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Long Island	7/15/13
BF16	150		Y		female	head and thorax	NA	<i>Erophylla</i>	<i>sezekorni</i>	NA	Long Island	7/15/13
KAS 158		Y					33089	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 160	151	Y	Y		female	punctured	33091	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 161		Y					33092	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 162		Y					33093	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 163	152	Y	Y		male	punctured	33094	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/14/13
KAS 163	153	Y	Y		female	head and thorax	33094	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/14/13
KAS 164		Y					33095	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/14/13
KAS 165		Y					33096	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/14/13
KAS 166	155	Y	Y		unknown	abdomen ruptured	33097	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 166	156	Y	Y		male	punctured	33097	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 168		Y					33099	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 169	157	Y	Y		male	punctured	33100	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 169	158	Y	Y		male	thorax ruptured and	33100	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 169	159	Y	Y		unknown	abdomen ruptured	33100	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 170		Y					33101	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 171		Y					33102	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 172	25	Y	Y			whole	33103	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/14/13
KAS 173		Y					33104	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/14/13
KAS 174	162	Y	Y		male	punctured	33105	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 175	163	Y	Y		female	abdomen ruptured	33106	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/14/13
KAS 176	22		Y			whole	33107	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 176	164		Y		male	punctured	33107	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 177	64			MK923998	male	whole	33108	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13

Field ID	Bat Fly Extraction ID	Bat Microsat.	Bat Fly Microsat.	Bat Fly COII	Bat Fly Sex	Bat Fly Specimen Type	FLMNH Catalogue Number	Genus	Species	Bat Sex	Island	Date Collected
KAS 177	65	Y	Y	MK923999	female	whole	33108	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 178	66		Y	MK924000	female	whole	33109	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 180		Y					33111	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 181	194	Y	Y				33112	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 182		Y					33113	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 183		Y					33114	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 184		Y					33115	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 185		Y					33116	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 186		Y					33117	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 187	67	Y	Y	MK924001	male	whole	33118	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 188	69	Y	Y	MK924002	female	whole	33119	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 189		Y					33120	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 190		Y					33121	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 191	195	Y	Y				33122	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 192	50	Y	Y		female	whole	33123	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 192	70	Y	Y	MK924003	male	whole	33123	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 192	71	Y	Y	MK924004	male	whole	33123	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 192	141	Y	Y		female	head and thorax	33123	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 193	142	Y	Y		male	punctured	33124	<i>Erophylla</i>	<i>sezekorni</i>	Female	Long Island	7/15/13
KAS 194	143		Y		male	punctured	33125	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 194	165		Y		male	abdomen and thora:	33125	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 216		Y					NA	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13
KAS 217		Y					NA	<i>Erophylla</i>	<i>sezekorni</i>	Male	Long Island	7/15/13

Table S2 – Primer sequence, repeat unit, and approximate length of amplified fragment for 9 polymorphic microsatellite loci. These are the unmodified versions of the primers used in this study, and do not include universal tags or pigtails.

Locus	Repeat Unit	Amplicon length	Forward Primer	Reverse Primer	Dye
TRFR1	2 (TC)	175-275	TGGTCATTAATATTTACACG	AATAGATACACCGATAAACG	6-FAM
TRFR4	2 (AT)	250-350	AATATCTCTGTA CTCTCAACG	TTATATGTCTCTCAGATGGG	VIC
TRFR13	2 (AT)	250-350	AATCTGATGGATAATTAACC	AATAAGTAATTTACCACACG	VIC
TRFR28	2 (AT)	150-250	AACTAATGAAGAATGATTGC	TACCAGTAGATGAATATCGC	NED
TRFR37	2 (TC)	150-250	GATGTAAATGAAGACAGACC	ATATGTTGTATCACACAGGC	6-FAM
TRFR38	4 (AATG)	200-300	ATAGAGACTGAGAGAGAGCG	CGTTGAAATAAATTACCG	PET
TRFR40	4 (AAAT)	250-350	ATATCGTGAATAATGACTGC	ATAAGAGATGCTACAGAACG	PET
TRFR43	4 (ACTG)	215-315	AAATGAAAAGAATGATGAGG	GCATCTGTATCTACCATACG	NED
TRFR45	4 (ATGG)	300-400	CAGTTATGTGATTATAGCCG	CTTTAAGGAATTATGAACG	PET

Table S3 – Estimates of population differentiation (Jost's D, G''_{ST} , F_{ST}) after removal of hypothesized null alleles of *E. sezekorni* and *T. frequens* when individuals are grouped into Little Bahama Bank and Great Bahama Bank clusters separated by the NPC. Values significantly different than random are indicated using asterisks ($P < 0.005$ is indicated by **).

	<i>Erophylla sezekorni</i>	<i>Trichobius frequens</i>
Jost's D	0.051**	0.159**
G''_{ST}	0.074**	0.229**
F_{ST}	0.017**	0.049**

Table S4 – Jost’s D (top number in each cell), G''_{ST} (middle number in each cell), and F_{ST} (bottom number in each cell) by island after removal of hypothesized null alleles of *Erophylla sezekorni* (white cells) and *Trichobius frequens* (grey cells). Values significantly different than random are indicated by asterisks (* $p < 0.05$, ** $p < 0.005$).

	Abaco	Grand Bahama	Eleuthera	Long Island
Abaco		0.00	0.139**	0.202**
		0.00	0.206**	0.294**
		0.007	0.050**	0.072**
Grand Bahama	0.002		0.174**	0.217**
	0.003		0.245**	0.306**
	0.010		0.061**	0.076**
Eleuthera	0.082**	0.050**		0.109*
	0.117**	0.070**		0.167*
	0.029**	0.019**		0.045**
Long Island	0.038*	0.092**	0.064**	
	0.058*	0.132**	0.091**	
	0.020*	0.031**	0.023**	

Table S5 – BayesAss results of 10 subsampled datasets of *Erophylla sezekorni* and *Trichobius frequens* when individuals are split into two populations, the Little Bahama Bank (LBB) and Great Bahama Bank (GBB). Results are given as the proportion of migrants from one population to another and the standard deviation around the mean. The columns labeled “LBB to LBB” and “GBB to GBB” indicated the proportion of non-migrants in the LBB and GBB, respectively.

	LBB to LBB	SD LBB to LBB	GBB to LBB	SD GBB to LBB	LBB to GBB	SD LBB to GBB	GBB to GBB	SD GBB to GBB
<i>Erophylla sezekorni</i>	0.99	0.01	0.01	0.01	0.07	0.03	0.93	0.03
	0.99	0.01	0.01	0.01	0.10	0.04	0.90	0.04
	0.99	0.01	0.01	0.01	0.11	0.04	0.89	0.04
	0.99	0.01	0.01	0.01	0.08	0.04	0.92	0.04
	0.99	0.01	0.01	0.01	0.09	0.04	0.91	0.04
	0.99	0.01	0.01	0.01	0.08	0.03	0.92	0.03
	0.99	0.01	0.01	0.01	0.13	0.05	0.87	0.05
	0.99	0.01	0.01	0.01	0.08	0.04	0.92	0.04
	0.99	0.01	0.01	0.01	0.14	0.05	0.86	0.05
	0.99	0.01	0.01	0.01	0.11	0.05	0.89	0.05
<i>Trichobius frequens</i>	0.97	0.02	0.03	0.02	0.03	0.02	0.97	0.02
	0.98	0.01	0.02	0.01	0.06	0.03	0.94	0.03
	0.97	0.02	0.03	0.02	0.05	0.02	0.95	0.02
	0.97	0.02	0.03	0.02	0.04	0.02	0.96	0.02
	0.98	0.01	0.02	0.01	0.06	0.02	0.94	0.02
	0.97	0.02	0.03	0.02	0.05	0.02	0.95	0.02
	0.98	0.02	0.02	0.02	0.03	0.02	0.97	0.02
	0.98	0.02	0.02	0.02	0.05	0.02	0.95	0.02
	0.97	0.02	0.03	0.02	0.06	0.02	0.94	0.02
	0.98	0.01	0.02	0.01	0.07	0.02	0.93	0.02

Table S6 – BayesAss results of 10 subsampled datasets of *Erophylla sezekorni* and *Trichobius frequens* when individuals are split into four populations: Abaco (A), Grand Bahama (GB), Eleuthera (E), and Long Island (LI). Results are given as the proportion of migrants from one population to another and the standard deviation around the mean. The columns where migrants are moving from and to the same population give the proportion of non-migrants in that population.

	A to A	SD A to A	GB to A	SD GB to A	E to A	SD E to A	LI to A	SD LI to A	A to GB	SD A to GB	GB to GB	SD GB to GB	E to GB	SD E to GB
<i>Erophylla sezekorni</i>	0.89	0.11	0.07	0.11	0.02	0.02	0.02	0.02	0.23	0.10	0.74	0.10	0.02	0.01
	0.90	0.09	0.06	0.09	0.02	0.01	0.02	0.02	0.23	0.09	0.74	0.09	0.02	0.02
	0.95	0.03	0.02	0.02	0.01	0.01	0.02	0.02	0.29	0.02	0.68	0.01	0.01	0.01
	0.92	0.07	0.03	0.06	0.02	0.02	0.02	0.02	0.27	0.07	0.71	0.06	0.02	0.01
	0.95	0.03	0.01	0.01	0.01	0.01	0.02	0.02	0.29	0.03	0.69	0.03	0.01	0.01
	0.95	0.03	0.01	0.01	0.01	0.01	0.03	0.02	0.29	0.02	0.68	0.01	0.01	0.01
	0.94	0.03	0.01	0.01	0.01	0.01	0.03	0.03	0.29	0.03	0.68	0.02	0.01	0.01
	0.69	0.05	0.28	0.05	0.01	0.01	0.02	0.02	0.02	0.05	0.95	0.05	0.02	0.02
	0.68	0.01	0.29	0.02	0.01	0.01	0.02	0.02	0.01	0.01	0.95	0.02	0.02	0.01
	0.95	0.03	0.01	0.01	0.01	0.01	0.02	0.02	0.29	0.02	0.68	0.02	0.01	0.01
<i>Trichobius frequens</i>	0.91	0.06	0.04	0.05	0.03	0.02	0.02	0.01	0.16	0.05	0.79	0.05	0.03	0.02
	0.90	0.06	0.05	0.06	0.03	0.02	0.02	0.02	0.16	0.05	0.78	0.05	0.03	0.02
	0.83	0.10	0.11	0.11	0.03	0.03	0.02	0.02	0.14	0.08	0.80	0.07	0.03	0.02
	0.87	0.09	0.08	0.09	0.04	0.03	0.02	0.01	0.18	0.07	0.77	0.07	0.03	0.02
	0.73	0.06	0.24	0.06	0.02	0.02	0.02	0.02	0.07	0.05	0.87	0.05	0.04	0.03
	0.87	0.06	0.07	0.06	0.05	0.03	0.02	0.02	0.18	0.07	0.76	0.06	0.03	0.02
	0.77	0.09	0.18	0.10	0.03	0.03	0.02	0.02	0.11	0.07	0.83	0.07	0.03	0.02
	0.88	0.09	0.07	0.09	0.02	0.02	0.02	0.02	0.15	0.07	0.80	0.07	0.02	0.02
	0.85	0.08	0.09	0.08	0.04	0.03	0.02	0.02	0.12	0.06	0.82	0.06	0.03	0.02
	0.87	0.10	0.09	0.10	0.02	0.02	0.02	0.02	0.15	0.07	0.79	0.07	0.02	0.02

Table S6, continued.

	LI to GB	SD LI to GB	A to E	SD A to E	GB to E	SD GB to E	E to E	SD E to E	LI to E	SD LI to E	A to LI	SD A to LI	GB to LI	SD GB to LI
<i>Erophylla sezekorni</i>	0.01	0.01	0.09	0.05	0.04	0.04	0.73	0.04	0.13	0.06	0.10	0.06	0.03	0.03
	0.01	0.01	0.09	0.05	0.05	0.04	0.69	0.03	0.17	0.05	0.09	0.05	0.02	0.02
	0.01	0.01	0.09	0.04	0.02	0.02	0.70	0.03	0.19	0.04	0.07	0.04	0.01	0.01
	0.01	0.01	0.10	0.05	0.03	0.03	0.70	0.03	0.18	0.05	0.09	0.05	0.02	0.02
	0.01	0.01	0.12	0.05	0.02	0.03	0.75	0.04	0.11	0.05	0.05	0.03	0.01	0.01
	0.01	0.01	0.16	0.06	0.02	0.02	0.74	0.04	0.08	0.05	0.05	0.04	0.01	0.01
	0.01	0.01	0.17	0.06	0.01	0.01	0.69	0.04	0.12	0.07	0.05	0.04	0.01	0.01
	0.02	0.01	0.02	0.03	0.15	0.06	0.78	0.06	0.05	0.05	0.02	0.02	0.08	0.04
	0.02	0.01	0.01	0.01	0.18	0.06	0.72	0.05	0.08	0.04	0.01	0.01	0.06	0.03
0.01	0.01	0.14	0.05	0.02	0.02	0.75	0.04	0.10	0.05	0.05	0.03	0.01	0.01	
<i>Trichobius frequens</i>	0.03	0.02	0.07	0.04	0.02	0.02	0.80	0.05	0.10	0.05	0.02	0.01	0.01	0.01
	0.03	0.02	0.09	0.04	0.03	0.02	0.77	0.04	0.11	0.04	0.02	0.02	0.02	0.02
	0.03	0.02	0.06	0.04	0.03	0.03	0.76	0.04	0.15	0.04	0.02	0.02	0.02	0.02
	0.03	0.02	0.04	0.03	0.04	0.03	0.78	0.05	0.14	0.04	0.02	0.02	0.02	0.01
	0.03	0.02	0.07	0.04	0.04	0.03	0.77	0.04	0.12	0.04	0.02	0.02	0.02	0.01
	0.03	0.02	0.07	0.04	0.04	0.03	0.75	0.04	0.14	0.04	0.02	0.01	0.02	0.01
	0.03	0.02	0.05	0.04	0.05	0.03	0.77	0.04	0.14	0.04	0.02	0.02	0.02	0.01
	0.03	0.02	0.04	0.03	0.04	0.03	0.79	0.05	0.13	0.06	0.02	0.02	0.02	0.02
	0.03	0.02	0.07	0.04	0.03	0.03	0.75	0.04	0.15	0.04	0.02	0.02	0.02	0.02
0.03	0.02	0.09	0.04	0.04	0.03	0.73	0.04	0.14	0.04	0.02	0.02	0.02	0.02	

Table S6, continued.

	E to LI	SD E to LI	LI to LI	sd LI to LI
<i>Erophylla sezekorni</i>	0.04	0.04	0.84	0.06
	0.03	0.02	0.86	0.05
	0.03	0.03	0.89	0.04
	0.04	0.03	0.86	0.05
	0.03	0.02	0.90	0.04
	0.03	0.03	0.90	0.04
	0.03	0.02	0.91	0.04
	0.03	0.02	0.88	0.04
	0.02	0.02	0.90	0.04
	0.04	0.03	0.90	0.04
<i>Trichobius frequens</i>	0.02	0.02	0.95	0.03
	0.03	0.02	0.94	0.03
	0.02	0.02	0.94	0.03
	0.02	0.02	0.95	0.03
	0.03	0.02	0.94	0.03
	0.02	0.02	0.95	0.03
	0.02	0.02	0.95	0.03
	0.05	0.05	0.91	0.06
	0.03	0.02	0.94	0.03
	0.02	0.02	0.95	0.03

Table S7 – Number of reads from 454 sequence data in *Trichobius frequens* and *T. sp. nov.* that matched to bacterial genera in the 16SMicrobe NCBI database. Only bacterial genera that had more than 4 reads were included.

Bacteria	<i>Trichobius frequens</i>	<i>Trichobius sp. nov.</i>
<i>Erythrobacter</i>	178	149
<i>Methanosarcina</i>	6	5
<i>Streptomyces</i>	38	26
<i>Wigglesworthia</i>	6	0
<i>Bavariicoccus</i>	15	17
<i>Stenotrophomonas</i>	8	0
<i>Mycobacterium</i>	6	7
<i>Mycoplasma</i>	11	29
<i>Acinetobacter</i>	6	0
<i>Staphylococcus</i>	10	8
<i>Pseudomonas</i>	6	6
<i>Roseobacter</i>	24	11
<i>Propionibacterium</i>	14	7
<i>Nonlabens</i>	5	0
<i>Paenibacillus</i>	17	7
<i>Desulfonatronum</i>	5	0
<i>Vibrio</i>	5	0
<i>Hymenobacter</i>	7	5
<i>Sphingomonas</i>	6	7
<i>Bacillus</i>	15	11
<i>Hydrogenophaga</i>	5	0
<i>Streptococcus</i>	6	0
<i>Bartonella</i>	48	0
<i>Burkholderia</i>	16	11
<i>Wolbachia</i>	40	0
<i>Lysobacter</i>	8	0
<i>Shewanella</i>	5	0
<i>Clostridium</i>	15	11
<i>Microbacterium</i>	22	25
<i>Prochlorococcus</i>	9	0
<i>Natrialba</i>	5	0
<i>Buchnera</i>	7	18
<i>Legionella</i>	0	5

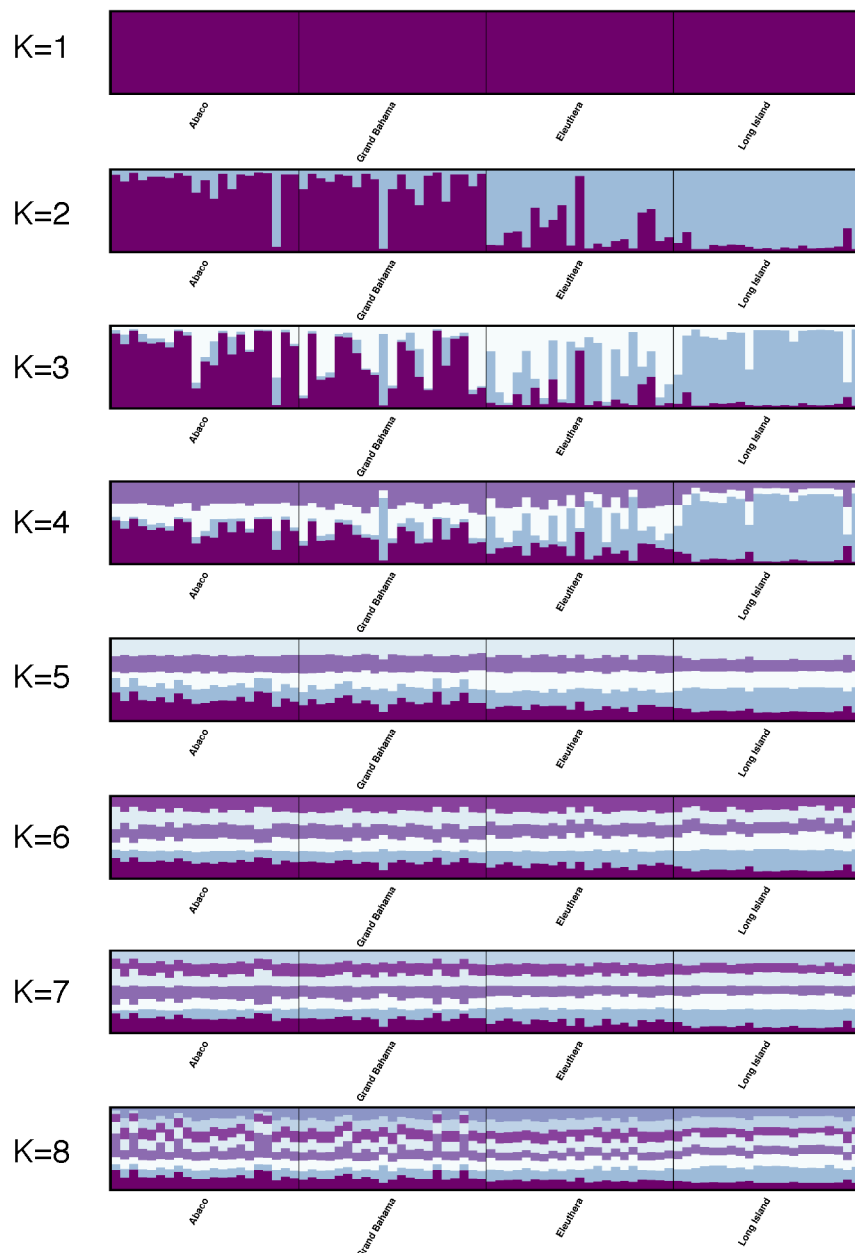


Figure S1 – CLUMPAK plots of Structure runs for *Trichobius frequens* under assumptions of $K=1-8$.

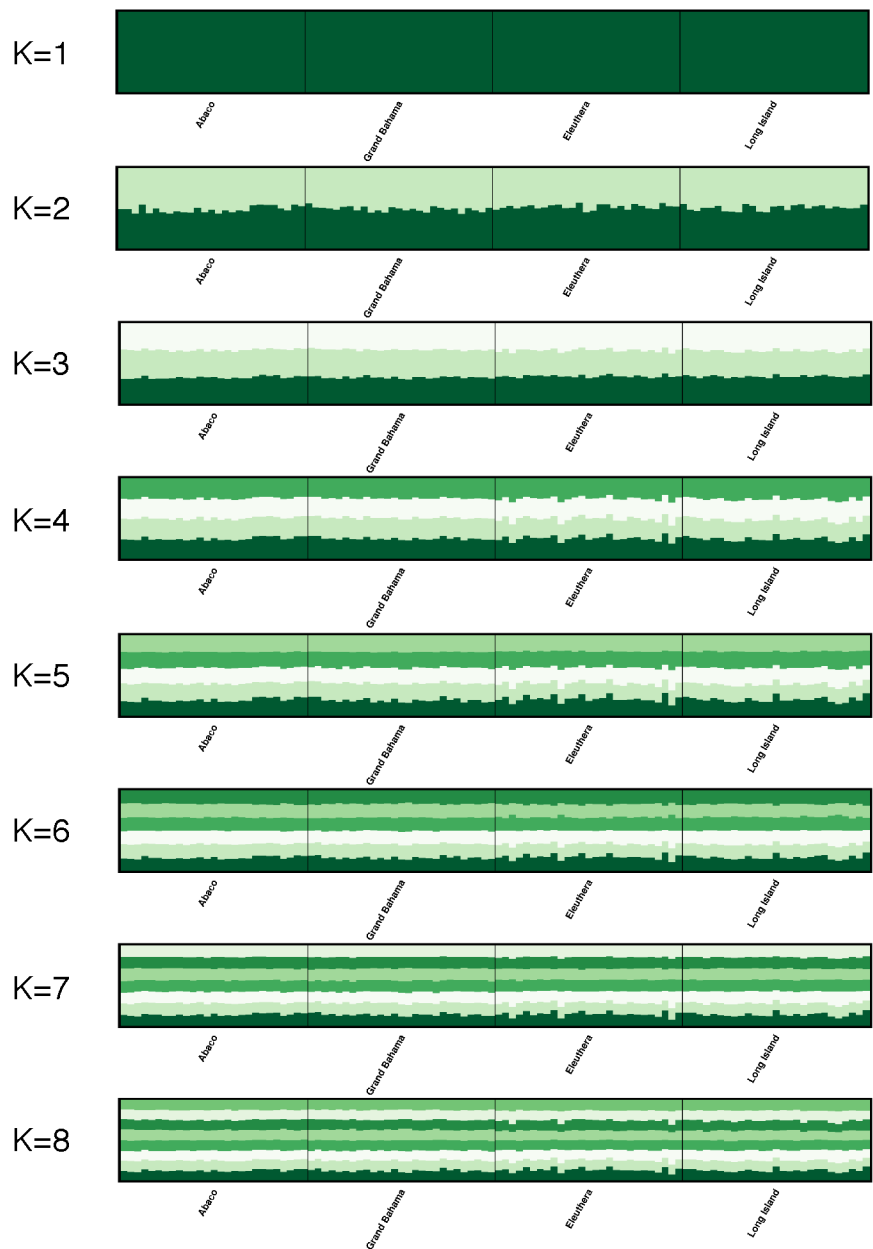


Figure S2 – CLUMPAK plots of Structure runs of *Erophylla sezekorni* under assumption of K=1-8.