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5 **Population collapse in viviparid gastropods of the Lake Victoria ecoregion started**
6 **before the Last Glacial Maximum**

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19

20 **Running title:** demographic collapse in African gastropods

21 **Abstract**

22 Ecosystems of Lake Victoria and riparian communities have been strongly disrupted by the
23 introduction of the invasive Nile perch and its fishing industry. Beyond this invasion and other recent
24 anthropogenic stressors, the Lake Victoria ecoregion also underwent phases of pronounced aridity
25 over the Late Pleistocene, lastly during the Last Glacial Maximum (LGM). The consequences of
26 recent and historic environmental change have been canvassed for the adaptive radiation of
27 haplochromine cichlids occupying the ecoregion, but their effect on freshwater invertebrate diversity
28 remains largely unknown. Here we use 15 microsatellite loci and approximate Bayesian computation
29 to test whether viviparid gastropods experienced a population bottleneck during the LGM, as did
30 cichlids. Clustering analyses support three viviparid gene pools in the Lake Victoria ecoregion,
31 gathering specimens from 1) Lake Albert and the White Nile, 2) the Victoria Nile and Lake Kyoga
32 and 3) Lake Victoria and tributaries. The last group contains the highest genetic diversity, but all
33 groups have a considerable number of private alleles and are inferred to predate the LGM.
34 Examinations of demographic history reveal a 190- to 500-fold population decline that started ~125-
35 150 ka ago, thus substantially before the LGM bottleneck documented in haplochromine cichlids.
36 Population collapses in viviparids are an order of magnitude more severe than declines in cichlids and
37 have not been halted by the re-establishment of freshwater ecosystems since the LGM. Recent
38 anthropogenic ecosystem deterioration is causing homogenization of previously diversified
39 microhabitats, which may contribute to (local) extinction and enhanced gene flow among species
40 within gene pools.

41

42 **Keywords:** Viviparidae, *Bellamyia*, phylogeography, genetic diversity, approximate Bayesian
43 computation

44

45 **Introduction**

46 Less than 1 % of the Earth's surface is covered by freshwater ecosystems, yet these habitats support
47 ~10 % of all known species, including approximately a third of the global vertebrate biodiversity
48 (Strayer & Dudgeon, 2010). The Lake Victoria ecoregion of the East African Rift System, which
49 contains among others Lakes Albert, Kyoga and Victoria, has rapidly accumulated extraordinary
50 freshwater biodiversity throughout the Quaternary, including almost 700 species of cichlid fishes
51 (Danley et al., 2012; Salzburger, Van Bocxlaer, & Cohen, 2014). The region also underwent major
52 geological and climatological changes during this period linked to the development of the East
53 African Rift, including several phases of aridity (Bishop & Trendall, 1966; Johnson, Kelts, & Odada,
54 2000; Lehman, 2009; Tryon et al., 2016). Additionally, human activities have exerted multifactorial
55 pressures on freshwater environments in the ecoregion over recent decades, through habitat
56 degradation, pollution, exploitation, the introduction of invasive species, ecosystem modifications and
57 climate change (Hecky, Mugidde, Ramlal, Talbot, & Kling, 2010; Johnson et al., 2000; Sayer, Máiz-
58 Tomé, & Darwall, 2018; Verschuren et al., 2002). As such, understanding diversification dynamics in
59 freshwater biota within the Lake Victoria ecoregion requires insight into the consequences of recent
60 and historic environmental change. The interplay of environment and diversification dynamics have
61 been canvassed for the remarkable evolutionary radiation of cichlid fishes in Lake Victoria while
62 addressing how the lake accumulated hundreds of endemic species despite having been dry ~15 ka
63 ago (Fryer, 2001, 2004; Johnson et al., 1996; Stager, Day, & Santini, 2004; Stager & Johnson, 2008;
64 Verheyen, Salzburger, Snoeks, & Meyer, 2003). Apart from cichlids and the schistosome-transmitting
65 snail genus *Biomphalaria* (Standley, Goodacre, Wade, & Stothard, 2014), the seemingly controversial
66 interplay between environment and diversity in the Lake Victoria ecoregion has not generated detailed
67 phylogeographic and demographic studies of freshwater taxa. This knowledge gap implies that the
68 effects of ecosystem changes on the community composition and demography of benthic organisms
69 remain poorly assessed, and that the effectiveness of currently implemented strategies for managing
70 fisheries and sustaining biodiversity is unstudied.

71 Beyond cichlids, several other freshwater organisms display elevated diversity throughout the Lake
72 Victoria ecoregion (Sayer et al., 2018), such as viviparid gastropods. Viviparidae has been proposed

73 to be particularly useful in reconstructing phylogeographic patterns due to poor dispersal in the absence
74 of hydrographic connections (Schultheiß, Van Bocxlaer, Riedel, von Rintelen, & Albrecht, 2014;
75 Stelbrink et al., 2020), and they are an important component of benthic ecosystems in general (Strong,
76 Gargominy, Ponder, & Bouchet, 2008; Van Bocxlaer & Strong, 2020), as illustrated in the Lake
77 Victoria ecoregion (Brown, 1994; Mandahl-Barth, 1954). The family has been studied on a rift-wide
78 scale at several occasions (Schultheiß et al., 2014; Schultheiß, Wilke, Jørgensen, & Albrecht, 2011;
79 Sengupta, Kristensen, Madsen, & Jørgensen, 2009), resulting in good knowledge on the
80 phylogeographic connectivity of drainage basins throughout the East African Rift. In contrast, the
81 relationships within clades occupying individual drainage basins remain largely unresolved in existing
82 phylogenetic analyses (Schultheiß et al., 2014; Sengupta et al., 2009). The observed polyphyly in
83 regional morphospecies and races may result from incomplete lineage sorting, from independent
84 recurrent mutations, or adaptive introgression between distant gene pools (Lee & Coop, 2017).
85 Studies of genetic diversity at the population level are thus required to obtain insight into regional
86 patterns of diversity and to link environmental and evolutionary history.

87 Here we study the population structure of the clade of *Bellamyia* gastropods that occupies the Lake
88 Victoria ecoregion, i.e. the ‘Victoria clade’ (Schultheiß et al., 2014), to relate past environmental
89 change with demography and diversification dynamics. *Bellamyia* is diploid, with separate sexes,
90 internal fertilization and ovovivipary (Van Bocxlaer & Strong, 2020), and the Victoria clade contains 13
91 geographical races, which have been grouped into 7 nominal species, 5 of which are endemic to Lake
92 Victoria (Brown, 1994; Mandahl-Barth, 1954). To examine the geographical structure of diversity we
93 first performed a network analysis using a fast evolving mitochondrial marker and increased
94 sampling. Subsequently, we used microsatellites to document how genetic diversity in Viviparidae of
95 the Lake Victoria ecoregion is structured in space and time. In light of the previous description of
96 geographical races and lake endemics, we hypothesized that the genetic diversity of viviparids in the
97 Lake Victoria ecoregion is geographically structured. Given the high morphological disparity and
98 elevated nominal species diversity in Lake Victoria, we hypothesized higher genetic diversity within
99 this lake and barriers to gene flow that reflect habitat divergence. Additionally, we used approximate
100 Bayesian computation (ABC) to test the hypothesis that individual gene pools of these benthic

101 gastropods experienced a population bottleneck during the Last Glacial Maximum (LGM), as did
102 cichlids (Elmer et al., 2009).

103

104 **Material and Methods**

105 **Sampling.** Material was collected in 2008-2010 throughout the Lake Victoria ecoregion by CA and
106 colleagues (Fig. 1), and was deposited in the Systematics and Biodiversity collection of the Justus
107 Liebig University Giessen (UGSB). For the network analysis we used sequence data on cytochrome *c*
108 oxidase subunit 1 (COI) from 60 specimens: one from Jørgensen, Kristensen, and Madsen (2008), 22
109 from Sengupta et al. (2009), 4 from Schultheiß et al. (2011), 16 from Schultheiß et al. (2014) and 17
110 sequences were newly generated (Fig. 1). Specimen information, including UGSB and NCBI
111 GenBank accession numbers, is provided in Table S1. Our microsatellite dataset consists in total of
112 321 individuals from 39 localities at Lake Victoria, its tributaries, the Victoria Nile, Lake Kyoga,
113 Lake Albert and the White Nile (Fig. 1). Specimen information is supplied in Table S2. Note that
114 *Bellamyia* is absent from three other large lakes in this ecoregion, i.e. Lakes George, Edward and Kivu
115 (Brown, 1994). Because we recovered few *Bellamyia* individuals at some of the sampling localities,
116 we pooled localities with small samples sizes within a 5-km radius into a regrouped dataset (282
117 specimens from 21 populations with ≥ 10 individuals per population) from which some isolated,
118 poorly-sampled localities were discarded. Depending on analytical requirements, we analysed the
119 total or regrouped dataset for a robust characterisation of patterns of genetic variation within and
120 between sampling localities. Regrouping did not alter the overall results and interpretation of our
121 analyses compared to analyses of the total dataset.

122

123 **Morphological identifications.** Morphological identifications to race and morphospecies were
124 performed with the identification key of Mandahl-Barth (1954), information in Brown (1994) and by
125 evaluating type specimens. All *Bellamyia* species and races currently recognized in the Lake Victoria
126 ecoregion (Brown, 1994; Mandahl-Barth, 1954) are represented in our dataset (see SI Text).
127 Construction of the regrouped dataset did not result in the exclusion of races or morphospecies, but
128 implied that the rare *B. phthinotropis* is only represented by three specimens. Morphological

129 identifications were used to interpret patterns of genetic diversity, but not as an input variable to guide
130 molecular data analyses.

131

132 **COI data collection and analysis.** We extracted genomic DNA following the protocol of Schultheiß
133 et al. (2014). We used the forward primer LCO1490 (Folmer, Black, Hoeh, Lutz, & Vrijenhoek,
134 1994) and the reverse primer COX-B7R (Schultheiß et al., 2011) for PCR amplification. The PCR
135 conditions were an initial denaturation step at 95 °C for 60 s, followed by 29 amplification cycles
136 (denaturation at 95 °C for 30 s, annealing at 52 °C for 30 s and elongation at 72 °C for 30 s) and a
137 final extension step at 72 °C for 180 s. Sequencing was performed on an ABI3730XL sequencer at
138 LGC Genomics (Berlin, Germany). The first base pairs following the 3' end of each primer were
139 difficult to read and therefore trimmed, leaving a 593 bp fragment. The sequences were unambiguously
140 aligned with ClustalW (Thompson, Higgins, & Gibson, 1994) in BioEdit v. 7.2.5 (Hall, 1999) and
141 visually inspected. We constructed a haplotype network using this alignment and an infinite site
142 model with functions from the package PEGAS v. 0.12 (Paradis, 2010) in the statistical environment R
143 v. 3.6.1 (R Core Team, 2019).

144

145 **Microsatellite data collection.** The here analysed microsatellite loci have previously been described
146 by Clewing et al. (2013). Genomic DNA was extracted, amplified and genotyped as outlined in
147 Clewing et al. (2013). In summary, PCR reactions were performed separately for each locus, and loci
148 were subsequently pooled in four groups depending on the expected fragment length and fluorescent
149 dyes used (pool 1: Bel_L10, Bel_L13, Bel_L15, Bel_L53, Bel_L25; pool 2: Bel_L18, Bel_L23,
150 Bel_L50; pool 3: Bel_L45, Bel_L47, Bel_L63; pool 4: Bel_L16, Bel_L31, Bel_L32, Bel_L48,
151 Bel_L56). These pools were sent to LGC Genomics for precision electrophoresis on a 16-capillary
152 3130xl Genetic Analyzer (Applied Biosystems). Genotypes were called by CC using GeneMarker® v.
153 1.85 (SoftGenetics LLC). First, chromatograms were visually inspected and custom panels of allele
154 sizes per locus were created with prior knowledge on the length of repeat motives for each locus.
155 Subsequently, the software automatically called genotypes based on the created panels. Allele calls
156 that did not correspond to the associated panel were verified manually. For two markers, Bel_L18 and

157 Bel_L56, chromatograms were sometimes difficult to read or occasionally included more than two
158 alleles, so these loci were excluded. Finally, individuals for which allele profiles were difficult to read
159 were excluded from the dataset. All automated genotype calls were verified manually by CC and a
160 subset of 15 % of individuals were genotyped twice, but as no inconsistencies occurred, we
161 considered our genotype calling robust for subsequent analyses. Size data for each of the 321
162 specimens and each of the 15 microsatellite loci was tabulated for subsequent analyses. All data and
163 analytical scripts have been uploaded to the Dryad Data Repository and are available via
164 <https://doi.org/10.5061/dryad.q83bk3jg2> (Van Boclaer et al., 2020).

165

166 **Examination of genetic variation within populations.** We examined the 15 microsatellites for the
167 presence of null alleles with the ApparentNulls method of the R package GENEPOP v.1.1.3 (Rousset,
168 2008) using the weighted average over all populations in the total and regrouped datasets. Subsequent
169 analyses were performed both including and excluding loci with null alleles. We studied genetic
170 variation within populations from the regrouped dataset. Genotypic linkage disequilibrium was
171 documented pairwise for all possible pairs of loci with a log-likelihood ratio test as implemented in
172 FSTAT v. 2.9.3.2 (Goudet, 2002). Significance was examined at a nominal level of $\alpha = 0.05$ and p -
173 values were corrected for multiple tests using the false discovery rate (FDR; Benjamini & Hochberg,
174 1995). Subsequently, we estimated genetic variation for the microsatellite loci by examining the
175 number of alleles, allelic richness, the observed and expected heterozygosity, and mean fixation
176 indices (F_{IS} , F_{IT} , F_{ST}) in FSTAT and the R package HIERFSTAT v. 0.04-22 (Goudet & Jombart, 2015).
177 Fixation indices were calculated following Weir and Cockerham (1984). The significance of
178 departures from zero for F_{IS} , F_{IT} , F_{ST} were examined in FSTAT with 1000 randomizations of alleles
179 within populations, alleles among populations, and individuals among populations, respectively.
180 Subsequently, we tested whether our loci are in Hardy-Weinberg equilibrium with χ^2 tests and exact
181 tests based on 1000 Monte Carlo permutations of alleles following Guo and Thompson (1992) with
182 functions from PEGAS. Genetic diversity was also examined per sampling locality using SPAGeDi
183 1.5a (Hardy & Vekemans, 2002) and HIERFSTAT.

184

185 **Spatial patterns of genetic structure.** Spatial patterns of molecular differentiation were identified
186 from the total dataset in three different ways. First, we subjected the centered matrix of genotypes to
187 principal component analysis (PCA) with the function ‘indpca’ of HIERFSTAT. The coordinates for all
188 individuals on PC1 and PC2 were then subjected to model-based clustering using Gaussian mixture
189 models with functions of the R package MCLUST v. 5.4 (Scrucca, Fop, Murphy, & Raftery, 2016).
190 MCLUST uses various models of variance-covariance structure to fit clusters to the data without *a*
191 *priori* assumptions of group entities. The model-fit for the various models is subsequently evaluated
192 with a Bayesian Information Criterion (BIC). Second, we performed Bayesian clustering analyses in
193 STRUCTURE v. 2.3.4 (Pritchard, Stephens, & Donnelly, 2000), using an admixture model with
194 correlated allele frequencies. Analyses were conducted for $K = 1-20$ with 30 independent runs per K .
195 Each Markov chain ran for 5 000 000 iterations with a burn-in of 200 000 iterations. The underlying
196 genetic structure was examined with the ΔK statistic (Evanno, Regnaut, & Goudet, 2005) in
197 CLUMPAK (Kopelman, Mayzel, Jakobsson, Rosenberg, & Mayrose, 2015). Finally, we performed a
198 discriminant analysis of principal components (DAPC) using the R package ADEGENET v. 2.1.1
199 (Jombart, 2008). We first evaluated the number of groups present in our dataset from the output of K -
200 means clustering with a BIC and subsequently performed DAPC on scenarios retained from the
201 clustering output. The results of DAPC were subsequently evaluated by examining the assignment
202 probability of individuals to molecular groups.

203 Subsequently, we documented the proportions of shared and private alleles for the obtained molecular
204 groups, i.e. gene pools, using the R package POPPR v. 2.8.1 (Kamvar, Tabima, & Grünwald, 2014)
205 and the regrouped dataset. Because substantial differences existed in the number of individuals per
206 molecular cluster, we resampled each molecular cluster to the smallest sample size with 1,000
207 replicates and tested for differences in the number of private alleles with a Kruskal-Wallis test
208 followed by FDR-corrected pairwise Wilcoxon rank sum tests. Recent migration rates among
209 populations in the regrouped dataset were assessed in BayesAss (Wilson & Rannala, 2003) from three
210 independent runs of 20,000,000 Markov chain Monte Carlo iterations with default mixing parameters,
211 a burn-in of 5,000,000 iterations and sampling every 10,000 iterations. We verified that the runs
212 achieved stationary and that the variance among runs was low.

213 Finally, we examined the processes underlying geographical differentiation in the regrouped dataset
214 by estimating the pairwise relatedness between individuals with a kinship coefficient, F_{ij} , in
215 SPAGeDi. Kinship coefficients were regressed on the spatial distances among sampling localities in
216 SPAGeDi, first for all localities together, and then for relevant subsets. This method is similar to
217 regressing F_{ST} [or $F_{ST}/(1 - F_{ST})$] on spatial distances, with the difference that kinship coefficients can
218 be established pairwise between individuals (used here) as well as between populations (see Fenster,
219 Vekemans, & Hardy, 2003; Van Bocxlaer, 2017). Summary statistics are based on tests with 1000
220 permutations and jackknife procedures. Because *Bellamyia* disperses very poorly in the absence of
221 hydrographic connections (e.g. Schultheiß et al., 2014; Van Bocxlaer, Verschuren, Schettler, &
222 Kröpelin, 2011) the distances between sampling localities were measured manually in Google Earth
223 Pro v. 7.3.2.5776 as the shortest path of dispersal along the hydrographic network.

224

225 **Examination of demographic history.** All analyses of demographic history were performed with the
226 regrouped dataset and ABC as implemented in the program DIYABC v.2.1.0 (Cornuet et al., 2014).
227 Because null alleles are treated as missing data in DIYABC, demographic analyses included all 15
228 loci. First, we examined the extent to which five anagenetic scenarios of demographic changes in N_e
229 were able to reproduce the patterns of genetic polymorphism observed in the empirical dataset (Fig.
230 2). Model 1) simulates constant N_e , 2) an increase in N_e , 3) a decline in N_e , 4) a bottleneck, and 5)
231 population increase followed by decline. The priors for each parameter of N_e were set as a uniform
232 distribution from 1 to 10,000,000 and for time parameters between 10 and 500,000 generations [with
233 1 generation \approx 1 year for *Bellamyia* (Brown, 1994)]; additional constraints are indicated in Fig. 2.
234 Subsequently, we designed cladogenetic models with all possible scenarios of hypothesized
235 phylogenetic relationships between the recognized molecular groups, and three demographic models
236 of changes in N_e upon divergence (Fig. S1): 1) divergence with constant N_e (3 time parameters, 1
237 parameters of N_e), 2) divergence with changing N_e upon each lineage split (3 time parameters, 5
238 parameters of N_e), and 3) divergence similar to 2) but allowing additional change in N_e along the
239 longest branch (4 time parameters, 6 parameters of N_e). These models were implemented with the
240 same priors as the anagenetic models and with additional constraints on the timing of population

241 splits: $t_2 > t_1$ and $t_2 > t_{1b}$. Change in N_e was unconstrained, so that increases or decreases were possible
242 as time progressed. All calculation with DIYABC were implemented with the Generalized Stepwise
243 Mutation model (Estoup, Jarne, & Cornuet, 2002), with the default parameters for microsatellite loci.
244 For each model 1 million data sets were simulated and subsequently compared to our empirical data
245 using 4 and 36 default summary statistics for anagenetic and cladogenetic simulations, respectively.
246 Parameters were estimated for retained models from the posterior distribution of raw parameter values
247 using the 1 000 ABC simulations that approximated the observed data best.

248 Some migration among gene pools was inferred in our analyses and, because the resulting gene flow
249 could lead to inferential bias (see e.g. Heller, Chikhi, & Siegmund, 2013), we examined its potential
250 effect on our ABC inferences in two ways. Because DIYABC cannot currently account for migration,
251 we first repeated our analyses excluding specimens that showed signs of admixture, i.e. those with an
252 assignment probability to their gene pool of <80% such as F_1 , F_2 or backcross hybrids. This strategy
253 allows estimating the influence of migration from distant gene pools on ABC inferences. Second, we
254 evaluated the effect of migration on our model comparisons by using a slightly different ABC
255 approach that can account for migration. Specifically, we simulated datasets for three demographic
256 scenarios (constant, declining and increasing population size, respectively) and 11 rates of migration
257 into the studied population (0-10 migrants per generation). For each combination of demographic
258 scenarios and migration rates ($n = 33$), we simulated 1 000 datasets with a coalescent simulator
259 (Hudson, 2002), after which we used ABC to document the relative support for each demographic
260 scenario under all 33 combinations. Population size was randomly drawn from a uniform distribution
261 between 100 and 5,000,000 diploids; the start of population decline or increase was randomly drawn
262 from a uniform distribution between 100 and 500,000 generations; for population decline model the
263 current population was randomly drawn from a uniform distribution between 0.0 and $0.5 \times$ the
264 ancestral N_e ; for population increase model the ancestral population was randomly drawn from a
265 uniform distribution between 0.0 and $0.5 \times$ the current N_e . Each simulated dataset consisted of 500
266 sampled loci for each of 10 individuals, for which we calculated the following summary statistics:
267 number of SNPs, diversity measured as π (Tajima, 1983), Watterson's θ (Watterson, 1975), Tajima's
268 D (Tajima, 1989), and the number of SNPs in each category describing the site frequency spectrum.

269 Model comparison was performed by first training a random forest from 20 000 simulations without
270 migration (RF; Pudlo et al., 2016) for each of the demographic models. This ABC RF is composed of
271 1 000 trained trees per demographic scenario and was used to estimate which of the demographic
272 scenarios was best supported for each of the 33,000 simulated datasets.

273

274 **Results**

275 **Haplotype network analysis.** Our COI dataset contained 52 haplotypes and like previous
276 phylogenetic studies (Schultheiß et al., 2014; Sengupta et al., 2009), our network analysis did not
277 reveal geographic structure in the haplotype diversity of *Bellamyia* from the Lake Victoria ecoregion
278 (Fig. S2).

279

280 **Linkage disequilibrium and genetic diversity.** The total and regrouped datasets display low null
281 allele frequencies ($\leq 5.0\%$) except for two of our 15 microsatellite loci, i.e. Bel_L50 and Bel_L45 (7.5
282 and 14.7 %, respectively). We removed these two loci from the dataset for the analyses reported
283 below (except for demographic analyses, which were performed with 15 loci as mentioned above),
284 although frequencies up to 8 % bias population genetic estimators only slightly (Putman & Carbone,
285 2014), and analyses with all 15 loci gave highly similar results. All analyses of genetic diversity have
286 thus been performed with the regrouped dataset and 13 loci. Examining pairwise linkage among our
287 loci did not reveal evidence for linkage disequilibrium, therewith enabling downstream demographic
288 inferences that assume independence among loci.

289 Our dataset contains substantial allelic richness and genetic diversity (Table S3). Three loci display a
290 deficit of heterozygotes (Bel_L23, Bel_L25 and Bel_L47; Table S3) and significant deviations from
291 Hardy-Weinberg equilibrium were observed for all but two loci (Bel_L13 and Bel_L53; Table S4),
292 implying the existence of population structure. Summary statistics of genetic diversity per sampling
293 locality in the regrouped dataset are illustrated in Table S5 and Fig. S3. We found significantly higher
294 allelic richness and genetic diversity in Lake Victoria ($A_r = 6.962$ among 14 gene copies; $H_E = 0.822$)
295 than in other waterbodies ($A_r = 6.068$; $H_E = 0.761$; Wilcoxon rank sum tests: A_r : $W = 82$, $p = 0.004$;
296 H_E : $W = 88.5$, $p < 0.001$; Fig. S3). Substantial differentiation exists among populations (global $F_{ST} =$

297 0.064, 95% CI = 0.048-0.082). Pairwise population differentiation ranges between $F_{ST} = 0.005$ and
298 0.150, and all but 9 of the 210 pairwise tests indicate significant differentiation after FDR-correction
299 (Fig. S4).

300

301 **Spatial patterns of genetic structure.** PCA on the centered matrix of genotypes followed by model-
302 based clustering with 14 models on the variance-covariance structure in the PCA revealed strong
303 support for three gene pools (Fig. 3A). Solutions with a different number of groups received much
304 less support ($\Delta BIC \geq 21.024$; Fig. 3B). Bayesian clustering with STRUCTURE and examination of
305 the ΔK statistic supported two to three genetic clusters (Fig. 3C). Analysis of molecular structure with
306 DAPC produced a four-group model, but with limited preference over models with three or five
307 groups ($\Delta BIC < 2.03$; Fig. S5). Overall assignment probabilities decreased substantially when more
308 than three groups were considered, however (99.7 %, 82.6 % and 68.5 % for models with three, four
309 and five groups, respectively), so that the three group DAPC model is considered most representative,
310 despite its slightly higher BIC score. In summary, our analyses of molecular structure jointly indicate
311 a three-group model, which is moreover corroborated by high population pairwise differentiation
312 among gene pools versus low differentiation within (Fig. S4; see below). These three groups display a
313 clear geographical pattern: 1) sampling localities in Lake Albert and the White Nile, 2) those in Lake
314 Kyoga and the Victoria Nile, and 3) those of Lake Victoria, with its tributaries, including Lake
315 Muhazi in Rwanda, and localities directly at the outflow of Lake Victoria into the upper Victoria Nile,
316 i.e. VN01 (Fig. 4). In what follows we label these gene pools as LAG, LKG, LVG, respectively, after
317 the principal lake in each group.

318 Pairwise F_{ST} values between LAG and LVG, between LVG and LKG, and between LAG and LKG
319 are 0.084, 0.078 and 0.108, respectively (regrouped dataset; all at $p < 0.001$). Beyond a higher allelic
320 richness and genetic diversity (see above), LVG has more private alleles than LAG and LKG, even
321 when resampled to identical sampling sizes (Kruskal-Wallis test; $\chi^2 = 2430.9$, $df = 2$, $p < 0.001$; Table
322 S6, Fig. S6). The molecular clusters reflect morphospecies and geographical races to some extent
323 (Fig. 3, 5): all individuals identified as *B. rubicunda* and most identified as *B. unicolor unicolor*
324 belong to LAG ($n = 41$), whereas LKG ($n = 29$) consists almost exclusively of *B. costulata ugandae*.

325 The most genetically diverse group, LVG ($n=212$), also displayed the highest morphological disparity
326 (11 races/morphospecies), but these races/morphospecies do not coincide with genetically distinct
327 subgroups within LVG (Fig. 3C, D, 5).
328 Overall, we found strong isolation-by-distance (IBD), i.e. a significant negative correlation between
329 kinship coefficients and geographic distances ($r^2 = 0.916$; $p < 0.001$; Fig. 6A), in *Bellamyia* throughout
330 the Lake Victoria ecoregion. There is no IBD within LVG (Fig. 6B; 16 localities) and 113 of the 120
331 related F_{ST} values range between 0.00 and 0.05 (Fig. S4), revealing that overall limited genetic
332 differentiation exists within LVG. Nevertheless, kinship coefficients within LVG are elevated at very
333 small spatial scales compared to those at intermediate and large spatial scales (Fig. 6B). Recent
334 migration rates estimated with BayesAss are low among gene pools: the fraction of individuals in a
335 population that are inferred to be migrants from a population of another gene pool is usually $\leq 1.1\%$.
336 Migration within each of the gene pools is elevated among at least some population pairs, however
337 ($>10\%$; Table S7).

338

339 **Demographic modelling indicates population collapse.** Using anagenetic ABC models and the
340 regrouped dataset we found that models simulating population decline (i.e. models 3 and 5 in Fig. 2)
341 obtained high support for all three gene pools (joint posterior probability of 76.1-86.3 %; Table 1).
342 Model 5, a past population expansion followed by population decline, consistently obtained the
343 highest support for all three gene pools. Model 3 also consistently received substantial support and
344 differs from model 5 by simulating a population at equilibrium, rather than under expansion, prior to
345 the subsequent decline. These two models are difficult to distinguish because the ongoing decline is
346 erasing the genetic signature of previous demographic events. The support for models of constant
347 effective population size (N_e) was much smaller (13.3 – 21.5 %), whereas models that include a
348 recent population expansion have very limited explanatory power (0.1 – 2.4 %). LKG experienced the
349 strongest population decline, with a ~ 500 -fold reduction in N_e over the last ~ 102 ka (95% CI: 10-387
350 ka; Table 2). Nevertheless, LAG and LVG also endured 240-fold and 190-fold declines in N_e ,
351 respectively, over the same period (LAG: 140 ka, 95% CI: 18-426 ka; LVG: 173 ka, 95% CI: 26-452
352 ka). In simulations of model 5 the average value of t_2 , the onset of population expansion, was ~ 300 ka

353 (95% CI: 70-490 ka) for each molecular group. At that time, expansions in N_e were about 2-fold for
354 each molecular group, and, hence, much more restricted than the subsequent population collapses.
355 None of the cladogenetic models tested with ABC (Fig. S2) fitted the empirical data well, so we do
356 not consider them further. In summary, the three gene pools display very similar demographic
357 histories indicating a tight link since differentiation from their most recent common ancestor
358 (MRAC). Their current population sizes represent only 0.2-0.6 % of those prior to ~125-150 ka ago.
359 Some migration among gene pools occurs in our dataset (Table S7), which warranted an analysis of
360 how the resulting gene flow may affect our ABC analyses. Specimens indicating admixture among
361 gene pools were found in LAG ($n = 1$) and LVG ($n = 16$; regrouped dataset) but not in LKG. Model
362 support remains very similar when these specimens are removed (Table S8), and also our estimates of
363 model parameters are robust (Table S9). Running ABC on simulated datasets without migration, 99.8
364 %, 99.1 % and 99.2 % of simulations were assigned correctly to the models of population decline,
365 population increase and a constant population size (Fig. S7). Including progressively increasing levels
366 of migration, the demographic history of populations with declining and increasing N_e remained
367 accurately reconstructed (correct assignment >97 %; Fig. S7A, B). Migration into populations at
368 equilibrium size resulted in ~17 % of correct assignment only, with bias in the ABC inferences
369 towards strongly inflated support for the population expansion model (~83 %; Fig. S7C). This bias
370 results from migration causing long branches in the coalescent model, which mimics the expected
371 coalescence under an expansion model. In conclusion, the model of population decline is not affected
372 by migration nor did migration cause erroneous support for population decline under models of
373 population increase and equilibrium. As such, our analysis of robustness indicates that the ABC
374 support obtained for population decline cannot be attributed to bias caused by gene flow from distant
375 gene pools.

376

377 **Discussion**

378 Our results indicate that three, geographically-structured gene pools exist in *Bellamyia* gastropods of
379 the Lake Victoria ecoregion, with the highest genetic diversity in LVG. We did not uncover barriers
380 to gene flow within gene pools that reflect habitat divergence, which is surprising for LVG, given the

381 recognition of several endemic species (Brown, 1994; Mandahl-Barth, 1954). Our study presents the
382 first examination of demographic history of freshwater invertebrates from the Lake Victoria ecoregion
383 with ABC and it evidences population collapse, which started before the Last Glacial Maximum.
384 Declines in viviparids are much more severe than in co-occurring haplochromine cichlids (Elmer et
385 al., 2009), they have started earlier and they are evidenced in all studied gene pools. Whereas
386 population collapse was initiated by historical environmental change, it appears to be intensified by
387 ongoing anthropogenic ecosystem change. Below we discuss all these aspects in the ecological
388 context of environmental change in the Lake Victoria ecoregion.

389

390 **Spatial patterns of genetic structure.** Our microsatellite dataset is the first to document three gene
391 pools in viviparid gastropods of the Lake Victoria ecoregion, which occupy distinct geographic
392 regions (see Fig. 4). Specimens of these gene pools had been included in rift-wide phylogenetic
393 analyses based on 6 nuclear and mitochondrial gene fragments (Schultheiß et al., 2014; Sengupta et
394 al., 2009), but these studies and our analysis of COI haplotypes (Fig. S2) did not uncover spatial
395 patterns of genetic structure. Our data suggest that a few critical barriers have driven dispersal
396 limitations. The main transition between LKG and LVG occurs ~20 km downstream of the outflow of
397 Lake Victoria, between sampling localities VN01 and VN02, which are historically separated by a
398 series of cascades, rapids and now also the Bujagali Hydropower Plant. Likewise, LAG and LKG are
399 separated by a series of rapids that includes the Karuma and Murchison Falls, which also prevent fish
400 migration (Hecky et al., 2010). Interestingly, all three gene pools contain substantial genetic diversity,
401 including private alleles, although during the LGM, Lake Victoria was dry (Johnson et al., 2000;
402 Johnson et al., 1996), Lake Albert experienced several low stands and potential desiccation (Beuning,
403 Talbot, & Kelts, 1997), and the Victoria Nile became a permanent overflow of Lake Victoria only
404 ~11.2 ka (Johnson et al., 2000).

405

406 **Putative erosion of adaptive divergence.** Genetic differentiation between the inferred viviparid gene
407 pools seems to have been caused mainly by dispersal limitation but, given the consistent
408 morphological differences among these gene pools, adaptive divergence may also have contributed

409 (Fig. 5). Adaptive divergence was previously only inferred within LVG, where morphological
410 disparity is largest (Fig. 3D). Indeed, morphological differentiation within LVG has been interpreted
411 as the result of ecological divergence related to different microhabitats within Lake Victoria (Brown,
412 1994; Mandahl-Barth, 1954), so that the Lake Victoria viviparids represent an evolutionary radiation
413 (Schultheiß et al., 2014; Sengupta et al., 2009). Therefore, we anticipated that our neutral genetic
414 markers would uncover clear traces of molecular divergence among morphospecies within LVG,
415 which was not the case despite high molecular diversity and morphological disparity. Nevertheless,
416 112 out of 120 pairwise population F_{ST} values (~93 %) within LVG indicate limited albeit significant
417 genetic differentiation. As such, subtle genetic differences exist in LVG, but they have not been
418 picked up in our analyses of genetic structure. Interestingly, our sampling indicates that many of the
419 morphospecies that were previously confined to different microhabitats within Lake Victoria currently
420 occur in sympatry (Table S2, S5). This observation and the result that kinship coefficients within
421 LVG are elevated at very small spatial scales (Fig. 6B) strongly suggest that gene flow occurs among
422 sympatric morphospecies. To examine this hypothesis, we compared individual inbreeding
423 coefficients for localities of LVG that contained one versus multiple morphospecies, which resulted in
424 no significant differences ($F_i = 0.026 \pm 0.048$ vs. 0.030 ± 0.041 [mean \pm sd], respectively; Wilcoxon
425 rank sum tests: $W = 32.5$, $p = 0.958$). Our data suggest that the anthropogenic homogenization of
426 previously differentiated microhabitats (Sayer et al., 2018) is promoting gene flow among
427 morphospecies (see below), which may also explain the deficit in heterozygotes observed for three
428 loci. We would expect inbreeding to trigger similar patterns of heterozygosity across loci, however,
429 and the uneven occurrence of null alleles in a few populations for these three loci (although being
430 overall infrequent), may have contributed to heterozygote deficiency. Surprisingly, morphological
431 differences currently persist among morphospecies of LVG that occur in sympatry, that share recent
432 gene flow, and that are not molecularly differentiated for the here studied loci. Ecophenotypic
433 plasticity is contradicted by regular sympatric co-occurrence and the observed morphological
434 disparity exceeds that expected under such plasticity (see Van Bocxlaer, Van Damme, & Feibel,
435 2008). If morphological differentiation indeed was adaptive then we would expect it to be linked to
436 regions of the genome that are/were under selection and where differentiation may persist in the face

437 of gene flow. If the size of such regions is restricted in comparison to that of the viviparid genome, we
438 would unlikely have sampled such regions with our microsatellite loci. More in-depth investigations
439 into the molecular diversity of the viviparids of Lake Victoria is warranted to further test this
440 hypothesis, which would best be undertaken with genome-wide, rapidly-evolving molecular markers
441 and samples that cover all shorelines of the lake (see e.g. Wagner et al., 2013).

442

443 **Comparison of phylogeography and demography with haplochromine cichlids.** The largest
444 intraspecific genetic differentiation in the mega-diverse species flock of haplochromine cichlids of the
445 Lake Victoria ecoregion occurs in Lake Kivu (Verheyen et al., 2003), from which other parts of the
446 ecoregion were subsequently colonized (Elmer et al., 2009; Nagl et al., 2000). Lake Kivu does not
447 harbor extant viviparid populations, and neither do Lakes Edward and George (Brown, 1994), but
448 otherwise phylogeographic patterns are highly similar in viviparids and cichlids. For example,
449 cichlids from tributaries of Lake Victoria are genetically more closely related to those of Lake
450 Victoria than to those of Lakes Albert and Kyoga (Elmer et al., 2009). Our results suggest that the
451 ancestral stock of viviparids from the Lake Victoria ecoregion either occurred in the geographic area
452 currently covered by LVG, or that it colonized this area well before colonizing the regions occupied
453 by LAG and LKG. The increase in viviparid N_e in ABC model 5 ~300 ka (95% CI 70-490 ka)
454 coincides broadly with the formation of the Lake Victoria Basin ~400 ka ago (Bishop & Trendall,
455 1966; Johnson et al., 2000; Lehman, 2009). That demographic expansion was only two-fold, which
456 indicates that large populations of *Bellamyia* were already existing in the ecoregion before the origin
457 of the Lake Victoria Basin. Indeed, the MRCA of the viviparids from the Lake Victoria ecoregion was
458 estimated to ~2.5 Ma (95% CI 1.5-4.3 Ma) (Schultheiß et al., 2014), which broadly overlaps with
459 estimates on the MRCA of the Lake Victoria haplochromines ~1.4 Ma (Nagl et al., 2000) or ~3.0 Ma
460 (95% CI 2.3-3.9 Ma; Elmer et al., 2009). As such, some genetic lineages of viviparids in the
461 ecoregion clearly predate the Late Pleistocene desiccation of Lake Victoria, which has, beyond
462 cichlids, also been reported for cyprinid fish (Rutaisire, Booth, Masembe, Nyakaana, & Muwanika,
463 2004), catfish (Mwita & Nkwengulila, 2008) and unionid bivalves (Ortiz-Sepulveda et al., 2020).
464 Furthermore, the current genetic differentiation, estimated as population pairwise F_{ST} values, is very

465 similar in viviparids (0.005-0.150) and cichlids (0.013-0.104; Elmer et al., 2009) of the Lake Victoria
466 ecoregion.

467 After formation of the basin, aquatic environments experienced three low stands, potentially related to
468 100,000-year glacial-interglacial cycles (Johnson et al., 2000). As mentioned, the last megadrought in
469 the Lake Victoria ecoregion occurred at the LGM ~18-15 ka and included a substantial interval during
470 which Lake Victoria, with a current surface area of almost 70,000 km², was completely desiccated.

471 Lake Albert experienced simultaneous low stands and potential desiccation, and the Victoria Nile was
472 only formed ~11.2 ka ago (Beuning et al., 1997; Johnson et al., 2000). Interestingly, none of the three
473 viviparid gene pools evidence a population expansion related to the re-establishment of aquatic
474 habitats in the Lake Victoria ecoregion after the LGM. Instead, our demographic modelling suggests
475 that the *N_e* of each of these viviparid gene pools remained relatively stable during recent ecosystem
476 calamities (Table 2). This diversity was potentially maintained in mountain-fed river systems along
477 the western branch of the East African Rift (Johnson et al., 2000). The penultimate phase of
478 megadrought in the Lake Victoria ecoregion transpired at the end of the last interglacial ~125 ka
479 (Tryon et al., 2016), and whereas the extent of aridity during this period is more uncertain in
480 comparison to the LGM (Johnson et al., 2000; Johnson et al., 1996), it corresponds broadly to the
481 onset of viviparid population decline estimated in our ABC simulations, suggesting at least a similar
482 level of aridity to that at the LGM.

483 Whereas we anticipated scenarios of early population expansion and subsequent decline to perform
484 well in simulations, based on earlier demographic studies of cichlids (Elmer et al., 2009), the early
485 onset of such decline and the magnitude of population collapse were unexpected. Indeed, the here
486 documented collapses in viviparids (Table 3) are an order of magnitude more severe than those
487 recorded in haplochromine cichlids (30- to 50- fold population declines), and they also started 100 ka
488 earlier (Elmer et al., 2009). Additionally, our evidence indicates that they affected all viviparid gene
489 pools in the Lake Victoria ecoregion simultaneously. Given the persistence and extent of population
490 collapses, it is likely that viviparid species have gone extinct in the Lake Victoria ecoregion over the
491 Late Pleistocene.

492 Paleoenvironmental studies in the Lake Victoria ecoregion focused primarily on the megadrought at
493 the LGM because it is geologically better constrained than previous phases of aridity (Johnson et al.,
494 1996), and because desiccation seemed counter-intuitive with cichlid evolution (Elmer et al., 2009;
495 Verheyen et al., 2003). Consequently, cichlid research addressing this seeming contradiction likewise
496 focused on the LGM, and responses in cichlid evolution to earlier ecological calamities may not have
497 been fully considered. The increase in haplotype diversity observed for haplochromines since the
498 penultimate phase of aridity ~125 ka (Nagl et al., 2000) suggests a simultaneous bottleneck for
499 cichlids and viviparids. The alternative explanation, i.e. that the LGM megadrought affected cichlids
500 more severely than viviparids, is unlikely given the limited dispersal abilities of viviparids compared
501 to cichlids. A search for genomic imprints of earlier megadroughts in other freshwater organisms
502 including other benthic invertebrates is warranted, especially because high-throughput sequencing
503 technology now allows the reconstruction of population history with unprecedented resolution.

504

505 **Recent ecological degradation.** The historical population decline in viviparid gastropods is
506 intensified by the ongoing ecological degradation resulting from multifactorial anthropogenic
507 pressures on freshwater ecosystems of the Lake Victoria ecoregion (Hecky et al., 2010; Sayer et al.,
508 2018; Van Damme, Seddon, & Carr, 2018). Indeed, as for cichlids (Elmer et al., 2009), no signs for a
509 potential recovery of allelic diversity have been observed in viviparids since the LGM. Algal blooms
510 and widespread bottom anoxia are becoming increasingly common in Lake Victoria (Hecky et al.,
511 1994; Stager & Johnson, 2008), which could result in a shoaling of gastropods (Christian Albrecht,
512 pers. obs.), as is occurring in Lakes Malawi and Tanganyika (Van Bocxlaer, Schultheiß, Plisnier, &
513 Albrecht, 2012). Viviparids were previously (19th and early 20th centuries) found to maximum depths
514 of 30 and 33 m in Lake Victoria (*B. trochlearis* and *B. phthinotropis*, respectively), and *B. rubicunda*
515 was recovered from a maximum depth of 18 m in Lake Albert (Brown, 1994; Mandahl-Barth, 1954).
516 In our surveys, no living *Bellamyia* specimens were retrieved from depths >6 m in Lake Albert. In
517 Lake Victoria *B. trochlearis* and *B. phthinotropis* were obtained from <15 m and usually in sympatry
518 with other *Bellamyia* species (see Table S5). At two localities living viviparids, i.e. *B. costulata*
519 *ugandae* and *B. unicolor meta*, which were previously reported up to depths of 10 and 12 m,

520 respectively, were collected between 15 and 23 m. Beyond mass mortality in fishes, as occasionally
521 reported (Ochumba, 1990), anoxia would asphyxiate large proportions of zoobenthos communities,
522 especially of taxa with low mobility such as viviparids. The toll of such events on mollusc populations
523 is evidenced by deposits of dead and moribund individuals along the shorelines of Lake Victoria (Van
524 Bocxlaer and Albrecht, pers. obs.). The consequences of ongoing degradation may differ among
525 shorelines, among the various habitats and among taxa. Some viviparid species, such as *B.*
526 *phthinotropis*, which was predominantly found in deeper waters (see above), are rare in recent surveys
527 and are reported to be critically endangered (Sayer et al., 2018).

528 The ongoing ecological degradation of Lake Victoria is homogenising environmental conditions
529 through the elimination of microhabitats, which may cause the reduction of endemic diversity in
530 various freshwater taxa through extinction and faunal homogenization (Sayer et al., 2018). Our data
531 indicate that habitat destruction has forced putatively differently adapted (incipient) viviparid species
532 to occupy increasingly more similar habitats, and that this renewed (ecological and geographical)
533 proximity is causing gene flow among them, which may erode genetic distinctiveness. Estimating the
534 extent to which reproductive barriers among viviparids have already been obliterated is currently
535 difficult, especially because it is unclear to what level such barriers existed prior to the onset of
536 ecological degradation and given the lack of dense genomic sampling. Nevertheless, reverse
537 speciation has previously been hypothesized for co-occurring cichlids (Seehausen, 2006), so
538 investigations as to how reproductive barriers have changed over time are warranted for other
539 freshwater biota in the Lake Victoria ecoregion. Our data suggests inbreeding among morphospecies
540 and therewith faunal homogenisation in aquatic invertebrates and we document the strongest
541 demographic collapse observed thus far in the Lake Victoria ecoregion. Given the current rate of
542 ecosystem change throughout the entire Lake Victoria ecoregion, and given the anticipated additional
543 anthropogenic pressure expected over coming decades (Sayer et al., 2018), further in-depth studies of
544 the viviparid species flock from Lake Victoria, and benthic invertebrate diversity in general, are
545 highly pressing. Indeed, understanding the consequences of ongoing, multifactorial ecosystem
546 transformations on freshwater communities will be critical for sustaining biodiversity and managing
547 fisheries in the Lake Victoria ecoregion over the coming decennia.

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756

757 **Data accessibility**

758 Various metadata are provided in Supplemental Information, including data on specimen vouchers
759 and NCBI GenBank accession numbers. All data files and the R script used for the analysis have been
760 deposited in the Dryad Data Repository and are available via
761 <https://doi.org/10.5061/dryad.q83bk3jg2>.

762

763 **Author contributions**

764 BVB and CA designed research; CA coordinated sampling; CC performed molecular biology; BVB,
765 AD and CR performed analyses; BVB wrote the paper, with help of all authors.

766

767 **Tables**

768 **Table 1.** Relative model support for the five anagenetic demographic models included in our ABC
769 simulations. Scenarios of effective population size through time for each of these models are
770 displayed in Fig. 2.

Group	Model 1	Model 2	Model 3	Model 4	Model 5	Model 3+5
Lake Albert Group	0.1468	0.0003	0.3591	0.0009	0.4930	0.8521
Lake Kyoga Group	0.1328	0.0000	0.3571	0.0041	0.5060	0.8631
Lake Victoria Group	0.2147	0.0030	0.3443	0.0214	0.4166	0.7609

771

772

773 **Table 2.** Estimates on the principal demographic parameters for the best supported ABC models. 95%
774 CI indicates the 95% confidence intervals. Given the high similarities in models 3 and 5, their
775 averaged outcome is presented under Model 3+5. N_e represents the number of diploid individuals in
776 the population and times t , t_1 and t_2 are expressed in number of generations [1 generation is \sim 1 year
777 for *Bellamyia* (Brown, 1994)].

	mean N_e	mode N_e	95% CI		mean t or t_1	mode t or t_1	95% CI		mean $N_{e_{big}}$	mode $N_{e_{big}}$	95% CI		mean t_2	mode t_2	mean $N_{e_{s_Anc}}$	mode $N_{e_{s_Anc}}$
Lake Albert Group																
Model 3	23 800	12 700	5 830	60 300	186 000	72 900	25 700	460 000	4.36×10^6	1.36×10^6	259 000	9.63×10^6	n.a.	n.a.	n.a.	n.a.
Model 5	19 800	9 220	4 840	51 400	98 600	51 600	15 000	308 000	6.06×10^6	8.60×10^6	1.12×10^6	9.82×10^6	291 000	323 000	2.81×10^6	503 000
Model 3+5	21 500	11 200	5 310	56 000	140 000	66 000	17 500	426 000	5.22×10^6	8.11×10^6	397 000	9.77×10^6	n.a.	n.a.	n.a.	n.a.
Lake Kyoga Group																
Model 3	9 860	4 080	2 210	27 100	116 000	28 500	11 000	411 000	4.26×10^6	2.49×10^6	239 000	9.58×10^6	n.a.	n.a.	n.a.	n.a.
Model 5	12 900	5 110	3 300	35 000	81 600	30 000	11 400	265 000	6.73×10^6	9.83×10^6	1.82×10^6	9.88×10^6	293 000	439 000	3.50×10^6	2.17×10^6
Model 3+5	11 700	5 570	2 750	32 700	102 000	40 700	9 690	387 000	5.58×10^6	7.75×10^6	484 000	9.82×10^6	n.a.	n.a.	n.a.	n.a.
Lake Victoria Group																
Model 3	27 800	12 800	6 800	72 900	213 000	85 000	35 900	470 000	4.19×10^6	1.50×10^6	158 000	9.63×10^6	n.a.	n.a.	n.a.	n.a.
Model 5	30 600	10 200	7 000	69 900	136 000	94 500	22 000	360 000	6.04×10^6	9.41×10^6	1.12×10^6	9.72×10^6	345 000	414 000	2.82×10^6	722 000
Model 3+5	27 000	11 700	6 870	70 000	173 000	78 300	25 500	452 000	5.18×10^6	8.95×10^6	348 000	9.71×10^6	n.a.	n.a.	n.a.	n.a.

778
779
780

781 **Figure captions**

782 **Figure 1.** Geographical context of this study with indication of the major lakes and sampling
783 localities (triangles for the COI dataset, circles for the microsatellite dataset). The Lake Victoria
784 ecoregion is demarcated. Lakes Albert and Kivu are currently considered to be part of the Upper Nile
785 and Lake Tanganyika ecoregions, respectively (see Abell et al., 2008), but their historic biogeography
786 is strongly connected with the Lake Victoria ecoregion. Therefore, we here consider them to be part
787 of the Lake Victoria ecoregion for practical reasons (dashed lines).
788

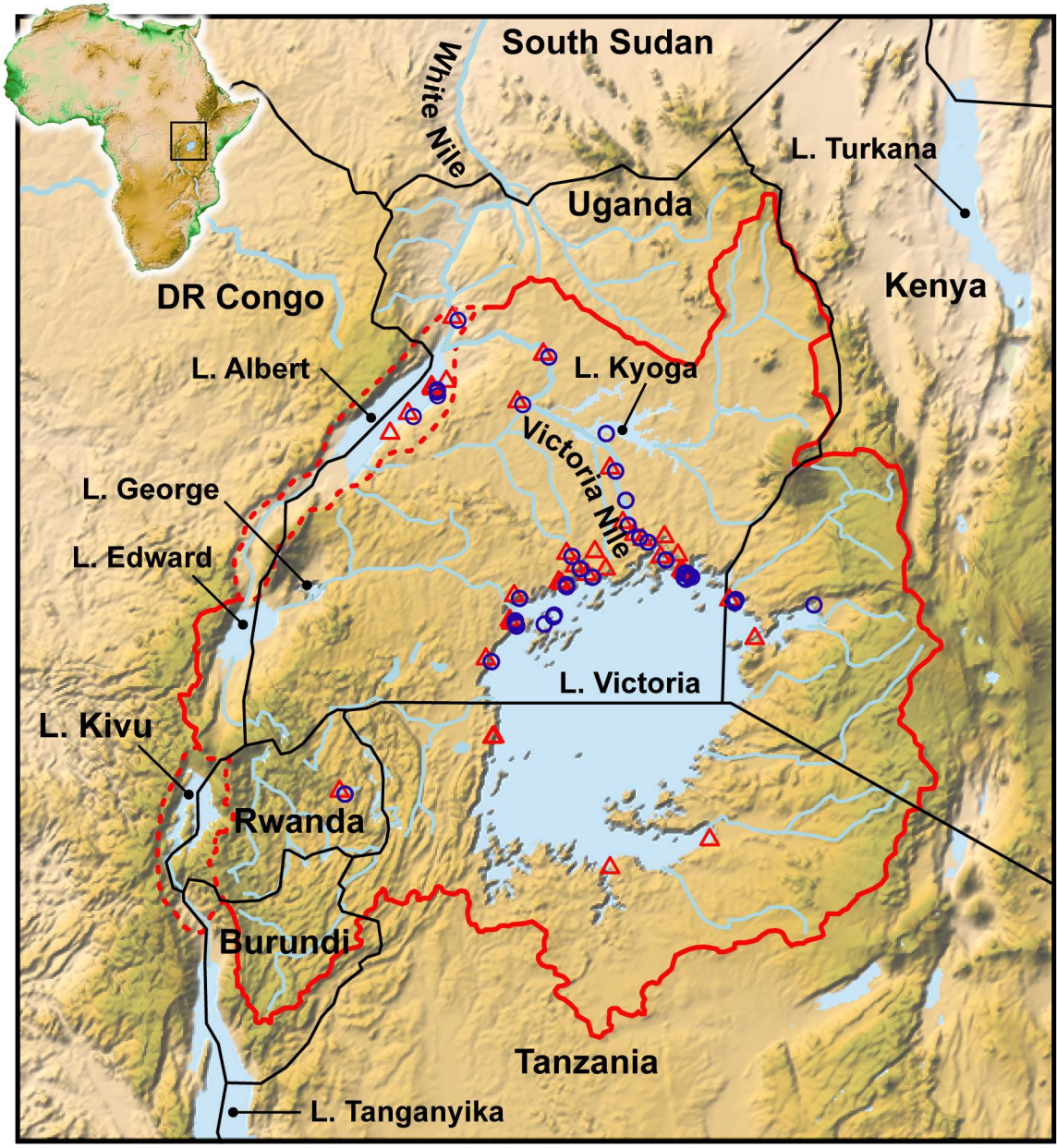
789 **Figure 2.** Five scenarios of anagenetic demographic change in effective population size (N_e) over
790 time (t), as implemented in approximate Bayesian computations. Scenario 1) indicates constant N_e ,
791 scenario 2) an expansion in N_e , scenario 3) a decline in N_e , scenario 4) a population bottleneck, and
792 scenario 5) population expansion followed by population decline. These scenarios are reflected in the
793 specified model conditions (see Methods).
794

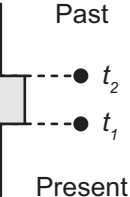
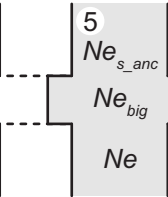
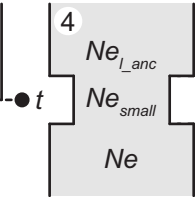
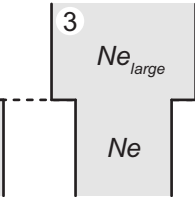
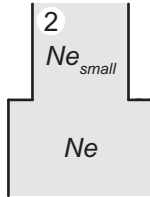
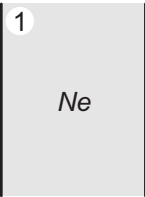
795 **Figure 3.** Structure of molecular diversity in *Bellamyia* from the Lake Victoria ecoregion. A) Principal
796 component analysis on the centered matrix of genotypes for the total dataset (39 populations; 321
797 individuals) with results of model-based clustering using 14 variance-covariance models (B; see
798 Methods). C) results of Bayesian clustering with STRUCTURE for $K = 2, 3$; the individuals of one
799 cluster that approach another cluster in A, correspond to the individuals that have mixed assignments
800 in C under scenario $K = 3$. D) the morphospecies belonging to each molecular group. LAG: *B.*
801 *unicolor unicolor* (a) and *B. rubicunda* (b); LKG: *B. costulata ugandae* (c) and *B. u. elatior* (d); LVG:
802 *B. c. ugandae* (e), *B. c. dagusiae* (f), *B. c. costulata* (g), *B. u. elatior* (h), *B. u. meta* (i), *B.*
803 *phthinotropis* (j), *B. jucunda altior* (k), *B. j. kisumiensis* (l), *B. j. jucunda* (m), *B. trochlearis* (n-p), *B.*
804 *constricta* (q).
805

806 **Figure 4.** Geographical distribution of sampling localities in the total dataset with pie charts
807 indicating the average assignment of individuals per sampling localities to the three gene pools
808 following the output of STRUCTURE.
809

810 **Figure 5.** Principal component analysis on the centered matrix of genotypes in our total dataset with
811 symbols indicating the race or morphospecies to which individuals have been assigned. Specimens
812 from LAG have been assigned to *B. rubicunda* and *B. unicolor unicolor*, whereas most specimens
813 from LKG were assigned to *B. costulata ugandae*. Most morphological disparity was found in LVG,
814 but these races/morphospecies do not coincide with genetically distinct subgroups (*B. c.* = *Bellamyia*
815 *costulata*, *B. j.* = *Bellamyia jucunda*, *B. u.* = *Bellamyia unicolor*).
816

817 **Figure 6.** Regression of kinship coefficients on geographic distance for the regrouped dataset
818 indicates a pattern of isolation-by-distance (IBD) over the entire ecoregion (A), but not for the Lake
819 Victoria group (LVG; 16 localities; B), although kinship coefficients are elevated over very short
820 geographical distances for LVG (blue vertical bar).





Conditions:

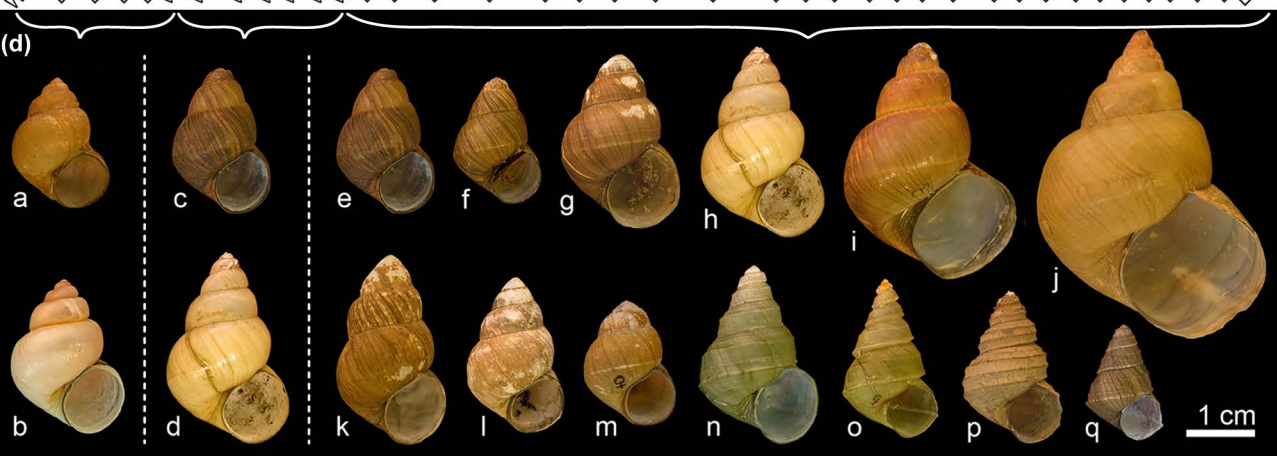
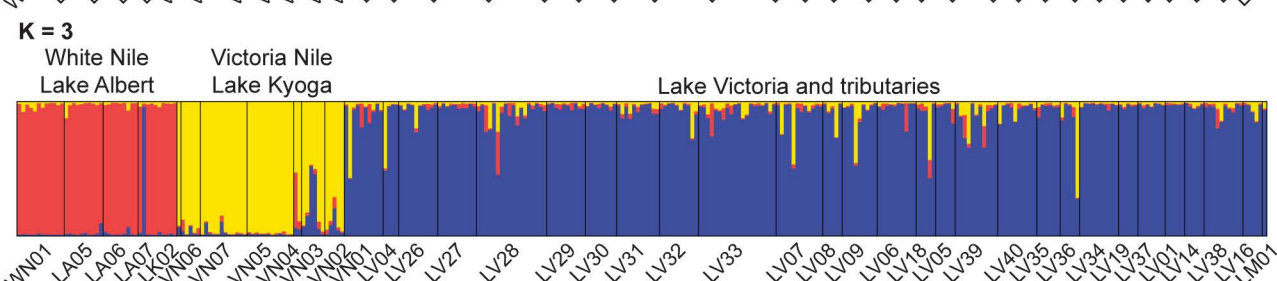
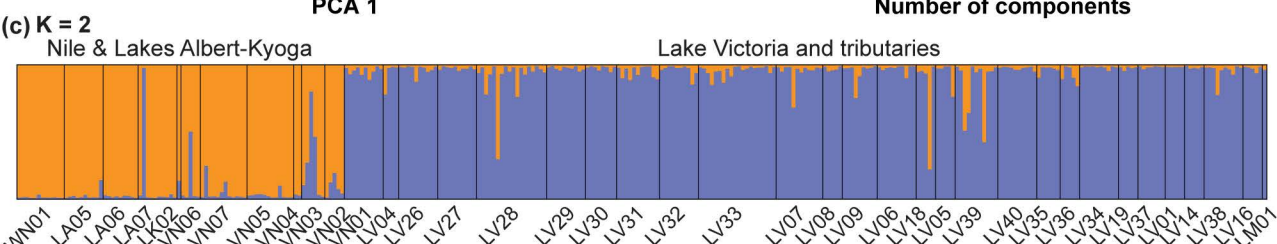
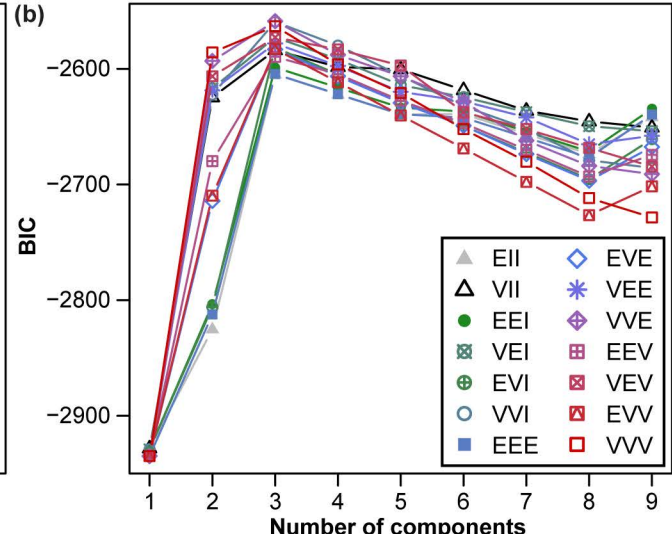
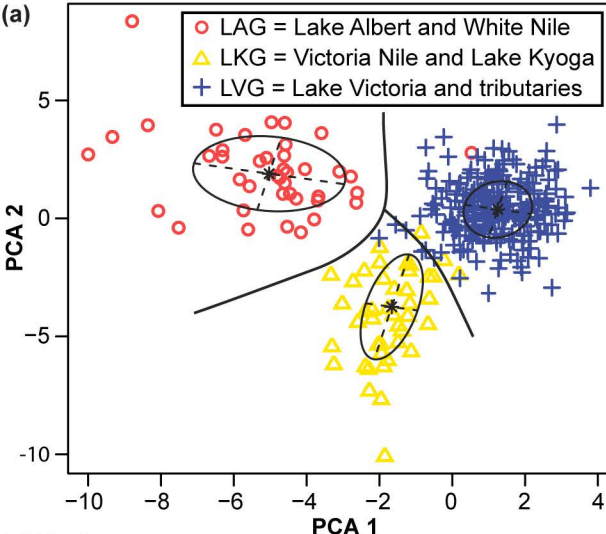
$Ne_{small} < Ne$

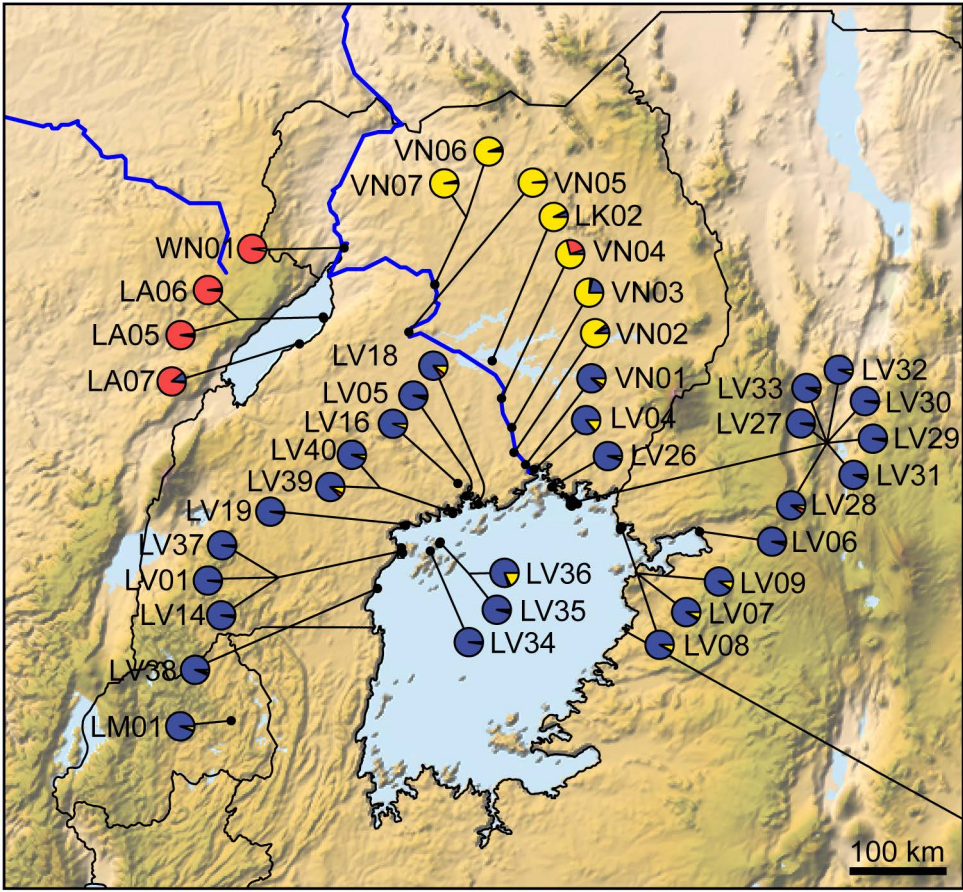
$Ne_{large} > Ne$

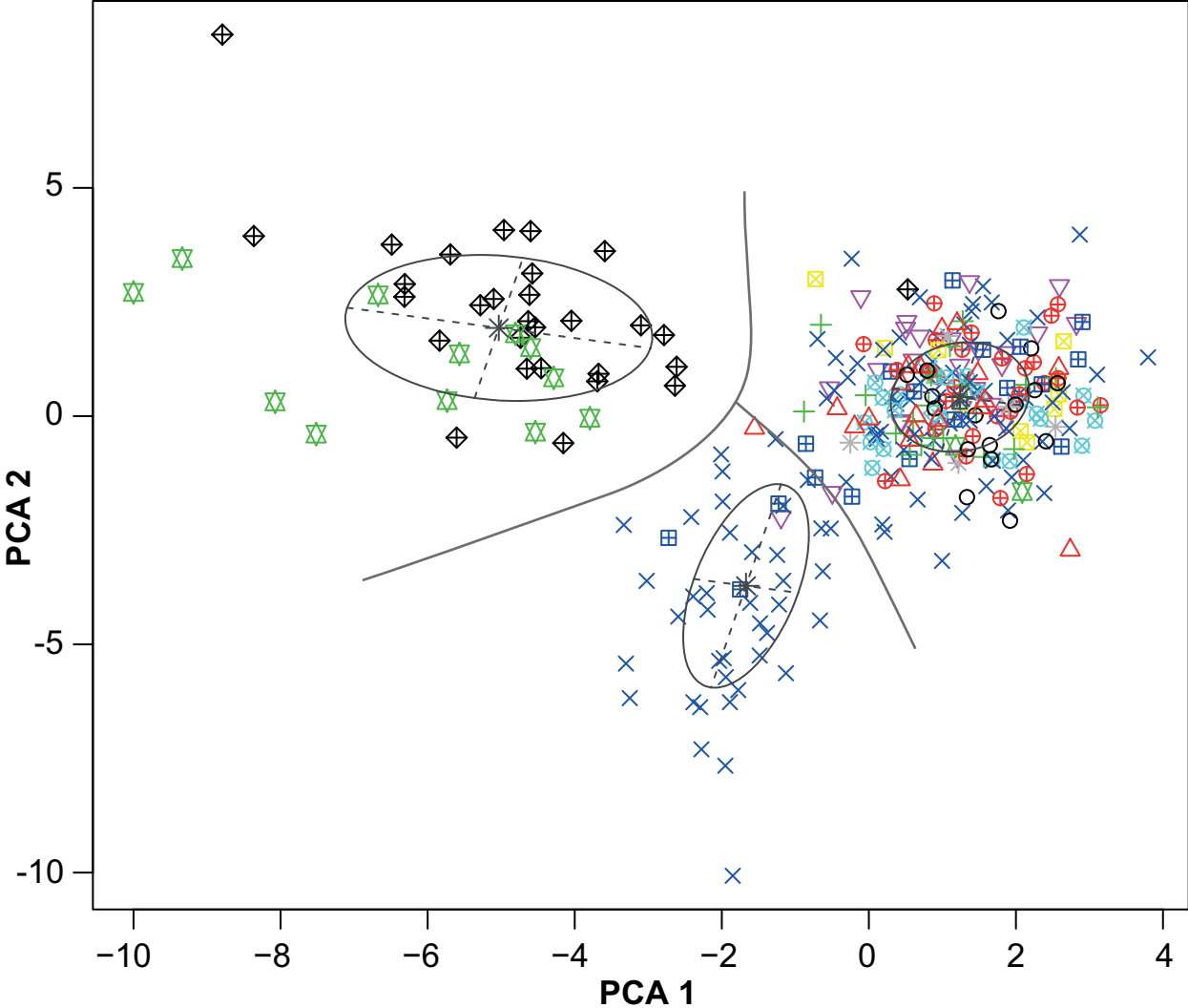
$Ne_{l_anc} > Ne_{small}$

$Ne_{s_anc} < Ne_{large}$

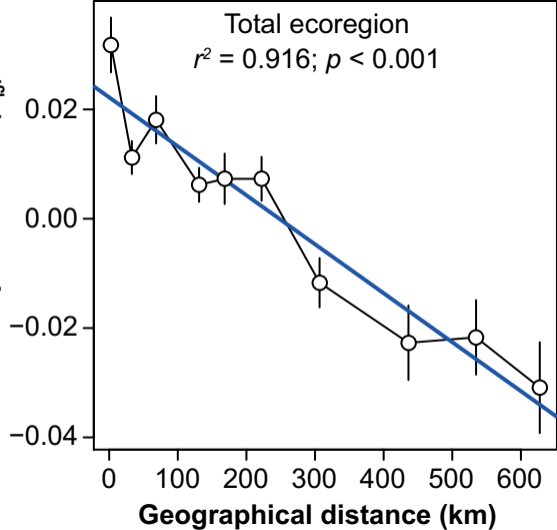
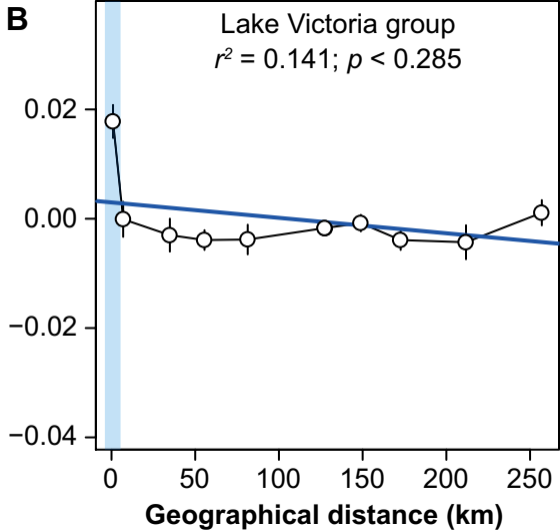
$t_2 > t_1$







- | | | | |
|-------------------------|----------------------------|--------------------------|------------------------|
| ◆ <i>B. rubicunda</i> | ⊞ <i>B. u. elatior</i> | ⊞ <i>B. u. meta</i> | ○ <i>B. constricta</i> |
| × <i>B. c. ugandae</i> | ▽ <i>B. j. jucunda</i> | △ <i>B. c. costulata</i> | |
| ⊞ <i>B. u. unicolor</i> | ⊞ <i>B. j. kisumiensis</i> | ◇ <i>B. j. altior</i> | |
| ⊕ <i>B. trochlearis</i> | * <i>B. phthinotropis</i> | + <i>B. c. dagusiae</i> | |

AKinship coefficient (F_{IJ})**B**Kinship coefficient (F_{IJ})

Supplemental Information for:

Population collapse in viviparid gastropods of the Lake Victoria ecoregion started before the Last Glacial Maximum

Bert Van Bocxlaer, Catharina Clewing, Anne Duputié, Camille Roux, Christian Albrecht

SI text**Morphological identifications**

Morphological identifications to species and/or races were performed with the identification key of Mandahl-Barth (1954) and these identifications were subsequently updated following Mandahl-Barth (1973) and Brown (1994). Because the identification key has some ambiguous steps, we additionally cross-validated our identifications using type specimens from the Natural History Museum in London and the Zoological Museum, Copenhagen, which houses the Mandahl-Barth collection. As multiple morphological transitions exist, the status of geographical races, nominal species and the assignment of races to species requires further taxonomic research. Nevertheless, all currently recognized races and species were represented in our total dataset, although some morphological variants of *B. trochlearis*, *B. phthinotropis* and *B. unicolor* are missing. Construction of the reduced dataset from the total dataset did not result in the exclusion of morphospecies, but it implied that *B. phthinotropis* is only represented by three specimens. This regrouping of the populations also implied three cases of lumping several morphospecies into joint populations. More specifically, it affects specimens of *B. constricta*, *B. costulata costulata* and *B. trochlearis* in the merge of LV01, LV14 and LV37; specimens of *B. costulata ugandae*, *B. jucunda altior*, *B. jucunda jucunda*, and *B. unicolor elatior* in the merge of LV29 and LV30; and specimens of *B. costulata costulata*, *B. jucunda altior*, *B. cf. phthinotropis*, *B. costulata ugandae*, *B. sp.* (juvenile) in the merge of LV35 and LV36. In none of these cases, however, did the merge result in drastically altered summary statistics.

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56 genotypes. *Genetics*, 163, 1177-1191.
- 57

58 **Tables**

59 **Table S1.** Sampling and collection information on all specimens in the cytochrome *c* oxidase subunit I
60 dataset: population code (Pop.), specimen code (Ind.), morphological identification, accession number
61 in the Systematics and Biodiversity collection of the Justus Liebig University Giessen (UGSB), the
62 DNA voucher number (DNA#), the NCBI GenBank accession number and sequence code. For each
63 locality sampling information is provided as well. The reference (Ref.) for the sequence data is: 1 =
64 Jørgensen, Kristensen, and Madsen (2008); 2 = Sengupta, Kristensen, Madsen, and Jørgensen (2009);
65 3 = Schultheiß, Wilke, Jørgensen, and Albrecht (2011); 4 = Schultheiß, Van Bocxlaer, Riedel, von
66 Rintelen, and Albrecht (2014); 5 = this study. Identifications of specimens from Schultheiß et al. (2014)
67 were updated: Specimens indicated with an * under identification were previously identified as *B.*
68 *unicolor*, that with ** as *B. trochlearis*. Individuals with bold specimen codes were included in the
69 microsatellite dataset.

Pop.	Ind.	Identification	UGSB	DNA#	GenBank	Seq code	Lat.	Long.	Waterbody	Country	Locality	Ref.
LV01	LV01/1	<i>B. trochlearis</i>	7933	n.a.	FJ405837	Btr837vi	-0.29431	32.02575	Lake Victoria	Uganda	Bukakata	2
LV02	LV02/1	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405872	Bsp872vi	0.48827	33.38524	Lake Victoria	Uganda	Buluba	2
LV03	LV03/1	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405862	Bsp862vi	0.05388	32.47012	Lake Victoria	Uganda	Entebbe	2
LV03	LV03/2	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405866	Bsp866vi	0.05388	32.47012	Lake Victoria	Uganda	Entebbe	2
LV04	LV04/1	<i>B. unicolor elatior</i>	7935	n.a.	FJ405848	Bun848vi	0.44008	33.23195	Lake Victoria	Uganda	Jinja	2
LV04	LV04/2	<i>B. unicolor elatior</i>	n.a.	n.a.	FJ405853	Bun853vi	0.44008	33.23195	Lake Victoria	Uganda	Jinja	2
LV05	LV05/1	<i>B. costulata/jucunda/unicolor</i>	7928	n.a.	FJ405849	Bsp849vi	0.19892	32.61540	Lake Victoria	Uganda	Kaazi	2
LV08	LV08/1	<i>B. costulata ugandae</i>	7064	15686	JX489237	Bco237vi	-0.10900	34.02031	Lake Victoria	Kenya	Usenge	2
LV08	LV08/2	<i>B. costulata ugandae</i>	7063	15685	MT834851	Bsp685VI	-0.10900	34.02031	Lake Victoria	Kenya	Usenge	5
LV10	LV10/1	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405850	Bsp850vi	0.19364	32.85216	Lake Victoria	Uganda	Kibanga Port	2
LV11	LV11/1	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405869	Bsp869vi	0.32119	33.50837	Lake Victoria	Uganda	Kityerea	2
LV12	LV12/1	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405868	Bsp868vi	0.35247	32.75374	Lake Victoria	Uganda	Kivindi	2
LV12	LV12/2	<i>B. trochlearis</i>	n.a.	n.a.	FJ405870	Btr870vi	0.35247	32.75374	Lake Victoria	Uganda	Kivindi	2
LV14	LV14/1	<i>B. trochlearis</i>	7930	n.a.	FJ405846	Btr846vi	-0.32093	32.03923	Lake Victoria	Uganda	Lambu	2
LV15	LV15/1	<i>B. sp.</i>	n.a.	n.a.	FJ405854	Bsp854vi	n.a.	n.a.	Lake Victoria	Uganda	Lomba	2
LV16	LV16/1	<i>B. trochlearis</i>	7934	n.a.	FJ405847	Btr847vi	0.31341	32.54089	Lake Victoria	Uganda	Lugala	2
LV17	LV17/1	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405852	Bsp852vi	-0.43713	34.20606	Lake Victoria	Uganda	Mbita	2
LV18	LV18/1	<i>B. costulata/jucunda/unicolor</i>	7929	n.a.	FJ405839	Bsp839vi	0.12303	32.72698	Lake Victoria	Uganda	Mpunge	2
LV19	LV19/1	<i>B. trochlearis</i>	7932	n.a.	FJ405855	Btr855vi	-0.06967	32.06489	Lake Victoria	Uganda	Ngombe	2
LV20	LV20/1	<i>B. costulata</i>	n.a.	7125	HQ012712	Bco712vi	-2.26658	33.79654	Lake Victoria	Tanzania	Speke Bay	3
LV21	LV21/1	<i>B. costulata/jucunda/unicolor</i>	n.a.	n.a.	FJ405845	Bsp845vi	n.a.	n.a.	Lake Victoria	Uganda	Nile Source	2
LV22	LV22/1	<i>B. costulata costulata</i>	13203	20330	MT834852	Bsp330VI	-2.52111	32.89134	Lake Victoria	Tanzania	Mwanza	5
LV23	LV23/1	<i>B. costulata costulata</i>	13204	20331	MT834853	Bsp331VI	-1.33525	31.82467	Lake Victoria	Tanzania	Bukoba	5
LV24	LV24/1	<i>B. constricta</i>	13206	20333	MT834854	Bsp333VI	-1.33076	31.83954	Lake Victoria	Tanzania	Bukoba	5
LV24	LV24/1	<i>B. sp. (juvenile)</i>	13207	20334	MT834855	Bsp334VI	-1.33076	31.83954	Lake Victoria	Tanzania	Bukoba	5
LV25	LV25/1	<i>B. costulata costulata</i>	13209	20336	MT834856	Bsp336VI	-1.33605	31.82361	Lake Victoria	Tanzania	Bukoba	5
LV26	LV26/1	<i>B. unicolor meta</i>	6261	15170	MT834857	Bsp170VI	0.28161	33.39454	Lake Victoria	Uganda	Lufu Island	5
LV26	LV26/2	<i>B. unicolor meta</i>	6262	15171	MT834858	Bsp171VI	0.28161	33.39454	Lake Victoria	Uganda	Lufu Island	5
LV26	LV26/3	<i>B. unicolor meta</i>	6264	15173	MT834859	Bsp173VI	0.28161	33.39454	Lake Victoria	Uganda	Lufu Island	5
LV30	LV30/1	<i>B. unicolor elatior</i>	6518	15261	JX489229	Bun229vi	0.14067	33.60258	Lake Victoria	Uganda	Simu Island	4
LV30	LV30/2	<i>B. costulata ugandae</i>	6517	15260	MT834860	Bun260VI	0.14067	33.60258	Lake Victoria	Uganda	Simu Island	5
LV32	LV32/1	<i>B. trochlearis</i>	6283	15192	JX489227	Btr227vi	0.16176	33.58264	Lake Victoria	Uganda	Dagusi Island NE	4
LV32	LV32/2	<i>B. trochlearis</i>	6284	15193	JX489228	Btr228vi	0.16176	33.58264	Lake Victoria	Uganda	Dagusi Island NE	4
LV38	LV38/1	<i>B. jucunda jucunda</i>	6578	15321	JX489231	Bju231vi	-0.64564	31.80791	Lake Victoria	Uganda	Ddimio	4
LV38	LV38/2	<i>B. jucunda jucunda</i>	6577	15320	MT834861	Bsp320VI	-0.64564	31.80791	Lake Victoria	Uganda	Ddimio	5
LV39	LV39/1	<i>B. unicolor elatior**</i>	6889	15494	JX489235	Btr235vi	0.03892	32.49402	Lake Victoria	Uganda	Entebbe S	4
LV39	LV39/2	<i>B. unicolor elatior</i>	6890	15495	JX489236	Bun236vi	0.03892	32.49402	Lake Victoria	Uganda	Entebbe S	4
LM01	LM01/1	<i>B. unicolor unicolor</i>	7123	15745	JX489240	Bun240mu	-1.84843	30.47826	Lake Muhazi	Rwanda	Gahini	4
VN01	VN01/6	<i>B. costulata ugandae</i>	6253	15162	MT834862	Bun162NI	0.48544	33.15524	Victoria Nile	Uganda	Bujagali Falls	5
VN01	VN01/9	<i>B. costulata ugandae*</i>	6256	15165	JX489226	Bun226ni	0.48544	33.15524	Victoria Nile	Uganda	Bujagali Falls	4
VN02	VN02/1	<i>B. unicolor elatior</i>	7931	n.a.	FJ405851	Bun851vi	0.59448	33.05258	Victoria Nile	Uganda	Kumucanga	2
VN04	VN04/1	<i>B. costulata ugandae*</i>	7085	15707	JX489238	Bun238ni	1.09002	32.93648	Victoria Nile	Uganda	Budali	4
LK01	LK01/1	<i>B. unicolor</i>	n.a.	n.a.	FJ405863	Bun863ky	n.a.	n.a.	Lake Kyoga	Uganda	Lyingo	2
VN05	VN05/1	<i>B. costulata ugandae*</i>	7111	15733	JX489239	Bun239ni	1.69255	32.09473	Victoria Nile	Uganda	Masindi Port	4
VN06	VN06/1	<i>B. costulata ugandae*</i>	7124	15746	JX489241	Bun241ni	2.12373	32.33107	Victoria Nile	Uganda	Mutunda	4
VN07	VN07/1	<i>B. costulata ugandae</i>	6692	15458	MT834863	Bsp458NI	2.12852	32.32919	Victoria Nile	Uganda	Mutunda	5
VN07	VN07/2	<i>B. costulata ugandae</i>	6695	15461	MT834864	Bsp461NI	2.12852	32.32919	Victoria Nile	Uganda	Mutunda	5
LA01	LA01/1	<i>B. rubicunda</i>	n.a.	6612	HQ012714	Bru714al	1.42904	30.89265	Lake Albert	Uganda	Kiabahamba	3
LA01	LA01/2	<i>B. rubicunda</i>	n.a.	6611	HQ012713	Bru713al	1.42904	30.89265	Lake Albert	Uganda	Kiabahamba	3
LA01	LA01/3	<i>B. rubicunda</i>	n.a.	6615	HQ012715	Bru715al	1.42904	30.89265	Lake Albert	Uganda	Kiabahamba	3
LA02	LA02/1	<i>B. rubicunda</i>	n.a.	n.a.	FJ405861	Bru861al	1.90188	31.40362	Lake Albert	Uganda	Bugoigo	2
LA03	LA03/1	<i>B. rubicunda</i>	n.a.	n.a.	FJ405836	Bru836al	1.80911	31.32299	Lake Albert	Uganda	Butiaba	2
LA04	LA04/1	<i>B. rubicunda</i>	n.a.	n.a.	EU274556	Bru556al	n.a.	n.a.	Lake Albert	Uganda	Rwangala	1

MOLECULAR ECOLOGY

Pop.	Ind.	Identification	UGSB	DNA#	GenBank	Seq code	Lat.	Long.	Waterbody	Country	Locality	Ref.
LA05	LA05/1	<i>B. rubicunda</i>	6303	15212	MT834865	Bru212AL	1.83060	31.31484	Lake Albert	Uganda	Butiaba	5
LA06	LA06/1	<i>B. rubicunda</i>	6877	15482	JX489233	Bru233al	1.81842	31.32021	Lake Albert	Uganda	Butiaba	4
LA06	LA06/2	<i>B. rubicunda</i>	6878	15483	JX489234	Bru234al	1.81842	31.32021	Lake Albert	Uganda	Butiaba	4
LA07	LA07/1	<i>B. rubicunda</i>	6569	15312	JX489230	Bru230al	1.58649	31.10057	Lake Albert	Uganda	Kiriamboga	4
WN01	RN07/1	<i>B. unicolor unicolor</i>	6710	15476	JX489232	Bun232ni	2.45933	31.50487	White Nile	Uganda	Pakwach	4
WN01	RN07/2	<i>B. unicolor unicolor</i>	6711	15477	MT834866	Bsp477NI	2.45933	31.50487	White Nile	Uganda	Pakwach	5
WN01	RN07/3	<i>B. unicolor unicolor</i>	6712	15478	MT834867	Bsp478NI	2.45933	31.50487	White Nile	Uganda	Pakwach	5

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72 **Table S2.** Sampling and collection information on all individuals included in our microsatellite dataset:
 73 population code (Pop.), specimen code (Ind.), morphological identification, accession number in the
 74 Systematics and Biodiversity collection of the Justus Liebig University Giessen (UGSB), the DNA
 75 voucher number (DNA#), and locality information. Information specific to the sampling event is
 76 identical for all specimens in a population and, therefore, it is only indicated on the first row for each
 77 population. Populations that have been pooled in the regrouped dataset are indicated with identical
 78 locality names, however, their geographic coordinates specify precise sampling locations.

Pop.	Ind.	Identification	UGSB	DNA#	Lat.	Long.	Waterbody	Country	Locality
LA05	LA05/1	<i>B. rubicunda</i>	6303	15212	1.83060	31.31484	Lake Albert	Uganda	Butiaba
	LA05/2	<i>B. rubicunda</i>	6295	15204					
	LA05/3	<i>B. rubicunda</i>	6296	15205					
	LA05/4	<i>B. rubicunda</i>	6297	15206					
	LA05/5	<i>B. rubicunda</i>	6298	15207					
	LA05/6	<i>B. rubicunda</i>	6299	15208					
	LA05/7	<i>B. rubicunda</i>	6301	15210					
	LA05/8	<i>B. rubicunda</i>	6302	15211					
	LA05/9	<i>B. rubicunda</i>	6305	15214					
	LA05/10	<i>B. rubicunda</i>	6306	15215					
LA06	LA06/1	<i>B. rubicunda</i>	6877	15482	1.81842	31.32021	Lake Albert	Uganda	Butiaba
	LA06/2	<i>B. rubicunda</i>	6878	15483					
	LA06/3	<i>B. rubicunda</i>	6879	15484					
	LA06/4	<i>B. rubicunda</i>	6880	15485					
	LA06/5	<i>B. rubicunda</i>	6881	15486					
	LA06/6	<i>B. rubicunda</i>	6882	15487					
	LA06/7	<i>B. rubicunda</i>	6884	15489					
	LA06/8	<i>B. rubicunda</i>	6886	15491					
	LA06/9	<i>B. rubicunda</i>	6887	15492					
	LA07	LA07/1	<i>B. rubicunda</i>	6569					
LA07/2		<i>B. rubicunda</i>	6567	15310					
LA07/3		<i>B. rubicunda</i>	6568	15311					
LA07/4		<i>B. rubicunda</i>	6570	15313					
LA07/5		<i>B. rubicunda</i>	6571	15314					
LA07/6		<i>B. rubicunda</i>	6572	15315					
LA07/7		<i>B. rubicunda</i>	6573	15316					
LA07/8		<i>B. rubicunda</i>	6574	15317					
LA07/9		<i>B. rubicunda</i>	6575	15318					
LA07/10		<i>B. rubicunda</i>	6576	15319					
LK02	LK02/1	<i>B. costulata ugandae</i>	7122	15744	1.43136	32.85360	Lake Kyoga	Uganda	Bukungu
LM01	LM01/1	<i>B. unicolor unicolor</i>	7123	15745	-1.84843	30.47826	Lake Muhazi	Rwanda	Gahini
LV01	LV01/2	<i>B. trochlearis</i>	7961	16549	-0.29431	32.02575	Lake Victoria	Uganda	Bukakata
	LV01/3	<i>B. trochlearis</i>	7962	16550					
	LV01/4	<i>B. trochlearis</i>	7963	16551					
	LV01/5	<i>B. trochlearis</i>	7964	16552					
	LV01/6	<i>B. trochlearis</i>	7965	16553					
	LV04	LV04/4	<i>B. unicolor elatior</i>	7972					
LV04/5		<i>B. jucunda jucunda</i>	7973	16561					
LV04/6		<i>B. jucunda jucunda</i>	7974	16562					
LV04/7		<i>B. jucunda jucunda</i>	7975	16563					
LV05	LV05/2	<i>B. jucunda jucunda</i>	7936	16524	0.19892	32.61540	Lake Victoria	Uganda	Kaazi
	LV05/3	<i>B. jucunda jucunda</i>	7937	16525					
	LV05/4	<i>B. jucunda jucunda</i>	7938	16526					
	LV05/5	<i>B. jucunda jucunda</i>	7939	16527					
	LV05/6	<i>B. jucunda jucunda</i>	7940	16528					
	LV06	LV06/1	<i>B. jucunda kisumiensis</i>	6493					
LV06/2		<i>B. jucunda kisumiensis</i>	6494	15237					
LV06/3		<i>B. jucunda kisumiensis</i>	6495	15238					
LV06/4		<i>B. jucunda kisumiensis</i>	6497	15240					
LV06/5		<i>B. jucunda kisumiensis</i>	6498	15241					
LV06/6		<i>B. jucunda kisumiensis</i>	6499	15242					
LV06/7		<i>B. jucunda kisumiensis</i>	6500	15243					
LV06/8		<i>B. jucunda kisumiensis</i>	6502	15245					
LV06/9		<i>B. jucunda kisumiensis</i>	6503	15246					
LV06/10		<i>B. jucunda kisumiensis</i>	6504	15247					
LV07	LV07/1	<i>B. costulata ugandae</i>	6505	15248	-0.09034	34.02106	Lake Victoria	Kenya	Usenge
	LV07/2	<i>B. costulata ugandae</i>	6506	15249					
	LV07/3	<i>B. costulata ugandae</i>	6507	15250					
	LV07/4	<i>B. costulata ugandae</i>	6508	15251					
	LV07/5	<i>B. costulata ugandae</i>	6509	15252					

MOLECULAR ECOLOGY

Pop.	Ind.	Identification	UGSB	DNA#	Lat.	Long.	Waterbody	Country	Locality
	LV07/6	<i>B. costulata ugandae</i>	6510	15253					
	LV07/7	<i>B. costulata ugandae</i>	6511	15254					
	LV07/8	<i>B. costulata ugandae</i>	6512	15255					
	LV07/9	<i>B. costulata ugandae</i>	6513	15256					
	LV07/10	<i>B. costulata ugandae</i>	6514	15257					
	LV07/11	<i>B. costulata ugandae</i>	6515	15258					
	LV07/12	<i>B. costulata ugandae</i>	6516	15259					
LV08	LV08/1	<i>B. costulata ugandae</i>	7064	15686	-0.10900	34.02031	Lake Victoria	Kenya	Usenge
	LV08/2	<i>B. costulata ugandae</i>	7063	15685					
	LV08/3	<i>B. costulata ugandae</i>	7065	15687					
	LV08/4	<i>B. costulata ugandae</i>	7066	15688					
	LV08/5	<i>B. costulata ugandae</i>	7068	15690					
LV09	LV09/1	<i>B. costulata ugandae</i>	7069	15691	-0.08075	34.03286	Lake Victoria	Kenya	Usenge
	LV09/2	<i>B. costulata ugandae</i>	7070	15692					
	LV09/3	<i>B. costulata ugandae</i>	7071	15693					
	LV09/4	<i>B. costulata ugandae</i>	7072	15694					
	LV09/5	<i>B. costulata ugandae</i>	7073	15695					
	LV09/6	<i>B. costulata ugandae</i>	7074	15696					
	LV09/7	<i>B. costulata ugandae</i>	7075	15697					
	LV09/8	<i>B. costulata ugandae</i>	7076	15698					
	LV09/9	<i>B. costulata ugandae</i>	7077	15699					
LV14	LV14/2	<i>B. costulata costulata</i>	7946	16534	-0.32093	32.03923	Lake Victoria	Uganda	Bukakata
	LV14/3	<i>B. costulata costulata</i>	7947	16535					
	LV14/4	<i>B. costulata costulata</i>	7948	16536					
	LV14/5	<i>B. costulata costulata</i>	7949	16537					
	LV14/6	<i>B. costulata costulata</i>	7950	16538					
LV16	LV16/2	<i>B. unicolor elatior</i>	7966	16554	0.31341	32.54089	Lake Victoria	Uganda	Lugala
	LV16/3	<i>B. unicolor elatior</i>	7967	16555					
	LV16/4	<i>B. costulata ugandae</i>	7968	16556					
	LV16/5	<i>B. costulata ugandae</i>	7969	16557					
	LV16/6	<i>B. costulata ugandae</i>	7970	16558					
LV18	LV18/2	<i>B. jucunda jucunda</i>	7941	16529	0.12303	32.72698	Lake Victoria	Uganda	Mpunge
	LV18/3	<i>B. jucunda jucunda</i>	7942	16530					
	LV18/4	<i>B. jucunda jucunda</i>	7943	16531					
	LV18/5	<i>B. jucunda jucunda</i>	7944	16532					
	LV18/6	<i>B. jucunda jucunda</i>	7945	16533					
LV19	LV19/2	<i>B. phthinotropis</i>	7956	16544	-0.06967	32.06489	Lake Victoria	Uganda	Ngombe
	LV19/3	<i>B. phthinotropis</i>	7957	16545					
	LV19/4	<i>B. trochlearis</i>	7958	16546					
	LV19/5	<i>B. trochlearis</i>	7959	16547					
	LV19/6	<i>B. trochlearis</i>	7960	16548					
LV26	LV26/1	<i>B. unicolor meta</i>	6261	15170	0.28161	33.39454	Lake Victoria	Uganda	Lufu Island
	LV26/2	<i>B. unicolor meta</i>	6262	15171					
	LV26/3	<i>B. unicolor meta</i>	6264	15173					
	LV26/4	<i>B. unicolor meta</i>	6260	15169					
	LV26/5	<i>B. unicolor meta</i>	6263	15172					
	LV26/6	<i>B. unicolor meta</i>	6265	15174					
	LV26/7	<i>B. unicolor meta</i>	6266	15175					
	LV26/8	<i>B. unicolor meta</i>	6267	15176					
	LV26/9	<i>B. unicolor meta</i>	6268	15177					
	LV26/10	<i>B. unicolor meta</i>	6270	15179					
LV27	LV27/1	<i>B. costulata costulata</i>	6541	15284	0.11627	33.56262	Lake Victoria	Uganda	Dagusi Island SW
	LV27/2	<i>B. costulata costulata</i>	6542	15285					
	LV27/3	<i>B. costulata costulata</i>	6543	15286					
	LV27/4	<i>B. unicolor elatior</i>	6544	15287					
	LV27/5	<i>B. unicolor meta</i>	6545	15288					
	LV27/6	<i>B. costulata ugandae</i>	6546	15289					
	LV27/7	<i>B. costulata ugandae</i>	6547	15290					
	LV27/8	<i>B. costulata ugandae</i>	6549	15292					
	LV27/9	<i>B. unicolor elatior</i>	6551	15294					
	LV27/10	<i>B. unicolor elatior</i>	6552	15295					
LV28	LV28/1	<i>B. costulata ugandae</i>	6271	15180	0.10460	33.57583	Lake Victoria	Uganda	Dagusi Island S
	LV28/2	<i>B. costulata ugandae</i>	6272	15181					
	LV28/3	<i>B. costulata ugandae</i>	6274	15183					
	LV28/4	<i>B. costulata ugandae</i>	6275	15184					
	LV28/5	<i>B. costulata ugandae</i>	6276	15185					
	LV28/6	<i>B. costulata ugandae</i>	6277	15186					
	LV28/7	<i>B. costulata ugandae</i>	6280	15189					
	LV28/8	<i>B. costulata ugandae</i>	6282	15191					

MOLECULAR ECOLOGY

Pop.	Ind.	Identification	UGSB	DNA#	Lat.	Long.	Waterbody	Country	Locality
	LV28/9	<i>B. sp.</i> (juvenile)	6553	15296					
	LV28/10	<i>B. sp.</i> (juvenile)	6554	15297					
	LV28/11	<i>B. sp.</i> (juvenile)	6555	15298					
	LV28/12	<i>B. sp.</i> (juvenile)	6556	15299					
	LV28/13	<i>B. sp.</i> (juvenile)	6557	15300					
	LV28/14	<i>B. sp.</i> (juvenile)	6558	15301					
	LV28/15	<i>B. sp.</i> (juvenile)	6559	15302					
	LV28/16	<i>B. sp.</i> (juvenile)	6560	15303					
	LV28/17	<i>B. sp.</i> (juvenile)	6561	15304					
	LV28/18	<i>B. sp.</i> (juvenile)	6562	15305					
LV29	LV29/1	<i>B. jucunda jucunda</i>	6644	15410	0.13707	33.60149	Lake Victoria	Uganda	Simu Island
	LV29/2	<i>B. jucunda altior</i>	6645	15411					
	LV29/3	<i>B. jucunda jucunda</i>	6646	15412					
	LV29/4	<i>B. jucunda jucunda</i>	6647	15413					
	LV29/5	<i>B. jucunda jucunda</i>	6649	15415					
	LV29/6	<i>B. jucunda jucunda</i>	6650	15416					
	LV29/7	<i>B. jucunda jucunda</i>	6651	15417					
	LV29/8	<i>B. jucunda jucunda</i>	6653	15419					
	LV29/9	<i>B. jucunda jucunda</i>	6654	15420					
	LV29/10	<i>B. jucunda jucunda</i>	6655	15421					
LV30	LV30/1	<i>B. unicolor elatior</i>	6518	15261	0.14067	33.60258	Lake Victoria	Uganda	Simu Island
	LV30/2	<i>B. costulata ugandae</i>	6517	15260					
	LV30/3	<i>B. costulata ugandae</i>	6519	15262					
	LV30/4	<i>B. unicolor elatior</i>	6520	15263					
	LV30/7	<i>B. costulata ugandae</i>	6525	15268					
	LV30/8	<i>B. unicolor elatior</i>	6526	15269					
	LV30/9	<i>B. unicolor elatior</i>	6527	15270					
	LV30/10	<i>B. unicolor elatior</i>	6528	15271					
LV31	LV31/1	<i>B. unicolor meta</i>	6656	15422	0.12456	33.62969	Lake Victoria	Uganda	Kaza Island E
	LV31/2	<i>B. unicolor meta</i>	6657	15423					
	LV31/3	<i>B. unicolor meta</i>	6658	15424					
	LV31/4	<i>B. unicolor meta</i>	6659	15425					
	LV31/5	<i>B. unicolor meta</i>	6660	15426					
	LV31/6	<i>B. unicolor meta</i>	6661	15427					
	LV31/7	<i>B. unicolor meta</i>	6662	15428					
	LV31/8	<i>B. unicolor meta</i>	6663	15429					
	LV31/9	<i>B. unicolor meta</i>	6665	15431					
	LV31/10	<i>B. unicolor meta</i>	6666	15432					
	LV31/11	<i>B. unicolor meta</i>	6667	15433					
LV32	LV32/1	<i>B. trochlearis</i>	6283	15192	0.16176	33.58264	Lake Victoria	Uganda	Dagusi Island NE
	LV32/2	<i>B. trochlearis</i>	6284	15193					
	LV32/3	<i>B. trochlearis</i>	6285	15194					
	LV32/4	<i>B. trochlearis</i>	6286	15195					
	LV32/5	<i>B. trochlearis</i>	6287	15196					
	LV32/6	<i>B. trochlearis</i>	6289	15198					
	LV32/7	<i>B. trochlearis</i>	6290	15199					
	LV32/8	<i>B. trochlearis</i>	6292	15201					
	LV32/9	<i>B. trochlearis</i>	6293	15202					
	LV32/10	<i>B. trochlearis</i>	6294	15203					
LV33	LV33/1	<i>B. costulata dagusiae</i>	6668	15434	0.15662	33.56414	Lake Victoria	Uganda	Dagusi Island NW
	LV33/2	<i>B. costulata dagusiae</i>	6669	15435					
	LV33/3	<i>B. costulata dagusiae</i>	6671	15437					
	LV33/4	<i>B. costulata dagusiae</i>	6672	15438					
	LV33/5	<i>B. costulata dagusiae</i>	6673	15439					
	LV33/6	<i>B. costulata dagusiae</i>	6674	15440					
	LV33/7	<i>B. costulata dagusiae</i>	6675	15441					
	LV33/8	<i>B. costulata dagusiae</i>	6676	15442					
	LV33/9	<i>B. costulata dagusiae</i>	6678	15444					
	LV33/10	<i>B. costulata dagusiae</i>	6679	15445					
	LV33/11	<i>B. costulata dagusiae</i>	6680	15446					
	LV33/12	<i>B. costulata dagusiae</i>	6681	15447					
	LV33/13	<i>B. costulata dagusiae</i>	6682	15448					
	LV33/14	<i>B. costulata dagusiae</i>	6683	15449					
	LV33/15	<i>B. costulata dagusiae</i>	6685	15451					
	LV33/16	<i>B. costulata dagusiae</i>	6687	15453					
	LV33/17	<i>B. costulata dagusiae</i>	6688	15454					
	LV33/18	<i>B. costulata dagusiae</i>	6689	15455					
	LV33/19	<i>B. costulata dagusiae</i>	6690	15456					
	LV33/20	<i>B. costulata dagusiae</i>	6691	15457					

MOLECULAR ECOLOGY

Pop.	Ind.	Identification	UGSB	DNA#	Lat.	Long.	Waterbody	Country	Locality
LV34	LV34/1	<i>B. trochlearis</i>	6307	15216	-0.30371	32.28927	Lake Victoria	Uganda	Kalangala
	LV34/2	<i>B. trochlearis</i>	6308	15217					
	LV34/3	<i>B. trochlearis</i>	6309	15218					
	LV34/4	<i>B. trochlearis</i>	6310	15219					
	LV34/5	<i>B. trochlearis</i>	6311	15220					
	LV34/6	<i>B. trochlearis</i>	6312	15221					
	LV34/7	<i>B. trochlearis</i>	6313	15222					
	LV34/8	<i>B. trochlearis</i>	6315	15224					
	LV34/9	<i>B. trochlearis</i>	6317	15226					
	LV34/10	<i>B. trochlearis</i>	6318	15227					
LV35	LV35/1	<i>B. cf. phthinotropis</i>	7091	15713	-0.23731	32.37333	Lake Victoria	Uganda	Serinya Island
	LV35/2	<i>B. cf. phthinotropis</i>	7092	15714					
	LV35/3	<i>B. cf. phthinotropis</i>	7093	15715					
	LV35/4	<i>B. costulata costulata</i>	7094	15716					
	LV35/5	<i>B. jucunda altior</i>	7095	15717					
	LV35/6	<i>B. costulata costulata</i>	7096	15718					
LV36	LV36/1	<i>B. sp. (juvenile)</i>	7097	15719	-0.22237	32.37996	Lake Victoria	Uganda	Serinya Island
	LV36/2	<i>B. sp. (juvenile)</i>	7098	15720					
	LV36/3	<i>B. costulata ugandae</i>	7099	15721					
	LV36/4	<i>B. costulata ugandae</i>	7100	15722					
	LV36/5	<i>B. costulata ugandae</i>	7102	15724					
LV37	LV37/1	<i>B. constricta</i>	7103	15725	-0.27263	32.02691	Lake Victoria	Uganda	Bukakata
	LV37/2	<i>B. constricta</i>	7104	15726					
	LV37/3	<i>B. constricta</i>	7105	15727					
	LV37/4	<i>B. constricta</i>	7106	15728					
	LV37/5	<i>B. constricta</i>	7107	15729					
	LV37/6	<i>B. constricta</i>	7108	15730					
	LV37/7	<i>B. constricta</i>	7109	15731					
LV38	LV38/1	<i>B. jucunda jucunda</i>	6578	15321	-0.64564	31.80791	Lake Victoria	Uganda	Ddimu
	LV38/2	<i>B. jucunda jucunda</i>	6577	15320					
	LV38/3	<i>B. costulata costulata</i>	6579	15322					
	LV38/4	<i>B. costulata costulata</i>	6580	15323					
	LV38/5	<i>B. costulata costulata</i>	6581	15324					
	LV38/6	<i>B. costulata costulata</i>	6582	15325					
	LV38/7	<i>B. costulata costulata</i>	6583	15326					
	LV38/8	<i>B. costulata costulata</i>	6585	15328					
	LV38/9	<i>B. jucunda kisumiensis</i>	6496	15239					
	LV38/10	<i>B. costulata costulata</i>	6584	15327					
LV39	LV39/1	<i>B. unicolor elatior</i>	6889	15494	0.03892	32.49402	Lake Victoria	Uganda	Entebbe S
	LV39/2	<i>B. unicolor elatior</i>	6890	15495					
	LV39/3	<i>B. unicolor elatior</i>	6891	15496					
	LV39/4	<i>B. costulata costulata</i>	6892	15497					
	LV39/5	<i>B. costulata costulata</i>	6894	15499					
	LV39/6	<i>B. costulata costulata</i>	6895	15500					
	LV39/7	<i>B. costulata costulata</i>	6896	15501					
	LV39/8	<i>B. costulata costulata</i>	6897	15502					
	LV39/9	<i>B. costulata costulata</i>	6899	15504					
	LV39/10	<i>B. costulata costulata</i>	6900	15505					
	LV39/11	<i>B. costulata costulata</i>	6893	15498					
LV40	LV40/1	<i>B. constricta</i>	6529	15272	0.05525	32.49198	Lake Victoria	Uganda	Entebbe N
	LV40/2	<i>B. constricta</i>	6530	15273					
	LV40/3	<i>B. constricta</i>	6531	15274					
	LV40/4	<i>B. constricta</i>	6532	15275					
	LV40/5	<i>B. constricta</i>	6533	15276					
	LV40/6	<i>B. constricta</i>	6534	15277					
	LV40/7	<i>B. unicolor unicolor</i>	6535	15278					
	LV40/8	<i>B. constricta</i>	6537	15280					
	LV40/9	<i>B. constricta</i>	6539	15282					
	LV40/10	<i>B. constricta</i>	6540	15283					
VN01	VN01/1	<i>B. costulata ugandae</i>	6247	15156	0.48544	33.15524	Victoria Nile	Uganda	Bujagali Falls
	VN01/2	<i>B. costulata ugandae</i>	6249	15158					
	VN01/3	<i>B. costulata ugandae</i>	6250	15159					
	VN01/4	<i>B. costulata ugandae</i>	6251	15160					
	VN01/5	<i>B. costulata ugandae</i>	6252	15161					
	VN01/6	<i>B. costulata ugandae</i>	6253	15162					
	VN01/7	<i>B. costulata ugandae</i>	6254	15163					
	VN01/8	<i>B. costulata ugandae</i>	6255	15164					
	VN01/9	<i>B. costulata ugandae</i>	6256	15165					
	VN01/10	<i>B. costulata ugandae</i>	6257	15166					

MOLECULAR ECOLOGY

Pop.	Ind.	Identification	UGSB	DNA#	Lat.	Long.	Waterbody	Country	Locality
VN02	VN02/2	<i>B. unicolor elatior</i>	7951	16539	0.59448	33.05257	Victoria Nile	Uganda	Kumucanga
	VN02/3	<i>B. jucunda jucunda</i>	7952	16540					
	VN02/4	<i>B. unicolor elatior</i>	7953	16541					
	VN02/5	<i>B. unicolor elatior</i>	7954	16542					
	VN02/6	<i>B. unicolor elatior</i>	7955	16543					
	VN03	VN03/1	<i>B. costulata ugandae</i>	7078					
VN03/2		<i>B. costulata ugandae</i>	7079	15701					
VN03/3		<i>B. costulata ugandae</i>	7080	15702					
VN03/4		<i>B. unicolor elatior</i>	7081	15703					
VN03/5		<i>B. costulata ugandae</i>	7082	15704					
VN03/6		<i>B. costulata ugandae</i>	7083	15705					
VN04	VN04/1	<i>B. costulata ugandae</i>	7085	15707	1.09002	32.93648	Victoria Nile	Uganda	Budali
	VN04/2	<i>B. costulata ugandae</i>	7084	15706					
VN05	VN05/1	<i>B. costulata ugandae</i>	7111	15733	1.69255	32.09473	Victoria Nile	Uganda	Masindi Port
	VN05/2	<i>B. costulata ugandae</i>	7110	15732					
	VN05/3	<i>B. costulata ugandae</i>	7112	15734					
	VN05/4	<i>B. costulata ugandae</i>	7113	15735					
	VN05/5	<i>B. costulata ugandae</i>	7114	15736					
	VN05/6	<i>B. costulata ugandae</i>	7115	15737					
	VN05/7	<i>B. costulata ugandae</i>	7116	15738					
	VN05/8	<i>B. costulata ugandae</i>	7117	15739					
	VN05/9	<i>B. costulata ugandae</i>	7118	15740					
	VN05/10	<i>B. costulata ugandae</i>	7119	15741					
	VN05/11	<i>B. costulata ugandae</i>	7120	15742					
	VN05/12	<i>B. costulata ugandae</i>	7121	15743					
VN06	VN06/1	<i>B. costulata ugandae</i>	7124	15746	2.12373	32.33107	Victoria Nile	Uganda	Mutunda
	VN06/2	<i>B. costulata ugandae</i>	7125	15747					
	VN06/3	<i>B. costulata ugandae</i>	7126	15748					
	VN06/4	<i>B. costulata ugandae</i>	7127	15749					
	VN06/5	<i>B. costulata ugandae</i>	7128	15750					
VN07	VN07/1	<i>B. costulata ugandae</i>	6692	15458	2.12852	32.32919	Victoria Nile	Uganda	Mutunda
	VN07/3	<i>B. costulata ugandae</i>	6693	15459					
	VN07/4	<i>B. costulata ugandae</i>	6694	15460					
	VN07/2	<i>B. costulata ugandae</i>	6695	15461					
	VN07/5	<i>B. costulata ugandae</i>	6696	15462					
	VN07/6	<i>B. costulata ugandae</i>	6697	15463					
	VN07/7	<i>B. costulata ugandae</i>	6698	15464					
	VN07/8	<i>B. costulata ugandae</i>	6699	15465					
	VN07/9	<i>B. costulata ugandae</i>	6700	15466					
	VN07/10	<i>B. costulata ugandae</i>	6701	15467					
	VN07/11	<i>B. costulata ugandae</i>	6702	15468					
	VN07/12	<i>B. costulata ugandae</i>	6703	15469					
WN01	WN01/1	<i>B. unicolor unicolor</i>	6710	15476	2.45933	31.50487	White Nile	Uganda	Pakwach
	WN01/2	<i>B. unicolor unicolor</i>	6711	15477					
	WN01/3	<i>B. unicolor unicolor</i>	6712	15478					
	WN01/4	<i>B. unicolor unicolor</i>	6704	15470					
	WN01/5	<i>B. unicolor unicolor</i>	6705	15471					
	WN01/6	<i>B. unicolor unicolor</i>	6706	15472					
	WN01/7	<i>B. unicolor unicolor</i>	6707	15473					
	WN01/8	<i>B. unicolor unicolor</i>	6708	15474					
	WN01/9	<i>B. unicolor unicolor</i>	6709	15475					
	WN01/10	<i>B. unicolor unicolor</i>	6713	15479					
	WN01/11	<i>B. unicolor unicolor</i>	6714	15480					
	WN01/12	<i>B. unicolor unicolor</i>	6715	15481					

81 **Table S3.** Estimates of nuclear genetic variation for our 15 microsatellite loci in the regrouped dataset
 82 (21 populations; 282 specimens). Note that loci *Bel_L045* and *Bel_L050* (in grey) are discarded from
 83 the results reported in the main text due to the presence of null alleles. A_n = number of alleles; A_r =
 84 allelic richness standardized to a sample size of 5 diploid individuals, H_o = observed heterozygosity;
 85 H_E = expected heterozygosity. The mean fixation indices F_{IS} , F_{ST} , F_{IT} are indicated with their standard
 86 error following Weir and Cockerham (1984).

Locus	A_n	A_r	H_o	H_E	F_{IS}	s.e. F_{IS}	F_{ST}	s.e. F_{ST}	F_{IT}	s.e. F_{IT}
<i>Bel_L53</i>	19	6.9	0.888	0.880	-0.005	0.020	0.038***	0.009	0.034*	0.022
<i>Bel_L25</i>	23	6.5	0.800	0.859	0.067**	0.034	0.033***	0.010	0.098***	0.032
<i>Bel_L48</i>	17	5.1	0.738	0.727	-0.014	0.027	0.107***	0.032	0.095**	0.046
<i>Bel_L16</i>	18	7.2	0.870	0.861	-0.016	0.020	0.067***	0.025	0.052**	0.026
<i>Bel_L63</i>	15	4.8	0.702	0.670	-0.036	0.036	0.108***	0.032	0.076**	0.050
<i>Bel_L13</i>	10	3.4	0.571	0.602	0.026	0.037	0.023*	0.017	0.048	0.043
<i>Bel_L10</i>	19	6.3	0.755	0.769	0.021	0.027	0.117***	0.035	0.136***	0.045
<i>Bel_L50</i>	24	7.4	0.734	0.883	0.147***	0.034	0.037***	0.010	0.178***	0.036
<i>Bel_L32</i>	30	8.1	0.907	0.924	0.010	0.018	0.031***	0.007	0.040**	0.017
<i>Bel_L23</i>	27	7.6	0.788	0.907	0.118***	0.033	0.037***	0.011	0.151***	0.030
<i>Bel_L47</i>	33	7.2	0.817	0.853	0.038*	0.025	0.064***	0.019	0.099***	0.029
<i>Bel_L15</i>	23	6.5	0.763	0.791	0.040	0.034	0.105***	0.026	0.141***	0.034
<i>Bel_L45</i>	28	6.3	0.574	0.852	0.314***	0.039	0.025***	0.011	0.332***	0.036
<i>Bel_L31</i>	33	7.3	0.833	0.864	0.035	0.023	0.050***	0.009	0.083***	0.022
<i>Bel_L17</i>	16	5.1	0.728	0.764	0.041	0.036	0.058***	0.019	0.096**	0.033

87 Significance scores for F_{IS} , F_{ST} and F_{IT} : * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

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90 **Table S4.** Tests whether genotype frequencies in the 13 retained microsatellite loci follow Hardy-
 91 Weinberg equilibrium. These tests, i.e. χ^2 tests and exact tests based on 1000 Monte Carlo permutations
 92 of alleles, were run on the regrouped dataset.

Locus	χ^2	<i>df</i>	Pr(χ^2)	Pr.exact
<i>Bel_L53</i>	152.7	171	0.839	0.073
<i>Bel_L25</i>	395.0	253	<0.001	0.002
<i>Bel_L48</i>	142.1	136	0.343	0.002
<i>Bel_L16</i>	182.6	153	0.051	0.031
<i>Bel_L63</i>	166.2	105	<0.001	<0.001
<i>Bel_L13</i>	52.0	45	0.220	0.225
<i>Bel_L10</i>	262.1	171	<0.001	<0.001
<i>Bel_L32</i>	507.8	435	0.009	0.012
<i>Bel_L23</i>	608.5	351	<0.001	<0.001
<i>Bel_L47</i>	920.1	528	<0.001	<0.001
<i>Bel_L15</i>	649.7	253	<0.001	<0.001
<i>Bel_L31</i>	708.9	528	<0.001	0.002
<i>Bel_L17</i>	194.3	120	<0.001	0.002

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95 **Table S5.** Locality information for the regrouped dataset (13 loci) including statistics of genetic
 96 diversity and the identification of specimens to species and/or race. A_n = number of alleles; A_r =
 97 expected allelic richness among 14 gene copies ($K = 14$), H_E = expected heterozygosity, i.e. gene
 98 diversity corrected for sample size (Nei, 1978), H_O = observed heterozygosity, F_i = individual
 99 inbreeding coefficient with asterisks indicating the level of significance for $F_i \neq 0$ from a two-sided test
 100 with 1000 randomizations of gene copies among individuals (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

Code	Morphospecies	Waterbody	Country	Latitude	Longitude	# ind.	A_n	A_r	H_E	H_O	F_i
LA05_LA06	<i>B. rubicunda</i>	Lake Albert	Uganda	1.82451	31.31753	19	10.00	6.68	0.787	0.765	0.029
LA07	<i>B. rubicunda</i>	Lake Albert	Uganda	1.58649	31.10057	10	7.77	6.65	0.786	0.729	0.076
LV01_LV14_LV37	<i>B. constricta</i> ; <i>B. costulata costulata</i> ; <i>B. trochlearis</i>	Lake Victoria	Uganda	-0.29596	32.03063	17	10.85	7.01	0.800	0.790	0.013
LV06	<i>B. jucunda kisumiensis</i>	Lake Victoria	Kenya	-0.12739	34.74232	10	7.85	6.63	0.791	0.754	0.050
LV07_LV08_LV09	<i>B. costulata ugandae</i>	Lake Victoria	Kenya	-0.09336	34.02474	26	12.62	7.14	0.820	0.782	0.048*
LV26	<i>B. unicolor meta</i>	Lake Victoria	Uganda	0.28161	33.39454	10	7.54	6.44	0.786	0.703	0.110**
LV27	<i>B. costulata costulata</i> ; <i>B. costulata ugandae</i> ; <i>B. unicolor elatior</i> ; <i>B. unicolor meta</i>	Lake Victoria	Uganda	0.11627	33.56262	10	7.15	6.45	0.808	0.774	0.044
LV28	<i>B. costulata ugandae</i> ; <i>B. sp. (juvenile)</i>	Lake Victoria	Uganda	0.10460	33.57583	18	10.92	7.18	0.831	0.853	-0.027
LV29_LV30	<i>B. costulata ugandae</i> ; <i>B. jucunda altior</i> ; <i>B. jucunda jucunda</i> ; <i>B. unicolor elatior</i>	Lake Victoria	Uganda	0.13887	33.60204	18	10.31	7.08	0.838	0.859	-0.027
LV31	<i>B. unicolor meta</i>	Lake Victoria	Uganda	0.12456	33.62969	11	8.38	6.98	0.831	0.788	0.056
LV32	<i>B. trochlearis</i>	Lake Victoria	Uganda	0.16176	33.58264	10	8.54	7.32	0.845	0.804	0.051
LV33	<i>B. costulata dagusiae</i>	Lake Victoria	Uganda	0.15662	33.56414	20	10.85	7.24	0.843	0.842	0.001
LV34	<i>B. trochlearis</i>	Lake Victoria	Uganda	-0.30371	32.28927	10	7.38	6.41	0.797	0.815	-0.024
LV35_LV36	<i>B. costulata costulata</i> ; <i>B. costulata ugandae</i> ; <i>B. jucunda altior</i> ; <i>B. phthinotropis</i> ; <i>B. sp. (juvenile)</i>	Lake Victoria	Uganda	-0.22984	32.37665	11	8.92	7.39	0.847	0.810	0.046
LV38	<i>B. costulata costulata</i> ; <i>B. jucunda jucunda</i> ; <i>B. jucunda kisumiensis</i>	Lake Victoria	Uganda	-0.64564	31.80791	10	8.00	6.78	0.798	0.747	0.067
LV39	<i>B. costulata costulata</i> ; <i>B. unicolor elatior</i>	Lake Victoria	Uganda	0.03892	32.49402	11	8.62	7.19	0.852	0.855	-0.005
LV40	<i>B. constricta</i> ; <i>B. unicolor unicolor</i>	Lake Victoria	Uganda	0.05525	32.49198	10	8.62	7.19	0.842	0.782	0.075*
VN01	<i>B. costulata ugandae</i>	Victoria Nile	Uganda	0.48544	33.15524	10	6.92	5.97	0.752	0.777	-0.035
VN05	<i>B. costulata ugandae</i>	Victoria Nile	Uganda	1.69255	32.09473	12	6.54	5.36	0.729	0.724	0.006
VN06_VN07	<i>B. costulata ugandae</i>	Victoria Nile	Uganda	2.12613	32.33013	17	7.85	5.74	0.747	0.709	0.052
WN01	<i>B. unicolor unicolor</i>	White Nile	Uganda	2.45933	31.50487	12	7.00	6.01	0.765	0.747	0.025

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103 **Table S6.** Locus-specific percentage of private alleles for each of the three molecular groups, i.e. LAG
 104 = the Lake Albert Group, LVG = the Lake Victoria Group and LKG = the Lake Kyoga group.

Locus	% LAG-private	% LVG-private	% LKG-private	% common
<i>Bel_L53</i>	0.00	0.32	0.00	0.68
<i>Bel_L25</i>	0.00	0.21	0.00	0.79
<i>Bel_L48</i>	0.00	0.42	0.05	0.53
<i>Bel_L16</i>	0.11	0.11	0.00	0.79
<i>Bel_L63</i>	0.05	0.26	0.00	0.68
<i>Bel_L13</i>	0.05	0.05	0.00	0.89
<i>Bel_L10</i>	0.05	0.21	0.00	0.74
<i>Bel_L32</i>	0.00	0.53	0.00	0.47
<i>Bel_L23</i>	0.05	0.26	0.05	0.63
<i>Bel_L47</i>	0.00	0.84	0.05	0.11
<i>Bel_L15</i>	0.21	0.42	0.00	0.37
<i>Bel_L31</i>	0.16	0.32	0.00	0.53
<i>Bel_L17</i>	0.00	0.42	0.05	0.53

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107 **Table S7.** Estimates of contemporary relative gene flow between pairwise populations of *Bellamyia*
 108 from the Lake Victoria ecoregion as inferred with BayesAss (Wilson & Rannala, 2003). Source
 109 populations appear in rows and receiving populations in columns, with diagonal values indicating the
 110 proportion of non-migrants. Other values indicate the fraction of individuals in the receiving population
 111 that are migrants from the source population. Represented values are averages from three independent
 112 runs, each with 20,000,000 Markov chain Monte Carlo iterations, a burn-in of 5,000,000 iterations and
 113 sampling every 10,000 iterations. Standard deviations among runs were negligible (<0.11 %). The
 114 greyscale background color of cells is proportional to values.

	LA05			LV01			LV07			LV29			LV35									
	WN01	06	LA07	14 37	LV06	08 09	LV26	LV27	LV28	30	LV31	LV32	LV33	LV34	36	LV38	LV39	LV40	VN01	VN05	VN06 07	
WN01	67.7 %	12.2 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	2.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %
LA05_06	0.8 %	82.4 %	0.8 %	0.9 %	0.8 %	0.9 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	1.7 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.9 %
LA07	1.1 %	10.8 %	67.7 %	1.1 %	1.1 %	2.2 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %
LV01_14_37	0.9 %	0.9 %	0.9 %	67.5 %	0.9 %	15.7 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %
LV06	1.1 %	1.1 %	1.1 %	1.1 %	67.8 %	11.8 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %
LV07_08_09	0.7 %	0.7 %	0.7 %	0.7 %	0.7 %	84.2 %	0.7 %	0.7 %	0.7 %	0.7 %	0.7 %	0.7 %	1.5 %	0.7 %	0.7 %	0.7 %	0.7 %	0.7 %	0.7 %	0.7 %	0.7 %	1.5 %
LV26	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	11.8 %	67.7 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %
LV27	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	8.9 %	1.1 %	67.8 %	1.1 %	1.1 %	1.1 %	1.1 %	4.0 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %
LV28	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	16.2 %	0.9 %	0.9 %	67.5 %	0.8 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %
LV29_30	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	13.7 %	0.9 %	0.9 %	0.9 %	67.5 %	0.9 %	0.9 %	3.4 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.8 %	0.9 %	0.9 %
LV31	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	12.6 %	1.0 %	1.0 %	1.1 %	1.0 %	67.7 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %
LV32	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	11.8 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	67.7 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %
LV33	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	14.6 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	69.9 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %	0.8 %
LV34	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	11.8 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	67.7 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %
LV35_36	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	12.4 %	1.0 %	1.0 %	1.1 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	67.7 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.1 %
LV38	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	11.8 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	67.7 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %
LV39	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	11.4 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	2.1 %	1.0 %	1.0 %	1.0 %	67.7 %	1.0 %	1.0 %	1.0 %	1.0 %	1.1 %
LV40	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	11.9 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	67.7 %	1.1 %	1.1 %	1.1 %	1.1 %
VN01	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	11.8 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	1.1 %	67.7 %	1.1 %	1.1 %	1.1 %
VN05	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	1.0 %	67.7 %	13.1 %
VN06_07	0.9 %	1.0 %	0.9 %	0.9 %	0.9 %	1.5 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	0.9 %	81.7 %

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117 **Table S8.** Relative support for the five anagenetic demographic models in our ABC simulations for
 118 LAG and LVG, excluding individuals that indicate admixture ($n = 1$ and 16 , respectively; in LKG all
 119 individuals have assignment probabilities to the gene pool $\geq 80\%$). Scenarios of effective population
 120 size through time for each of these models are displayed in Fig. 2.

Group	Model 1	Model 2	Model 3	Model 4	Model 5	Model 3+5
Lake Albert Group	0.1700	0.0004	0.3933	0.0006	0.4357	0.8290
Lake Victoria Group	0.2378	0.0109	0.3492	0.0199	0.3822	0.7314

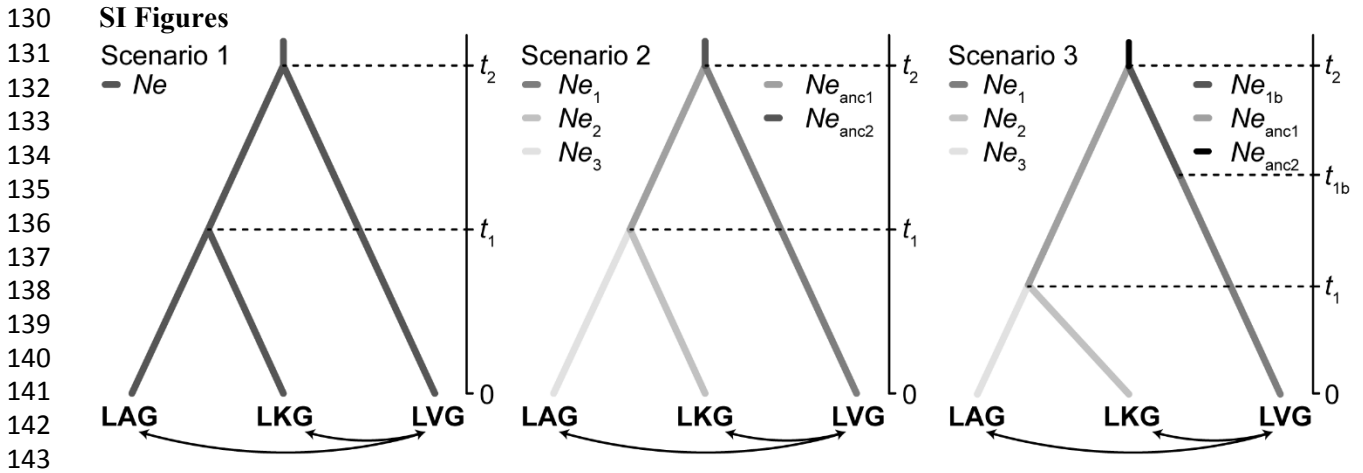
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123 **Table S9.** Estimates on the principal demographic parameters for the best supported ABC models on
 124 LAG and LVG excluding individuals that indicate admixture. 95% CI indicates the 95% confidence
 125 intervals. Given the high similarities in models 3 and 5, their averaged outcome is presented under
 126 Model 3+5. N_e represents the number of diploid individuals in the population and times t , t_1 and t_2 are
 127 expressed in number of generations [1 generation is \sim 1 year for *Bellamyia* (Brown, 1994)].

	mean N_e	mode N_e	95% CI		mean t or t_1	mode t or t_1	95% CI		mean $N_{e_{big}}$	mode $N_{e_{big}}$	95% CI		mean t_2	mode t_2	mean $N_{e_{s,Anc}}$	mode $N_{e_{s,Anc}}$
Lake Albert Group (no admixture)																
scenario 3	16 400	7 500	4 360	43 400	148 000	48 600	18 700	433 000	3.92×10^6	1.11×10^6	203 000	9.46×10^6	n.a.	n.a.	n.a.	n.a.
scenario 5	21 100	8 270	4 450	43 400	100 000	39 500	14 800	308 000	6.20×10^6	9.69×10^6	1.38×10^6	9.84×10^6	299 000	339 000	3.02×10^6	405 000
scenario3+5	16 800	7 110	4 400	43 000	123 000	32 700	13 900	406 000	5.13×10^6	3.70×10^6	401 000	9.73×10^6	n.a.	n.a.	n.a.	n.a.
Lake Victoria Group (no admixture)																
scenario 3	29 000	12 300	7 360	78 200	210 000	77 200	33 500	473 000	4.47×10^6	378 000	187 000	9.64×10^6	n.a.	n.a.	n.a.	n.a.
scenario 5	47 600	11 200	7 310	85 300	134 000	78 900	17 800	358 000	6.10×10^6	8.97×10^6	1.28×10^6	9.85×10^6	316 000	406 000	2.64×10^6	238 000
scenario3+5	35 500	12 700	7 570	78 600	173 000	74 600	24 600	451 000	5.28×10^6	9.12×10^6	362 000	9.80×10^6	n.a.	n.a.	n.a.	n.a.

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144 **Figure S1.** Schematic representation of the 9 examined phylogenetic DIYABC models, including three
 145 possible topological relationships between the three molecular groups, i.e. the Lake Albert Group
 146 (LAG), the Lake Kyoga Group (LKG), and the Lake Victoria Group (LVG) for each of three scenarios.
 147 From scenario 1 to 3 the number of parameters as to effective population size (Ne) increases, allowing
 148 with each new parameter new combinations of change (increase or decrease) in Ne .
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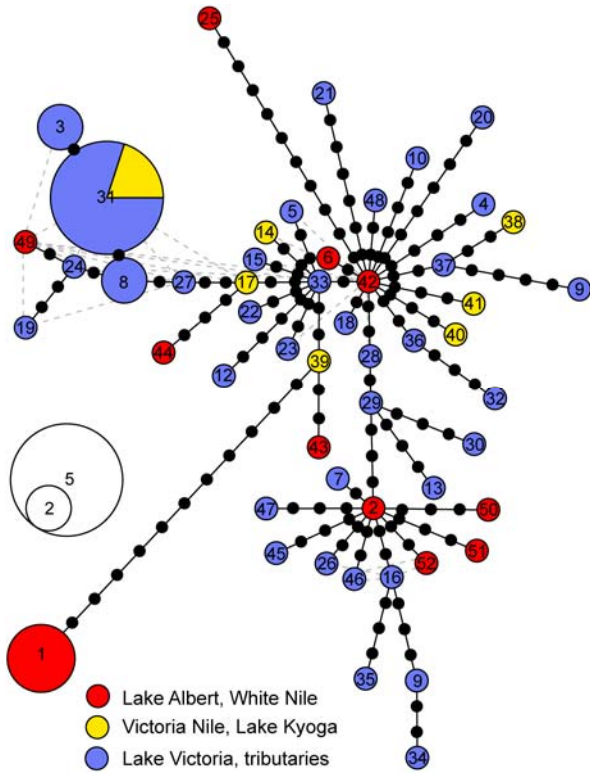


Figure S2. Haplotype network of 52 *Bellamyia* haplotypes obtained from 60 sequences of the cytochrome oxidase subunit I (593 bp; see Table S1) belonging to specimens of the Lake Victoria ecoregion, i.e. the ‘Victoria clade’ of Schultheiß et al. (2014). Dashed light grey edges indicate alternative relationships (mutations, at most 2 mutations/edge, are not indicated for these edges).

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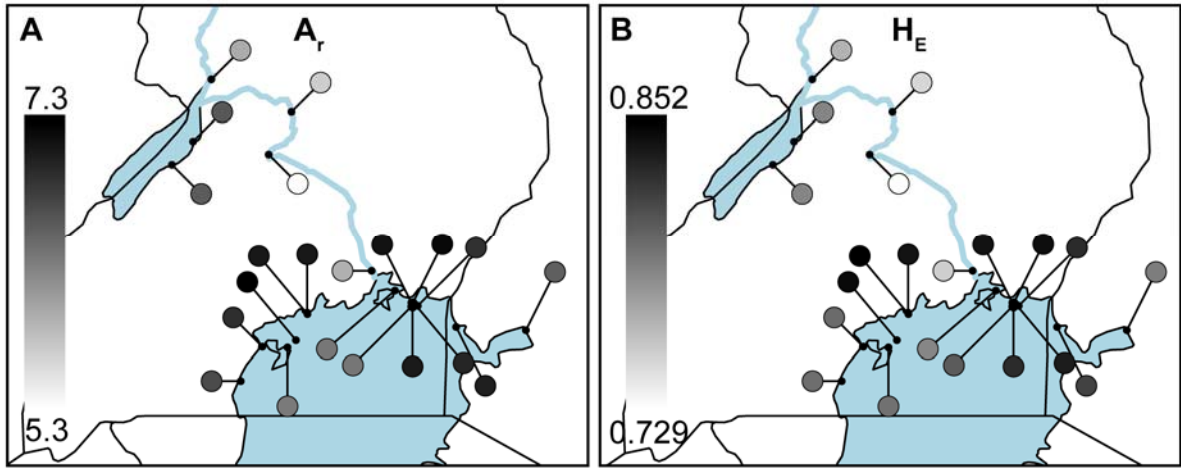


Figure S3. Geographic variation in allelic richness among 14 gene copies (A) and expected heterozygosity (B) in the regrouped dataset of *Bellamya* from the Lake Victoria ecoregion.

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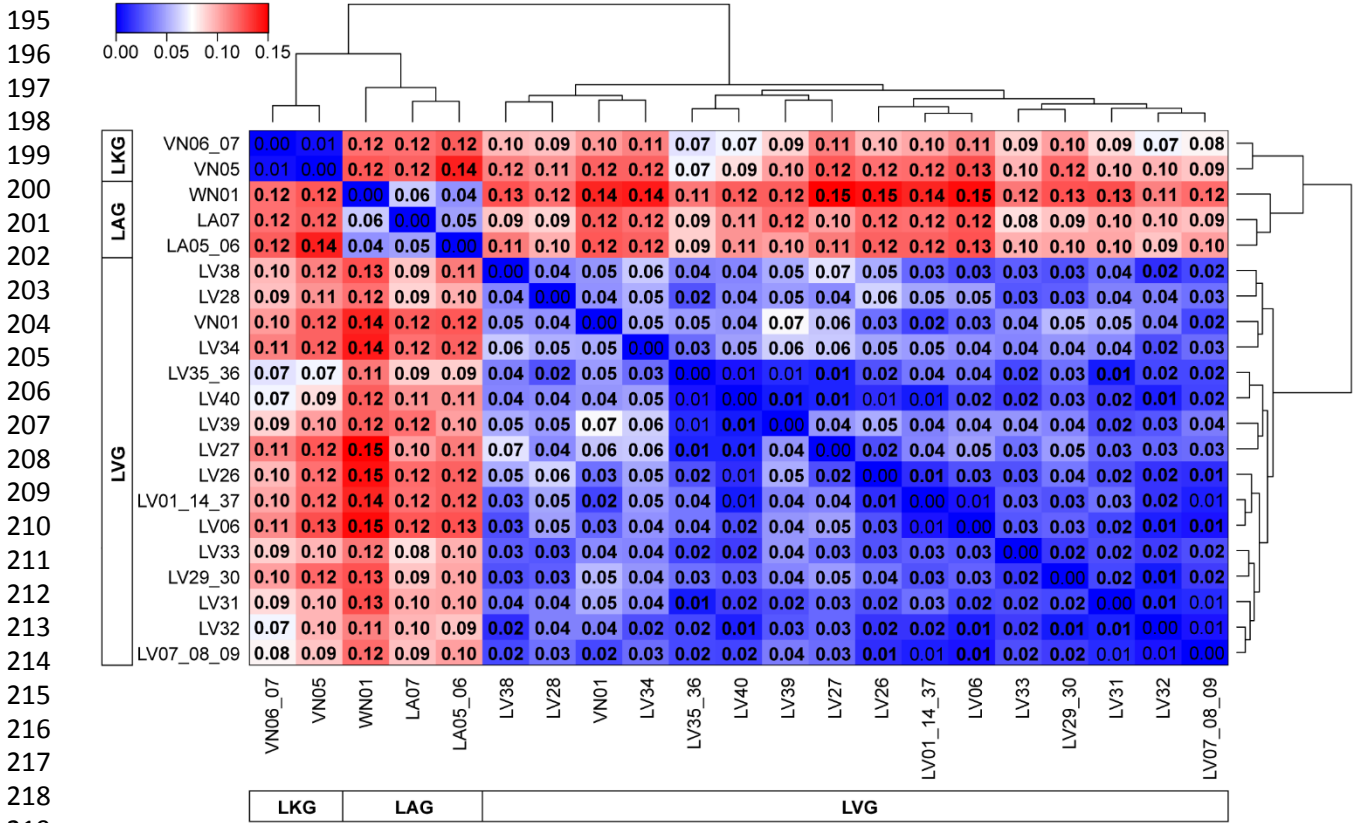


Figure S4. Heatmap of population pairwise F_{ST} values with clustering dendrograms revealing the three molecular groups (= gene pools) of specimens in the Lake Victoria ecoregion. High F_{ST} values are observed between gene pools (red), whereas F_{ST} values within gene pools (blue) are lower.

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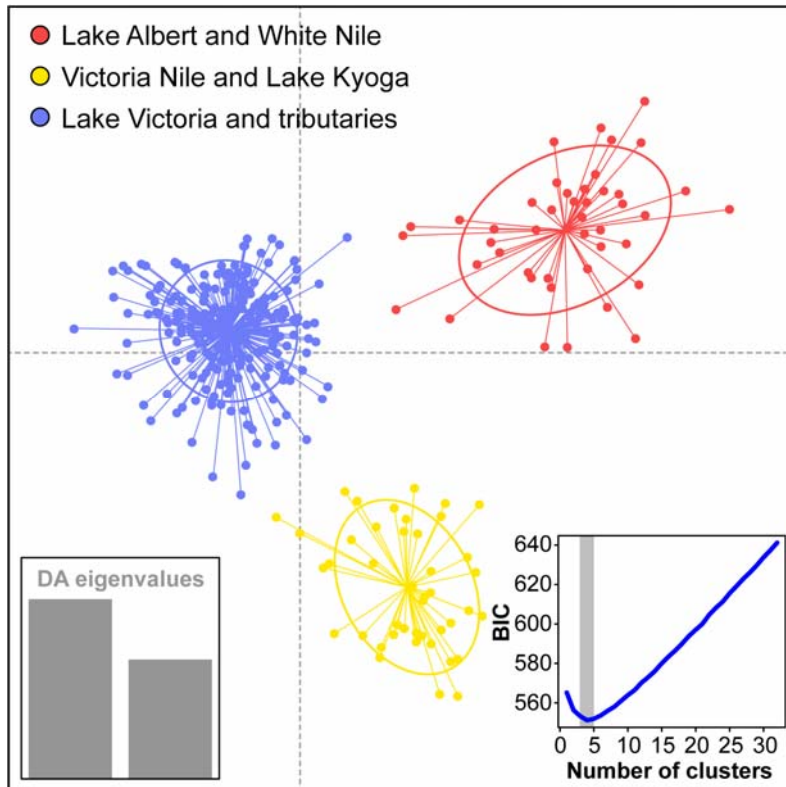
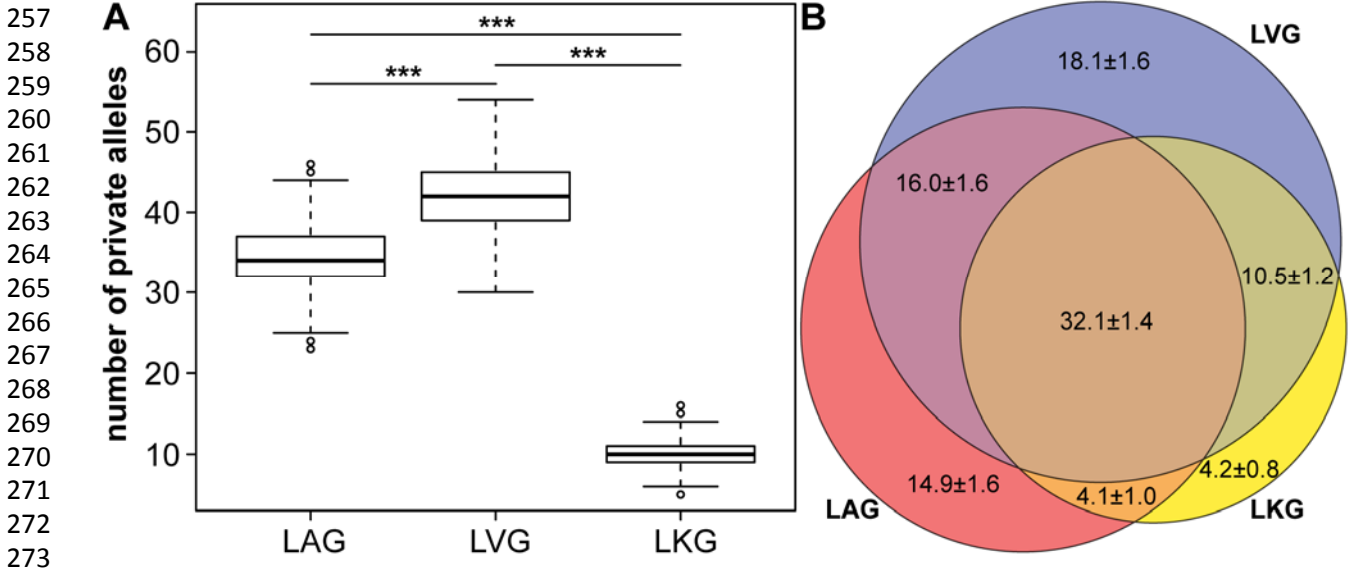
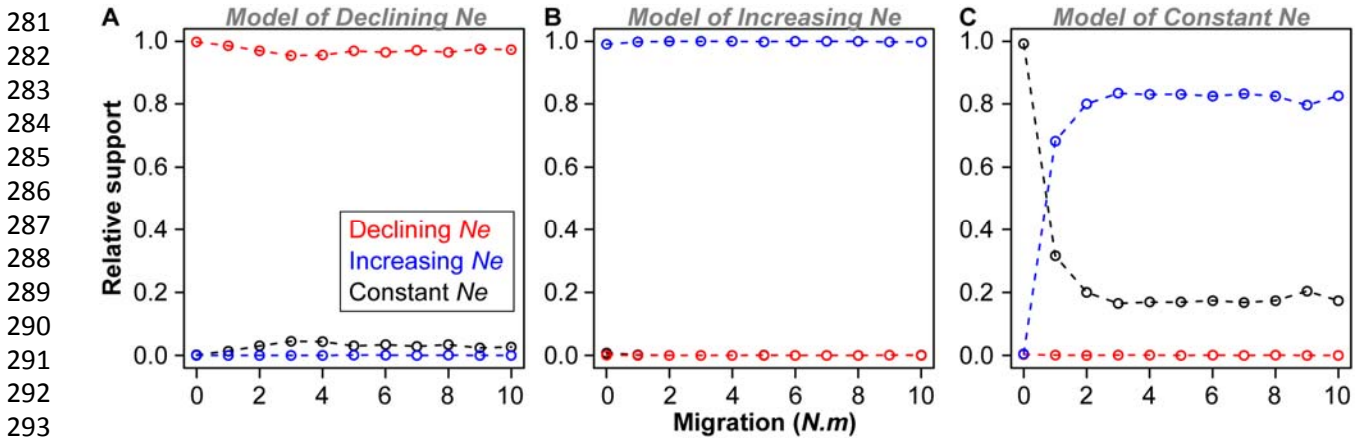


Figure S5. Discriminant analyses of molecular components on the microsatellite dataset (13 loci) of *Bellamyia* from the Lake Victoria ecoregion. The analysis indicates highest support from the Bayesian information criterion (BIC) for four groups, which resulted in poor assignment probabilities for two of these four groups, however. The here depicted three-group solution has still high BIC support and consistently high assignment probabilities. Therefore, it represents a more robust clustering solution. As with the other two clustering methods illustrated in the main text, a few individuals were assigned to geographic clusters that are inconsistent with their sampling locality (not shown). See main text and Fig. 3A, C for more information on this topic.



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 274 **Figure S6.** A) Total number of private alleles from 13 microsatellite loci for 1000 random subsamples
 275 of 29 individuals (the number of individuals in the regrouped dataset assigned to the smallest genetic
 276 cluster, LKG) for each molecular cluster. Differences between these three distributions were tested with
 277 FDR-corrected Wilcoxon tests, and are highly significant. B) Relative proportions (in %, mean ± sd) of
 278 private and shared alleles among the three molecular groups following the same subsampling scheme
 279 under (A).
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294 **Figure S7.** Analysis of how migration into the studied population affects approximate Bayesian
295 computation (ABC) for populations with a decline in N_e (A), an increase in N_e (B) and constant N_e (B)
296 over time. Migration is indicated as the number of immigrants per generation into the studied population
297 ($N.m$). Migration does not bias ABC inferences for populations that are declining or increasing in N_e ,
298 however, it is expected to bias conclusions for populations of constant N_e .
299