

Founder effects determine the genetic structure of the water flea *Daphnia* in Ethiopian reservoirs

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1 Founder effects determine the genetic structure of the water flea *Daphnia* in Ethiopian reservoirs

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17 Running headline: Founder effects in zooplankton populations

18

19 **Abstract**

20 Founder effects introduce stochasticity in the genetic structure of species at the regional scale. To
21 the extent that founder effects are important that they will result in a reduced signature of space,
22 time and environmental variation in landscape genetic data. We studied the metapopulation
23 genetic structure of recently founded populations of the microcrustacean *Daphnia sinensis* in ten
24 Ethiopian water reservoirs. We used three different approaches of estimating the number of
25 effective founders applied to two independent genetic marker sets to investigate the role of
26 founder effects and to estimate effective size of the founding population. Estimates of founding
27 sizes rarely exceeded eight individuals but were most often limited to less than four individuals.
28 No associations of genetic identities, gene frequencies, measures of genetic diversity or
29 differentiation with environmental and spatial variables were found. Age and size of the
30 reservoirs were not correlated with genetic diversity measures or number of founders in these
31 reservoirs. These findings indicate that neither strong selection, nor dispersal limitation are
32 responsible for the observed pattern of genetic variation. Our results suggest a regional
33 population structure that is strongly impacted by founder events, reflecting colonization by just a
34 few founders per water body, and not noticeably influenced by subsequent dispersal and gene
35 flow. Our results show that rapid colonization of empty habitats and fast population growth by a
36 handful of founders can result in strong founder effects, even in relatively large habitats
37 (estimated populations sizes of several million individuals) that are likely regularly reached by
38 new immigrants.

39 **Keywords:** colonization, *Daphnia sinensis*, effective population size, founder effects,
40 metapopulation, monopolization, zooplankton

41

42 **Introduction**

43 Metapopulation theory describes the interplay between colonization and extinction rates on patch
44 occupancy as a function of death, birth and dispersal rates ([Hanski 1998](#); [Levins 1969](#)).
45 Population genetics, on the other hand considers occupied patches, and considers how gene flow
46 and population size interact to influence genetic structure within and among demes of a
47 metapopulation ([Wright 1951](#)). In reality, both extinction-colonization dynamics of local
48 populations and changes in genetic diversity by gene flow and drift within these local populations
49 act simultaneously. Dispersal, which is one of the most fundamental processes in ecology, affects
50 many aspects of evolution and population genetics if translated into successful colonization
51 ([Bilton et al. 2001](#)). Dispersal allows individuals to establish new populations in an empty patch
52 and promotes range expansion following colonization of new sites.

53 In a metapopulation genetics context, the colonization of an empty habitat patch by
54 founders can be considered as a special case of gene flow. As the new local population grows in
55 size to carrying capacity, new neutral immigrants (having equal expected fitness) can still enter
56 the population, but their relative contribution to the local gene pool is expected to decrease as
57 local population size at the time of immigration becomes larger. In this initial colonization
58 scenario at least two processes are responsible for successful colonization and establishment of a
59 population in an empty patch. First, the response of the immigrants to the local environmental
60 conditions of the habitat they colonize. Second, differences in their time of arrival at the site,
61 which generates a numerical advantage to the first colonizers over late-comers ([Boileau et al.](#)
62 [1992](#); [De Meester et al. 2002](#)). In contrast to the relative ease of establishment of founders, which
63 experience no to a little competition, individuals attempting to immigrate into an established
64 population close to carrying capacity are faced with strong intraspecific competition by the
65 resident population and low levels of resources. Due to this, realized rates of gene flow may be

66 much lower than expected based on the rates of dispersal ([De Meester et al. 2002](#)). This reduced
67 establishment success may strongly contribute to prolonged persistence of founder effects
68 ([Boileau et al. 1992](#); [De Meester et al. 2002](#); [Ventura et al. 2014](#)). Because founder effects
69 represent a type of sampling error, they introduce stochasticity in the genetic structure at the
70 regional scale, which tends to result in a reduced signature of space and environmental variation
71 in the genetic data ([Orsini et al. 2013](#)).

72 Estimates of the number of founders represent baseline estimates for ecological dispersal
73 rates (m_c , the observed number of migrants), which represent the maximal potential for gene flow
74 (m_e , the effective number of migrants) among populations. Gene flow, the realized effect of
75 ecological dispersal on genetic structure, can be estimated indirectly through population genetics
76 as well ([Broquet & Petit 2009](#)). Although we know from many population genetic studies in
77 zooplankton that gene flow (m_e) is often much lower than expected, we have relatively few good
78 estimates of ecological dispersal rates (m_c), because they are so hard to measure directly ([Bilton
79 et al. 2001](#)). Nevertheless, good dispersal estimates provide baseline information for a broad
80 array of ecological and evolutionary studies ([Broquet & Petit 2009](#)). Distinguishing between
81 dispersal and gene flow is essential, especially for biological conservation of populations and
82 species.

83 Here we take advantage of the recent creation of water reservoirs in Northern Ethiopia
84 and the colonization of these water bodies by zooplankton to estimate the number of founders of
85 populations of a zooplankton species using genetic methods. The reservoirs studied here are
86 young (6-18 years) and two to three orders of magnitude larger than most other systems studied
87 so far on founder effects in zooplankton and small invertebrates ([Boileau et al. 1992](#); [Haag et al.
88 2006](#); [Louette et al. 2007](#)). Specifically, we present patterns of genetic composition and
89 differentiation of the water flea *Daphnia sinensis* in reservoirs that range in size from 1.8 to 45.4

90 hectare. Using variation at nuclear (nDNA) and mitochondrial (mtDNA) genetic markers, we
91 estimate allele frequencies, within-population genetic variation and among-population genetic
92 differentiation, and relate genetic variation and genotype composition to spatial, environmental
93 and temporal variables. We use various methods to independently estimate founding population
94 sizes, and thereby provide baseline estimates of dispersal rates. Using information on the
95 observed genetic structure (F_{ST}) and the associated expected gene flow at various levels of
96 migration-drift equilibrium and ages of populations, we show that the dispersal rates (m_c) are
97 orders of magnitude higher than the actual gene flow rates (m_e).

98

99 **Methods**

100 **Study region and sampling**

101 The studied reservoirs are part of a set of reservoirs constructed between 1984 and 2001 in the
102 highlands of Tigray Regional State, Northern Ethiopia. The rainfall in Tigray region is seasonal
103 and erratic resulting in moisture stress that hampers the rain-fed agriculture ([Haregeweyn et al.
104 2006](#)). To solve this problem agricultural development through irrigation has been a priority for
105 the Regional Government of Tigray. Hence, the target of the construction of reservoirs was
106 mainly to bring food self-sufficiency to the area through irrigation but also to use the water for
107 household consumptions ([Asmelash et al. 2007](#)). Thirty-two of these reservoirs have been the
108 subject of a detailed limnological survey ([Asmelash et al. 2007](#); [Dejenie et al. 2008](#)). Apart from
109 a single natural lake, not inhabited by the focal species of this study, *Daphnia sinensis*, no similar
110 large and deep aquatic systems are known from Tigray ([Dejenie et al. 2008](#)). Naturally, this
111 species occurs in temporary pools and ponds as well as larger temporary ponds and lakes ([Gu et
112 al. 2013](#)). The rapid colonization of these reservoirs shortly after their creation by a considerable
113 number of zooplankton taxa, including typical lake species ([Dejenie et al. 2008](#)), despite a
114 regional lack of similar habitats suggests that dispersal rates are relatively high and long-distance
115 dispersal events are rather frequent. Water birds (members of the Podicipidae, Pelecanidae,
116 Ciconiidae, Anatidae and Charadriidae family) are common in and alongside the reservoirs
117 ([Asmelash et al. 2007](#)) and are probably important vectors of dormant propagules of zooplankton
118 ([Figuerola & Green 2002](#)).

119 Thirty-two reservoirs were sampled for zooplankton in September 2005 ([Dejenie et al.
120 2008](#)). Ten of these samples contained *D. sinensis* in large enough numbers for population
121 genetic analyses (see Table S1, Supporting information). In addition, five temporary natural
122 wetlands were sampled, two of which contained *D. sinensis* (henceforth called T1 and T3),

123 bringing the total number of independent samples to twelve. All *Daphnia* samples were preserved
124 in 100% ethanol until further processing. Although previously identified as *D. carinata* King by
125 Dejenie *et al.* (2008), DNA barcoding indicates that individuals from these reservoirs belong to
126 *D. sinensis*, a member of the *Daphnia similis* species complex (Popova *et al.* 2016).
127 Measurements of geographic position and morphometric, physical, chemical, and biotic variables
128 were recorded for each sampled reservoir (see Table S1, Supporting information; Dejenie *et al.*
129 2008). Age of the reservoirs was expressed as number of years at sampling time since
130 construction of the reservoir. The two natural populations T1 and T3 were first excluded from all
131 age related analysis, and were in a second analysis arbitrarily given the same age as the oldest
132 reservoir.

133

134 **Genotyping**

135 DNA of individual *Daphnia* was extracted using the HotShot protocol (Montero-Pau *et al.* 2008)
136 Sample sizes ranged from 6 to 35 individuals per population for mtDNA (Table 1; 10 out of 12
137 samples with 17 or more individuals) and from 15 to 34 individuals per population for nDNA
138 (Table 2). Differences in sample sizes between both markers are due to unsuccessful
139 amplification with either approach. A fragment of 341 nucleotides of the mtDNA cytochrome
140 oxidase gene, subunit 1 (*COI*) was amplified using primers *SCoxIF1* (GGC CCC AGA TAT
141 GGC TTT) and *SCoxIR2* (GCT CCA GCT AAT ACT GGT AAA CTT), specifically designed
142 for this study. The polymerase chain reaction mix of 25 µl contained 2 µl DNA, 2.75µl 10x PCR
143 buffer (10 mM Tris-HCl; pH 8.3; 50 mM KCl), 0.4 µM of each primer, 2.2 mM MgCl₂, 0.2 mM
144 of each dNTP, and 1 unit Silverstar *Taq* DNA polymerase (Eurogentec[®], Liege Belgium). PCR
145 cycling conditions, PCR product purification and sequencing followed the methods of Mergeay *et*
146 *al.* (2007). The purified fragments were sequenced using 3.2 pmol of *SCoxIF1* primer and the

147 ABI Big Dye Terminator Kit. Sequences were aligned and trimmed in Mega 4.1 ([Kumar et al.](#)
148 [2008](#)).

149 Variation at six microsatellite loci using primers originally developed for the related
150 species *Daphnia magna* (*B088*, *B172*, *B087*, *S6-38*, *B064* and *Dma15* ([Agostini et al. 2010](#);
151 [Jansen B et al. 2011](#)) was assessed in a single multiplex PCR reaction of 10 µl consisting of 5 µl
152 HotStar *Taq* DNA polymerase buffer (Qiagen[®], Hilden Germany), 0.15 µM, 0.5 µM, 0.3 µM, 0.2
153 µM, 0.1 µM and 0.3 µM of each primer of locus *Dma15*, *B087*, *B064*, *S6-38*, *B088* and *B172*,
154 respectively, and 2 µl of template DNA. Cycling conditions were 15' hot start denaturation at
155 95°C followed by 30 cycles of 30" for each step at 95°C, 56°C and 72°C, and a final elongation
156 step at 60°C for 30'. Polymorphism was assessed on an ABI PRISM[®] 3130 genetic analyser
157 (Applied Biosystems[®], Foster City, CA, USA), using an internal Liz Gene-scan size standard by
158 means of the Genemapper 4.0 software (Applied Biosystems[®], Foster City, CA, USA).

159

160 **Population genetic data analysis**

161 Nucleotide diversity of the sequenced *COI* fragments was calculated in DNAsp version
162 4.5 ([Rozas et al. 2003](#)). Because we were not interested in the evolutionary relationships among
163 haplotypes that originated thousands of years prior to the colonization of these reservoirs, no
164 attempts were made to construct haplotype networks or to calculate genetic differentiation among
165 populations based on haplotype identity. The observed haplotype frequencies were primarily used
166 to estimate the number of founders involved in the colonization of each reservoir. We calculated
167 observed haplotype richness (HR) for each sample as well as haplotype diversity (HD). HD was
168 calculated as the true diversity equivalent of the Simpson concentration ([Jost 2007](#)). These values
169 were compared to expected HR and HD under the null hypothesis that all reservoirs form one
170 panmictic population, using 10^4 permutations in Partition ([Veech & Crist 2009](#)). This yields alpha

171 (local gene diversity) and beta (average differentiation) estimators that are converted to their true
172 diversity equivalents ([Jost 2007](#)).

173 Standard measures of genetic diversity (number of alleles, allelic richness per locus and
174 per population across all loci, observed heterozygosity and expected heterozygosity) at six
175 microsatellite loci were assessed in R using diveRsity package ([Keenan et al. 2013](#)). Identical
176 multilocus genotypes, on the basis of the combined information of six microsatellite loci, in a
177 given water body were considered to belong to a single clone. Clonal diversity (CD) was
178 expressed as the true diversity equivalent of the Simpson concentration, clonal richness (CR) as
179 the number of multilocus genotypes per water body. Moreover, relative clonal richness was
180 calculated per sample corrected for sample size expressed as proportion of clones to total
181 individuals genotyped as $R = (G-1) / (N-1)$, where G is the number of genotypes and N indicates
182 sample size. We used HWclon ([De Meester & Vanoverbeke 1999](#)) to estimate whether or not
183 observed levels of CD and CR were significantly different from a random distribution, given the
184 genetic diversity and allelic polymorphism in the population ([De Meester & Vanoverbeke 1999](#);
185 [Vanoverbeke & De Meester 1997](#)).

186 The standardized genetic variance among populations (F_{ST}) was calculated according to
187 Weir & Cockerham([1984](#)). We used 500 bootstrap pseudoreplicates to estimate 95% confidence
188 intervals of the F_{ST} values. Genetic structure was assessed using the unbiased estimators of Nei &
189 Chesser ([1983](#)) of the overall gene diversity (H_T) and subpopulation gene diversity (H_S).

190

191 **Spatial, environmental and temporal correlates of genetic differentiation**

192 To investigate the role of spatial and environmental variables separately and to
193 disentangle the unique contribution of each variable matrix to the genetic structure of the studied
194 populations we used redundancy analyses (RDA, a linear constrained ordination technique [Dray](#)

195 [et al. 2006](#)). In a multivariate variation partitioning analysis, the contributions of local
196 environmental predictors (n= 16 variables provided in Table S1, Supporting information) and
197 spatial predictors are tested by generating adjusted redundancy statistics (R^2_{adj}) in an RDA
198 analysis. A significant effect of environment would imply sorting of clones with different traits
199 and niches along environmental gradients.

200 Under a model of persistent founder effects, we expect genetic structure to be mainly
201 caused by chance events as dispersal is likely not limiting at the investigated spatial scale. Hence,
202 we expect to find at most a weak spatial genetic structure in the data ([Orsini et al. 2013](#)). To test
203 this, with the nDNA allele frequency data we performed a principle coordinates analysis (PCoA)
204 and then used the population loadings of the first six PCoA axes as dependent variables in a
205 distance-based redundancy analysis (db-RDA). In this RDA we attempted to explain the observed
206 genetic variation as a function of distance-based eigenvector maps (dbMEM) ([Dray et al. 2006](#)).
207 This analysis allows to find spatial patterns in the genetic data other than linear ones, making this
208 a more powerful approach with lower type II error rates than Mantel tests ([Legendre & Fortin](#)
209 [2010](#)). Five positive dbMEM eigenvectors were retained and were used as explanatory variables
210 in a forward selection procedure. Although this particular approach has the risk of identifying a
211 false positive spatial signal (see [Blanchet et al. 2008](#)), the double stop criterion of Blanchet *et al.*
212 ([2008](#)) is very conservative with regard to small datasets. Here we take a more liberal approach,
213 involving forward selection of spatial variables without prior testing of the overall spatial model,
214 to make sure that any lack of a detectable spatial signal is not due to the use of conservative
215 statistical methods.

216 In parallel, we performed a separate RDA relating the mtDNA data to the spatial data
217 (dbMEM). These mtDNA data were Hellinger-transformed to allow the use of linear regression
218 analyses in zero-inflated data ([Legendre & Gallagher 2001](#)).

219 Using non-parametric correlation (Spearman's rho) analyses, we related diversity
220 measures (H_e , AR, HR, HD, CR, CD, number of founders at mtDNA, and number of founders at
221 nDNA) to age, depth and size of the reservoirs. Under a model of persistent founder effects,
222 genetic diversity should not be related to age or size of the reservoir, as late-arriving immigrants
223 are expected to have little impact on the genetic structure compared to the very first founders. If
224 founder effects still persisted at the time of sampling, we expect that old and large populations do
225 not differ in genetic structure from younger and/or smaller populations. Specifically, we tested if
226 a model of population structure including reservoir age, reservoir size or their interaction
227 explained the genetic structure better than the null model not including age or size using Geste v.
228 2 ([Foll & Gaggiotti 2006](#)). Geste calculates a specific F_{ST} value for each population that
229 represents the population specific contribution to the total genetic differentiation in the
230 metapopulation. Then, the effect of age and/or size on these F_{ST} values is evaluated using
231 generalized linear models. The posterior probability of each model was used to select the model
232 with the highest probability given our data.

233

234 **Estimating the number of effective founders**

235 We used three different approaches to estimate the number of effective founders, which
236 reflects how many individuals contributed to the observed genetic diversity in each local
237 population. First, we used a general approach based on F-statistics from microsatellite data, using
238 the principle that the inbreeding coefficient among populations just after colonization is
239 $F_{ST} = (2K)^{-1}$, with K the average number of founders per population ([Boileau *et al.* 1992](#); [Wade
240 & McCauley 1988](#)). Confidence intervals (95% CI) for F_{ST} were calculated by bootstrapping over
241 loci (500 replicates). This method provides the average effective size of the founding population.

242 Second, we used a general simulation approach in the programming environment R (R 2.14; The
243 R Foundation for Statistical Computing, 2014) to calculate the expected HR and HD under a
244 model of random colonization from a regional gene pool with 1, 2... 10, 15 and 20 founders.
245 Expected HR and HD values were calculated by randomly sampling 10^4 times the pre-set number
246 of founders in 200 populations from an estimated regional frequency distribution, which was
247 based on the actual haplotype counts over all water bodies, or on presence-absence data for each
248 haplotype per water body. For each of the random samples we calculated the probability that the
249 expected average HR or HD, over the 200 population, was smaller or larger than the values
250 observed in our empirical dataset. The product of these values provides the overall probability
251 that the observed HD or HR is achieved by the corresponding number of founders. The R-script
252 is available as supplementary information (Table S2, Supporting information), and provides the
253 average census size of the founding population. Third, we used a population-specific approach
254 for which we used the Colonize script ([Mergeay *et al.* 2007](#); [Vanoverbeke & Mergeay 2007](#)).
255 This is a standalone command-line tool that calculates the likelihood that a predefined number of
256 founders from a predefined source population established the focal population, given the gene
257 frequency distribution of the source and the sink populations. The number of founders associated
258 to the highest likelihood score provides the best estimate for the founding propagule size of that
259 population. Again, this provides the census size of the founding population, which ignores that
260 some individuals contributed less to the genetic structure of the founding population than other
261 individuals. For each water body, we calculated likelihood scores for one to thirty founders, and
262 set both the number of batches and the number of random samples to 500. Ideally, one has
263 multiple putative source populations from which to sample, so as to assign the most likely source
264 population as well (see Mergeay *et al.* 2007, for an example). Here we have no such prior
265 information, and hence we use the regional gene pool (the average over all our samples) as the

266 overall source population. To increase the overall robustness of this approach, three different
267 prior allele frequency distributions were used. 1) Using the regional frequency of each allele over
268 the pooled data of all investigated water bodies (distribution = Freq.). Here we used the rare allele
269 correction in Colonize to account for extremely rare alleles. 2) Using presence-absence of each
270 allele per population and counting the frequency of occurrence of each allele over all populations
271 (distribution = Rich.). This approach gives less weight to alleles that dominate in certain
272 populations but are rare in other populations. 3) Using three abundance classes for the regional
273 allele frequencies (1: frequency <15%; 2: frequency 15-30%; 3: frequency >30%). This approach
274 (distribution = Level) gives even more weight to rare alleles. Analyses with Colonize were
275 performed separately for the mtDNA data and for the nDNA data in order to obtain independent
276 estimates for both marker types. Overall, these three approaches yield one overall estimate based
277 on F_{ST} (first method), two overall estimates based on mtDNA haplotype richness and haplotype
278 distributions (second method), and per reservoir three estimates based on mtDNA and three based
279 on nDNA (third method).

280

281 **Testing assumptions**

282 All of the outlined methods to estimate the number of founders rely on similar
283 assumptions, but vary in their sensitivity to violations thereof. Here we outline how we tested for
284 violations of the assumptions. First, we assume that genetic drift has not yet strongly affected
285 allele frequency distributions (especially fixation or loss of alleles), given that they were founded
286 at most 6 to 18 years before sampling. Second, we assume that all founders are genetically
287 independent.

288 The main source of genetic drift in cyclical parthenogens like *Daphnia* is clonal selection

289 (reduction in clonal and genetic diversity as a result of selection among clones in the population)
290 ([De Meester et al. 2006](#)), which may erode genetic diversity considerably and thereby reduce our
291 estimates of founding population sizes. To assess whether clonal population structure (leading to
292 a similar signal as genetic bottlenecks) has affected our results, we performed a Spearman Rank
293 order correlation between clonal diversity (CD) and clonal richness (CR) versus the estimated
294 number of founders per population. This was performed for all estimates of the number of
295 founders, which have different sensitivities for common and rare alleles. Significant correlations
296 would reflect that clonal erosion affects our estimates of founding population sizes. Furthermore,
297 because drift reduces richness faster than diversity ([Cornuet & Luikart 1996](#)), founding
298 population size estimates based on richness should be lower than those based on diversity indices
299 if genetic drift is really important. Next, genetic drift affects mitochondrial genetic structure
300 stronger than nuclear genetic structure, because the effective population size at mitochondrial
301 genes is smaller ([Hamilton 2011](#)). Hence our founding number estimates should be lower when
302 using mitochondrial data if these were strongly influenced by genetic drift. We used the Student
303 t-test to test for differences among all these cases.

304 **Results**

305 *Genetic diversity*

306 Among a total of 285 sequences we found 25 polymorphic positions out of 299 nucleotide
307 positions in the *COI* gene fragment. This resulted in six distinct mitochondrial haplotypes. Two
308 of these haplotypes, H5 and H6, were singletons detected from Adi Gela and Adi Kenafiz,
309 respectively. Four haplotypes were common, with overall frequency of occurrence of 36.0, 33.0,
310 20.3 and 9.70 % for H2, H1, H3 and H4, respectively (Table 1 and Fig. 1). Most populations,
311 including both natural systems, were dominated by one or two haplotypes (average HD = 1.74).
312 Overall, the observed haplotype diversity or richness in a given population was always
313 significantly lower (X^2 test, $p < 0.0001$) than the expected diversity or richness assuming a
314 panmictic regional metapopulation (Table 1). Pairwise nucleotide diversity among haplotypes
315 ranged from 0.003 to 0.047 (overall nucleotide diversity = 0.021).

316 For the microsatellite markers, we found an average of 5.3 ± 3.6 (\pm standard deviation)
317 alleles per locus over the whole metapopulation, whereas the mean allelic richness per locus was
318 2.58 ± 0.5 per population. The number of alleles per locus ranged from 2 to 11, with a total of 32
319 alleles scored over the six microsatellite loci combined. The total number of alleles observed
320 across all loci per population ranged from 11 to 20, with a mean allelic richness of 2.32 alleles
321 per locus (Table 2). The observed heterozygosity for the 12 relatively young *Daphnia*
322 populations ranged from 0.21 to 0.57 whereas the expected heterozygosity (H_e) ranged from 0.24
323 to 0.54 per population (Table 2 and Table S3, Supporting information).

324 In total, we found 183 unique multilocus genotypes (MLGs) out of 293 individuals
325 successfully genotyped. The majority of those MLGs (88%) were represented by a single
326 individual whereas 5% of the MLGs ($n = 10$) were represented by two individuals. Only a small

327 number of MLGs ($n = 18$) was shared between reservoirs. The highest clonal richness ($CR = 27$)
328 and clonal diversity ($CD = 22.3$) was observed for Gum Selasa (Table 2). The difference between
329 the observed clonal richness/diversity and expected clonal richness/diversity was not statistically
330 different at $\alpha = 0.05$ for all the 12 populations studied, indicating that there is no substantial
331 clonal erosion (Table 2).

332 All values of pairwise genetic differentiation (F_{ST}) were significant ($p < 0.05$). Nearby
333 population pairs were not more related to each other than distant pairs (Table S4, Supporting
334 information). The highest pairwise F_{ST} value was observed in the comparison between T1 and
335 Adi Kenafiz ($F_{ST} = 0.585$), while the lowest pairwise F_{ST} value ($F_{ST} = 0.037$) was between Gereb
336 Awso and Dibla (Table S4, Supporting information).

337 None of the RDA analyses yielded a model with one or more spatial or environmental
338 explanatory variables that could significantly ($p < 0.05$) explain the variation in the genetic data,
339 either in the distribution of the mtDNA haplotypes, or in the allele frequency data of the
340 microsatellite loci. Exclusion of the two natural systems did not affect the general pattern. Mantel
341 tests between pairwise genetic distance (Nei's genetic distance) and geographic distances or
342 environmental distances yielded correlation coefficients of $r = -0.114$ ($p = 0.658$) and $r = 0.181$
343 ($p = 0.212$), respectively, thus confirming the absence of any spatial trend in the genetic data
344 (Fig. 2).

345

346 **Number of founders**

347 *Method 1: F_{ST} -based.* The overall among-population fixation index (F_{ST}) was 0.237, with 95%
348 confidence intervals (CI) ranging from $0.180 < F_{ST} < 0.342$. Without T1 and T3, F_{ST} equalled
349 0.219 (95% CI: $0.169 < F_{ST} < 0.309$). Since $F_{ST} \approx 1/2N$ at colonization, this reflects average
350 effective founding population sizes of 2.3 individuals (95% CI: $1.6 < N_e < 3.0$). Put differently,
351 the average genetic diversity we observed corresponds to a mean effective founding population
352 size of 1.6 to 3.0 individuals.

353
354 *Method 2: Comparing observed to expected richness and diversity estimates.* We found an
355 average observed haplotype richness $HR = 2.5$ and an average observed haplotype diversity
356 $HD = 1.74$ (Table 1). When comparing the average observed levels of HR and HD to expected
357 HR and HD, we found that average founding population size estimates smaller than two and
358 larger than eight are improbable at $p\text{-value} = 0.05$ (Table S5, Supporting information). The
359 highest probability scores were obtained with 4, 3, 3 and 4 founders for the four types of
360 simulations (Table S5, Supporting information).

361
362 *Method 3: Population-specific simulations.* We used population-specific simulations using
363 mtDNA and nDNA, based on three prior theoretical allele frequency distributions (Freq, Rich,
364 and Level, in descending order of sensitivity to rare alleles). For mtDNA, all three prior allele
365 frequency distributions yielded very comparable estimates (Table 3 and Table S6, Supporting
366 information), with averages ranging between 3.5 and 4 founders ($1 \leq \text{range} \leq 8$). This didn't
367 change appreciably when the natural systems were excluded (results not shown). For nDNA,
368 similar average (2.8 to 5.5) values were found ($2 \leq \text{range} \leq 13$), although the estimate using the
369 Freq. prior distribution was somewhat higher and was positively skewed due to higher estimates

370 for two populations (Table 3 and Table S6, Supporting information). Confidence in the prior
371 distribution of regional allele frequencies (Freq.) was unacceptably low (highest observed
372 likelihood score < 0.05) in six cases for nDNA and two cases for mtDNA. The prior distribution
373 based on local richness of alleles (Rich) yielded one estimate at nDNA with too low likelihood
374 scores (Table 3 and Table S6, Supporting information). All these estimates indicate that founding
375 population sizes were typically smaller than five individuals, and very rarely exceeded ten
376 individuals.

377

378 **Effect of size and age of the reservoir**

379 There was no significant relation ($p > 0.05$) between H_e and surface area or log (surface
380 area) of the water body ($S = 183.28$, Spearman rank $r = 0.3563$, p -value = 0.126) or with age of
381 the reservoir ($S = 342.35$, Spearman rank $r = -0.197$, p -value = 0.730, Figs S1, Supporting
382 information). The only significant correlation found in a total of 42 associations tested (age,
383 depth, area, versus AR, H_e , H_o , HR, HD, CR/N, CD/N, F_{IS} , number of founders at mtDNA
384 (Colonize-Rich), and number of founders at nDNA (Colonize-Rich)) was between H_e and
385 average depth ($r = -0.79$, $p < 0.001$). However, after Bonferroni correction, this p -value was
386 larger than 0.05. All other correlations were extremely weak and statistically insignificant at
387 $\alpha=0.05$ (absolute value of $r < 0.15$, uncorrected $p > 0.10$; Figs S1, Supporting information).
388 Inclusion of size and/or age of the reservoir did not provide a better model (Geste v. 2) for
389 genetic structure than the more parsimonious null model. All of these results support the
390 hypothesis that founder effects are the main drivers of genetic structure and indicate that clonal
391 genetic drift did not markedly influence our estimates of founding population sizes. In addition,
392 none of the tests we did could show a significant difference between founding population size
393 estimates based on mitochondrial versus nuclear genetic data, or based on richness versus

394 diversity estimates (all p values > 0.05). Thus, we have no indication that the assumptions
395 concerning genetic drift were violated (see Table S7 and Fig. S1, supporting information).

396
397

398 **Discussion**

399 Although we included a broad set of environmental and spatial variables, we found no
400 pattern with environmental variation, space and time (age) in the distribution of genetic variation
401 of the studied *Daphnia sinensis* populations inhabiting reservoirs in Tigray. Both the nuclear and
402 mitochondrial markers that we used are expected to behave neutrally. As such, we expected a
403 stronger signature of space than of environment. Still, a correlation with environmental variables
404 may result when particular haplotypes would hitchhike with particular genotypes or fixed allele
405 combinations that are favoured under certain conditions. Two studies on strictly asexual
406 zooplankton with comparable sample sizes and statistical power found clear environmental
407 and/or spatial structuring in their studies ([Aguilera et al. 2007](#); [Pantel et al. 2011](#)) suggesting that
408 the lack of patterns in our dataset is not merely a consequence of insufficient statistical power.
409 Evolution-mediated priority effects, the key feature of the monopolisation hypothesis ([De](#)
410 [Meester et al. 2002](#); [De Meester et al. 2016](#)), are expected to be less important in asexual taxa
411 than in similar sexual taxa, due to a reduced ability for rapid local adaptation in the asexuals. As a
412 consequence, it is expected that fitness differences among dispersed clones will lead to a match
413 between environmental gradients and landscape genetic structure in asexual taxa, similar to
414 species sorting in communities ([De Bie et al. 2012](#); [Leibold et al. 2004](#)). Conversely, if the
415 colonizing propagules of a sexual species harbours sufficient genetic variation to allow local
416 genetic adaptation, the increased fitness of resident populations may reduce establishment
417 success of new immigrants and thus reduce gene flow ([De Meester et al. 2016](#)). As a result, the
418 match between environmental and genetic variation is expected to be less strong in sexual than in
419 asexual species, which is the emergent pattern from our study on a cyclically parthenogenetic
420 *Daphnia* species and contrasts with the two aforementioned studies that focused on obligately
421 parthenogenetic *Daphnia*.

422 To investigate the number of founders typically involved in the colonization of new
423 moderately-sized freshwater systems (ranging from 1.8-45.4 ha in size), we used three different
424 approaches that rely on different test statistics with varying prior parameters, applied on two
425 independent sets of genetic markers. All approaches indicated that typically less than five
426 founders per habitat were responsible for the observed pattern of genetic diversity in the studied
427 reservoirs. Irrespective of whether we used estimates based on richness data or more detailed
428 frequency data, we obtained very similar estimates, showing that our results are robust to strong
429 allele frequency changes that may have occurred since colonization. Admittedly, the different
430 approaches we used all rely on similar assumptions, including an absence of genetic drift since
431 colonization, and genetic independence of each founder. The second assumption that the founders
432 are genetically independent from each other may have been violated to some extent. Birds, for
433 example, may disperse more than one dormant stage at the same time from a single source,
434 thereby introducing multiple related propagules. Especially results from mtDNA are expected to
435 be prone to such bias, given the much lower local and regional genetic variation compared to the
436 levels of variation found at nDNA. Estimated numbers of founders for nDNA and mtDNA were,
437 however, very similar.

438 We have detected high genetic differentiation among population ($F_{ST}= 0.232$) and no
439 isolation by dispersal limitation. This indicates low levels of gene flow among populations.
440 Furthermore, we failed to detect isolation-by-environment (IBE), which rules out the possibility
441 that sorting of genotypes along environmental gradients similar to species sorting in communities
442 ([Leibold *et al.* 2004](#)) might have driven the observed high genetic differentiation among
443 populations. Thus, our results support the idea that colonization dynamics in a newly created
444 metapopulation are strongly affected by founder effects exerted by a limited number of founding
445 genotypes. The founder effects observed here indicate that metapopulation and colonization

446 dynamics in this species resemble a lottery model ([Sale 1977](#)). In Sale's (1977) lottery model,
447 individuals compete for a limited number of discrete resources and once a resource is claimed, an
448 individual cannot be usurped from it. The classic lottery model was formulated at the community
449 level and with respect to microsites. However, it here acts at the level of genetic variants of a
450 species, and at the habitat level in a metapopulation. Populations are thus founded by a small
451 number of individuals from a varied array of regional sources. As long as a local genetic variant
452 persists (also if persistence is mediated through dormant stages; ([Mergeay et al. 2007](#)), the niche
453 space will continue to be occupied by these local variants, thereby pre-empting niche space for
454 immigrants. Several empirical studies focusing on colonization of novel habitats have shown that
455 dispersal rates in zooplankton are high ([Cáceres & Soluk 2002](#); [Jenkins & Buikema 1998](#);
456 [Louette & De Meester 2005](#)). The lack of spatial genetic patterns in our dataset also suggests that
457 dispersal per se is not limiting at the spatial scale here studied.

458 The sole environmental variable that showed a significant but negative correlation with
459 genetic diversity was average lake depth. One may speculate that the negative correlation
460 between depth and H_e reflects a species-specific preference for shallow waters, thereby reducing
461 the likelihood that a colonizing propagule will survive in deep reservoirs. This is indeed expected
462 from an organism that seems to naturally inhabit shallow pools. In that case, however, we would
463 also expect a similar negative relation between depth and number of founders, or other measures
464 of genetic diversity, which was not the case. An alternative explanation is that deeper lakes result
465 in more stable habitat conditions and therefore in populations that survive year-round and are
466 thus less dependent on dormant egg banks for survival. It is well known that more permanent
467 populations in *Daphnia* exhibit lower genetic diversity because of ongoing clonal erosion ([De](#)
468 [Meester et al. 2006](#); [Hebert 1987](#)).

469 Earlier studies ([Boileau et al. 1992](#); [Haag et al. 2006](#)) already showed that founder events

470 can strongly determine metapopulation structure, but the habitats they studied were very small
471 (less than $<100\text{ m}^2$). The systems we study are thousand times larger than the typical size of the
472 small habitats studied earlier, with associated differences in carrying capacity, effective
473 population size, genetic drift and inbreeding. Although the results shown here should be
474 interpreted with some caution given that the limited number of reservoirs that was inhabited by
475 the studied *Daphnia* species resulted in a reduced statistical power in detecting spatial and
476 environmental patterns, our analyses strongly indicate that zooplankton populations of these new
477 large water bodies are typically founded by just a handful of individuals. Interestingly, the
478 number of founders in these reservoirs (on average 4-6) is strikingly similar to the range found in
479 ponds with population sizes that are up to a thousand times smaller ([Boileau et al. 1992](#); [Louette](#)
480 [et al. 2007](#)). Similarly, the local recolonization by *Daphnia barbata* of the 150 km^2 large Kenyan
481 Lake Naivasha happened most likely by no more than nine individuals from an old dormant egg
482 bank ([Mergeay et al. 2007](#)).

483 Inbreeding effective population size (N_e) in populations is a function of the number of
484 founders and is thus generally small in our zooplankton population. It seems that in zooplankton,
485 habitat size per se, at least within given boundaries, may have little influence on the effective
486 population size. Next to the low number of founders that seem typically involved, our results
487 indicate that these founder effects were equally high irrespective of the age of the reservoirs.
488 Several case studies on the propagule banks of *Daphnia* populations have demonstrated high
489 local genetic stability over periods of 50-150 years ([Decaestecker et al. 2007](#); [Mergeay et al.](#)
490 [2007](#)). Recently, Ventura et al. ([2014](#)) even provided empirical evidence for founder effects
491 lasting thousands of years. All this evidence indicates that zooplankton populations primarily
492 have founder-controlled populations ([Okamura & Freeland 2002](#)), similar to founder-controlled
493 communities ([Sale 1977](#)). In such populations, dispersal contributes little to gene flow and is

494 mostly prevalent during the initial phase of colonization of empty or newly created habitats.
495 While dormant propagules are the main unit of dispersal in most zooplankton, their most
496 pervasive impact on landscape genetic structure may be their role in the short-term and long-term
497 local persistence of populations as well as in fostering colonization of empty habitats rather than
498 that they contribute to continuous gene flow among populations. Even seemingly extinct
499 populations may still be recolonized by local dormant egg banks once the habitat becomes
500 suitable again after decades ([Mergeay et al. 2007](#)). This has profound consequences for our view
501 on metapopulation biology of zooplankton and other micro-organisms, as these species often
502 share the lack of landscape genetic structure reflecting strong isolation-by-distance ([Okamura &
503 Freeland 2002](#)). More specifically, we should not equal high potential for dispersal into high rates
504 of gene flow ([De Meester et al. 2016](#)). In very small water bodies, however, negative effects of
505 genetic drift and inbreeding can be pronounced, and the positive influence on fitness of
506 immigrant alleles or genotypes from immigrants may then promote immigration and gene flow
507 ([Ebert et al. 2002](#)). One might therefore expect a shift from a gene flow dominated system in
508 extremely small populations (Ebert et al 2002) to metapopulations that are more strongly
509 dominated by local processes combined with extinction-recolonization dynamics in somewhat
510 larger systems such as the reservoirs studied here, shallow lakes and the sometimes much smaller
511 (approx. 100 m²) farmland ponds ([De Meester et al. 2002](#); [Louette et al. 2007](#); [Vanoverbeke &
512 De Meester 1997](#)).

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521 **Data Accessibility**

522 Sampling locations, raw environmental data for each reservoir and microsatellite genotype data is
523 stored in in Dryad[®].

524

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640
641

642 List of tables

643 Table 1: Genetic diversity in mtDNA haplotypes: observed frequencies (expressed as fractions)
 644 of each haplotype per water body and diversity descriptors. N: number of individuals extracted
 645 per sampling site. HR: haplotype richness. HD-Si: true haplotype diversity measured with the
 646 Simpson index. Average observed alpha diversity is the average observed within-sample
 647 diversity weighted by sample size. Average expected alpha diversity gives the expected value of
 648 HR or HD given a panmictic population over all water bodies, using 10,000 permutations. The
 649 range of the expected values shows the lowest and highest value among all permutations over
 650 individuals. All observed values deviate significantly ($p < 0.0001$) from expected values. True beta
 651 diversity is calculated as γ/α .
 652

Water body	N	Haplotype n°						HR	HD-Si
		1	2	3	4	5	6		
Adi Gela	17	0	0.71	0.06	0.18	0.06	0	4	1.86
Adi Kenafiz	18	0	0	0.39	0.56	0	0.06	3	2.16
Dibla	27	0.26	0.07	0.67	0	0	0	3	1.93
Gereb Awso	35	1.00	0	0	0	0	0	1	1.00
Gereb Mihiz	31	0.45	0.16	0.39	0	0	0	3	2.63
Gum Selasa	33	0.27	0.06	0.27	0.39	0	0	4	3.25
Haiba	6	0.83	0	0.17	0	0	0	2	1.38
Mai Leba	29	0.03	0.93	0	0.03	0	0	3	1.15
Meala	32	0.97	0.03	0	0	0	0	2	1.06
Tsinkanet	12	0	1.00	0	0	0	0	1	1.00
Temp 1 (T1)	22	0.14	0.36	0.50	0	0	0	3	2.49
Temp 3 (T3)	23	0	1.00	0	0	0	0	1	1.00
Overall frequency		0.33	0.36	0.203	0.097	0.005	0.005		
Average observed (alpha)		0.38	0.30	0.19	0.12	0.01	0.01	2.5	1.74
Total diversity (gamma)								6	3.43
Average expected alpha								4	3.40
Range expected alpha								3.7-4.2	3.01-3.67
True beta diversity								2.4	2.10

653

654 Table 2: Clonal and genetic diversity based on microsatellite loci (nDNA). N: sample size; n: number of individuals with complete
 655 genotypic information (6 loci) on which calculations of clonal richness (CR) and clonal diversity (CD) were based. CR=clonal
 656 richness; CD=clonal diversity.

Water body	Observed				Expected [§]									
	N	n	CR	CD	CR/n	CD/n	CR ± S.e	CD ± S.e	A	AR	Ho	He	HWE [¥]	F _{IS}
AG	30	20	19	18.18	0.95	0.91	20.92±0.09	20.86±0.02	20	2.97	0.38	0.54	0.001	0.302
AK	30	20	15	11.11	0.75	0.56	12.04±0.03	11.40±0.05	11	1.76	0.39	0.34	0.335	-0.164
DIB	30	27	19	12.79	0.70	0.47	25.13±0.05	22.86±0.08	15	2.29	0.41	0.32	0.085	-0.29
GA	32	31	13	8.50	0.42	0.27	21.35±0.06	16.10±0.08	14	1.95	0.34	0.27	0.108	-0.242
GM	36	34	19	6.64	0.56	0.20	28.09±0.10	25.05±0.08	19	2.46	0.43	0.39	0.001	-0.106
GS	40	32	27	22.26	0.84	0.70	22.93±0.03	22.08±0.05	18	2.63	0.38	0.47	0.000	0.19
HA	16	16	16	16.00	1.00	1.00	14.99±0.01	14.98±0.01	17	2.62	0.35	0.41	0.001	0.145
ML	29	23	22	21.16	0.96	0.92	23.68±0.02	23.42±0.03	13	2.13	0.57	0.47	0.012	-0.19
MA	30	20	3	1.23	0.15	0.06	21.71±0.04	20.67±0.06	13	1.85	0.51	0.29	0.000	-0.755
TS	18	15	11	7.76	0.73	0.52	14.99±0.01	14.98±0.01	18	2.92	0.39	0.52	0.000	0.258
T1	26	23	15	8.97	0.65	0.39	18.37±0.04	14.58±0.06	14	2.10	0.21	0.24	0.272	0.138
T3	32	32	31	30.12	0.97	0.94	29.63±0.04	28.52±0.06	14	2.13	0.45	0.47	0.335	0.032

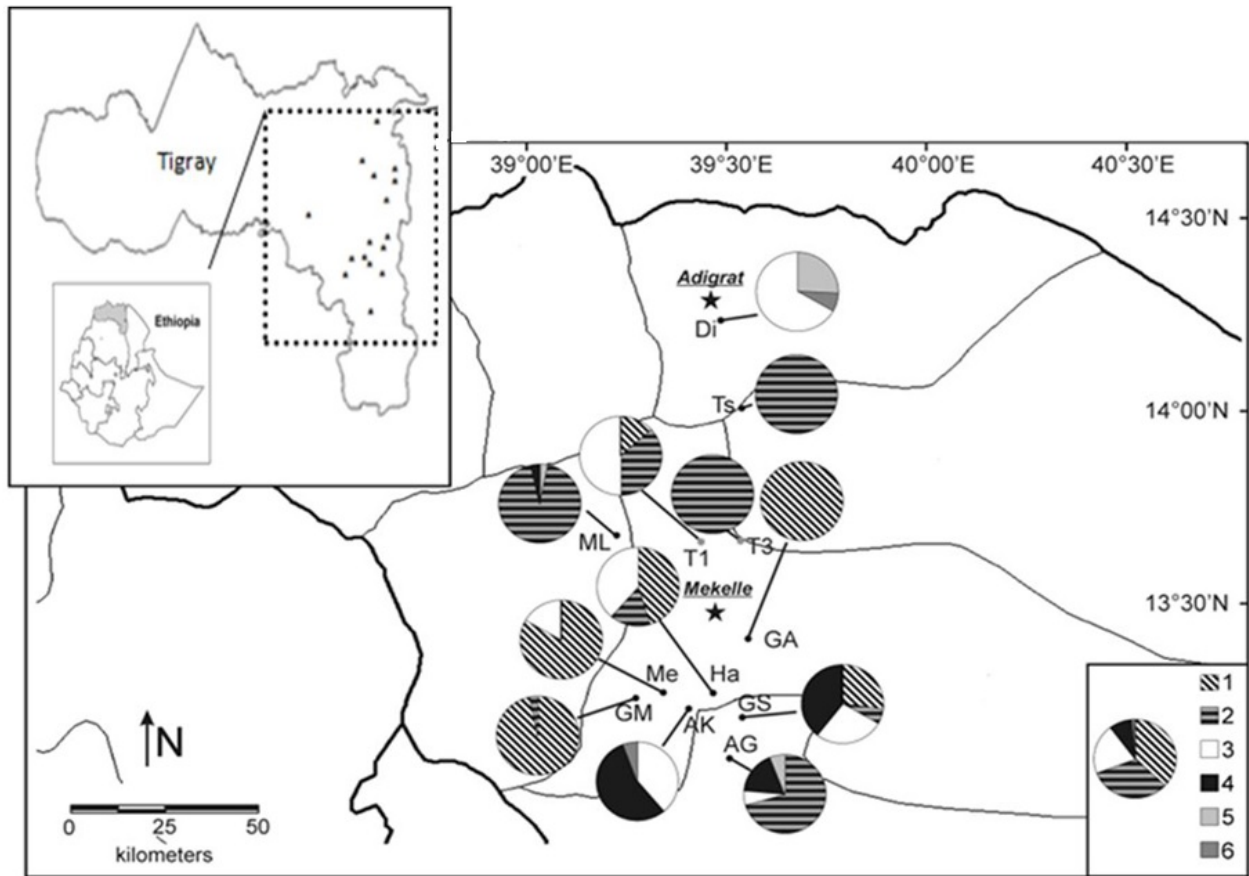
657 CR/n and CD/n refers to clonal richness and diversity, respectively, corrected for sample size expressed as proportion of clones to total
 658 individuals genotyped. A = number of alleles; Ar = allelic richness; H_o = observed heterozygosity; H_e = expected heterozygosity; F_{IS} =
 659 fixation index between individuals within local populations. [¥]The numbers are the p-value from a goodness of fit to HWE expectations
 660 test using Fisher's exact test method. [§]refers to the expected clonal richness (CR) and clonal diversity (CD) under Equilibrium using
 661 randomisation tests implemented in Hwclon ([De Meester & Vanoverbeke 1999](#)) There is no significant difference (at α= 0.05) between
 662 Observed CR/CD and expected CR/CD values for all population comparisons

663 Table 3: Summary results of Colonize analyses with three prior allele frequency distributions
 664 (Freq, Rich, Level; see main text for explanation), showing the most likely number of founders
 665 for each population, based on either mtDNA or nDNA data, for each population and averaged
 666 over all populations. Sd: standard deviation. Values with asterisk indicate that the likelihood
 667 score was too low ($p < 0.05$) to represent a reliable estimate. Non-integer values represent the
 668 average of shared highest scores.
 669

Water body	N° of founders with highest likelihood score (Colonize)					
	mtDNA			nDNA		
	Freq	Rich	Level	Freq	Rich	Level
Adi Gela	4*	4	4	2*	2	2
Adi Kenafiz	5*	8	7	7*	7	5
Dibla	5	4	4	5	3	2
Gereb Awso	1	1	1	5	2	2
Gereb Mihiz	5	6	4	12.5	4	4
Gum Selasa	8	8	7.5	13	5	4
Haiba	2.5	2	2	3*	2	2
Mai Leba	4	3.5	3	5	3	2
Meala	2	2	2	2*	2	2
Tsinkanet	1	1	1	3*	3*	4
T1	5	5	5	3*	2	2
T3	1	1	1	6	3	2
Average	3.63	3.79	3.46	5.54	3.17	2.75
Standard deviation	2.17	2.55	2.23	3.71	1.53	1.14

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Figure 1: Geographic location of the sampling sites and mtDNA haplotype frequencies in each

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population. Major cities are indicated with a star. Inset on the right shows the overall regional

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frequency of the six encountered haplotypes. AG = Adi Gela; AK = Adi Kenafiz; Di = Dibla; GA

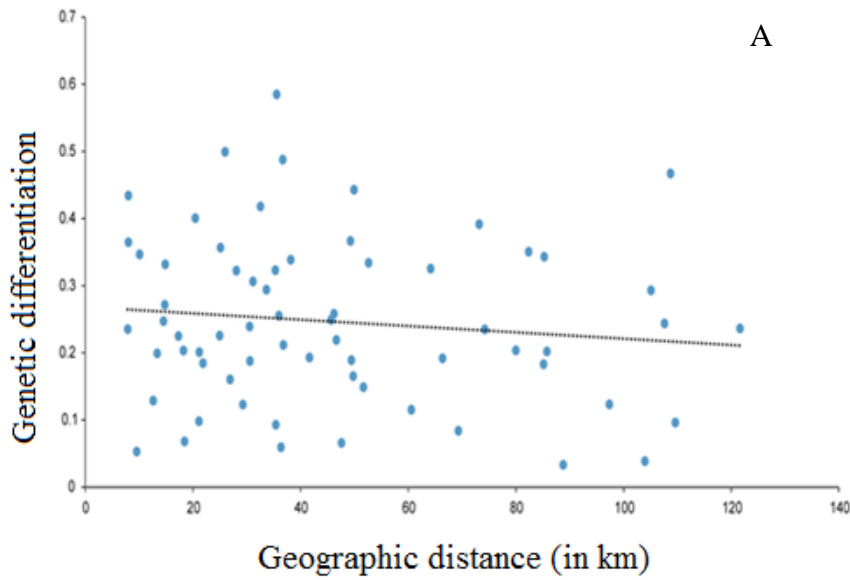
677

= Gereb Awso; GM = Gereb Mihiz; Ha = Haiba; ML = Mai Leba; Me = Meala; Ts = Tsinkanet;

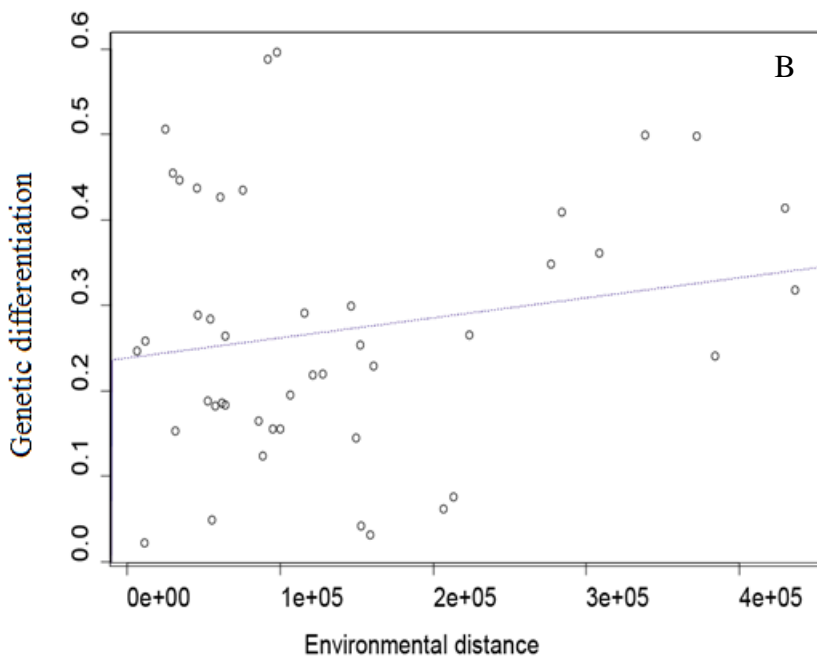
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T1 = Temporary pond 1; T3 = Temporary pond 3.

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682 Figure 2. Relationship between Nei's genetic distance and geographic distance (panel A; testing
 683 for an isolation-by-distance and thus for dispersal limitation; $r = -0.114$; $p = 0.662$) and the
 684 Euclidean distance for environmental variables (panel B; testing for isolation-by-environment; $r =$
 685 0.181 ; $p = 0.212$).

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