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1 **Mate choice of an endogeic earthworm revealed by microsatellite markers.**

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14 **Running title:** Mate choice of an endogeic earthworm

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26 **Summary**

27 Endogeic earthworms are difficult study subjects due to the cryptic medium in which they
28 live; thus, only the behaviour of epigeic and anecic earthworms has been studied before. We
29 used microsatellite markers as a tool to elucidate the mate choice processes of *Hormogaster*
30 *elisiae*, an endogeic earthworm. It was shown to normally mate with two partners, preferably
31 of the same size, that are found in close proximity thereby eliminating the need for long-
32 distance dispersion, which could explain the previously observed high genetic differentiation
33 between populations. The genetic analyses of the sperm within each of its four spermathecae
34 showed a uniform distribution with no signs of differential storage of sperm from different
35 partners.

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38 **Keywords:** Mate choice, endogeic earthworm, sperm, spermathecae, microsatellite markers.

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52 **Introduction**

53 Partner preference and mating behaviour have been studied in epigeic (*Eisenia fetida* by
54 Monroy et al., 2005; *E. andrei* by Tato et al., 2006) and anecic (*Lumbricus terrestris* by
55 Nuutinen and Butt, 1997; Butt and Nuutinen, 1998; Michiels et al., 2001; Sahm et al., 2009)
56 earthworms, but no attention has been given to endogeic earthworms, whose biological cycles
57 and vital strategies are substantially different. Endogeic earthworms inhabit the sub-surface
58 layers of the soil, rarely reaching the surface (Valle et al., 1999), which makes observation
59 and consequently, behavioural studies extremely difficult. Nevertheless, endogeic earthworms
60 probably have their own reproductive strategies because their life cycles are much longer and
61 their rates of cocoon production are lower than those of epigeic or anecic earthworms
62 (Edwards and Bohlen, 1996; Díaz-Cosín et al., 2009); hence, it is interesting to investigate
63 their unknown mating behaviour and partner preference.

64

65 *Hormogaster elisae* is a typical endogeic earthworm. It is an obligate out-crossing
66 hermaphrodite, endemic to the central Iberian Peninsula, and may represent a complex of
67 cryptic species, according to Novo et al. (2009). *H. elisae* needs, on average, 484 days for
68 clitellum development from hatching, and its cocoon production rate ranges from 0.9 to 2.29
69 cocoons earthworm⁻¹ year⁻¹ (Díaz-Cosín et al., 2009).

70

71 Because endogeic earthworms live in a very cryptic medium, analysis of molecular markers,
72 such as microsatellites, is a good way to unravel some of their behavioural and reproductive
73 characteristics. These markers have been used recently by Sahm et al. (2009) to study mating
74 preferences in *L. terrestris*, and specific primers are available for the species *H. elisae* (Novo
75 et al., 2008).

76

77 We address some questions on pre-copulatory sexual selection, such as: (1) What is the
78 average number of partners? (2) Do worms choose partners according to the size of the mate?
79 and (3) Does the mating success of the studied earthworms depend on their size or their
80 genetic variability?

81

82 A different strategy, known as sperm competition (Parker, 1970) or cryptic female choice
83 (Thornhill, 1983), is possible after copulation (Birkhead and Pizzari, 2002) when multiple
84 copulation partners exist. Two possible mechanisms of sperm competition in earthworms are
85 old sperm digestion (Richards and Fleming, 1982) or a differential storage pattern within the
86 spermathecae. We tested the second hypothesis in *H. elisae*, which has two pairs of large
87 tubular spermathecae. The posterior pair of spermathecae has been found to contain more
88 allosperm than the anterior pair (Garvin et al., 2003). Other Hormogastrid earthworms exhibit
89 much smaller spermathecae, and, in some cases, different chambers are found within each
90 spermatheca (Qiu and Bouché, 1998). Given that *H. elisae* has no tissue subdivision inside the
91 spermathecae, we tested whether they use the different spermathecae to achieve the function
92 of different chambers and store sperm from different partners.

93

94 There is no information about the movements of *H. elisae* individuals under the soil, and it
95 remains unknown whether they relocate to seek a partner or whether they stay within a certain
96 home range. The latter behaviour was observed in the anecic *L. terrestris*, which is known to
97 be anchored in its burrows (Michiels et al., 2001). Nevertheless, the burrow system that *H.*
98 *elisae* uses is possibly more complex, as endogeic earthworms normally build semi-
99 permanent or temporary gallery systems (Lavelle and Spain, 2001). By sampling different

100 points within a population we tried to infer the dispersal capacity of *H. elisae* and detect its
101 genetic structure at a microgeographical scale.

102

103 **Materials and methods**

104 Sampling and earthworm dissection.

105 A total of 75 sexually mature clitellate individuals of *Hormogaster elisae* were collected by
106 digging and manual sorting at a micro-geographical scale in El Molar, Madrid, Spain (GPS:
107 N40°44'22.9'' W3°33'53.1'') in January 2008. The climatic and edaphic characteristics of the
108 site are fully described in Valle et al. (1997) and Gutiérrez et al. (2006). Earthworms were
109 collected from nine different 1m² plots, each separated by 8 m, within a square of 64 m². Six
110 to ten individuals were collected from each plot (see below), which is a relatively high density
111 but assured the possibility of choice among different partners within one square meter.

112

113 After being washed with distilled water, the individuals were preserved in absolute ethanol at
114 -20 °C. They were dissected, and five different samples were taken from each specimen: a
115 portion of their tegument (0.025 g) was carefully cleaned and their four spermathecae were
116 isolated under the stereomicroscope, resulting in a total of 375 samples.

117

118 **Microsatellite analysis**

119 DNA from the tegument and spermathecae was isolated using the DNeasy Tissue Kit
120 (QIAGEN) and stored at 4°C.

121 Four loci (Table 1) with high polymorphism were selected from the microsatellite markers
122 developed for *H. elisae* by Novo et al. (2008). PCR amplifications were carried out in 20 µl
123 reaction volumes with 5 ng of DNA, 1X PCR buffer (Biotools), a locus-specific MgCl₂

124 concentration (Table 1), 1 mM of dNTPs, 0.5 μ M of each primer (0.25 μ M for Hem 194b)
125 and 1 U *Taq* DNA polymerase (Biotools) on a Perkin Elmer 9700 thermal cyclers.

126 The PCR profile was 94 °C (1 min), 30 cycles of [94 °C (30 s), 60 °C (15 s), 72 °C (15 s)] and
127 a final extension of 3 min at 72 °C. For the locus Hem193, the PCR profile was 94 °C (5 min),
128 35 cycles of [94 °C (1 min), 60 °C (1 min), 72 °C (1 min)] and a final extension of 7 min at 72
129 °C.

130 The amplified products were first checked on a 1% agarose gel and then analysed on a 3730
131 DNA Analyzer (Applied Biosystems) following the manufacturer's instructions. The alleles
132 were sized using the GS-500 LIZ size standard and Peak Scanner Software v. 1.0 (Applied
133 Biosystems).

134

135 Micro-geographical genetic analysis

136 The program Arlequin v. 3.1 (Excoffier et al., 2005) was used to obtain results on overall
137 genetic diversity from tegument samples. The allele number (NA), and the observed (H_o) and
138 expected heterozygosity (H_e) were calculated for each locus. Hardy–Weinberg equilibrium
139 (HWE) was tested following the procedure described in Guo and Thompson (1992), and tests
140 for linkage disequilibrium were conducted following Slatkin (1994). Polymorphism
141 information content (PIC) was calculated using the Excel Microsatellite Toolkit (Park, 2001).

142

143 The genetic variation in samples, including mean unbiased expected heterozygosity (H_e) and
144 allelic richness (A), were estimated using Fstat v. 2.9.3 (Goudet, 2001). For A , Fstat estimates
145 the number of alleles in a sample corrected to the smallest sample size, as recommended by El
146 Mousadik and Petit (1996).

147

148 We examined the existence of a genetic structure within the studied area using a hierarchical
149 analysis of molecular variance (AMOVA) framework (Excoffier et al., 1992), as implemented
150 in Arlequin 3.1 (Excoffier et al., 2005). Weir and Cockerham's (1984) F-statistics were
151 calculated: pairwise F_{st} values (as estimates of genetic differentiation between sample plots)
152 and F_{is} values (inbreeding coefficients within sample plots).

153

154 A pattern of isolation by distance was tested with a Mantel (1967) test, which correlates the
155 matrix of genetic distances between sample plots (F_{st}) with geographical distance (the length
156 of a straight line between sample plots). The significance of correlation between the matrices
157 was evaluated with 10,000 random permutations in Arlequin v.3.1 (Excoffier et al., 2005).

158

159 Sexual selection analysis

160 The alleles of each spermatheca were scored separately in order to observe whether there was
161 a differential sperm storage pattern in the four spermathecae. Alleles from the tissue samples
162 of the focal individual were removed from the analysis because the spermathecae walls had
163 been included in the DNA extraction. Then, all the alleles from the four spermathecae were
164 combined to calculate the minimum number of partners for each individual. The locus that
165 exhibited the maximum number of alleles was considered for the estimate, and this number
166 was divided by two, as *H. elisae* is diploid.

167

168 Mating probabilities were calculated following Sahm et al. (2009). For each individual of a
169 given sample plot, the probability of having received sperm from all the other individuals
170 from that plot was calculated. For that purpose, the presence (1) or absence (0) of the
171 tegument alleles from each of the potential donors in the DNA from the recipient's
172 spermathecae was scored. We estimated the probability that an allele observed in the

173 spermatheca of the focal individual arrived there due to sperm donation from another
174 individual. This probability is high if the pertinent allele frequency in the rest of the
175 population is low. So the probability of any particular spermatheca allele being donated was
176 estimated by subtracting its frequency in the population from unity (probability = 1 - allele
177 frequency) . Finally, the average of the probabilities that the two alleles were donated was
178 calculated for each locus, and then the average of the probabilities for all four loci was
179 determined. The mating probability between two individuals was calculated as the average of
180 the probabilities of each individual receiving sperm from the other.
181 The mating success of each individual was estimated and expressed as the global probability
182 of receiving and giving sperm, and the global probability of copulation (the average value of
183 the previous two probabilities).

184

185 Correlation analyses were implemented in STATISTICA v. 6.1 (StatSoft, Inc;
186 www.statsoft.com). The mating probabilities between individuals were tested for a correlation
187 with their differences in size (expressed as weight). A correlation between global probabilities
188 of mating success (donation, reception and copulation) and weight of individuals was
189 explored. An ANOVA was also performed to explore the possibility that the mating
190 probabilities of individuals depended on their degrees of heterozygosity (categories: number
191 of heterozygous loci). This analysis was controlled for their weights with an ANCOVA.

192

193 **Results**

194 Microgeographical genetic analysis

195 Total genetic diversity values for each microsatellite locus are shown in Table 1. The loci
196 exhibited high polymorphism, and the number of alleles detected ranged from 12 to 24. The

197 heterozygosity ranged from 0.41 to 0.91. The polymorphism information content was from
198 0.80 to 0.93. The loci showed differences between observed and expected heterozygosities.

199

200 Analysis of linkage disequilibrium yielded two significant cases (HEM07 vs. HEM188, $P =$
201 0.031; HEM188 vs. HEM193, $P = 0.017$) out of 6 pairwise comparisons. None of these
202 remained significant after Bonferroni correction (critical significance level of $P=0.008$),
203 indicating that the loci used are unlinked.

204

205 The genetic variability within each sample point and the F_{is} values are shown in Table 2. The
206 inbreeding coefficients were all positive and ranged from 0.096 to 0.234. There was no
207 significant genetic structure (Table 3) within the studied area, and the differentiation between
208 plots explained only 3.14% of the genetic variation found, which was explained mostly by
209 differences between and within individuals.

210 Pairwise F_{st} values between samples ranged from -0.01049 to 0.10343, exhibiting low genetic
211 differentiation (Table 4).

212 The Mantel test indicated that the pairwise genetic distances between sample sites (F_{st}) and
213 the distance between sites in metres were significantly correlated ($P= 0.03$, $r= 0.34$).

214

215 Mate choice analysis

216 Most of the individuals (62.66%) stored sperm from a minimum of two partners, whereas
217 18.67% of the earthworms copulated with a minimum of one partner, and the remainder
218 (18.67%) stored sperm from at least three different individuals.

219

220 There were no differences in the pattern of sperm storage between the four spermathecae, and
221 the same alleles were generally found in all the spermathecae from one individual.

222 A significant negative correlation was found between the mating probability and the
223 difference in weight of the specimens ($r = -0.22$, $P < 0.05$), thus indicating that individuals
224 prefer to mate with partners of similar weights to themselves.

225 No significant results were found in the remaining statistical analyses.

226

227 **Discussion**

228 Microgeographical genetic analysis

229 Overall genetic diversity values were high, similar to the ones found by Velavan et al. (2009)
230 for *L. terrestris* and even higher with respect to average allelic richness. Departure from the
231 HWE was detected, as in a previous study by Novo et al. (2008). Their hypothesis for
232 explaining these significant departures was a possible population sub-structuring (i.e.
233 Wahlund effect) that could lead to inbreeding. Indeed, positive FIS values indicated a
234 moderate amount of inbreeding within the sampled plots, but the inbreeding was not very
235 pronounced, permitting high genetic diversity. The AMOVA indicated no genetic sub-
236 structuring, but the significant result of the Mantel test indicated isolation by distance.
237 Therefore, it seems that individuals of *H. elisae* are rather sedentary and do not relocate over
238 long distances to find mating partners. Sahm et al. (2009) found that distance was the most
239 important factor for mate choice in *L. terrestris*, but because endogeic *H. elisae* is not
240 anchored to vertical burrows and does not copulate at the surface, it was not expected to have
241 this pattern. *H. elisae* individuals are not exposed to predators during copulation, and so they
242 can move underground to seek appropriate partners. Nevertheless, these results could lead us
243 to two hypotheses, namely that *H. elisae* earthworms could be somehow linked to a
244 permanent or semi-permanent burrow system or that, due to a high density of individuals in
245 the studied area (Table 2), they do not need to move long distances to find partners.

246 This reduced capacity for mobility has been also found in other earthworm species that have
247 observed natural dispersal rates of only 1.4–9 m/year (Ligthart and Peek, 1997; Hale et al.,
248 2005) and could explain the deep genetic isolation between populations found by Novo et al.
249 (2009) that led to cryptic speciation. Deep genetic splits between populations of earthworms
250 are also observed in *Lumbricus rubellus* (which has a surface-active activity), (see Andre et
251 al., 2010), and is in contrast with other soil invertebrates such as Collembola, in which
252 populations are structured on a scale extending to several kms (Van der Wurff et al., 2003).

253

254 Sexual selection

255 It seems that, on average, individuals of *H. elisae* copulate with two partners. Nevertheless,
256 this finding could represent only their very recent mating history if only the sperm of the last
257 mating partners are maintained for future use. In fact, a histological study of spermathecae
258 from *H. elisae* (in prep.) has shown that there were degrading sperm loads in the central areas
259 of the spermathecae. Richards and Fleming (1982) found spermatozoal phagocytosis by the
260 spermathecae of *Dendrobaena subrubicunda* and other lumbricids that was probably related
261 to ageing or aberrant sperm removal during the months when cocoon production was
262 minimal. Butt and Nuutinen (1998) observed that *L. terrestris* was capable of successfully
263 maintaining received sperm for up to 6 months, and Meyer and Bouwman (1994) reported
264 that *E. fetida* continued cocoon production for up to 12 months after the earthworms were
265 isolated from their partners, although the viability of the cocoons was not measured.

266

267 No differences in the pattern of sperm storage between the four spermathecae were found,
268 which indicates that if sperm competition is present in these animals it should be orchestrated
269 by mechanisms inside each spermatheca. Grove and Cowley (1926) observed that
270 transmission of sperm in *E. fetida* normally occurs on both sides of the individual, whereas in

271 *L. terrestris* some individuals were found with spermatophores in only one side of their
272 bodies (Butt and Nuutinen, 1998). Future histochemical studies are necessary to unravel such
273 mechanisms.

274

275 A negative correlation was found between weight differences and mating probabilities, which
276 means that *H. elisae* individuals select partners with similar weights. This selection was
277 already discussed by Michiels et al. (2001) who found that pairs of similarly-sized anecic *L.*
278 *terrestris* earthworms copulated earlier than pairs with different sizes in laboratory
279 experiments. It was also found by Monroy et al. (2005) that the epigeic *Eisenia fetida* showed
280 size-assortative mating in the field with individuals choosing similarly-sized partners. This
281 selection could be explained for epigeic and anecic earthworms as a trade-off between
282 choosing a larger partner, given that female fecundity (as measured by cocoon production,
283 cocoon size and hatchling size) is related to body size (Meyer and Bowman, 1995, 1997), and
284 choosing a smaller partner that would decrease predation risk. However, as endogeic *H. elisae*
285 copulates underground, larger partners could be expected to be selected. The proposal that
286 assortative mating could be constrained by physical incompatibility of the copula among
287 partners of different sizes (Michiels et al., 2001) could explain the similar-sized selection in
288 *H. elisae*, although this incompatibility would be caused only by excessive size differences.
289 Therefore, it is more plausible that this pattern is caused by the conflict of every earthworm
290 seeking a larger partner that finally led to an equilibrium of similar weight partners, thus
291 balancing expectations of both mates on female and male functions.

292

293 Conclusions

294 This is the first time that sexual behaviour has been studied in an endogeic earthworm.

295 Different questions arise from the findings of this study, but in general, it seems that *H. elisae*

296 has multiple matings and generally maintains the sperm of two individuals mixed in four
297 spermathecae. Individuals prefer same-sized partners that are found nearby with no need for
298 long-distance dispersion.

299

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304

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452 **Table 1.** Details of the microsatellite markers used in the study of *Hormogaster elisae* and
453 overall genetic diversity for each locus.

Repeat motif	Primer sequence(5' - 3')	Mg ⁺⁺	Tag*	GenBank Accession	Size range (bp)**	N	NA	Ho	He	HWI P-val†
(CT) ₂₆ †	F:CTGTTCTCCGTGACTTCGAG R:CAGGGAGTCAGACAGGCAGT	2.5	FAM	AM902182	134-202 (156,164)	75	24	0.89	0.94	0.000
b (GTCTCT) ₄	F:GCCCCATCCCCGCTTCTTTGTAT R:GCGCACCAAAATAAAGCCACACTAGTA	2.5	VIC	AM902190	154-244 (154)	75	12	0.91	0.83	0.002
‡ (CT) ₂₄	F:CCGGGAGCCTCATGCAACAG R:CCGATAAACTCAGAAAAACGCATAAACT	1.5	VIC	AM902188	222-310 (256)	75	20	0.41	0.91	0.000
‡ (GT) ₄₃ †	F:CAGTTATGTATGTGTTTTGCGTGGGTGTA R:CAAAGAGAGCTCCGCCAGTTACGTAGAC	3	FAM	AM902189	124-178 (148)	75	17	0.67	0.88	0.000

454

†: Microsatellites contain interruptions among repeats

455

Mg⁺⁺: Magnesium ion concentration in mM used for PCR amplifications

457

*: Fluorescence label at 5' - end of primer

458

** : Numbers in parentheses are the most frequent allele(s) sizes.

459

N: Number of individuals analysed

460

NA: Number of alleles

461

Ho: Observed heterozygosity

462

He: Expected heterozygosity

463

HWE: Hardy–Weinberg equilibrium

464

PIC: Polymorphism Information Content

465

466

467 **Table 2.** Mean genetic variability expressed as mean allelic richness (A), mean expected
 468 heterozygosity (He), and inbreeding coefficients (Fis) within each sample plot (Pn) of
 469 *Hormogaster elisae* at four microsatellite loci.

470

Sampling point	N	A	He	Fis
P1	7	6.55	0.87	0.189*
P2	6	6.50	0.85	0.234*
P3	9	7.13	0.89	0.161*
P4	9	5.76	0.78	0.121
P5	8	6.68	0.88	0.195*
P6	10	6.05	0.84	0.174*
P7	10	6.43	0.87	0.173*
P8	8	7.16	0.87	0.185*
P9	8	6.63	0.86	0.096
Total	75	7.32	0.89	0.191

471

472 N: Number of individuals analysed
 473 Asterisks in Fis represent significant coefficients at $P < 0.05$

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478 **Table 3.** Results of analysis of molecular variance (AMOVA) in *Hormogaster elisae* at four
 479 microsatellite loci. Partitioning of genetic variance at three hierarchical levels is shown.
 480 Corresponding fixation indices (Weir and Cockerham, 1984) and their P-values are given.

481

Source of variation	d.f.	Sum of squares	Variance components	Fixation indices	P-values	Percentages of variation
Among sites	8	23.61	0.056	0.031 (FST)	0.76	3.14
Among individuals within sites	66	133.31	0.290	0.168 (FIS)	0.00	16.23
Within individuals	75	108.00	1.440	0.193 (FIT)	0.00	80.63

482

483 d.f.: degrees of freedom

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488

489 **Table 4.** Average pairwise Fst values between sample plots (Pn) of *Hormogaster elisae* based
 490 on four microsatellite loci.

491

	P1	P2	P3	P4	P5	P6	P7	P8
P1	-							
P2	0.05532	-						
P3	0.07034*	0.02812	-					
P4	0.02113	0.10343*	0.09370	-				
P5	0.02027	0.02211	0.02609	0.04499*	-			
P6	0.06941*	0.05501*	0.02140	0.09478*	0.03096	-		
P7	0.02947	0.03361	0.04114*	0.04915*	0.02298	0.03029	-	
P8	0.05222*	0.02526	0.03913	0.08298*	0.00657	-0.01049	0.02871	-
P9	0.06820*	0.00164	0.02461	0.09595*	0.01037	0.02564	0.04721*	0.01520

492

493 Asterisks in Fst represent significance at $P < 0.05$

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