

1 **Sampling scale can cause bias in positive assortative mating estimates: The first**
2 **evidence in two intertidal snails**

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4 Terence P. T Ng¹, Gray A. Williams¹, Mark S. Davies², Richard Stafford³, E.
5 Rolán-Alvarez^{4*}

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7 ¹ *The Swire Institute of Marine Science and School of Biological Sciences, The*
8 *University of Hong Kong, Pokfulam Road, Hong Kong SAR, China*

9 ² *Faculty of Applied Sciences, University of Sunderland, Sunderland, U.K.*

10 ³ *Faculty of Science and Technology, Bournemouth University, U.K.*

11 ⁴ *Faculty of Biology, University of Vigo, 36310 Vigo, Spain*

12

13 *Correspondence: E. Rolán-Alvarez, Faculty of Biology, University of Vigo, 36310
14 Vigo, Spain; e-mail: rolan@uvigo.es

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16 Abstract

17 Assortative mating in the wild is commonly estimated by correlating between traits

18 in mating pairs (e.g. size of males and females). Unfortunately such an approach

19 may suffer from considerable sampling bias when the distribution of different

20 expressions of a trait in the wild is non-random; for example, when segregation of

21 different size classes of individuals occur in different microhabitats or areas.

22 Consequently, any observed trait correlation in the wild can be an artifact of pooling

23 heterogeneous samples of mating pairs from different microhabitats or areas rather

24 than true non-random matings. This bias in estimating trait correlations due to

25 sampling scale is termed the scale-of-choice effect (SCE). Here we use two intertidal

26 littorinid species from Hong Kong to show how the SCE can bias size-assortative

27 mating estimates from mating pairs captured in the wild, empirically demonstrating

28 the influence of this effect on measures of positive assortative mating. This finding

29 cautions that studies that have overlooked SCE may have misinterpreted the

30 magnitude and the cause of assortative mating, and we provide a new analytical
31 approach to protect against this potential bias in future studies.

32

33 Keywords: SCE; mate choice; mating pair; size-assortative mating; mating
34 preference; *Echinolittorina* spp.

35

36 **Introduction**

37 The decisions that dioecious organisms take in choosing their mates has key
38 evolutionary importance, as these choices influence the probability of allele
39 transmission and distribution of genotypes in the next generation (Lewontin et al.,
40 1968; Coyne and Orr, 2004; Gavrillets, 2004). Mating preferences can be investigated
41 by detecting deviations from random mating (i.e. assortative mating) in traits which
42 are used to distinguish between individuals such as size and colour (Jiang et al., 2013).
43 Perhaps the most simple and common approach to detect non-random mating in the
44 wild is by studying any correlation between traits (assessed using Pearson's r) of the
45 observed mating pairs (Crespi, 1989; Arnqvist et al., 1996; Jiang et al., 2013). Trait
46 correlations can be positive or negative, when there is a tendency of individuals
47 mating preferentially with members of the opposite sex with similar or dissimilar trait
48 values, respectively. Observed correlation of traits in mating pairs in the wild can,
49 however, be the result of a variety of processes such as mating preferences and mating
50 constraints (Crespi, 1989). Non-random distribution of different expressions of a trait
51 may, however, also influence observed mating patterns (Arnqvist et al., 1996; Jiang et
52 al., 2013), and a recent study has illustrated how such spatial patterns can lead to
53 sampling bias and hence confound the assessment of mating patterns in the wild. This
54 effect has been termed the scale-of-choice effect (SCE; Rolán-Alvarez et al., 2015),

55 and occurs when the sample of mating pairs is measured at a larger spatial scale than
56 the scale of mate choice in the organism and when there is spatial heterogeneity in
57 trait distribution at the true scale of mate choice (see Figure 1a). In the example (Fig.
58 1a), positive size-assortative mating may be ‘detected’ because different sized pairs
59 from different localities (e.g. sections of a seashore) have been measured and pooled
60 during estimation. This pooling of samples over an spatial scale inappropriate to the
61 movement range of the mating individuals will lead to a biased estimate of correlation,
62 or other similar statistics that may be used to estimate assortative mating
63 (Rolán-Alvarez et al., 2015), calculated at the wrong spatial scale for the hypothesis
64 being tested (Hassler and Thadewald, 2003). The practical consequence of this
65 phenomenon is that many correlation coefficients estimated from measurements in the
66 wild may be subject to this effect and, therefore, their support for the hypotheses
67 tested, and subsequent interpretation could be misleading, as the SCE can obscure the
68 true nature of any trait correlation.

69 Although the true scale of choice is usually unknown in most species, grouping
70 mating data according to the frequency of different expressions of a trait (e.g.
71 according to size classes or shell colour) of individuals surrounding mating pairs can
72 reduce the influence of spatial heterogeneity and, therefore, diminish or eliminate the
73 bias caused by SCE. As the SCE has two necessary conditions; firstly that there is a
74 mismatch between the scale over which individuals can make a choice and the scale at
75 which sampling occurs; and secondly that there is spatial heterogeneity at the scale of
76 sampling; diminishing or eliminating the effects of either condition will affect the
77 magnitude of SCE (Rolán-Alvarez et al., 2015), and therefore the bias affecting the
78 estimated correlation coefficient (r). Rolán-Alvarez et al., (2015), for example, have
79 shown that pooling samples of mating pairs of the intertidal snail, *Littorina fabalis*,

80 from three localities with similar trait (colour) frequency increased the estimated r
81 when compared with non-pooled samples. The true strength of the negative mating
82 preference for distinct shell colours was, therefore, accentuated due to the
83 inappropriate analysis of the pairs. As such, a systematic bias in any meta-analysis on
84 assortative mating may occur whenever the studied species has small dispersion
85 ranges and the SCE is expected to be high. In reality, negative assortative mating is
86 apparently a rare phenomenon in natural populations (Jiang et al., 2013), but
87 generality may be an artifact of SCE which has not been accounted for in previous
88 meta-analyses (Rolán-Alvarez et al., 2015). It is also desirable to investigate whether
89 the SCE can also bias cases of positive assortative mating.

90 Positive size-assortative mating is common in gastropods and many other
91 organisms (Erlandsson and Johannesson, 1994; Staub and Ribi, 1995; Erlandsson and
92 Rolán-Alvarez, 1998; Rolán-Alvarez et al., 1999; Zahradnik et al., 2008; Avaca et al.,
93 2012; Ng & Williams, 2012; see Jiang et al., 2013 for a review). In intertidal snails
94 this mating pattern may be caused by males following female mucus trails in a
95 size-dependent manner, which would result in positive assortative mating for size
96 (Conde-Padín et al., 2008; Johannesson et al., 2008; Ng et al., 2013; Ng & Williams,
97 2014), but other mechanisms based on preferential mating can also be invoked to
98 explain this pattern (Saur, 1990; Hull, 1998; Johannesson et al., 2008; Zahradnik et al.,
99 2008; Saltin et al., 2013). Given their limited locomotion capacity relative to the
100 habitat they occupy, it is reasonable to assume that snail species exhibit their choice at
101 rather small scales, and therefore there is a strong potential for SCE to influence
102 estimates of trait correlation coefficients using mating pairs captured in the wild. This
103 theory was investigated using two tropical intertidal snails to determine whether SCE
104 might influence assessment of their assortative mating patterns.

105

106 **Material and Methods**

107

108 **Study localities and sampling approach**

109 *Echinolittorina malaccana* and *E. radiata* are common grazers on the high shore and
110 their distributions on the shore overlap, with *E. malaccana* generally found above *E.*
111 *radiata* (Mak, 1996). Measurements were made in August 2015, during the snails
112 reproductive season (Mak, 1996) at Cape D' Aguilar Marine Reserve (22° 12' 27" N,
113 114° 15' 33" E) and Shek O (22° 13' 44" N, 114° 15' 22" E), Hong Kong (Fig. 1b).
114 These two species were scored at seven localities (CD1 to CD7) in Cape D' Aguilar
115 and one in Shek O (SO) with relatively high densities of either one or both species (all
116 localities for *E. malaccana*, and CD1, 2, 6 and 7 for *E. radiata*, Fig. 1b). These
117 localities were all within 10-m stretches of the shoreline, and were separated by 10s to
118 1000s of metres in order to investigate the SCE (Fig. 1a).

119 Mating pairs were collected within the same tidal phase at each locality. In
120 addition to the mating pairs, the four closest unmated conspecifics surrounding each
121 mating pair were also scored to define a microarea unit (within a ~250 mm radius of
122 each mating pair representing a small portion of area in each locality). Every mating
123 pair plus the four unmated conspecifics, therefore, represents a different microarea
124 replicate. All (4-80 microarea replicates among the localities) mating and nonmating
125 snails were taken to the laboratory where sex (determined by the presence or absence
126 of a penis as seen under dissection microscope) and shell length (\pm 0.1 mm, vernier
127 calipers) were recorded. Previous studies have demonstrated very low parasite loading
128 of littorinids in Hong Kong (maximum 0.6%, Tang, 1995), and hence this possible
129 confounding effect on mating behaviour and mating pattern was considered to be
130 insignificant. All snails collected were returned to their original shores after

131 investigation.

132

133 **Statistical analyses**

134 Size-assortative mating was estimated by Pearson's correlation coefficient (r) among
135 the observed mating pairs, and the significance evaluated by the non-parametric
136 Kendall-tau-b test. The SCE is defined as the correlation coefficient of a trait in the
137 pooled sample (r_{pooled}) minus the averaged correlation (r_{averaged}) of the trait among
138 homogeneous sets of data (Rolán-Alvarez et al., 2015 see Figure 1a), and in this case,
139 r_{pooled} refers to the correlation coefficient between sizes derived from pooled mating
140 pairs of all localities in both Cape D' Aguilar and Shek O, whereas r_{averaged} refers to
141 the mean correlation coefficient derived from mating pairs in each homogeneous set
142 of size classes (i.e. microareas that share similar sizes classes of individuals including
143 the mated and unmated conspecifics). As such, SCE estimates the possibility of bias
144 in estimating the correlation coefficient due to non-random distribution of different
145 size classes among the localities by taking into account individual sizes in each
146 microarea. Three to five homogeneous sets of size classes were used in the analyses,
147 derived from the mean individual size in each microarea. The r_{averaged} was, therefore,
148 calculated over these three to five homogeneous sets of size classes. The significance
149 of the SCE was evaluated by comparing the r_{averaged} against the r_{pooled} value as null
150 value by a t test. All analyses were performed with SPSS 20.0 (SPSS Inc., Chicago,
151 IL, U.S.A).

152

153 **Results and Discussion**

154 When SCE was not considered by grouping data into homogenous sets of size classes,
155 the calculated correlations supported the presence of positive size-assortative mating

156 in both species (Table 1). The averaged r across all localities was positive and
157 significant ($p < 0.05$) in *E. radiata* and positive and marginally non significant ($p =$
158 0.053) in *E. malaccana*. In addition, there was at least one locality where significant,
159 positive size-assortative mating was recorded in both species (Table 1) and the pooled
160 samples among different homogeneous sets of size classes clearly demonstrated
161 size-assortative mating. This pattern is typical for many littorinid species, and positive
162 size-assortative mating is assumed to be the underlying mechanism (Erlandsson and
163 Johannesson, 1994; Erlandsson and Rolán-Alvarez, 1998; Johnson, 1999;
164 Rolán-Alvarez et al., 1999; Ito and Wada, 2006; Zahradnik et al. 2008; Ng & Williams,
165 2012). This assumption, however, may be incorrect if sampling biases such as the
166 SCE are not taken into account (Rolán-Alvarez et al., 2015). Grouping the mating
167 pairs in three to five homogeneous sets of size classes within the two study sites, for
168 example, indicated close to random mating patterns in the two species (Table 1). The
169 Pearson correlation coefficient averaged across the homogeneous sets of size classes
170 was 0.21 (for 3 classes), 0.12 (for 4 classes) and 0.06 (for 5 classes) in *E. malaccana*,
171 with 3 out of 6 estimates being significantly different from r_{pooled} , and the other 2 out of 6
172 being marginally different, with the probability being close to 0.05. The SCE, and
173 hence the bias in the estimation of correlation coefficients based on five homogeneous
174 sets of size classes, was as large as 0.5 and 4.7 in Shek O and Cape' D Aguilar
175 respectively in *E. malaccana* (Table 1). The SCE was even more clear in *E. radiata*,
176 as the correlation coefficients across averages was always significantly different from
177 the pooled estimate, yielding a SCE of 0.54 (Table 1). In both species, therefore, the
178 assumed trend towards positive assortative mating when mating pairs are pooled from
179 multiple localities was likely an artifact due to the pooling of heterogeneous samples
180 (i.e. mating pairs from different microareas consisting with individuals of different

181 size classes) rather than a true non-random mating pattern. To try and avoid this bias,
182 we propose that investigators should analyse mating pairs in homogeneous subgroups,
183 which can reveal whether the SCE is contributing to the estimates of correlation
184 coefficients to detect relationships between traits. This approach requires large sample
185 sizes as well as information about conspecifics close (i.e. within their movement
186 range) to the mating pairs. Although the calculated correlation coefficients and hence
187 SCEs are somewhat sensitive to the number of homogeneous subgroups used (3 to 5
188 in the present case; Table 1), this approach does provide an appropriate method to
189 evaluate the potential bias due to the scale of sampling area.

190 As previous authors have pointed out, the study of assortative mating and its
191 causes seems fraught with difficulties, especially as the problem has been defined and
192 considered in different ways from theoretical and empirical frameworks (Gavrilets,
193 2004; Roff and Fairbairn, 2015). Theoretical mathematical functions to simulate
194 assortative mating *in silico*, for example, have recently suggested that assortative
195 mating can be a consequence of either an increase of mating preference *per se*, or by a
196 drift in the distribution of the trait being used to describe the preference
197 (Carvajal-Rodríguez et al., 2014). The difference between these two mechanisms in
198 driving assortative mating is subtle but rather important in evolutionary terms, since
199 only a genetic change in mating preference is evolutionary relevant for reinforcement
200 (Kirkpatrick, 2000), speciation and/or sexual selection (Gavrilets, 2004), and we
201 presently do not have the tools that distinguish between these phenomena
202 (Carvajal-Rodríguez et al., 2014). Although the analytical approach provided here,
203 which estimates assortative mating independently of the trait distribution, is not a
204 perfect solution it does, however, provide an estimate of sampling bias and this alone
205 is a considerable advantage over more traditional approaches (Jiang et al., 2013).

206 While this study demonstrates the need to consider sampling bias in estimating
207 assortative mating, even greater efforts will be needed in the future to understand the
208 true causes of this mating pattern.

209

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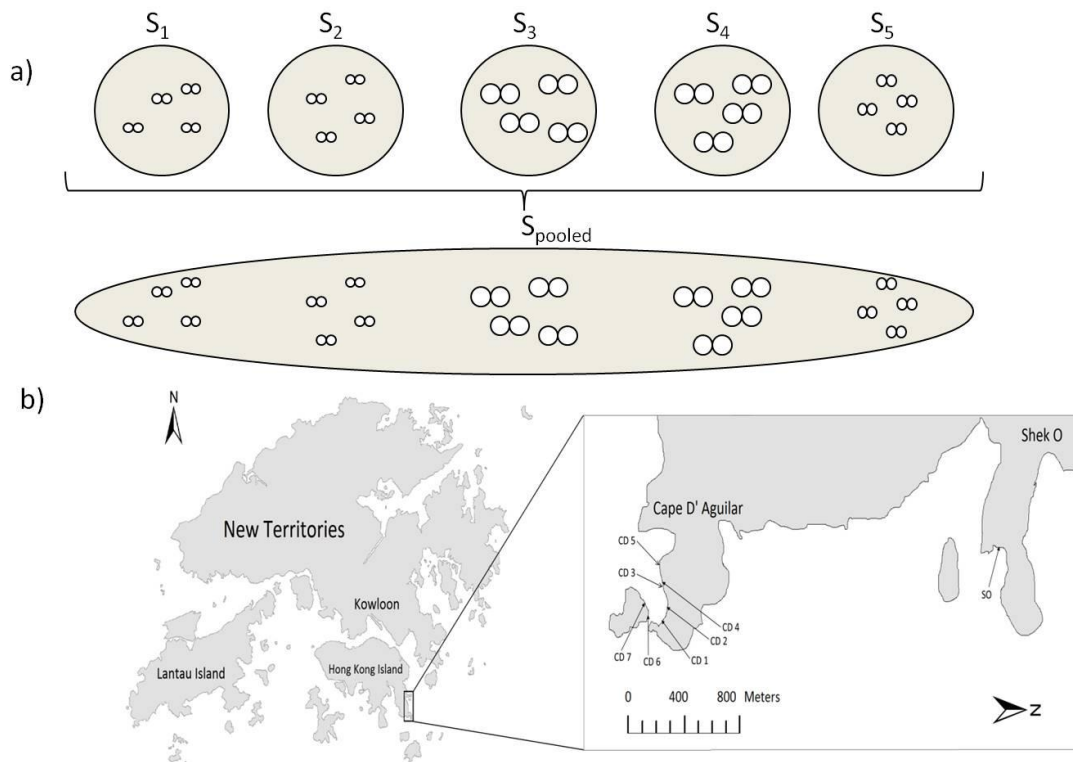
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297

298

299 Figure 1. 1_a) The scale-of-choice effect (SCE) results in this example when pooling
 300 a heterogeneous sets of subsamples (S_1 to S_5) with random mating within each
 301 (represented by the pairs within circles), causing an overall positive assortative
 302 mating in the pooled set of samples (S_{pooled} ; represented by the ellipse). Note that the
 303 analytical approach proposed here consists of estimating correlation coefficients
 304 ($r_{averaged}$) from homogenous sets of size classes (Class₁= S_1 , S_2 and S_5 ; Class₂= S_3 and
 305 S_4 in this example). The SCE would be r_{pooled} minus $r_{averaged}$. 1_b) Sampled
 306 distribution of mating pairs captured in Shek O (SO) and Cape D' Aguilar (CD,
 307 inset), Hong Kong.

308 **Table 1.** Analysis of the scale-of-choice effect (SCE) for size assortative mating in *Echinolittorina malaccana* and *E. radiata*. The Pearson
 309 correlation coefficient ($r \pm SD$) for size of mates is provided within sample, pooled samples and different homogeneous sets (3-5) of samples
 310 within localities (SO or CD). The significance of the correlation coefficient, r , is given by the non-parametric Kendall-tau-b correlation test
 311 within sample and pooled (r and r_{pooled}), and by a t-test for means (r_{averaged} ; checking the null hypothesis = r_{pooled}). SCE is only calculated for the
 312 case when mating pairs are grouped according to five homogeneous sets of size classes.

| Species | Locality | All samples | | N | r_{pooled} | r_{averaged} across homogeneous sets of size classes | | | SCE ₅ |
|---------------------|----------|---------------|---------|-----|---------------------|---|----------------|---------------|------------------|
| | | N | r | | | 5 classes | 4 classes | 3 classes | |
| <i>E. malaccana</i> | SO | 40 | 0.52*** | 228 | 0.52*** | 0.03* ± 0.293 | 0.20? ± 0.238 | 0.07? ± 0.225 | 0.49 |
| | CD1 | 13 | 0.21 | | | | | | |
| | CD2 | 40 | -0.21 | | | | | | |
| | CD3 | 4 | 0.46 | | | | | | |
| | CD4 | 23 | -0.1 | | | | | | |
| | CD5 | 58 | 0.195 | | | | | | |
| | CD6 | 80 | 0.229 | | | | | | |
| | CD7 | 10 | 0.673 | | | | | | |
| | mean | 0.25? ± 0.300 | | | | | | | |
| <i>E. radiata</i> | CD1 | 6 | 0.90* | 49 | 0.67*** | 0.13** ± 0.166 | 0.08** ± 0.173 | 0.22 ± 0.295 | 0.54 |
| | CD2 | 31 | 0.13 | | | | | | |
| | CD6 | 4 | 0.016 | | | | | | |
| | CD7 | 8 | 0.379 | | | | | | |
| | mean | 0.36* ± 0.395 | | | | | | | |

313 * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$; ? $p \leq 0.10$