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Intensive genetic assessment of the mating system and reproductive success in a semi-closed population of the mottled sculpin, *Cottus bairdi*

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**Abstract**

Most genetic surveys of parentage in nature sample only a small fraction of the breeding population. Here we apply microsatellite markers to deduce the genetic mating system and assess the reproductive success of females and males in an extensively collected, semi-closed stream population of the mottled sculpin fish, *Cottus bairdi*. In this species, males guard nest rocks where females deposit the eggs for fertilization. The potential exists for both males and females to mate with multiple partners and for males to provide parental care to genetically unrelated offspring. Four hundred and fifty-five adults and subadults, as well as 1259 offspring from 23 nests, were genotyped at five polymorphic microsatellite loci. Multilocus maternal genotypes, deduced via genetic analyses of embryos, were reconstructed for more than 90% of the analysed nests, thus allowing both male and female reproductive success to be estimated accurately. There was no genetic evidence for cuckoldry, but one nest probably represents a takeover event. Successful males spawned with a mean of 2.8 partners, whereas each female apparently deposited her entire clutch of eggs in a single nest (mean fecundity = 66 eggs/female). On average, genetically deduced sires and dams were captured 1.6 and 9.3 metres from their respective nests, indicating little movement by breeders during the spawning season. Based on a ‘genetic mark–recapture’ estimate, the total number of potentially breeding adults (c. 570) was an order-of-magnitude larger than genetically based estimates of the effective number of breeders (c. 54). In addition, significantly fewer eggs per female were deposited in single than in multidam nests. Not only were perceived high-quality males spawning with multiple partners, but they were receiving more eggs from each female.

**Keywords**: effective number of breeders, mark–recapture, maternity, parentage analysis, paternity

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**Introduction**

Genetic analyses of fish reproduction in nature have provided insights into broader aspects of animal mating system evolution (reviewed in Avise 2001; Avise et al. 2002). Molecular markers have been used to quantify reproductive success of fishes that exhibit such diverse phenomena as egg thievery (Jones et al. 1998), alloparental care of embryos (Munehara & Takenaka 2000) and alternative mating tactics and morphs of breeding adults (DeWoody & Avise 2001; Neff 2001). Genetic parentage analyses in fishes and other taxonomic groups have also been used to estimate population parameters such as gene flow (Kameyama et al. 2001), mutation rates and patterns (Jones et al. 1999), heritabilities of quantitative traits (King et al. 2003) and the nature and intensity of sexual selection (Greene et al. 2000; Jones et al. 2000, 2001a,b).

Most genetic studies of fish parentage have surveyed relatively open populations and sampled only a small proportion of the potential breeders. In addition, one sex (that which tends the dozens to thousands of embryos in a nest) is often represented disproportionately in the collected
Materials and methods

Field collections

Fish were collected from an approximately 150-m section of Shope Fork Creek within Coweeta Hydrological Laboratory in Otto, North Carolina. The population was semi-closed: the downstream point was marked by a pipeline crossing the creek (creating a 0.5-m waterfall), and the upstream end was blocked by a weir about 50 m beyond the study area. To facilitate locating the exact position of each fish and nest, permanent markers were placed at two meter intervals along both banks.

Twenty-three nests and 79 adults were collected between 22 and 25 April, 1999, via snorkelling (27 total hours in the water and three passes through the stream) using aquarium dip-nets. The locations of captured (or missed) individuals and nests were marked with numbered weights, and exact spatial relationships within the stream were reconstructed by triangulation from the bank markers. An additional 376 individuals and one nest were collected using a backpack electro-fisher (two passes on 27 April), and the locations of these samples were recorded to within four stream-metres. Live standard lengths and weights of the fish were measured, individuals were sexed via internal examination and adult tissues were stored in 95% EtOH for DNA analysis.

Parentage analyses

For most nests, a total of 48 embryos (equal numbers from each egg mass) were genotyped at the five polymorphic loci. From brood simulations (DeWoody et al. 2000b), this number of offspring was determined to provide adequate statistical power for detecting the allelic contributions of at least eight females, assuming that they contributed equally to a nest. For nests containing fewer than 48 eggs, all offspring were analysed. In addition, two nests (N015 and N012) were sampled more extensively, with 68 of 355 embryos and 209 of 210 embryos analysed, respectively.

Microsatellite analysis

A size selected genomic library for C. bairdi was constructed according to standard protocols (Choudhary et al. 1993) and then screened with multiple di-, tri-, and tetranucleotide probes. Positive clones were sequenced on an ABI 310 automated sequencer and PCR primer pairs were developed from the flanking sequences. In addition, 12 primer sets developed for Cottus gobio (Englbrecht et al. 1999) were assayed for polymorphism in C. bairdi.

From adults and post-hatching juveniles, DNA was extracted using standard phenol/chloroform methods (Maniatis et al. 1982); from embryo-containing eggs, DNA extractions were based on a modified fly buffer protocol (Gloor & Engels 1992; DeWoody et al. 2000a). PCR amplifications were conducted according to the thermal conditions in Table 1 using 0.1 unit Promega Taq polymerase, 1× PCR buffer, 1.5 mM MgCl₂, 0.3 mM of each primer, 0.1 mM of each dNTP and 1 µL DNA template. Loci Chs14 and Chs51 were multiplexed; all other reactions were performed separately. Markers which proved consistently scorable and polymorphic on radioactive gels were run on an ABI 377 sequencer using fluorescent primers, and genotypes were classified using the associated software. All five loci, distinguishable by their fluorescent colours and nonoverlapping sizes, were assayed together on single gels.

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Nest-guarding males were excluded genetically as the biological sire when they were inconsistent with offspring genotypes at multiple loci. For nests at which no guardian male was captured, multilocus paternal genotypes were deduced and matches were made to potential sires in the adult population. If multilocus maternal genotypes could not be reconstructed (see below), the minimum number of dams contributing to a nest was estimated by directly counting the number of distinct, maternally derived alleles in the progeny array (Parker & Kornfield 1996).

Mark–recapture estimates of population size

Data from parentage studies can be utilized in ‘genetic mark–recapture’ analyses to estimate the contemporary size of a breeding population (for details see Jones & Avise 1997; Pearse et al. 2001). By applying a corrected Lincoln–Peterson estimator (Pollock et al. 1990), that population size is calculated as:

\[
N = \frac{(n_1 + D)(n_2 + D)}{(m_2 + 1)} 
\]

where \(n_1\) is the number of reconstructed multilocus parental genotypes (i.e. the number of marked individuals), \(n_2\) is the number of adults subsequently captured, and \(m_2\) is the number of matches of captured adults to the genetically deduced parents (i.e. the number of recaptures). The variance of this estimate (Pollock et al. 1990), used to generated the 95% confidence limits, is given by:

\[
\text{Var}(N) = \frac{(n_1 + 1)(n_2 + 1)(n_1 - m_2)(n_2 - m_2)}{(m_2 + 1)^2(m_2 + 2)} .
\]

Table 1 Primer sequences and PCR conditions for the five microsatellite loci in mottled sculpins. PCR conditions began with a 2-min denaturing at 94 °C, followed by 30 cycles of the respective thermal profile. Thermal profiles represent times (in seconds) spent denaturing at 94 °C, annealing at the appropriate temperature, and extending at 72 °C with a final extension (in minutes) at 72 °C.

<table>
<thead>
<tr>
<th>Primer*</th>
<th>Fluorescent label</th>
<th>Sequence</th>
<th>Thermal profile</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chs14F</td>
<td>5’ FAM</td>
<td>5’-TTGCTGACACAGCATTTTGTG-3’</td>
<td>30, 30, 30 @ 55 °C, 2-min extension</td>
</tr>
<tr>
<td>Chs14R</td>
<td>5’-ACAAGTCCAGTCCACGACG-3’</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chs42F</td>
<td>5’-AAGATGTCAGCGTCTCCCTG-3’</td>
<td>30, 30, 30 @ 60 °C, 2-min extension</td>
<td></td>
</tr>
<tr>
<td>Chs42R</td>
<td>5’-AGGGAAGGACGAGAAGG-3’</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chs51F</td>
<td>5’-ATCAACCGCAGCTACGAGA-3’</td>
<td>30, 30, 30 @ 55 °C, 2-min extension</td>
<td></td>
</tr>
<tr>
<td>Chs51R</td>
<td>5’-CTGGGAGCTACGAGATC-3’</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cgp18ZimF</td>
<td>5’ FAM</td>
<td>described in Englbrecht et al. (1999)</td>
<td>45, 45, 45 @ 49 °C, 10-min extension</td>
</tr>
<tr>
<td>Cgp18ZimR</td>
<td>5’ HEX</td>
<td>described in Englbrecht et al. (1999)</td>
<td>45, 45, 45 @ 49 °C, 10-min extension</td>
</tr>
<tr>
<td>Cgp42ZimF</td>
<td>5’ FAM</td>
<td>described in Englbrecht et al. (1999)</td>
<td>45, 45, 45 @ 49 °C, 10-min extension</td>
</tr>
<tr>
<td>Cgp42ZimR</td>
<td>5’ HEX</td>
<td>described in Englbrecht et al. (1999)</td>
<td>45, 45, 45 @ 49 °C, 10-min extension</td>
</tr>
</tbody>
</table>

*Sequenced clones for Chs14, Chs42 and Chs51 have GenBank accession nos AFS19795, AFS19796 and AFS19797, respectively.

Only individuals two years or older (based on otolith ageing; Grossman et al. unpublised) were included in the count of \(t_2\), as they represent the potential breeders.

Estimates of the effective number of breeders

The effective population size, \(N_e\), can often be used as a surrogate for the effective number of breeders, \(N_b\). By applying a corrected Lincoln–Peterson estimator to calculate the effective number of breeders (\(N_b\)). It is important to recognize that the adult-to-progeny measure of \(N_b\) that we have calculated here is not the same as a single generation \(N_b\) estimate because C. bairdi maintains overlapping generations. For consistency, we have presented the formulae as they appear in the original publications. Here, \(N_b\) was estimated in two ways. In the first approach, based on variances in reproductive success among individuals, \(N_{b_{\text{en}}}\) and \(N_{b_{\text{em}}}\) are the effective numbers of breeding males and females, respectively (Kimura & Crow 1963). In the present study, the effective number of males was computed as:

\[
N_{b_{\text{en}}} = \frac{N_{b_{\text{km}}} - 1}{\frac{1}{\tilde{k}_m} + \frac{V_{m_{\text{en}}}}{\tilde{k}_m^2}} ,
\]

where \(N_{b_{\text{km}}}\) is the census number of breeding males, \(\tilde{k}_m\) is the mean number of offspring produced per male (deduced from the genetic paternity analyses in conjunction with census numbers of eggs per nest), and \(V_{m_{\text{en}}}\) is the variance in male reproductive success; an analogous formula yields the effective number of breeding females. Then, \(N_{b_{\text{em}}}\) was estimated as:

\[
N_{b_{\text{em}}} = \frac{4N_{b_{\text{en}}}N_{b_{\text{ef}}}}{N_{b_{\text{en}}} + N_{b_{\text{ef}}}} ,
\]

where \(N_{b_{\text{ef}}}\) is the census number of breeding females.

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In the second approach, \( N_e \) was estimated from temporal changes in allele frequency (Nei & Tajima 1981; Pollak 1983; Waples 1989), in this case from the parental to the offspring generation. The standardized variance in allele frequency change between generations (\( F_k \)) is given by:

\[
\frac{\sum (x_i - y_i)^2}{K - 1} (x_i + y_i)/2
\]

where \( K \) is the number of segregating alleles at a locus and \( x_i \) and \( y_i \) are the frequencies of the \( i \)th allele in the adults and progeny, respectively (Pollak 1983; Waples 1989). Allele frequencies in the progeny were estimated as the weighted average from within each nest. For multiple loci, the weighted mean of the single locus values is calculated according to:

\[
\frac{\sum (K_j - 1)\bar{F}_j}{\sum (K_j - 1)}
\]

for \( K_j \) alleles at the \( j \)th locus (Tajima & Nei 1984; Waples 1989). Under sampling plan I as defined by Waples (1989), the estimated effective population size (i.e. the effective number of breeders) is:

\[
N_e = \frac{t}{2[\bar{F}_k - 1/(2S_0) - 1/(2S_t) + 1/N]}
\]

where \( t \) is the number of generations traversed (one, in our case), \( S_0 \) and \( S_t \) are the sample sizes at times 0 and \( t \) (here, the adult and offspring generations), and \( N \) is the census size in the generation previous to the earliest sampled (assumed to be the same as the potential adult breeders, as estimated from the genetic mark–recapture analyses; see above). Confidence intervals were generated as described in Waples (1989).

Results

Population and nest characteristics

Of the 455 free-swimming individuals captured, 117 were less than 2 years old (based upon otolith ageing; Grossman et al. unpublished) and, thus, probably were not yet reproductively mature. Among the 338 adults, the sex ratio was 1.3:1 (females:males).

The DNA in embryos from one nest failed to amplify. Characteristics of the remaining nests are summarized in Table 2. For nine of the 23 nests, a male was captured tending the nest rock. In eight additional nests, a potential sire was captured within 1 m of the nest rock at the same time as the nest was discovered (i.e. in the immediate vicinity of the nest rock). All embryos were ‘eyed’ and showed little variation in size, either within or between nests. The mean

Table 2 Characteristics of the 23 analysed nests of the mottled sculpin

<table>
<thead>
<tr>
<th>Nest</th>
<th>Guarding male present?</th>
<th>No. egg masses</th>
<th>Total no. healthy eggs (per mass)</th>
<th>No. fungal-infected eggs in each egg mass</th>
</tr>
</thead>
<tbody>
<tr>
<td>N003</td>
<td>yes</td>
<td>3</td>
<td>331 (164, 95, 72)</td>
<td>0, 0</td>
</tr>
<tr>
<td>N012</td>
<td>yes</td>
<td>4</td>
<td>210 (61, 43, 30)</td>
<td>0, 0, 0</td>
</tr>
<tr>
<td>N015</td>
<td>nearby</td>
<td>3</td>
<td>355 (280, 80, 45)</td>
<td>0, 0, 0</td>
</tr>
<tr>
<td>N017</td>
<td>yes</td>
<td>3</td>
<td>279 (161, 98, 20)</td>
<td>= 30, 0, 90</td>
</tr>
<tr>
<td>N027</td>
<td>nearby</td>
<td>1</td>
<td>48</td>
<td>0</td>
</tr>
<tr>
<td>N033</td>
<td>yes</td>
<td>3</td>
<td>240 (139, 63, 38)</td>
<td>0, 0, 0</td>
</tr>
<tr>
<td>N034</td>
<td>nearby</td>
<td>2</td>
<td>191 (102, 89)</td>
<td>6, 8</td>
</tr>
<tr>
<td>N041</td>
<td>yes</td>
<td>1</td>
<td>30</td>
<td>13</td>
</tr>
<tr>
<td>N046</td>
<td>no</td>
<td>4</td>
<td>263 (116, 51, 50, 46)</td>
<td>4, 1, 6, 0</td>
</tr>
<tr>
<td>N058</td>
<td>nearby</td>
<td>1</td>
<td>135</td>
<td>6</td>
</tr>
<tr>
<td>N059</td>
<td>nearby</td>
<td>1</td>
<td>89</td>
<td>4</td>
</tr>
<tr>
<td>N063</td>
<td>yes</td>
<td>1</td>
<td>40</td>
<td>0</td>
</tr>
<tr>
<td>N064</td>
<td>no</td>
<td>1</td>
<td>105</td>
<td>0</td>
</tr>
<tr>
<td>N065</td>
<td>yes</td>
<td>3</td>
<td>127 (62, 35, 30)</td>
<td>= 35, 25, 2</td>
</tr>
<tr>
<td>N067</td>
<td>no</td>
<td>2</td>
<td>85 (48, 37)</td>
<td>3, 4</td>
</tr>
<tr>
<td>N070</td>
<td>nearby</td>
<td>3</td>
<td>158 (27, 54, 27)</td>
<td>2, 20, 1</td>
</tr>
<tr>
<td>N071</td>
<td>nearby</td>
<td>2</td>
<td>262 (153, 109)</td>
<td>2, 1</td>
</tr>
<tr>
<td>N078</td>
<td>nearby</td>
<td>4</td>
<td>345 (122, 103, 83, 37)</td>
<td>7, 5, 4, 18</td>
</tr>
<tr>
<td>N083</td>
<td>yes</td>
<td>1</td>
<td>120</td>
<td>2</td>
</tr>
<tr>
<td>N095</td>
<td>no</td>
<td>1</td>
<td>53</td>
<td>0</td>
</tr>
<tr>
<td>N100</td>
<td>yes</td>
<td>2</td>
<td>173 (118, 55)</td>
<td>0, 0</td>
</tr>
<tr>
<td>N101</td>
<td>no</td>
<td>3</td>
<td>273 (155, 60, 58)</td>
<td>0, 0, 0</td>
</tr>
<tr>
<td>N108</td>
<td>no</td>
<td>2</td>
<td>220 (156, 64)</td>
<td>12, 3</td>
</tr>
</tbody>
</table>
At 2.1, this would yield a rough estimate of the mutation rate per offspring. As these offspring were genotyped at 5 loci, the deduced genotypes of three unsampled parents were reconstructed exactly, and perfect genetic matches were found for 35 of these (59%) in the collection of females from the adult population. In two nests (N017 and N070), however, the deduced genotypes of three unsampled parents were reconstructed as null heterozygotes. Based on the reconstructed multilocus genotypes it was estimated that $d_n$ mutations occurred in 13 of the 1259 sampled offspring. As these offspring were genotyped at 5 loci, this would yield a rough estimate of the mutation rate at $2.1 \times 10^{-7}$ per locus per meiosis, which is consistent with published estimates for other microsatellite loci (see Ellegren 2000).

### Paternity

A total of 1259 embryos were analysed from the 23 nests (Table 4). In 22 of those nests (96%), all the progeny were consistent with having been sired by a single male. The one exception (N059) registers a probable nest takeover event. Here, two sires contributed to the nest and each had spawned with a different, unique female. Although neither sire was captured guarding this nest, one of the two males was captured 1 m upstream.

Additionally, the embryos in nest 064 were consistent with being full-sib progeny, except for two analysed individuals who differed at multiple loci. As none of the genetically decided parents of this nest was captured, it could not be deduced whether these two progeny register low-level cuckoldry or a case where one of two females deposited only a few eggs into the nest. Given the complete absence of cuckoldry in the other sculpin nests, in subsequent analyses we assumed provisionally that nest 064 had been sired by a single male (Table 4).

Unique matches for 14 of the 24 genetically deduced males (58%) were identified among the sampled adults and there was no evidence that males spawned in more than one nest. All nine males captured guarding a nest were identified as the true sire of their respective embryos. Thus, no alloparental care was observed.

### Maternity

In many (but not all) cases, the genotypes of embryos within each "discrete" egg mass were consistent with their being full-sibs and, thus, the multilocus genotype of each contributing female could be reconstructed easily. The mean number of genetically deduced dams per nest was 2.8 ($\pm 0.3$ SE; range 1–6) (Table 4). Overall, at least 65 females contributed to the sculpin progeny arrays assayed, and often in varying proportions (Table 4). Of these, a total of 59 multilocus maternal genotypes could be reconstructed exactly, and perfect genetic matches were found for 35 of these (59%) in the collection of females from the adult population. In two nests (N017 and N070), however, genotypes of the progeny were distributed more randomly among the egg masses that we had delineated, and multilocus maternal genotypes could not be deduced with confidence. Although the number of egg masses was a useful predictor of the number of dams ($r = 0.7$, $P < 0.001$), it fell significantly below the genetically deduced estimates of females contributing to a nest ($P < 0.001$, paired $t$-test).

It appears probable that each female deposited most or all of her eggs in the nest of a single male. First, in no case

### Table 3 Marker polymorphism in mottled sculpins. Shown are the number of alleles, expected ($H_e$) and observed ($H_o$) heterozygosities and exclusion probabilities (under the ‘neither parent known’ or ‘one parent known’ models).

<table>
<thead>
<tr>
<th>Locus</th>
<th>No. alleles</th>
<th>$H_e$</th>
<th>$H_o$</th>
<th>$P_e$ (neither known)</th>
<th>$P_e$ (1 known)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chs14</td>
<td>9</td>
<td>0.77</td>
<td>0.81</td>
<td>0.39</td>
<td>0.57</td>
</tr>
<tr>
<td>Chs42</td>
<td>4</td>
<td>0.57</td>
<td>0.58</td>
<td>0.16</td>
<td>0.30</td>
</tr>
<tr>
<td>Chs51</td>
<td>16</td>
<td>0.73</td>
<td>0.64</td>
<td>0.37</td>
<td>0.56</td>
</tr>
<tr>
<td>Cgo18Zim</td>
<td>23</td>
<td>0.88</td>
<td>0.85</td>
<td>0.62</td>
<td>0.76</td>
</tr>
<tr>
<td>Cgo42Zim</td>
<td>8</td>
<td>0.75</td>
<td>0.74</td>
<td>0.36</td>
<td>0.54</td>
</tr>
<tr>
<td>mean</td>
<td>12</td>
<td>0.74</td>
<td>0.72</td>
<td>0.24</td>
<td>0.99</td>
</tr>
</tbody>
</table>

*Calculated using equation 1a from Jamieson & Taylor (1997).
†Calculated using equation 1a from Jamieson & Taylor (1997).
‡Cumulative exclusion probability across all loci, calculated using equation 4 from Jamieson & Taylor (1997).
was the same reconstructed multilocus maternal genotype present in more than one nest. Second, a plot of total embryo numbers in each nest against the deduced number of dams demonstrates that estimates of genetically deduced female fecundity agree well with those from ovarian counts (Fig. 2). The mean number of embryos contributed by each dam in this study was 66 (± 4.6 SE; range 4–168 eggs/female) compared to 71 (± 2 SE; range 9–166) calculated using ovarian counts from Grossman et al. (2002).

Interestingly, significantly more eggs per female were deposited in multidam nests (70 ± 4.9 SE) than in nests with only a single mother (46 ± 2.8 SE) (Fig. 3). Male guardians of single- vs. multidam nests did not differ significantly in body size, but mothers of the single-dam nests were smaller than those of multidam nests (P = 0.004; one-tailed t-test assuming unequal variances, total n = 57).

<table>
<thead>
<tr>
<th>Nest</th>
<th>Genetically deduced sire</th>
<th>Sire captured?</th>
<th>No. of analysed progeny sired by male</th>
<th>No. of genetically deduced dams</th>
<th>Relative contributions of females (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>N003</td>
<td>CB003 on nest</td>
<td></td>
<td>48 of 48</td>
<td>4</td>
<td>50, 22, 19, 9</td>
</tr>
<tr>
<td>N012</td>
<td>CB012 on nest</td>
<td></td>
<td>209 of 209</td>
<td>4</td>
<td>40, 22, 20, 18</td>
</tr>
<tr>
<td>N015</td>
<td>MM015 not captured</td>
<td></td>
<td>48 of 48</td>
<td>6</td>
<td>48, 20, 13, 11, 4, 4</td>
</tr>
<tr>
<td>N017</td>
<td>CB017 on nest</td>
<td></td>
<td>68 of 68</td>
<td>minimum of 3*</td>
<td>not deduced</td>
</tr>
<tr>
<td>N027</td>
<td>CB248 –11 m away</td>
<td></td>
<td>48 of 48</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>N033</td>
<td>CB033 on nest</td>
<td></td>
<td>48 of 48</td>
<td>4</td>
<td>47, 26, 16, 11</td>
</tr>
<tr>
<td>N034</td>
<td>CB039 +1 m away</td>
<td></td>
<td>48 of 48</td>
<td>3</td>
<td>46, 34, 20</td>
</tr>
<tr>
<td>N041</td>
<td>CB041 on nest</td>
<td></td>
<td>30 of 30</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>N046</td>
<td>CB321 –9 m</td>
<td></td>
<td>48 of 48</td>
<td>4</td>
<td>37, 26, 19, 18</td>
</tr>
<tr>
<td>N058</td>
<td>MM058 not captured</td>
<td></td>
<td>48 of 48</td>
<td>2</td>
<td>62, 38</td>
</tr>
<tr>
<td>N059#</td>
<td>CB055 +1 m away</td>
<td></td>
<td>15 of 48</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td></td>
<td>MM059 not captured</td>
<td></td>
<td>33 of 48</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>N063</td>
<td>CB063 on nest</td>
<td></td>
<td>40 of 40</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>N064</td>
<td>MM064 not captured</td>
<td></td>
<td>48 of 48</td>
<td>2</td>
<td>96, 4$</td>
</tr>
<tr>
<td>N065</td>
<td>CB065 on nest</td>
<td></td>
<td>48 of 48</td>
<td>4</td>
<td>28, 24, 24, 24</td>
</tr>
<tr>
<td>N067</td>
<td>MM067 not captured</td>
<td></td>
<td>48 of 48</td>
<td>2</td>
<td>56, 44</td>
</tr>
<tr>
<td>N070</td>
<td>CB182 0 m away, not guarding</td>
<td></td>
<td>48 of 48</td>
<td>minimum of 3*</td>
<td>not deduced</td>
</tr>
<tr>
<td>N071</td>
<td>MM071 not captured</td>
<td></td>
<td>48 of 48</td>
<td>3</td>
<td>41, 32, 27</td>
</tr>
<tr>
<td>N078</td>
<td>MM078 not captured</td>
<td></td>
<td>48 of 48</td>
<td>4</td>
<td>30, 29, 22, 19</td>
</tr>
<tr>
<td>N083</td>
<td>CB083 on nest</td>
<td></td>
<td>48 of 48</td>
<td>2</td>
<td>54, 46</td>
</tr>
<tr>
<td>N095</td>
<td>MM095 not captured</td>
<td></td>
<td>48 of 48</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>N100</td>
<td>CB100 on nest</td>
<td></td>
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<td>3</td>
<td>48, 32, 20</td>
</tr>
<tr>
<td>N101</td>
<td>MM101 not captured</td>
<td></td>
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<td>3</td>
<td>56, 25, 19</td>
</tr>
<tr>
<td>N108</td>
<td>MM108 not captured</td>
<td></td>
<td>48 of 48</td>
<td>3</td>
<td>56, 29, 15</td>
</tr>
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</table>

*The multilocus female genotypes could not be reconstructed, so the number of females was estimated via the single-locus minimum method (Parker & Kornfield 1996).
†The nest was composed of two, full-sib progeny arrays. Male CB005 mated to female CB125 and male MM059 mated to female CB155. Neither male was observed guarding the nest.
‡The nest consistent with a full-sib progeny array, excepting two offspring (at multiple loci). Neither the deduced male(s) nor the female(s) were captured and, thus, cuckoldry could not be definitively invoked. The nest was assumed to have been sired by a single male and dammed by two females.
mean standard lengths of females were 53 (±1.0 SE) mm and 59 (±1.3 SE) mm, respectively, for nests with single and multiple maternity. In addition, mating pairs appeared to be random with respect to the standard body length ($r^2 = 0.06$, $P > 0.1$) and weight ($r^2 = 0.12$, $P > 0.1$).

Relative locations

As expected, given that males in this species tend nests, there was an almost perfect correlation ($r^2 = 0.99$, $P < 0.001$) between the nest location and the collection locale of the genetically deduced sires (Fig. 4). Although females were never captured guarding a nest, there was also a strong correlation ($r^2 = 0.92$, $P < 0.001$) between nest sites and the location of the genetically deduced dams (Fig. 4). On average, sires and dams were captured only 1.6 (±1.0 SE) m and 9.3 (±1.8 SE) m from their respective nests.

Population size and effective number of breeders

Based on the mark-recapture calculations, there were 243 potentially breeding males (95% confidence limits, 172–314) and 323 potentially breeding females (95% confidence limits, 264–382) in the local population, or about 566 adults total. By contrast, the estimated effective number of breeders ($N_{e}$) was an order-of-magnitude lower. The ‘variance in reproductive success’ approach estimated 60 effective individuals (18 males and 99 females) whereas the ‘temporal method’ estimated 48 effective individuals (95% 

![Fig. 2](image2.png)  
**Fig. 2** Total number of eggs per nest as a function of the number of genetically deduced dams. The line represents the predicted number of eggs (assuming that each female deposited all her eggs in one nest) based on a mean of 71 eggs per female from direct ovarian counts (Grossman et al. 2002).

![Fig. 3](image3.png)  
**Fig. 3** Mean number of eggs deposited per female in single- vs. multidam nests. Bars show standard errors. This difference between these two classes of nests is significant ($P < 0.001$; one-tailed $t$-test assuming unequal variances).

![Fig. 4](image4.png)  
**Fig. 4** Locations of mottled sculpin nests (in stream-metres from the starting point) vs. the location of the genetically deduced sires (above) and dams (below). The lines represent what would be observed if the nest and parent were from exactly the same site. For specimens captured via electrofishing, distance from the starting point was calculated as the midpoint of the 4-m section (see text).
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Summary

In this study, we employed microsatellite DNA markers to characterize the genetic mating system of mottled sculpins, Cottus bairdi. Our results suggest that mottled sculpins are polygynous, with males guarding multiple nests and siring offspring. We observed a high degree of paternal certainty, with 96% of nests sired by a single male and 98% of offspring consistent with a single sire. These findings are consistent with previous studies that have documented high levels of paternal certainty in other species, such as the striped darter and the sand goby.

Discussion

Previous studies have suggested that mottled sculpins deposit all of their eggs into one nest. Here, we have confirmed this observation and provide new insights into the sculpin mating system and potential factors influencing mate choice.

Microsatellite markers

Mills et al. (2000) suggested using the mean probability of identity (PI) to determine the utility of markers for genetic mark-recapture studies. The PI was indeed suitably low in the current study (4.6 x 10^-9). Given the number of possible pairwise comparisons (162 165) between the estimated 570 potential sculpin breeders, fewer than one such pair might be expected to share a multilocus genotype by chance and, empirically, no instances of genotypic sharing were observed for the adult males and females sampled. However, the reconstructed genotype of one dam did match a male (CB449) in the collection, an outcome that is almost certainly spurious. For the nest in question (N100), the reconstructed genotype of one dam did represent a potential nest takeover, but neither of the genetically deduced sires was captured tending the embryos (although male CB005 was within 1 m of the nest). Overall, 96% of the nests were sired by a single male and 98% of the offspring analysed were consistent with a single sire per nest. This latter level of paternity assurance is higher than documented in several other cavity-spawning species: 85% in the sand goby (Jones et al. 2001a,b) and 84% in the striped darter (DeWoody et al. 2000a) and 86% in the tessellated darter (DeWoody et al. 2000b).

Effective number of breeders

The effective number of breeders is a useful measure of differential reproductive success among adults. We found that mottled sculpins are sedentary during the nonbreeding season (Brown & Downhower 1982b), and have estimated home ranges of less than 20 m (Hill & Grossman 1987; Petty 1998). Here we demonstrate restrictive travels during the breeding season as well. When captured, genetically deduced sires and dams were on average only 1.6 and 9.3 m away from their respective nests. Such strong correlations provide additional compelling evidence that the multilocus maternal genotypes were accurately reconstructed. Limited excursions by males are expected, because sires tend the nest-rock and provide offspring care. Given that females probably visit multiple males before spawning (Downhower & Brown 1979), the nests visited must often be proximate.
to its estimation either in managed populations (Perez-Enriquez et al. 1999; Hasen et al. 2000) or in nature (Scribner et al. 1997; Garant et al. 2001).

This study is among the first to estimate \( N_e \) for a natural fish population based on genetic parentage data. The genetically deduced effective number of breeders (\( N_e \approx 54 \)) in the mottled sculpin population was much smaller than the census size of potential breeders (\( N = 570 \)). Mottled sculpins have overlapping generations, so this discrete-time estimate of \( N_e \) (from adults to progeny) is not equivalent to the effective population size (\( N_e \)) across a single generation (see Nunnery 1993; Waite & Parker 1996; methods section). Nonetheless, the small \( N_e \) combined with the observation that adults have limited movements, imply that genetic drift could rapidly produce genetic heterogeneity of sculpin populations even among nearby streams.

It is important to recognize that multiple factors could influence the estimate of the effective number of breeders. First, a failure to sample some nests could yield underestimates of \( N_e \). Given that C. bairdi nests are fairly conspicuous (G. Grossman, pers. obs.), and given that we completed three snorkelling passes through the stream with only one nest being located on the final pass, we are confident that most nests were sampled. Second, an extended breeding season, coupled with limited temporal collections, also could lead to reductions in the calculated \( N_e \). Mottled sculpins, however, tend to have very short spawning seasons (Downhower & Brown 1980), a conclusion supported further by the lack of developmental variation observed among embryos of the surveyed nests.

Finally, the time at which the estimates of \( N_e \) are made can affect the calculated value. In this study we have analysed genetically late-stage eggs from each nest to determine: (a) the allele frequencies among the offspring, and (b) the variance in progeny number among reproductive adults. Short of spawning observations on marked fish, this may be the earliest tractable time to estimate \( N_e \). Time, and specifically natural selection operating from the point of egg-laying to the age at maturation, may make estimates of \( N_e \) calculated with older age classes very different from those presented in this study.

Indeed, such deviations, if they could be accurately quantified, might yield valuable insights into influencing selection in this species. Consider the following simplified example. If \( N_e \) estimates calculated using older individuals are larger than those using younger individuals, this might suggest the operation of either balancing or frequency dependent selection. If, however, the converse were true, this might suggest strong directional selection favouring only a small subset of families. Although the theoretical framework for such comparisons is currently lacking, such approaches may enlighten future research endeavors.

**Polygyny and fitness**

From the genetic maternity data, guardian males who had spawned with multiple females sired more embryos (i.e. received more eggs) per female than did sires who spawned with only one dam. Also, females who deposited eggs in multidam nests were larger, on average, than those who deposited eggs in single-maternity nests, and this finding is consistent with the positive correlation between standard length and fecundity previously reported for C. bairdi (Grossman et al. 2002). This finding is also consistent with the observation that smaller females tended to spawn with bachelor males (Downhower et al. 1987). In contrast, we did not find evidence for positive size assortative mating as did Downhower et al. (1983, 1987).

Females of many fish species prefer to mate with males whose nests already contain eggs (Constantz 1985; Maronato & Biaszza 1986; Unger & Sargent 1988). This observation has been proposed as an adaptive explanation for allopatrial care (Constantz 1985; Unger & Sargent 1988), as well as for the evolution in some species of male morphological features (such as knobs on the tips of fins) that mimic eggs in appearance (Knapp & Sargent 1989; Page & Bart 1989; Porter et al. 2002). However, for mottled sculpins, Downhower & Brown (1981) did not find a female preference for males who were guarding eggs. These results are consistent with the notion that females may sometimes prefer to spawn with a bachelor. Although established nests may be reflective of quality sires (Sargent 1988), additional considerations may well behave a female to weigh all potential costs and benefits in her final choice of spawning partner.

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**References**


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This study is part of the authors’ ongoing endeavour to assess genetic mating systems of fishes in nature. A former graduate student in the Avise laboratory, Anthony Fiumera explored theoretical and empirical methods to estimate genetic structure. Brady Porter, a postdoctoral associate in Avise’s laboratory, is currently using molecular markers to address ecological, phylogenetic and conservation issues in fishes. Gary Grossman, Professor of Animal Ecology, studies population and community ecology of aquatic ecosystems.