Genetic dissimilarity predicts paternity in the smooth newt (Lissotriton vulgaris)

Robert Jehle1,2,*, Marc Szstatecsny3, Jochen B. W. Wolf4, April Whitlock2, Walter Hödl3 and Terry Burke2

1Department of Evolutionary Biology, University of Bielefeld, Morgenbrede 45, Bielefeld 33615, Germany
2Department of Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield S10 2TN, UK
3Department of Evolutionary Biology, University of Vienna, Althanstrasse 14, Vienna 1090, Austria
4Department of Evolution Genetics, Institute for Genetics, University of Köln, Zülzicherstraße 47, Köln 50674, Germany
*Author for correspondence (robert.jehle@uni-bielefeld.de).

Under sperm competition, paternity is apportioned by polyandrous females according to the order of matings and the genetic quality of the inseminating males. In order to distinguish between these two effects, we sequentially paired 12 female smooth newts (Lissotriton vulgaris) with each of two males and, where possible, repeated the same procedure in reverse order of the identical males after assumed sperm depletion. For a total of 578 offspring, amplified fragment length polymorphisms genetic markers revealed multiple paternities in all matings, without significant first- or second-male sperm precedence. The paternity share of individual males was transitive across the two trials with male order switch, and successful males had a significantly higher genetic dissimilarity to the female than expected by chance. We argue that patterns of paternity in natural newt populations are determined through a combination of good genes and relatedness.

Keywords: amplified fragment length polymorphisms; genetic compatibility; paternity; sperm competition; Lissotriton vulgaris

1. INTRODUCTION

Female mate choice is a key concept in evolutionary biology and has vast consequences for male and female reproductive success. Females can either favour males that signal high quality through condition-dependent traits (good genes hypothesis) or select partners whose genotypes fit best with their own genetic make-up (genetic compatibility hypothesis, Zeh & Zeh 1997). The degree of genetic compatibility depends on specific female–male combinations, and thus represents a relative rather than absolute criterion for mate quality; the genetic basis of compatibility can however be quantified in a rather straightforward way, for example, through measures of genotypic dissimilarity (Mays & Hill 2004). The aquatic courtship display of European newts (formerly genus Triturus, see Steinfaatz et al. 2007) is characterized by a combination of visual and olfactory cues; sperm is transferred via spermatophores, and fertilization is internal. Studies on the mating system of the smooth newt (Lissotriton vulgaris) were among the first to comprehensively reveal the mechanisms of sexual selection and female choice in an amphibian (for a summary see Halliday (1998)). However, as the genetic mating system of L. vulgaris remained unstudied, it is yet unclear to what extent mating strategies are governed by sperm mixing, and/or genetic compatibility mechanisms (as demonstrated for the closely related Mesotriton alpestris, Rafinski & Osikowski (2002) and Garner & Schmidt (2003)).

The reproductive fitness of males with differing genetic backgrounds is often compared by measuring their paternity share after sequential insemination of a single female. However, in such a situation, the males under study compete under differential sperm competition regimes, and a more absolute measure of male quality can only be achieved with methods that disrupt the natural courtship sequence such as artificial fertilization (Birkhead et al. 2004). In this study, we conducted classical sperm competition experiments by sequentially mating one female L. vulgaris with two males. In order to distinguish genetic effects from mating-order effects on the paternity share, we then repeated this experiment for each female after sperm depletion, switching the order of the same two males. Using genetic markers, we document the patterns of sperm precedence in L. vulgaris and demonstrate that the more genetically dissimilar male has a higher paternity share, regardless of the order of access to the female.

2. MATERIAL AND METHODS

(a) Mating experiments

To ensure that the study individuals were unmated, they were captured in March 2003 at a breeding pond east of Vienna (Austria) before entering the water. Mating trials were conducted in April–May 2003 and 2004, but no individuals were used successively in both years. For the mating experiments, a single female was placed in an aquarium (50 × 30 × 30 cm) and an arbitrarily chosen male was added. After successful spermatophore transfer, the male was removed and a second male was placed into the tank for a second insemination on the following day (completing ‘trial 1’). Thereafter, females (n=12) were housed singly in individual aquaria furnished with anchored plastic strips in which their eggs were wrapped. They immediately started to lay eggs, ceasing after a maximum of approximately 30 days. At least one week after the last egg was laid, we attempted the same procedure as described above, with the same males but switching their order of insemination (‘trial 2’), again with a 1-day interval between the two matings; however, only 8 out of 12 females readily re-mated with both males). Eggs of both trials were raised independently in 1 l plastic units until larvae hatched. No carry-over of paternity was observed in trials of females mated successively with two different pairs of males (n=5 females, set-up as described above, data not given), supporting our assumption that they had become sperm depleted.

(b) Genotyping

A random subset of offspring was collected immediately after hatching, and toe-clips were taken from adults and stored in absolute ethanol for subsequent DNA extraction. For paternity determination and relatedness estimates, we applied amplified fragment length polymorphisms (AFLPs), using the fluorescently labelled primer combinations T108, T204, T205 and procedures as outlined in Whitlock et al. (2006). PCRs were performed in Bio-Rad thermal cyclers, and AFLP fragments were separated and visualized using an ABI 3730 capillary sequencer, followed by analysis using the software GENEMAPPER v. 3.5.
Table 1. Relatedness and paternity in experimental matings of *L. vulgaris*. (SM, relatedness coefficient (Wang 2004) to the female, with standard deviations in parenthesis. In trials 1 and 2, two identical males are mated with one female in both possible orders. The absolute number of genotyped embryos assigned to the respective males is given.)

<table>
<thead>
<tr>
<th>female</th>
<th>relatedness coefficient (SM)</th>
<th>offspring, trial 1</th>
<th>offspring, trial 2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>male 1</td>
<td>male 2</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>−0.28 (0.15)</td>
<td>0.39</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>−0.36 (0.16)</td>
<td>0.50 (0.13)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.05</td>
<td>0.03 (0.15)</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>−0.55 (0.15)</td>
<td>−0.01 (0.16)</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>−0.40 (0.16)</td>
<td>0.38 (0.14)</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>−0.59 (0.16)</td>
<td>−0.36 (0.15)</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>−0.59 (0.13)</td>
<td>0.22 (0.15)</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>0.26 (0.13)</td>
<td>0.07 (0.15)</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>0.04</td>
<td>−0.20 (0.13)</td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>0.24 (0.15)</td>
<td>0.02 (0.14)</td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>−0.13 (0.14)</td>
<td>0.06 (0.15)</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>−0.32 (0.15)</td>
<td>−0.16 (0.15)</td>
<td></td>
</tr>
</tbody>
</table>

* For these males, the AFLP profiles were not sufficiently scorable across the whole size range, and SM was set to the population average (zero). Paternity determination was possible based on partial AFLP screens.

3. RESULTS

We scored an AFLP size range of 70–280 bp, in which 53 out of 249 (21.3%) loci across three primer combinations were polymorphic across the adult individuals; pairwise relatedness coefficients SM ranged from −0.59 to 0.50, with standard deviations not exceeding 0.16 (table 1). Overall, we assigned the paternity of 578 offspring to their parents. Multiple paternities were observed in all 20 trials conducted with 12 females, with the relative paternity share of the first male averaging at 0.50 (range: 0.14–0.81). The null model focusing on male identity had considerably more support than a model which

![Figure 1. Difference in relatedness coefficient (SMdiff) for those male smooth newts (*L. vulgaris*), which sired more offspring than the competitor when inseminating one female. The dotted line indicates the expected average when relatedness plays no role in determining paternity. Circles represent trial 1 and squares represent trial 2 (see text). Colour indicates mating order (white, first male; grey, second male). Symbol size scales linearly with total number of offspring.](http://rsbl.royalsocietypublishing.org/article-pdf/10.1098/rsbl.2006.1217/527)
with *L. vulgaris*. Moreover, although last-male sperm precedence was suggested based on morphological evidence (Sever *et al.* 1999), we show that the paternity share between two competing males is independent of their order of insemination.

Given our modest sample size and accounting for the fact that several factors are potentially confounding any genetic effects (for example, we had no information about the number of sperm transferred by each male), the influence of genetic dissimilarity seems surprisingly strong. Out of 20 cases, only one male with higher paternity share was strikingly more closely related to the female than the competitor; in three other cases, \( S_{	ext{M}} \text{diff} \) of the more successful male was only marginally positive (figure 1). This suggests that paternity is more likely to be determined by a threshold effect rather than in a gradual way. Female sensitivity to differences in genetic dissimilarity of their mating partners is unexpectedly high. As typical effective population sizes in European newts are approximately 10–20 individuals (Jehle *et al.* 2005), it is possible that we created experimental matings between closely related individuals. Indeed, SM values between 12 known mother–offspring relationships (one offspring for each female used) were between 0.21 and 0.55 (mean 0.36). It is possible, albeit unlikely, that setting SM of three males to zero biased our results: in two cases (involving females 1 and 9), known SM values of the competing males are several standard errors below the population average (−0.20 and −0.28 at s.e. = 0.068), rendering it probable that the unknown SM values are above these values; excluding the case where the known male has an SM value close to the average (involving female 3), for example, results in an overall \( p \) value of 0.034.

Mate choice decisions are generally assumed to be shaped by both good and compatible genes in a complementary way (Mays & Hill 2004; Neff & Pitcher 2004). In natural situations, however, the temporal gaps between matings are more variable, and females have the opportunity to mate with more than two males; we are therefore uncertain whether the strong dissimilarity effects we obtained in our experiments are directly translatable to field populations. As our experiments excluded the possibility of overt mate choice, we also cannot draw conclusions on the efficiency of trading up for good genes in *L. vulgaris* (see Gabor & Halliday 1997). Future research should look into a potential influence of condition-dependant traits on the outcome of paternity under sperm competition, whether the importance of dissimilar genes is related to population size and inbreeding regimes, and whether the differential paternity share is due to the differential mortality of offspring, and/or cryptic female choice.

The study was supported by FWF grant P-14799. We thank Klaus Reinhold for constructive comments and Andreas Baierl for statistical advice.


