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**Article:**

Immler, S., Saint-Jalme, M., Lesobre, L. et al. (3 more authors) (2007) The evolution of sperm morphometry in pheasants. *Journal of Evolutionary Biology*. ISSN 1420-9101

<https://doi.org/10.1111/j.1420-9101.2007.01302.x>

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### Published paper

Immler, S., Saint-Jalme, M., Lesobre, L., Sorci, G., Roman, Y. and Birkhead, T.R. (2007) *The evolution of sperm morphometry in pheasants*. Journal of Evolutionary Biology.

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1 The evolution of sperm morphometry in pheasants

2

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22 Running title: Sperm morphometry and function in pheasants

1 **ABSTRACT**

2 Postcopulatory sexual selection is thought to be a potent evolutionary force driving the  
3 diversification of sperm shape and function across species. In birds, insemination and  
4 fertilisation are separated in time and sperm storage increases the duration of sperm-  
5 female interaction and hence the opportunity for sperm competition and cryptic female  
6 choice. We performed a comparative study of 24 pheasant species (Phasianidae,  
7 Galliformes) to establish the relative importance of sperm competition and the duration of  
8 sperm storage for the evolution of sperm morphometry (i.e. size of different sperm traits).  
9 We found that sperm size traits were negatively associated with the duration of sperm  
10 storage but were independent of the risk of sperm competition estimated from relative  
11 testis mass. Our study emphasises the importance of female reproductive biology for the  
12 evolution of sperm morphometry particularly in sperm storing taxa.

13

14

15

16 Keywords: sperm competition, female reproductive biology, sperm storage duration,  
17 sperm morphometry, pheasants, comparative study

## 1 **1. INTRODUCTION**

2 Postcopulatory sexual selection consisting of sperm competition (Parker, 1970;  
3 Birkhead & Parker, 1997) and cryptic female choice (Eberhard, 1996) is thought to be an  
4 important evolutionary force for many reproductive traits including sperm morphometry  
5 (Simmons, 2001; Miller & Pitnick, 2002; Snook, 2005). However, it is often difficult to  
6 disentangle male and female influences on sperm form and function. One reason for this  
7 is the difficulty of investigating the interaction between sperm and the female  
8 reproductive tract after insemination.

9 Morphometric sperm traits, including sperm length and midpiece volume are  
10 known to be influenced by sperm competition in a variety of taxa. Total sperm length is  
11 associated with the risk of sperm competition in insects (Gage, 1994; Morrow & Gage,  
12 2000) amphibians (Byrne *et al.*, 2003), fishes (Stockley *et al.*, 1997; Balshine *et al.*,  
13 2001), birds (Johnson & Briskie, 1999) and mammals (Gomendio & Roldan, 1991;  
14 Breed & Taylor, 2000; but see Hosken, 1997; Gage & Freckleton, 2003). Similarly,  
15 midpiece size is positively related to the risk of sperm competition in mammals  
16 (Anderson & Dixson, 2002; Anderson *et al.*, 2005; but see Gage & Freckleton, 2003).  
17 On the other hand, in taxa where females store sperm after insemination (Birkhead &  
18 Møller, 1993a, b) there is growing evidence for the influence of female reproductive  
19 biology and cryptic female choice on the evolution of sperm morphometry: the  
20 coevolution of the size (and number) of sperm storage organs and sperm size has been  
21 demonstrated in beetles (Dybas & Dybas, 1981), drosophilids (Miller & Pitnick, 2002),  
22 stalk-eyed flies (Presgraves *et al.*, 1999), Scatophagidae (Minder *et al.*, 2005), snails  
23 (Beese *et al.*, 2006) and birds (Briskie & Montgomerie, 1992; Briskie *et al.*, 1997).

1           The aims of this study were twofold: first, to test the hypothesis that sperm  
2 morphometry has evolved in response to the risk of sperm competition (inferred from  
3 relative testis mass; Møller, 1991; Møller & Briskie, 1995) in pheasants (Phasianidae,  
4 Galliformes). Pheasants typically exhibit intense precopulatory sexual selection  
5 characterised by polygynous, promiscuous or lek mating systems (Johnsgard, 1986;  
6 McGowan, 1994; Höglund & Alatalo 1995) and the risk of sperm competition may  
7 therefore vary markedly across species. Second, to test the hypothesis that sperm  
8 morphometry has evolved in response to female reproductive biology, specifically in  
9 response to the duration of sperm storage inferred from clutch size and the interval  
10 between successive eggs. Across a wide range of bird species, a significant relationship  
11 exists between sperm storage duration and the duration of egg laying (Birkhead &  
12 Møller, 1992). In many bird species, copulation ceases before egg laying starts and  
13 females store sperm for days or weeks prior to fertilise their eggs (Birkhead & Møller,  
14 1993a, b). Therefore, in species with larger clutch size sperm have to survive longer to  
15 ensure the fertilisation of all eggs. In the peafowl for example, females cease copulating  
16 12 days before the first egg is laid (Birkhead & Møller, 1993b); and females lay five to  
17 six eggs on average at two day intervals (Birkhead & Petrie, 1995). Sperm therefore have  
18 to survive for an average of 26 days inside the female tract. In contrast, female Palawan  
19 peacock pheasants *Polyplectron emphanum* lay only two eggs at two day intervals  
20 (McGowan, 1994) and sperm have to survive for a much shorter period. Sperm storage  
21 duration has two implications for postcopulatory sexual selection both of which depend  
22 strongly on copulation frequency: sperm storage duration may (i) influence the  
23 likelihood that sperm of rival males meet inside the female reproductive tract (Parker,

1 1970) and (ii) may be a way for females to select high quality (e.g. long lived) sperm  
2 (Birkhead *et al.*, 1993).

3

## 4 **2. MATERIAL & METHODS**

### 5 *Data collection*

6 We collected sperm samples from 24 pheasant species. "Males used for this study  
7 were all bred in captivity and held in the "Parc zoologique de Clères". Several species  
8 belong to populations managed by the European Endangered Programmes (EEP) to  
9 avoid inbreeding effects (Saint Jalme, 2002; Saint Jalme, *et al.* 2003; see also: Gomendio  
10 *et al.*, 2000; Gage *et al.*, 2006). Ejaculates were collected using the massage technique  
11 described in Saint Jalme *et al.* (2003). Data on sperm traits, testis mass and clutch size  
12 are summarised in the electronic Appendix 2. Data on testis mass and some  
13 morphometric sperm traits were not available for some species which explains variation  
14 in sample size in the analyses.

15

### 16 *a) Sperm morphometry*

17 Sperm from one ejaculate from one male per species were fixed in a 5% formalin  
18 solution. Intraspecific and intra-male repeatabilities (Lessells & Boag, 1987) for  
19 morphometric sperm traits were high, justifying the assumption that a single male is  
20 representative for a species (see Electronic Appendix Table 2). Furthermore, we  
21 compared the species mean for total sperm length obtained from an earlier dataset  
22 derived from several males per species by M. Saint Jalme (unpublished data) with the  
23 data from a single male per species used in this study. MSJ's species means and the data

1 used in the present study were highly correlated ( $r = 0.94$ ,  $p < 0.0001$ ,  $N = 25$ ) and not  
2 significantly different (paired sample  $t$  test:  $t_{10} = 1.17$ ,  $p = 0.27$ ).

3 For morphometric analyses, a sub-sample of sperm was placed on a microscope  
4 slide and stained using the fluorescent dye Mitotracker green FM (Molecular Probes) to  
5 make the midpiece evident for measurement. Two digital pictures of fifteen sperm per  
6 male were taken at 400x magnification: one picture was taken using bright-field and one  
7 picture was taken using fluorescence. The following sperm traits were measured using  
8 the image analysis software Leica IM50 Image manager: (i) the length of the head, (ii)  
9 the length of the midpiece, and (iii) the length of the flagellum including the part  
10 wrapped by the midpiece. Total sperm length was calculated by adding head length and  
11 flagellum length.

12

### 13 *b) Testis mass, body mass and sperm storage duration*

14 Testis mass and body mass were measured during the peak breeding season of  
15 each species from the same males used for sperm measurements. Testis mass was  
16 obtained by measuring testis dimensions and converting volume into mass using Møller's  
17 formula (1991). This method is widely used and provides an accurate measurement of  
18 testis mass if applied properly (Calhim & Birkhead, in press). Testis dimensions were  
19 obtained using laparotomy: maximum testis length and width were measured by inserting  
20 an endoscope and a calliper through the abdominal air sac wall. Only the left testis was  
21 measured to minimise stress. The measurements of the dimensions of both testes in one  
22 Indian peacock *Pavo cristatus* revealed minimal differences between left and right testis  
23 (right testis: 2.34g and left testis: 2.46; see also Friedmann, 1927; Kimball *et al.*, 1997).

1 For each species the left testis was measured and multiplied by two to obtain an index of  
2 total testis mass.

3 Information on clutch size and the mean interval between successive egg was  
4 obtained from the literature (Johnsgard, 1986; McGowan, 1994; MSJ, unpubl. data) and  
5 was used to estimate the duration of sperm storage: average clutch size was multiplied  
6 with the mean interval between subsequent eggs and one subtracted at the end.

7

## 8 *Statistical analyses*

### 9 a) *Comparative methods*

10 To control for statistical non-independence of traits due to phylogeny in our  
11 analyses (Felsenstein, 1985; Harvey & Pagel, 1991) we used the approach of generalised  
12 least-squares in a phylogenetic framework (GLS: Pagel, 1999; Freckleton *et al.*, 2002).  
13 The GLS approach allows the performance of regression and correlation analyses and the  
14 use of maximum-likelihood models takes phylogeny into account by referring to an  
15 internal matrix of expected covariances among species based on their degree of shared  
16 ancestry. The maximum-likelihood approach also allows the estimation of the  
17 phylogenetic dependence parameter  $\lambda$  which ranges between zero and one indicating the  
18 relative importance of phylogeny in explaining the similarities between traits. Values of  
19  $\lambda$  close to zero indicate that traits are likely to have evolved independently of phylogeny  
20 whereas values of  $\lambda$  close to one indicate strong phylogenetic relationships of traits.  
21 Analyses were performed using a code developed by R. Freckleton for the statistical  
22 package R V.2.1.0 (R Foundation for Statistical Computing 2005). The phylogeny used

1 in the analyses was obtained from Kimball *et al.* (1999, 2001) and Randi *et al.* (2000:  
2 Electronic appendix).

3

#### 4 b) *Multiple regression analyses*

5 We performed multiple regression analyses in a phylogenetic framework (GLS) as  
6 described above. Morphometric and functional sperm traits were included separately as  
7 dependent variables and testis mass, body mass and clutch size as independent variables.  
8 Stepwise removal of non-significant terms resulted in the minimal adequate model. The  
9 performance of multiple regression analyses including testis mass, body mass and clutch  
10 size allowed to control for possible allometry between both testis mass and body mass  
11 (Dunn *et al.*, 2001) and clutch size and body mass (Bennett & Owens, 2002). We tested  
12 for collinearity between specific independent variables (body mass and testis mass, body  
13 mass and clutch size) as described in Belsley *et al.* (1980). The highest condition index  
14 was 6.65 and only condition indices >30 indicate collinearity to be a problem. Where  
15 necessary, data were normalised using the appropriate transformation to obtain optimal fit  
16 of the GLS model.

17 In addition, we examined the inter-relationships among functional sperm traits,  
18 among morphometric sperm traits and between sperm functional and morphometric  
19 sperm traits using GLS. To assess the allometric relationships between morphometric  
20 sperm traits we calculated the slope  $\nu$  of a Reduced Major Axis regression (RMA:  
21 Ricker, 1973; McArdle, 1988). As an approximation we used the standard error of the  
22 GLS regression (Sokal & Rohlf, 1995) to perform a  $t$  test of  $\nu$  against one.

1           The use of Bonferroni correction seemed inappropriate as it enhances the chance  
2 of Type II errors since  $p$  values strongly depend on sample size (Nakagawa, 2004). We  
3 calculated the effect size  $r$  from  $t$  values from the multiple regression analyses (Cohen,  
4 1977; Nakagawa, 2004) and used Cohen's (1988) benchmarks to estimate the strength of  
5 the observed pattern. 95% non-central confidence limits (CL) for  $r$  indicate statistical  
6 significance if zero is not included in the CLs (Smithson, 2003).

7

### 8 **3. RESULTS**

#### 9 *Sperm morphometry*

10           None of the morphometric sperm traits showed any relationship with relative testis  
11 mass either when including testis mass, body mass and sperm storage duration or when  
12 excluding sperm storage duration (Table 1; Figure 1). Flagellum length showed a  
13 negative association with sperm storage duration which was significant when testis mass  
14 and body mass were removed from the model (Table 1; Figure 1). Similarly, total sperm  
15 length was also significantly negatively associated with sperm storage duration in both  
16 the model including testis mass, body mass and sperm storage duration and in the model  
17 including sperm storage duration only. The model AICs suggested that the minimum  
18 models including sperm storage duration only were more adequate than the maximum  
19 model including all three independent variables (flagellum: maximum model AIC = -  
20 40.3; minimum model AIC = -46.1; sperm total length: maximum model AIC = -41.9;  
21 minimum model AIC = -46.5). Head length and midpiece length showed no relationship  
22 with sperm storage duration. Effect sizes for flagellum length and total sperm length

1 were medium to large indicating that the association between sperm morphometry and  
2 sperm storage duration was substantial (Table 1).

3 Maximum likelihood (ML) values of  $\lambda$  were low for head length and high for  
4 midpiece length, flagellum length and total sperm length when testing the relationship  
5 between morphometric traits and testis mass and body mass. However, they were  
6 intermediate when testing the relationship between both flagellum length and total sperm  
7 length against sperm storage duration indicating that factors other than phylogeny plays  
8 an important role in explaining the observed pattern (Table 1).

9

#### 10 *Inter-relationships between sperm traits*

11 The GLS regression slope  $b = 0.78 (\pm 0.37 \text{ s.e.})$  and the RMA regression slope  $\nu =$   
12 2.16 indicated a positive relationship between midpiece length and flagellum length with  
13 a slope ( $\nu$ ) was significantly different from one ( $t = 3.13, P < 0.01$ ), indicating a positive  
14 allometric relationship between these two traits.

15

## 16 **4. DISCUSSION**

17 In pheasants, female reproductive biology seems to have a major influence on the  
18 evolution of sperm morphometry whereas we found no evidence for an influence of  
19 sperm competition on sperm morphometry. Our results suggest that the duration of  
20 sperm storage inferred from clutch size and spread of laying may have a major impact on  
21 pheasant sperm morphometry. To our knowledge, this is the first evidence for a  
22 relationship between sperm morphometry and sperm storage duration. A relationship  
23 between the evolution of sperm morphometry and female reproductive biology has also

1 been demonstrated in passerine birds where sperm size was found to have coevolved  
2 with the number and size of female sperm storage tubules rather than with sperm  
3 competition *per se* (Briskie & Montgomerie, 1992; Briskie *et al.*, 1997).

4       The lack of a relationship between sperm morphometry and the risk of sperm  
5 competition inferred from relative testis mass might be due to a possible lack of variation  
6 in sperm competition risk across pheasants. Although mating systems vary markedly  
7 across species ranging from monogamy to polygyny (Johnsgard, 1986; McGowan,  
8 1994), females appear to copulate only once or twice for a single clutch and hence the  
9 risk of sperm competition might be low and variation across species minimal. On the  
10 other hand, we found no evidence that variation in relative testis mass between species  
11 was any less in pheasants than in other avian taxa (S. Immler & T. R. Birkhead, unpubl.  
12 data).

13       A trade-off between sperm size and sperm longevity has been suggested in  
14 mammals and fish (Gomendio & Roldan, 1991; Stockley *et al.*, 1997; Gage, 1998). Such  
15 a trade-off would be a plausible explanation for the negative relationship between the  
16 size of sperm traits and sperm storage duration in pheasants. In mammals, no relationship  
17 between sperm size and oestrus length (as an index of sperm survival inside the female  
18 reproductive tract) has been found (Hosken, 1997, 1998; Gage, 1998). This contrasts  
19 with an earlier finding in mammals where sperm lifespan inside the female reproductive  
20 tract and fertility span of females were positively correlated (Gomendio & Roldan,  
21 1993). A possible explanation for this discrepancy is that the relative timing of  
22 copulation and ovulation varies across species (Asdell, 1964) and mechanisms  
23 controlling ovulation might influence the evolution of sperm longevity. The role of

1 sperm longevity after insemination is crucial for our understanding of the mechanisms in  
2 postcopulatory sexual selection and more detailed investigation is needed on the factors  
3 influencing sperm longevity.

4       The biological mechanisms underlying the trade-off between sperm size and  
5 longevity are highly debated (Cardullo & Baltz, 1991; Gage, 1998; Immler & Birkhead,  
6 in press). In mammals, it has been suggested that sperm longevity is influenced by the  
7 negatively allometric relationship between midpiece size and flagellum length which  
8 results in a relatively higher metabolic rate in longer sperm and thus a reduced lifespan  
9 (Cardullo & Baltz, 1991; Gage, 1998). However, in pheasants, the allometric relationship  
10 between midpiece length and flagellum length is positive, which means that unlike  
11 mammals, longer sperm have a relatively longer midpiece. The reason suggested for  
12 mammals, that increased metabolic rate accounts for reduced lifespan of longer sperm,  
13 therefore cannot apply to pheasants. One possibility is that midpiece size *per se*  
14 influences sperm longevity rather than the relationship between midpiece size and  
15 flagellum length (see also Immler & Birkhead, in press). In fowl, *Gallus gallus*  
16 *domesticus*, the duration of sperm storage appears to be determined in part at least by  
17 sperm metabolism, which in turn may be determined by mitochondrial (midpiece)  
18 function (Froman, 2003). The negative relationship between midpiece size and sperm  
19 storage duration in pheasants might indicate that a larger midpiece dissipates energy  
20 sooner than a smaller midpiece. However, the relationship between sperm size and sperm  
21 longevity needs further investigation in pheasants as well as in other taxa.

22       The influence of female reproductive biology including female reproductive  
23 anatomy, physiology and behaviour on the evolution of sperm morphometry is still

1 poorly understood. Several studies have addressed the relationship between sperm size  
2 and various aspects of female reproductive biology: in some sperm storing taxa, sperm  
3 size was found to be positively related with the size and/or number of sperm storage  
4 organs (passerine birds: Briskie *et al.*, 1997; insects: Dybas & Dybas, 1981; Miller &  
5 Pitnick, 2002; Presgraves *et al.*, 1999; Morrow & Gage, 2000; Minder *et al.*, 2005;  
6 snails: Beese *et al.*, 2006). However, in sperm storing bats no relationship between  
7 female reproductive tract dimensions and sperm size was found (Hosken, 1997, 1998)  
8 possibly because unlike the other taxa, female bats do not appear to have specific sperm  
9 storage structures. These contrasting results emphasize the need for more detailed  
10 investigation of the interactions between sperm and the female reproductive tract.

11

## 12 **Conclusions**

13 As in other sperm storing taxa, sperm morphometry in pheasants appears to have  
14 evolved in response to female reproductive biology and to sperm storage duration in  
15 particular. Sperm storage is likely to be a strong selective pressure favouring sperm traits  
16 such as sperm survival and longevity rather than sperm swimming velocity.

17 Fundamental differences in female reproductive biology may lead to marked  
18 differences in the evolution of sperm morphometry between taxonomic groups. Future  
19 studies should attempt to disentangle the relative importance of sperm competition and  
20 cryptic female choice for the evolution of sperm morphometry and function.

21

22

23

1 **ACKNOWLEDGEMENTS**

2 We thank Didier Cateville and Cyrille Dumais keepers of the Parc de Clères for technical  
3 help. We also thank Shinichi Nakagawa for statistical advice and Charlie K. Cornwallis,  
4 Stuart P. Sharp and two anonymous referees for useful comments on earlier drafts of the  
5 manuscript. This study was funded by a grant of the Roche Research Foundation to SI  
6 and TRB and by grants of the BRG and MNHN to MSJ.

7

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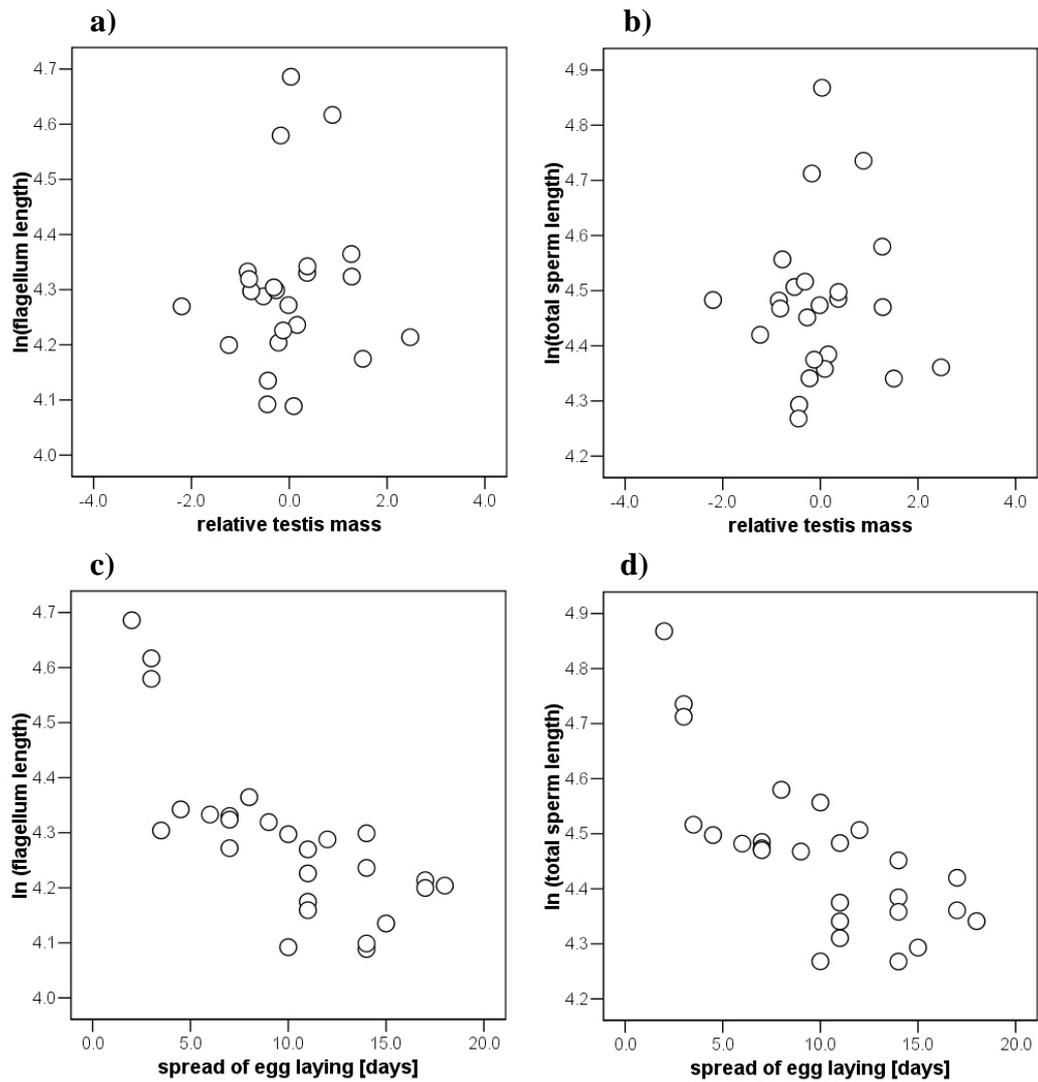
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## TABLES, FIGURES & LEGENDS:

**Table 1:** Multiple regression analyses controlling for phylogeny (GLS) to test the relationship between sperm morphometry and testis mass, body mass and sperm storage duration (storage dur.) across pheasant species. For head length and midpiece length results for maximum models are shown. For flagellum length and total sperm length results from separate models including (i) testis mass and body mass and (ii) sperm storage duration only are shown as indicated by broken line. The  $t$  values result from a test of the slopes against zero. The model including the maximum likelihood (ML) value for  $\lambda$  is compared against the models including  $\lambda = 1$  and  $\lambda = 0$  and superscripts after the ML value of  $\lambda$  indicate significance levels of the likelihood ratio tests (first position: against  $\lambda = 1$ ; second position:  $\lambda = 0$ ; significance levels: \* =  $P < 0.05$ ; \*\* =  $P < 0.01$ ). We also calculated effect size  $r$  and 95% non central confidence limits (CL) from the  $t$  value given in the GLS analysis to test for the strength of the association between traits (lower CL: LCL, upper CL: UCL). CLs excluding zero indicate a significant relationship whereas CLs including zero indicate no statistical significance.

trait	slope	$t$	$P$	$\lambda$	n	effect size		
						$r$	LCL	UCL
<b>head</b>								
				<0.001 <sup>**</sup> .n.s.	22			
testis mass	-0.13	1.41	0.18			0.32	-0.12	0.78
body mass	0.23	1.74	0.10			0.38	-0.05	0.85
storage dur.	-0.12	1.86	0.08			0.40	-0.03	0.87
<b>midpiece</b>								
				1.00 <sup>n.s.</sup> **	22			
testis mass	-0.07	1.04	0.31			0.24	-0.21	0.69
body mass	-0.12	1.04	0.31			0.24	-0.21	0.69
storage dur.	-0.01	0.08	0.94			0.02	-0.43	0.47
<b>flagellum</b>								
				0.90 <sup>n.s.</sup> **	24			
testis mass	-0.01	0.64	0.53			0.14	-0.29	0.57
body mass	-0.05	1.21	0.24			0.26	-0.16	0.69
storage dur.	-0.10	2.93	0.008	0.77 <sup>n.s.</sup> *		0.53	0.16	1.02
<b>total length</b>								
				0.86 <sup>n.s.</sup> **	24			
testis mass	-0.04	1.54	0.14			0.32	-0.10	0.76
body mass	-0.001	0.49	0.63			0.11	-0.32	0.54
storage dur.	-0.11	3.20	0.004	0.66 <sup>**</sup>		0.56	0.21	1.06



**Figure 1:** Association between morphometric sperm traits and (i) relative testis mass and (ii) sperm storage duration inferred from spread of egg laying. Relative testis mass indicates residual testis mass obtained from a regression between testis mass and body mass. Figures are not controlled for phylogeny: **a)** no significant association between flagellum length and relative testis mass ( $b = -0.01$ ,  $t = 0.64$ ,  $P = 0.53$ ,  $\lambda = 0.90$ ,  $n = 22$ ); **b)** no significant association between total sperm length and relative testis mass ( $b = -0.04$ ,  $t = 1.54$ ,  $P = 0.14$ ,  $\lambda = 0.86$ ,  $n = 22$ ); **c)** significant negative association between flagellum length and spread of egg laying ( $b = -0.10$ ,  $t = 2.93$ ,  $P = 0.008$ ,  $\lambda = 0.77$ ,  $n = 24$ ); **d)** significant negative association between total sperm length and spread of egg laying ( $b = -0.11$ ,  $t = 3.20$ ,  $P = 0.004$ ,  $\lambda = 0.86$ ,  $n = 24$ ).