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1 Title:

# 2 Greater sperm complexity in the Australasian old endemic rodents (Tribe:

## 3 Hydromyini) associates with increased levels of intermale sperm competition

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### 15 Abstract

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17 The male gamete, the spermatozoon, exhibits considerable interspecies morphological variation 18 across mammals, especially among murid rodents. In Australasia most murids in the Tribe 19 Hydromyini have a spermatozoon with a highly complex head that has, in addition to an apical hook 20 characteristic of most murids, two further projections that extend from its upper concave surface, 21 the ventral processes. Here we performed a phylogenetically controlled comparison of sperm 22 morphology across 44 species of hydromyine rodents to test the hypothesis that the length and 23 angle of both the ventral processes and apical hook, as well as the dimensions of the sperm tail, 24 increase with relative testes mass as a proxy for differences in levels of intermale sperm 25 competition. Although both sperm head protrusions exhibited considerable variation in their length 26 and angle across species, only the angles increased significantly in relation to relative testes mass. 27 Significant positive relationships were also evident between relative testes mass and lengths of the 28 sperm midpiece and flagellum. These results suggest that in the sperm head of hydromyine rodents, 29 the angle of the ventral processes, as well as that of the apical hook, together with the sperm tail 30 length, are likely to be under sexual selection. The possible functional significance of these findings 31 is discussed.

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## 34 Introduction

35 The spermatozoon is the most morphologically variable type of cell known to occur in vertebrates 36 (Cohen 1977; Pitnick et al. 2009). The reason(s) for this are not clear although differences in both the 37 mode of fertilisation and phylogeny have been suggested (Franzén 1970; Jamieson 1987). It is, 38 however, becoming increasingly evident that sexual selection also plays a major role in determining 39 the species specific form of the spermatozoon (for reviews see Pitnick et al. 2009; Simmons and 40 Fitzpatrick 2012) with mounting evidence suggesting that both sperm size and shape co-vary with 41 differences in levels of intermale sperm competition (see Snook 2005; Pitnick et al. 2009; Simmons 42 and Fitzpatrick 2012; Fitzpatrick and Lüpold 2014 for reviews). Within a species, sperm morphology 43 also appears to respond to experimentally manipulated levels of sperm competition (e.g. LaMunyon 44 and Ward 2002; Palopoli et al. 2015), and has been found to contribute to fertilisation success under 45 competitive conditions (e.g. LaMunyon and Ward 1998; Miller and Pitnick 2002; Oppliger et al. 2003; García-González and Simmons 2007; Firman and Simmons 2008; Lüpold et al. 2012; Bennison et al. 46 47 2015).

A spermatozoon consists of a head, with a nucleus housing a haploid set of chromosomes and an
enzyme-filled acrosome, and a tail for motility with the energy-generating mitochondria being
present in its midpiece. Across species, the midpiece and total flagellum length tend to positively
associate with sperm swimming speed (Gomendio & Roldan, 2008; Fitzpatrick *et al.*, 2009; Lüpold *et al.*, 2009; Gómez Montoto et al., 2011; Tourmente, Gomendio & Roldan, 2011) which is particularly
evident when the size and shape of the sperm head is also taken into account (Higdon, 1979;
Humphries et al. 2008).

Compared to most mammalian taxa, the morphology of the spermatozoon in murid rodents is highly
diverse across species in both its size and the shape of its head (Breed, 2004, 2005; Gomendio,

57 Tourmente & Roldan, 2011; Tourmente et al., 2011). Within the subfamily Murinae most, but not all, species have a sperm head with an apical hook whereas most rodents of the Australasian old 58 59 endemic tribe Hydromyini have an even more complex sperm form with two further extensions, the 60 ventral processes, protruding from its upper concave surface. Suggested functions of the apical hook 61 include facilitating temporary binding of the spermatozoon to the oviduct epithelium (Smith & 62 Yanagimachi, 1990; Firman & Simmons, 2009; Gómez Montoto et al., 2011) and/or in aiding in the 63 formation of sperm aggregates or "trains" to enhance motility under high levels of intermale sperm 64 competition (Moore et al., 2002; Immler et al., 2007; Fisher & Hoekstra, 2010) whereas the function 65 of the sperm ventral processes may be to facilitate sperm binding to, and penetration of, the coat 66 that surrounds the egg, the zona pellucida (Breed and Leigh, 1991; Drew et al. 2014). 67 In the current study, we tested the hypothesis that the length and angle of the sperm head ventral 68 processes, that are characteristic morphological feature of the spermatozoon of most of the 69 hydromyine rodents, are sexually selected traits and increase as the level of sperm competition is 70 enhanced. We examined morphological data of sperm obtained from 44 species of hydromyine 71 rodents in a phylogenetically controlled framework using relative testes mass as a proxy for sperm 72 competition (Soulsbury 2010).

73

## 74 Materials and Methods

The taxonomy of the Australasian Old Endemic rodents used in the current study follows that of
Musser and Carleton (2005) and Lecompte *et al.* (2008). Thus, within the Tribe Hydromyini six
divisions are recognised: Hydromys, Xeromys, Uromys, Pogonomys, Lorentizmys, and Pseudomys.

78 Specimens and Sample Preparation

79 Sperm samples were obtained from 44 species that included representatives from all of the 6

80 hydromyine divisions (for a full list of species and source of the material see Supplementary Table 1).

Sperm were obtained from the cauda epididymides that had been fixed in 10% buffered formalin.
The testis weight was determined and, when only one testis was available, its weight was doubled to
provide an approximate combined testes mass for the individual. Slides of sperm smears were
prepared by teasing apart the cauda epididymides with forceps under a dissecting microscope and
extruding sperm from the ducts. Body mass data came from either museum or laboratory records of
the relevant individuals or from the literature (e.g. Breed & Taylor, 2000; see Supplementary Table 1
for details).

88 Sperm Parameters

89 To indicate qualitative differences in sperm head morphology across species, and in particular the

90 interspecific variation in the length and orientation of the apical hook and ventral processes,

91 scanning electron microscopy of the sperm was carried out as previously described (see Breed, 1983,
92 1984; Breed & Leigh, 2010).

93 For quantification of trait variation, light microscopical images of morphologically intact sperm were 94 captured with a Nikon digital camera (Olympus SC100) attached to a Nomarski light microscope 95 (Olypus BH2), and 10 sperm per individual were measured using the image analysis program NIS-96 Elements BR, calibrated to 0.09  $\mu$ m/pixel. Sperm were selected at random and photographically 97 archived. Sperm head length was measured from the base of the sperm head to the base of the 98 apical hook, and head width across the widest part of the head perpendicular to head length. The 99 ventral process and hook length was determined by drawing a line at the base of the ventral 100 processes, when present, and the apical hook. The lengths of the apical hook and ventral processes 101 were measured from the base to the tip by tracing the centre line using a segmented line tool. 102 Where two ventral processes were discernible and differences in length were evident, the longer of 103 the two processes was recorded. The angle of the apical hook and ventral processes was measured 104 as the reflective angle between the tangent of a line drawn through their rostral tip along the 105 concave surface and the main longitudinal axis of the sperm head (see Immler et al., 2007).

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106 Midpiece length was measured from the connecting piece to either the cytoplasmic droplet and/or 107 to a discernible narrowing of tail width. The lengths of the principal and end pieces were combined 108 and measured from the posterior end of the midpiece to the tip of the tail. The total flagellum 109 length was the sum of the midpiece, principal piece and end piece lengths. Sperm with discernible 100 breaks were precluded from the analysis.

### 111 Statistical Analysis

Statistical analyses were performed using the statistical package R v.3.1.1 (R Core Team, 2014). Nonnormal data distributions were logarithmically transformed and relative testes mass (RTM) was used as a proxy for sperm competition (e.g. Soulsbury, 2010) by including both combined testes mass and body mass as predictor variables in all analyses of sperm traits against the level of sperm competition.

117 Phylogenetic general linear models (PGLM) were used to account for statistical non-independence of 118 the data due to shared common ancestry (Pagel, 1999; Freckleton, Harvey & Pagel, 2002), based on 119 a molecular phylogeny of the Australasian old endemic rodents (P. Smissen & K. Rowe, unpublished; 120 see Supplementary Fig. 1). The phylogenetic scaling parameter  $\lambda$ , estimated by the PGLM, was used 121 to determine the level of phylogenetic dependence of the relationships. In brief, values of  $\lambda$  close to 0 indicate that the association between the traits under examination is largely independent of 122 phylogeny, whereas  $\lambda$  values close to 1 suggest strong phylogenetic dependence. Likelihood ratio 123 124 tests were used to compare the maximum likelihood estimates of  $\lambda$  of a given PGLM to models 125 where  $\lambda$  was set to 0 or 1, respectively, and the corresponding *P*-values are shown as superscripts 126 following  $\lambda$  (first superscript for  $\lambda$ =0, second for  $\lambda$ =1). We report the strength of all relationships 127 (i.e., effect sizes) as the partial correlation coefficients, r, with 95% non-central confidence intervals (95% CI), calculated from the *t*-statistic of the PGLM (Nakagawa & Cuthill, 2007). 128

### 130 Results

132 The species investigated exhibited marked differences in relative testes mass (RTM) (for details see 133 Supplementary Table 1). The smallest RTM occurred in the three species of Notomys (N. alexis, N. 134 fuscus and N. mitchelli) which were between 0.14% and 0.16% of body mass, whereas the largest 135 RTM occurred in Pogonomys species, Mastocomys, and several species of Pseudomys where it 136 ranged from 2.7% to 5.5% of body mass. Considerable interspecific variation in RTM was observed 137 within the one genus Pseudomys where it ranged from 0.4% in P. novaehollandiae to 3.4% in P. 138 fumeus hence spanning most of the interspecific variation for RTM throughout the hydromyine 139 species investigated (see also Breed & Taylor, 2000). 140 Scanning electron microscopy showed that in five out of six divisions of hydromyine rodents most 141 species have a sperm head with two ventral processes (Figs. 1 and 2). However, their length and 142 angle, as well as that of the apical hook, varied across species (e.g. compare Fig. 1 a-d, g-i with Fig. 143 2a-e, g-i) even though they were generally fairly consistent within a species. Within the Pseudomys 144 division, P. novaehollandiae (Fig. 1e) was the only species with no ventral processes but a single 145 apical hook, whereas *P. shortridgei* had neither an apical hook nor ventral processes (see Fig. 1j). 146 Furthermore, the presence of ventral processes was highly variable within *N. alexis*, but, when 147 present, the apical hook and these processes were always very short (see Fig. 1j). The Pogonomys 148 division also had interspecies variation in the presence of ventral processes with some exhibiting 149 clear processes (Fig. 2 g to i) whereas others lacked them (Table S1). 150 Based on quantitative light microscopical measurements, the length of the sperm head ranged from 151 around 4.3 µm in Hydromys chrysogaster to a mean of 9.2 µm in Abeomelomys sevia, and its 152 maximum width ranged from 1.6 µm in *Mallomys rothschildi* to around 4 µm in *Notomys fuscus* (Fig. 153 2i) and Anisomys imitator (see Suppl. Table 2). When the apical hook on the sperm head was

154 present, its length ranged from 2 μm, or less, in sperm of *Notomys alexis* (Fig. 1j) to 14 μm in A.

155 sevia, with most sperm having an apical hook length of between 4 and 9 μm . The angle also varied

across species and ranged from 218° in *N. alexis* (Fig. 1j) to exceeding 340° in two species of

157 *Paramelomys* (e.g. Fig. 2c) (see Suppl. Table 2 for details).

158 Ventral processes were present on the sperm head of 36 out of all 44 species (Figs. 1, 2). However, in

159 *N. alexis,* when present, they measured no more than 1.0 μm. By contrast the ventral processes

160 exceeded 6 μm in several species including those of *Pseudomys desertor* (Fig. 1a), *P. australis*, *P.* 

161 gracilicaudatus, P. higginsi, Leporillus conditor, and Mastocomys fuscus (see Suppl. Table 2). The

angle of these processes varied from 204° in *N. alexis* to 360° in *Paramelomys levipes*, although the

163 majority fell between300° and 330° (see Suppl. Table 2).

Finally, midpiece lengths ranged from about 20 µm in *H. chrysogaster* to 55 µm in *Chiruromys vates*,
whereas the principal and end piece lengths varied between about 70 µm in *N. fuscus* and 126 µm in *Abeomelomys sevia*.

167 Phylogenetically controlled general linear models revealed several statistically significant 168 relationships between sperm traits and relative testes mass (RTM) (see Table 1 for details). For 169 example, the ratio of head length to width, a measure of how streamlined the sperm head is, 170 covaried positively with RTM (N = 44, partial r = 0.58, p < 0.001) (Fig. 3a). The length of both the 171 apical hook and ventral processes also tended to increase with RTM. Both these associations were, 172 however, largely driven by N. alexis and, after removing this species from the analysis, neither P-173 values were statistically significant (partial  $r \le 0.18$ ,  $P \ge 0.25$ ). The angles of both the apical hook and 174 ventral processes were also positively correlated with RTM (partial  $r \ge 0.63$ , P < 0.001) with these 175 effects remaining statistically significant after removing the three influential data points (apical hook 176 angle: N = 44, partial r = 0.71, P < 0.001; ventral process angle: N = 36, partial r = 0.63, P < 0.001) (see 177 Fig. 3 b, c). In addition, midpiece length tended to increase with RTM, albeit not significantly so 178 (partial r = 0.27, P = 0.07), whereas the lengths of the combined principal and end pieces and the

total flagellum length were positively associated with RTM (partial  $r \ge 0.50$ , P < 0.001) (Fig. 3d).

180 None of the ratios between sperm components were significantly correlated with RTM (partial  $|r| \le$ 181 0.25,  $P \ge 0.09$ ).

182

#### 183 Discussion

Most of the old endemic hydromyine rodents of Australasia have a highly complex sperm head in which two cytoskeletal processes, the ventral processes, extend from its upper concave surface. There are differences in length and orientation of these processes across the species and here we tested the hypothesis that their length and orientation have evolved as a result of sexual selection.

188 Most murid rodents have elongated sperm heads with an apical hook into which the nucleus, 189 acrosome with an elongated region of cytoskeleton, the perforatorium into which part of the 190 nucleus, acrosome and cytoskeleton extend (Fawcett, 1975; Oko & Clermont, 1988; Breed, 2004), 191 and it has previously been found that the length and angle of this apical hook increases in length 192 with increase of RTM (Immler et al. 2007, Sandera et al 2013). Our current study using 44 species in 193 the murid tribe, Hydromyini, shows that, in addition to the apical hook, most species have a sperm 194 head that has, in addition to an apical hook, two ventral processes which, unlike the apical hook, are 195 largely composed of cytoskeletal material (Flaherty and Breed 1983, 1987; Breed et al., 2000). The 196 present results show that these ventral processes have a more reflective angle in species with a high 197 RTM. A finding that suggests that their angle, like that of the apical hook, is a sexually selected trait 198 that has evolved under high levels of intermale sperm competition.

Across the species of hydromyine rodents there are, nevertheless, marked differences in overall sperm head size and shape, as well as in the length of the apical hook and ventral processes. For instance in *Notomys fuscus*, unlike most hydromyines, the sperm head is around half as wide as it is long with the apical hook being relatively much shorter than that of most other species with the 203 ventral processes also being either very short or nonexistent. These divergent features were even 204 more evident in the sperm of a closely related species, that of *N. alexis*, which has a highly variable 205 sperm head shape (e.g. see Suttle et al., 1988; Bauer and Breed, 2006) with the ventral processes 206 often being absent and the curvature of the apical hook being considerably less than that of the 207 other species. These two species of Notomys have the smallest relative testes mass of all species 208 investigated and, at least in N. alexis, the efficiency of production of sperm per gram testis is 209 comparatively low (Peirce and Breed, 2001; Bauer and Breed, 2008). These features suggest that 210 intermale sperm competition in these species is weak or even lacking, and this has resulted in highly 211 variable sperm morphology that occurs within and between males in these species similar to the 212 situation in the greater bandicoot rat Bandicota indica (Thitipramote et al 2011) and naked mole rat 213 Heterochephalus glaber (Van der Horst et al 2011) in which it has been suggested that due to 214 minimal sperm competition "degenerative" sperm traits and high levels polymorphism has evolved 215 (Van der Horst and Maree 2014).

216 Previous work on the functional and evolutionary significance of the apical hook of murine sperm 217 has suggested that in the wood mouse, Apodemus sylvaticus, the hook may facilitate the formation of highly progressive motile groups of sperm, or "sperm trains", with sperm attaching to each other 218 219 by way of their apical hook (Moore et al., 2002). This finding was subsequently observed in sperm of 220 the laboratory rat, Rattus norvegicus (Immler et al., 2007) as well as in a species of deer mouse, 221 Peromyscus maniculatus (Fisher & Hoekstra, 2010). Within the hydromyine rodents, the only 222 published study addressing this question is that of Firman et al. (2013) using sperm from the Sandy 223 Inland mouse, Pseudomys hermannsburgensis, in which no sperm grouping was observed in spite of 224 a well-developed apical hook being present. However, more recent observations on sperm with 225 similar morphology, those of *P. australis*, have indicated that sperm do indeed aggregate upon 226 release from the epididymis into culture medium, but this was not found to occur in sperm of N. 227 alexis, which lack lack a long hook and ventral processes (Kathrine Ferres and Bill Breed, unpublished 228 observations). Based on the comparison between these two species it may be that the ventral

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processes facilitate sperm aggregation although further evidence of the ventral processes beinginvolved in sperm behaviour is clearly needed.

231 Apart from supporting sperm aggregation, the sperm head ventral processes may also facilitate 232 sperm binding to the egg coat. For example, studies on sperm-egg interactions in vitro show that in 233 P. australis the ventral processes enhance the area of sperm binding to the egg coat (Drew et al., 234 2014), and in vivo observations indicate that these processes enlarge the size of the penetration slit 235 in the zona (Breed & Leigh, 1991). The significance of variation in the angle of the ventral processes 236 in relation to zona pellucida binding and penetration is unknown but it may be that sperm with more 237 reflective ventral processes form tighter initial attachment to the egg coat. Even though the function 238 of these processes remains unclear at the present time, the present study clearly shows that their length and orientation are generally similar to that of the apical hook; a feature that suggests that 239 240 these structures have coevolved.

241 In addition to sperm head variation, a significant positive relationship between relative testes mass 242 and the sperm flagellum length was also evident, a finding that is consistent with a broader range of 243 rodents (Gomendio et al., 2011). The prevailing explanation for a positive association with relative 244 testes size is that sperm with a relatively long flagellum and/or larger midpiece are favoured by 245 sexual selection because they have a competitive advantage by achieving greater swimming velocity 246 than sperm with relatively shorter tails (Katz, Drobnis & Overstreet, 1989; Cardullo & Baltz, 1991; 247 Gómez Montoto et al., 2011). Despite relatively little evidence within species (reviewed in 248 Humphries et al., 2008; Simmons & Fitzpatrick, 2012), such a link between sperm morphology and sperm velocity is supported by comparative studies using various vertebrate taxa, including cichlid 249 250 fishes (Fitzpatrick et al., 2009), passerine birds (Lüpold et al., 2009, but see Kleven et al., 2009), and 251 mammals (Gomendio & Roldan, 1991; Tourmente et al., 2011; Gómez Montoto et al., 2011). If such 252 a link between sperm form and function also holds for hydromyine sperm, our comparative data

would suggest that selection on sperm tail length through sperm competition may be mediated byits effects on the speed of sperm swimming.

255 In conclusion, our results suggest that the complex sperm morphology of hydromyine rodents is, at 256 least in part, a result of postcopulatory sexual selection. These findings extend previous reports of 257 Immler et al., (2007) and Šandera et al. (2013) on the apical hook of murine sperm and show that 258 the additional ventral processes on the sperm head of the Australasian old endemic rodents may 259 also have evolved under sexual selection. Similarly, sperm tail dimensions co-vary positively with 260 relative testes mass, which might be the result of sperm competition selecting for faster sperm, 261 mediated by relatively longer tails. Further studies are now required to gain more in-depth insight 262 into the adaptive significance of the ventral processes that are such a characteristic feature of the 263 sperm head of most of the hydromyine species of Australasia.

264

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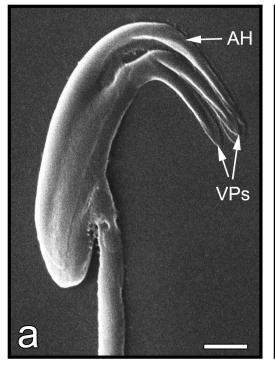
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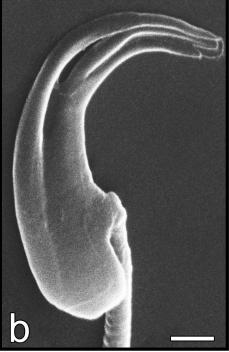
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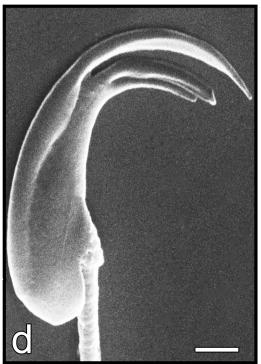
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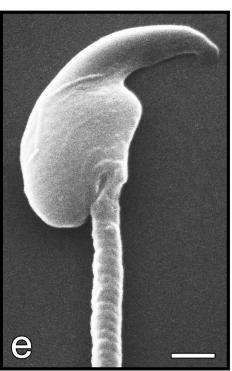
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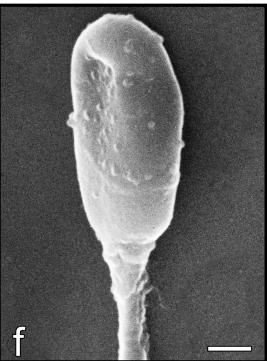




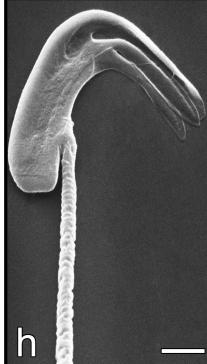


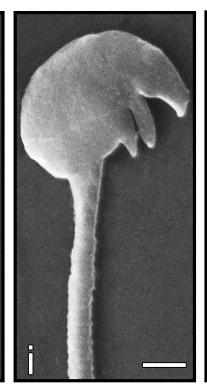


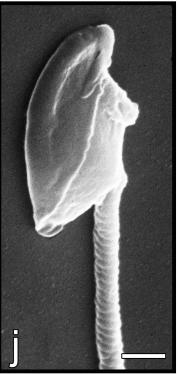


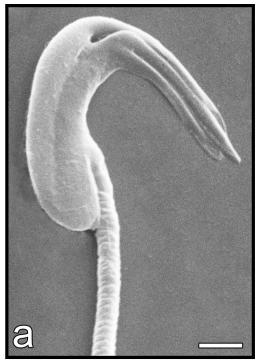


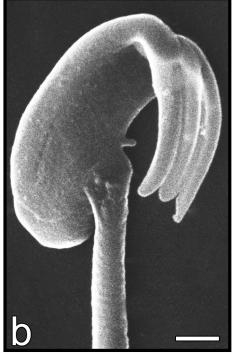


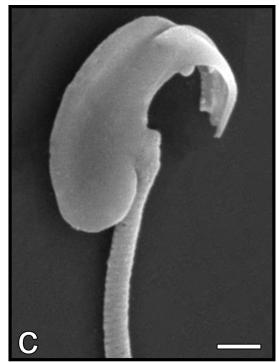


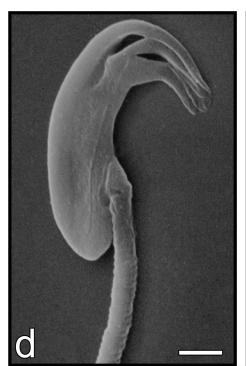


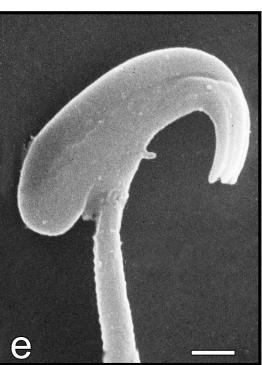


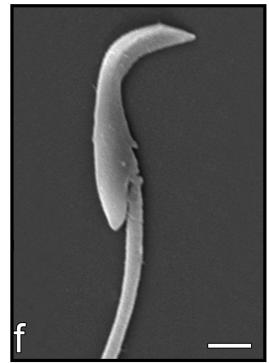


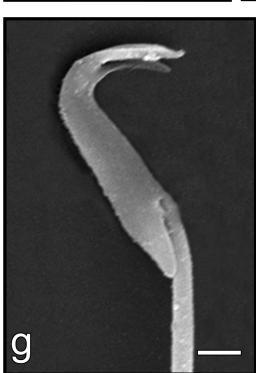


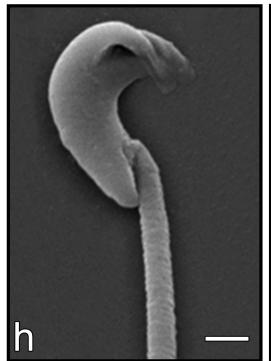












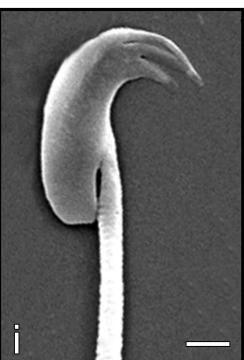


Table 1: Phylogenetically controlled associations between sperm morphological traits and testes mass corrected for body mass; all variables are log-transformed. Effect sizes(?) are shown as the partial correlation coefficients *r* along with their lower (LCL) and upper (UCL)

Commented [SL1]: Yes, this is correct. This is a statistical term referring to a statistic (in this case partial r) that expresses the strength (and direction) of an effect (or relationship).

95% confidence limits.

I

Sperm Trait	Predictors	df	partial r	(LCL, UCL)	t	Р	λª
Head Length: Width	Testes Mass	42	0.41	(0.13, 0.61)	2.89	0.006	0.76<0.001, <0.001
Ratio	Body Mass	42	-0.27	(-0.51, 0.03)	-1.81	0.08	0.70
Apical Hook Length	Testes Mass	41	0.29	(-0.01, 0.52)	1.94	0.06 <sup>b</sup>	0.38 <sup>0.12, &lt;0.001</sup>
	Body Mass	41	-0.08	(-0.36, 0.22)	-0.51	0.61	
Apical Hook Angle	, Testes Mass	41	0.72	(0.55, 0.82)	6.68	<0.001	< 0.001 <sup>1.0, &lt; 0.001</sup>
	Body Mass	41	-0.50	(-0.67, -0.23)	-3.66	<0.001	
Ventral Process Length	Testes Mass	33	0.36	(0.03, 0.59)	2.22	0.03 <sup>b</sup>	0.24 <sup>0.31, &lt;0.001</sup>
	Body Mass	33	-0.16	(-0.45, 0.18)	-0.93	0.36	
Ventral Process Angle	Testes Mass	33	0.63	(0.39, 0.77)	4.72	<0.001	< 0.001 1.0, < 0.001
	Body Mass	33	-0.32	(-0.57, 0.01)	-1.95	0.06	
Midpiece Length	Testes Mass	42	0.08	(0.22, 0.36)	1.84	0.61	1.00<0.001, 1.0
	Body Mass	42	-0.40	(-0.47, 0.08)	-1.46	0.15	
Principal and End Piece	Testes Mass	42	0.34	(0.05 <i>,</i> 0.56)	2.35	0.02	0.82 <sup>0.001, 0.05</sup>
Length (PEL)	Body Mass	42	-0.22	(-0.47, 0.08)	-1.49	0.14	
Total Flagellum Length	Testes Mass	42	0.34	(0.05 <i>,</i> 0.56)	2.33	0.02	0.91<0.001, 0.22
(TFL)	Body Mass	42	-0.27	(-0.51, 0.03)	-1.81	0.08	
PEL:TFL Ratio	Testes Mass	42	0.23	(-0.07, 0.47)	1.52	0.14	0.94<0.001, 0.39
	Body Mass	42	-0.04	(-0.32, 0.26)	-0.24	0.81	
Midpiece:TFL Ratio	Testes Mass	42	-0.24	(-0.49, 0.06)	-1.62	0.11	0.90<0.001, 0.22
	Body Mass	42	-0.04	(-0.25, 0.33)	-0.29	0.77	
Flagellum:Head Ratio	Testes Mass	42	0.24	(-0.06, 0.49)	1.63	0.11	< 0.001 <sup>1.0, 0.05</sup>
	Body Mass	42	-0.30	(-0.53, 0.00)	-2.04	0.05	

<sup>a</sup> Superscripts following the phylogenetic scaling parameter  $\lambda$  estimates denote significance levels of likelihood ratio tests (first superscript: against  $\lambda$  = 0; second superscript: against  $\lambda$  =

1). <sup>b</sup> These positive trends are not statistically significant after removal of a single influential data point (*Notomys alexis*; both partial  $r \le 0.18$ ,  $P \ge 0.25$ ). Statistically significant *P*-values (at  $\alpha = 0.05$ ) are highlighted in bold.