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Additive genetic variance and developmental plasticity in growth trajectories in a wild cooperative mammal

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Keywords:
cooperative breeding;
early environmental effects;
growth trajectories;
heritability;
meerkats;
Suricata suricatta.

Abstract
Individual variation in growth is high in cooperative breeders and may reflect plastic divergence in developmental trajectories leading to breeding vs. helping phenotypes. However, the relative importance of additive genetic variance and developmental plasticity in shaping growth trajectories is largely unknown in cooperative vertebrates. This study exploits weekly sequences of body mass from birth to adulthood to investigate sources of variance in, and covariance between, early and later growth in wild meerkats (Suricata suricatta), a cooperative mongoose. Our results indicate that (i) the correlation between early growth (prior to nutritional independence) and adult mass is positive but weak, and there are frequent changes (compensatory growth) in post-independence growth trajectories; (ii) among parameters describing growth trajectories, those describing growth rate (prior to and at nutritional independence) show undetectable heritability while associated size parameters (mass at nutritional independence and asymptotic mass) are moderately heritable ($0.09 \leq h^2 < 0.3$); and (iii) additive genetic effects, rather than early environmental effects, mediate the covariance between early growth and adult mass. These results reveal that meerkat growth trajectories remain plastic throughout development, rather than showing early and irreversible divergence, and that the weak effects of early growth on adult mass, an important determinant of breeding success, are partly genetic. In contrast to most cooperative invertebrates, the acquisition of breeding status is often determined after sexual maturity and strongly impacted by chance in many cooperative vertebrates, who may therefore retain the ability to adjust their morphology to environmental changes and social opportunities arising throughout their development, rather than specializing early.

Introduction
Individual variation in growth is unusually high in cooperative breeding societies that are characterized by morphological divergence in adults, where breeders are larger and heavier than helpers (Wilson, 1971; O’Riain & Jarvis, 1998; O’Riain et al., 2000; Clutton-Brock, 2009). In eusocial insects with castes, workers are sterile and provision extraordinarily fecund queens that are much larger and live much longer than them. Divergent morphological development of queens and workers starts shortly after hatching and is often irreversible and triggered by early nutritional differences (Wheeler, 1986; Beekman et al., 2006). Such divergence is thought to reflect developmental plasticity, here defined as environmentally induced variability during early development within a single genotype (Piersma & Drent, 2003), with long-lasting phenotypic effects.
Less is known regarding mechanisms responsible for the emergence of rank-related size differences commonly observed in cooperative vertebrates (O’Riaain et al., 2000; Heg et al., 2004; Russell et al., 2004; Wong et al., 2008; Young & Bennett, 2010). The best example of alternative morphotypes in cooperative vertebrates comes from the naked mole-rat Heterocephalus glaber (O’Riaain et al., 2000; Dengler-Crish & Catania, 2007), a subterranean rodent where the queen monopolizes reproduction in a large colony over many years (Jarvis, 1981; Bennett & Faulkes, 2000) and is much larger and heavier than same-sex subordinates (O’Riaain et al., 2000). Fast growth may facilitate dominance acquisition, as females fight fiercely over dominance and success may be size dependent (Clarke & Faulkes, 1997). Similarly, field studies of meerkats, a cooperative carnivore, suggest that individual variation in growth may reflect wider life-history trajectories: heavier females have better chances of reaching dominance and of breeding successfully (Clutton-Brock et al., 2006; Hodge et al., 2008), and early growth predicts future chances of acquiring breeding status (Russell et al., 2007; English et al., 2013b). Consequently, individuals may, as in cooperative insects, specialize in early life as a result of developmental plasticity and follow different developmental pathways leading to breeding vs. helping phenotypes.

However, it is also possible that cooperative vertebrates may avoid early specialization and retain the ability to adjust their developmental trajectories to short-term variation in their ecological or social environment. First, they live longer than invertebrates and may often face a greater range of environmental conditions over their lifetime. Second, breeding positions are generally acquired late, often after sexual maturity, and their inheritance is often largely impacted by chance. For example, in meerkats, breeding vacancies often go to the oldest subordinate female of the group (Hodge et al., 2008). Finally, recent evidence indicates that there is no early behavioural specialization in meerkats, as investment in cooperative behaviour in early life does not predict ultimate breeding status (Carter et al., 2014), suggesting that there is no general syndrome of early phenotypic specialization encompassing behaviour, morphology and life history. As a result, the development of phenotypic specialization in cooperative vertebrates and invertebrates may profoundly differ, and the role of developmental plasticity may be weaker in more ‘totipotent’ vertebrates.

Understanding the evolution of morphological divergence in cooperative breeding vertebrates requires identifying the factors underlying variation in early growth, as well as the mechanisms connecting early growth performance with later fitness-related traits such as body mass. Early growth is highly sensitive to environmental variation and particularly to maternal environment (e.g. Maestripieri, 2011). For example, studies in wild red squirrels (Tamiasciurus hudsonicus) suggest that maternal environment can account for up to 80% of the variance in early growth (McAdam et al., 2002). Although maternal effects on growth may be weaker in cooperatively breeding societies where they may be offset by helper care (Holekamp & Dloniak, 2009; Russell & Lummaa, 2009), studies of wild cooperative carnivores indicate that other sources of variations in the early social environment, like the size of the helping cohort, may play a crucial role in regulating growth, especially during the provisioning period (reviewed by Holekamp & Dloniak, 2009). The quality of the abiotic environment may also exert a large influence on early growth variation. In Damaraland mole-rats (Cryptomis damaensis), seasonal fluctuations in resource availability may mediate divergent developmental trajectories, as pups from early born litters grow faster, have higher asymptotic weight and contribute less to cooperative activities than pups from later litters (Bennett & Faulkes, 2000; Bennett & Navarro, 2009).

Early determination of growth trajectories can also reflect genetic variation. Additive genetic variance in growth is substantial in many vertebrates, as growth rates have been successfully targeted by animal breeding programmes (e.g. Hernández et al., 2004; Krumah et al., 2007; Elzo et al., 2012) and biomedical studies have revealed substantial additive genetic variance in children’s growth trajectories (Choh et al., 2011; Johnson et al., 2011). Studies on wild vertebrates, including on some cooperative breeders, have shown that the additive genetic variance of morphometric traits measured at various developmental stages is often significant and substantial (e.g. Réale et al., 1999; Wilson et al., 2005, 2006; Nielsen, 2013), suggesting that growth may retain a genetic component even in natural populations where environmental variation is extensive.

Detecting genetic variance consistently across life stages in the developmental sequence of a trait does not, however, imply that genetic variance is primarily responsible for the phenotypic covariance observed in this trait across life stages. Instead, measuring the genetic and environmental components of the covariance between early growth and later growth may help to determine whether an early growth effect on adult size is primarily a consequence of genetic variation or plasticity, respectively. Whereas no study has examined genetic and environmental sources of covariance between early and later growth in wild vertebrates, some studies have examined genetic sources of covariance in body mass or size at various developmental stages and indicate that genetic correlations across ages are generally strong and positive (Cheverud et al., 1983; Kirkpatrick & Losvold, 1992; Wilson et al., 2006), suggesting that genetic effects contribute to mediate the covariance between early and later mass or size.
However, sources of covariance between early and later growth may differ from sources of covariance among size or mass at different ages, as growth during a given developmental window may be less affected by carry-over effects from previous stages than age-related size. Recent studies of eusocial insects suggest that the quality of early environment may determine alternative growth trajectories corresponding to different social quality of early environment may determine alternative carry-over effects from previous stages than age-related a given developmental window may be less affected by among size or mass at different ages, as growth during later growth trajectories, especially adult size, would be mediated by early environmental (rather than additive genetic) effects.

This study aims at quantifying the relative importance of genetic and environmental sources of variance in, and covariance between, early growth rate (EGR) and later growth trajectories of wild cooperative meerkats inhabiting the Kalahari Desert. Despite living in a highly seasonal environment, meerkats breed throughout the year. Reproduction is largely monopolized by the alpha pair, and group size ranges from 3 to 50 individuals (Clutton-Brock, 2009). Pups are provisioned by helpers for approximately 2 months following their emergence from the natal burrow, about 1 month after birth (Clutton-Brock et al., 2001; Clutton-Brock, 2009), and recent studies have shown that abiotic (rain and season), maternal (age and rank) and social (number of helpers and littermates) factors affect individual growth trajectories (Russell et al., 2002; English et al., 2012, 2013a). Finally, morphological traits (body mass and skeletal size) show moderately heritable variation that increases with age (Nielsen, 2013).

We examine several genetic and environmental (group, maternal, litter identity and birth year) sources of variance in and covariance between EGR (during the provisioning period) and each of three parameters describing the growth curve between nutritional independence and adulthood (body mass at nutritional independence, growth rate at nutritional independence and asymptotic body mass). We use a high-resolution longitudinal and multigenerational phenotypic data set based on weekly weight measures together with quantitative genetic models to ask three questions. First, do individual growth trajectories diverge early in life? If so, we expect a positive phenotypic covariance between EGRs and subsequent growth parameters. Second, is individual variation in growth trajectories heritable? If so, we expect a significant additive genetic variance in growth parameters. Finally, are additive genetic effects responsible for any early divergence in growth trajectories? If so, we expect the phenotypic covariance between early growth and subsequent growth trajectories to be primarily driven by genetic, rather than by early environmental effects.

Materials and methods

Study species and population

Individual data were collected between 1998 and 2011 as part of a long-term study of a wild meerkat population at the Kuruman River Reserve in the Northern Cape, South Africa (26°58S, 21°49E). Further details on the study site and population are described elsewhere (Clutton-Brock et al., 1998, 1999a; Russell et al., 2002). Meerkats live in groups comprising 3–50 individuals, including a dominant breeding pair and subordinate individuals of both sexes (Clutton-Brock, 2009). Groups were visited on average three times per week in order to record life-history events (birth, death, immigration, emigration) as well as group composition. All individuals in the population were tagged with unique subcutaneous transponder chips and were identifiable in the field through dye marks on their fur. When they first emerge from the natal burrow (at approximately 3 weeks of age), a 2- to 5-mm tissue biopsy from the tail tip of each pup is taken for genetic analysis (Spong et al., 2008). All sampled individuals have been genotyped at up to 18 variable microsatellite loci so that genetic data were available for 86% of the total recorded population (Nielsen et al., 2012). Meerkats were fully habituated to human observers and were regularly (about twice per week) weighed to the nearest gram in the field using a portable balance, on which they were trained to climb in return for a small reward of water or crumbs of hard-boiled egg. Data used here were all collected in the morning, soon after meerkats emerge from their sleeping burrow, to avoid short-term fluctuations in mass owing to variation in foraging success. Growth trajectories presented here are exclusively based on longitudinal weight records, as additional developmental measures such as skeletal size were only collected opportunistically during captures (requiring anaesthesia), generating no or few repeated records per individual at heterogeneous points in time.

Rainfall was measured daily (in mm) using a standard rain gauge. When daily records were missing (< 1% of days), we used rainfall data from a remote-sensing data set provided by the NASA GES DISC (Goddard Earth Sciences Data and Information Services Center) Giovanni online data system (described in Acker & Leptoukh, 2007). Comparing the KMP records with the remote-sensing records on days where both were available indicated a strong positive correlation (Pearson’s correlation, \( r_p = 0.71, \text{d.f.} = 1481, P < 10^{-4} \)).

Modelling growth

Our modelling approach followed previous work (English et al., 2012) in this population, which compared the fits of several standard growth curves (monomolecular, von Bertalanffy, Gompertz, logistic, and Richards)
described by Gaillard et al. (1997) and Zullinger et al. (1984) to long-term changes in meerkat body mass, identifying the monomolecular model as the best description of meerkat growth trajectories. The extent to which environmental parameters, such as rainfall and season, may affect variation in meerkat body mass was investigated, revealing that incorporation of accumulated rainfall over 9 months, as well as seasonality, substantially improved the growth curve fits. Finally, this previous study also revealed that fitting a biphasic monomolecular model, accounting for differential growth before and after nutritional independence, substantially improved the model fit, thereby suggesting that processes influencing growth differ across these periods. Based on these findings, we chose to quantify growth before and after nutritional independence using distinct models, to ensure that parameter estimates for growth before and after nutritional independence may not directly constrain or influence each other during model fitting, allowing us to examine their biological covariance.

**Early growth (1–3 months)**

We calculated growth rates between 1 and 3 months for 1329 individuals born between 1998 and 2011, including 702 males and 627 females. The mean number of weight measures available per individual between 0 and 2 months was 13.3 ± 7.0, and between 2 and 4 months was 32.9 ± 15.5. To limit error due to missing data or variation in sampling effort, we calculated an interpolated monthly mass measure for each individual at 1 and 3 months of age (see Ozgul et al., 2010 for a similar approach). As weight is a simple quadratic function of age between 1 and 3 months of age (see Fig. S1), this measure was calculated by fitting linear mixed-effect models, for all individuals, to mass measurements for 1 month before and after each monthly age, with age and age$^2$ as fixed effect terms, and individual as a random term. These models were then used to predict each individual’s weight for its exact monthly age. Early growth was then computed as the difference between weight predictions obtained at one and at 3 months of age, providing a single-parama-

ter measure that was recently shown to predict a key fitness component in this population, the probability to acquire breeding status (English et al., 2013b).

**Lifetime growth (3–24 months)**

To quantify lifetime growth in meerkats, we analysed mass data on individuals who survived at least 2 years (730 days) and modelled mass from 3 months until 2 years, the age by which most individuals have reached adult weight (English et al., 2012). Individual mass time series were truncated at 2 years to ensure that individual differences in longevity would not affect the shape of the trajectories, although this does not ensure a random sample of individuals. We also excluded data for (i) pregnant females from their conception dates [approximately 70 days prior to parturition or 40 days prior to the first day of detectable pregnancy in cases where abortions occurred (Clutton-Brock et al., 1998)] until birth or abortion (removing 2796 out of 145 673 mass records for 169 females: < 2% of data) and (ii) individuals with fewer than 80 data points within the considered time frame ($n = 24$), to ensure that growth parameters were estimated with accuracy. In total, we analysed mass data for 531 individuals (270 males, 261 females) with an average of 271 body mass records per individual (range 81–417).

We fitted a monomolecular model to body mass records of each individual in our data set in order to calculate nonlinear least square estimates of the parameters of a monomolecular model (Fig. 1) using the ’nls’ function implemented in R 2.15.0. Parameter estimation was therefore independent from one individual to the next. We made several decisions in the implementation of this analysis, mainly based on the empirical questions addressed. We re-parameterized the monomolecular model as well as incorporated rainfall and season effects as formulated by English et al. (2012) when calculating individual growth parameters (see Appendix S1 for details). This procedure served, in effect, to correct the fitted mass for total rainfall over the preceding 9 months, as well as for the day of the year, in order to, first, increase the precision of individual parameter estimation by increasing the overall model fit and, second, to limit noise when examining genetic determinants of between-individual variation in growth by correcting for basic seasonal fluctuations affecting individual growth trajectories.

The final function used to model individual growth trajectories was thus as follows:

$$
\text{Mass} = A - (A - m_0) \cdot e^{-k_0 (\text{age} - 90)/\text{(A-m0)}} + s \cdot \sin \left( \frac{2\pi(\text{date} - d)}{365.25} \right) + R \cdot \text{rain}
$$

with $A$ the asymptotic mass, $m_0$ the initial mass (at 90 days of age), $k_0$ the initial growth rate (at 90 days of age), $s$ the amplitude of the seasonal oscillation, $d$ the time phase shift and $R$ the rainfall effect estimate (for the last three parameters, we used estimates from English et al., 2012; see Appendix S1). All these analyses were run using software R 2.15.0 (R Development Core Team 2012).
Pedigree and inbreeding coefficients

The pedigree for this study population was reconstructed using a combination of microsatellite data and phenotypic descriptors and two parentage inference programs: COLONY2 (Wang, 2004; Wang & Santure, 2009) and MASTERBAYES (Hadfield et al., 2006). Full details of the molecular and pedigree construction and structure can be found elsewhere (Nielsen et al., 2012). In brief, the full pedigree contains 2147 individuals, spans up to eight generations, and contains 1531 individuals with both parents known and a further 411 individuals with only maternity known (see Table S1). The section of the full pedigree which is informative with respect to the analyses presented here (‘pruned’ pedigree) is described in Table S1. Wright’s (1921) inbreeding coefficients ($F$) were calculated for each individual using PEDIGREEVIEWER (http://www-personal.une.edu.au/~bkinghor/pedigree.htm) (Kinghorn, 1994), under the assumption that all founders and immigrants were unrelated (Nielsen et al., 2012).

Partitioning phenotypic variance in growth

Two growth parameters, $k_0$ and $A$, were log-transformed to satisfy normality assumptions. The phenotypic variance was then partitioned for each growth parameter by running a univariate animal model, a mixed-effect model allowing us to estimate additive genetic variance and heritability, the proportion of phenotypic variance explained by additive genetic variance (Kruuk, 2004), and fitted using restricted maximum likelihood with the R package ASReml-R. The univariate model investigating sources of variance on early growth included 1329 individuals for which early life data were available, whereas the three univariate models investigating sources of variance in later growth included 531 individuals for which lifetime growth trajectories were available. We minimized the number of fixed effects in the model in order to partition the variance of the raw phenotypes on which natural selection operates. We nevertheless included two fixed effects: sex and inbreeding coefficients. Sex was fitted as a fixed effect to account for potential sexual dimorphism in growth rates, whereas inbreeding coefficient was included as a fixed effect since some studies have suggested that these nonadditive genetic effects may occasionally interfere with estimates of additive genetic variance in traits suffering from substantial inbreeding depression (Reid et al., 2006), which is the case for meerkat growth (Nielsen et al., 2012). Variance components (random effects) were initially estimated from univariate animal models built as follows:

$$ y = Xb + Z_a + Z_{bl} + Z_m + Z_{bg} + Z_{by} + e $$

where $y = \text{vector of observed phenotypic values}$; $b = \text{vector of fixed effects}$; $a = \text{vector of additive genetic effects}$; $bl = \text{vector of birth litter effects}$; $m = \text{vector of maternal effects}$; $bg = \text{vector of birth group effects}$; $by = \text{vector of birth year effects}$; $e = \text{vector of residual effects}$; $X$ and $Z_{1-5}$ = corresponding data-based design matrices.

For each trait, the phenotypic variance ($V_p$) that was unexplained by the fixed effects was thus partitioned as follows in the full model:

$$ V_p = V_A + V_{bl} + V_m + V_{bg} + V_{by} + V_R $$

where $V_p = \text{total phenotypic variance}$; $V_A = \text{additive genetic effect variance}$; $V_{bl} = \text{birth litter effect variance}$; $V_m = \text{maternal effect variance}$; $V_{bg} = \text{birth group effect variance}$; $V_{by} = \text{birth year effect variance}$; $V_R = \text{residual effect variance}$.

The proportion of variance attributed to each source of variance was then calculated by dividing the relevant variance component by the total phenotypic variance conditional on the fixed effects (e.g. heritability $h^2 = V_A/V_p$).

Although the significance of the fixed effects was evaluated by a $F$-test using a hypothesis-testing framework, we used Akaike Information Criterion (AIC) to select the models that best described the data while maintaining the lowest number of explanatory variables (parsimony principle) in the variance component analyses, as we had no a priori expectation regarding the
relative importance of the sources of variance and covariance. Two models differing by less than two units of AIC were considered to receive equal statistical support (Burnham & Anderson, 1998). The full set of alternative models considered is presented in Tables S2 and S3.

Next, we ran six bivariate models, each containing two of the four growth parameters [early growth, \(m_0\), \(\log(k_0)\), \(\log(A)\)] as response terms, aimed at simultaneously partitioning the sources of variance and covariance among those terms, in order to test whether observed phenotypic covariance among parameters is primarily of genetic or of environmental origin. These models were fitted on the intersection data set of individuals for which both early and later growth parameters had been estimated (\(n = 523\)). We initially attempted to fit trivariate models but these failed to converge. We included in bivariate models all random terms found to be significant in at least one of the two univariate models analysing variation in the two response terms. The parsimony of including a source of covariance (for additive genetic variance or a given environmental effect) between parameters in bivariate models was evaluated by comparing the AIC values of a model including this covariance with a model where the considered covariance was fixed to 0.

**Results**

**Do growth trajectories diverge early in life?**

Early growth rate significantly predicted subsequent growth trajectories, through a strong positive phenotypic correlation with estimated mass at nutritional independence \(m_0\) (Pearson’s correlation, \(n = 531\), \(r_s = 0.72, P < 10^{-3}\)), a weak negative phenotypic correlation with growth rate at nutritional independence \(k_0\) (Pearson’s correlation, \(n = 531\), \(r_s = -0.11, P < 10^{-3}\)) and an intermediate positive phenotypic correlation with asymptotic mass \(A\) (Pearson’s correlation, \(n = 531\), \(r_s = 0.22, P < 10^{-3}\); Table 1, Fig. 2). Overall, individuals with a fast early growth ended up with a higher asymptotic mass, despite a negative correlation between early growth and \(\log(k_0)\) that reflected the occurrence of post-independence compensatory growth for individuals that started with a slow early growth. Growth trajectories showed little differences between the sexes: males grew slightly faster than females shortly after nutritional independence as shown by a slight sex difference in \(\log(k_0)\) (\(F_{1,385} = 24.70, P < 10^{-3}\)), but there was no sex difference for \(EGR, m_0\) and \(\log(A)\) (\(P > 0.05\) in all cases, see Table 1). Finally, \(EGR\) was negatively affected by inbreeding (\(F_{1,240} = 4.90, P < 10^{-3}\)), as was

![Fig. 2](image.png) Early growth rate predicts subsequent growth trajectories. Lighter grey dots correspond to weight records from individuals with fast early growth falling above the first quartile of the distribution of growth before nutritional independence. Darker grey dots correspond to weight records from individuals with slow early growth falling below the third quartile of the distribution of growth before nutritional independence. The grey dashed line represents the average growth rate before nutritional independence followed by the composite of the monomolecular mixed model after nutritional independence for the individuals with fast early growth, and the black solid line represents the average growth rate before nutritional independence followed by the composite of the monomolecular mixed model after nutritional independence for individuals with slow early growth. The vertical dashed line at 90 days denotes the approximate age of nutritional independence. Only individuals for which both early and later growth parameters were available (\(n = 523\)) are shown here.

<table>
<thead>
<tr>
<th>Mean ± SD</th>
<th>(m_0)</th>
<th>(\log(k_0))</th>
<th>(\log(A))</th>
</tr>
</thead>
<tbody>
<tr>
<td>Males</td>
<td>3.12 ± 0.67</td>
<td>246.40 ± 57.16</td>
<td>0.55 ± 0.39</td>
</tr>
<tr>
<td>Females</td>
<td>3.12 ± 0.59</td>
<td>251.72 ± 56.58</td>
<td>0.41 ± 0.36</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Correlations</th>
<th>(m_0)</th>
<th>(\log(k_0))</th>
<th>(\log(A))</th>
</tr>
</thead>
<tbody>
<tr>
<td>(m_0)</td>
<td>(r_s = 0.72, P &lt; 10^{-3})</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>(\log(k_0))</td>
<td>(r_s = -0.11, P &lt; 10^{-3})</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>(\log(A))</td>
<td>(r_s = 0.22, P &lt; 10^{-3})</td>
<td>(r_s = -0.42, P &lt; 10^{-3})</td>
<td>(r_s = -0.44, P &lt; 10^{-3})</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>EGR</th>
<th>(m_0)</th>
<th>(\log(k_0))</th>
<th>(\log(A))</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean ± SD</td>
<td></td>
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</tr>
</tbody>
</table>

Table 1 Mean values and correlations among growth parameters.

\(EGR\), early (pre-independence) growth rate (g/j); \(m_0\), mass at independence (g); \(k_0\), post-independence growth rate (g/j); and \(A\), asymptotic mass (g).

Correlations were calculated using Pearson’s correlations using 531 individuals.
mass at independence \( m_0 \) \((F_{1,344} = 5.48, \ P = 0.021)\). Inbreeding effects were not detected later in life \([P > 0.05\) for \( \log(k_0)\) and \( \log(A)\)]).

**Are growth trajectories heritable?**

Additive genetic variance was retained in the best univariate models for mass at independence \( m_0 \) and for transformed asymptotic mass \( \log(A) \), but not for pre-independence or transformed post-independence growth rates \( \log(k_0) \) indicating that the latter two parameters are not heritable (Tables 2 and S2, Fig. 3). The heritability of \( m_0 \) and \( \log(A) \) was 17 ± 8% and 23 ± 9%, respectively. The effect of group and maternal identity was not significant in any of the models considered. In contrast, litter identity accounted for most of the phenotypic variance in early growth and \( m_0 \), for nearly half of the variance for \( m_0 \) and \( \log(k_0) \) and for about one-quarter for \( \log(A) \) (Table 2, Fig. 3). Birth year was present in the final model for each parameter and accounted for 5–30% of the phenotypic variance (Table 2, Fig. 3).

**Are additive genetic or early environmental effects responsible for early divergence in growth trajectories?**

Additive genetic variance appeared as a significant source of positive phenotypic covariance between \( \text{EGR} \) and \( \log(k_0) \), whereas shared early environment – as measured by a common birth litter and year – did not play any significant role in the covariance between these two parameters (Fig. 4 and Tables S3–S10). There was significant positive genetic covariance between mass at independence and asymptotic mass. Sources of phenotypic covariance between all other parameters were exclusively environmental and mostly due to birth litter identity (Fig. 4 and Tables S3–S10). Specifically, birth litter mediated the negative phenotypic covariance between \( \text{EGR} \) and \( \log(k_0) \), which suggests

**Table 2** Variance component analysis summary from the most parsimonious univariate model for each growth parameter.

<table>
<thead>
<tr>
<th>Random effect</th>
<th>Variance</th>
<th>SD</th>
<th>CV</th>
<th>Ratio variance component/V_p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early growth</td>
<td>VA</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>( n = 1329 ) individuals</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Litter</td>
<td>0.2920</td>
<td>0.0253</td>
<td>0.0940</td>
<td>0.737 ± 0.038</td>
</tr>
<tr>
<td>Birth year</td>
<td>0.0260</td>
<td>0.0171</td>
<td>0.0084</td>
<td>0.065 ± 0.041</td>
</tr>
<tr>
<td>Residual</td>
<td>0.0779</td>
<td>0.0039</td>
<td>0.0250</td>
<td>0.197 ± 0.017</td>
</tr>
<tr>
<td>Lifetime growth</td>
<td>( n = 531 ) individuals</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( m_0 )</td>
<td>VA</td>
<td>540.00</td>
<td>254.00</td>
<td>1.0172</td>
</tr>
<tr>
<td>Birth year</td>
<td>1920.00</td>
<td>236.00</td>
<td>0.9451</td>
<td>0.588 ± 0.067</td>
</tr>
<tr>
<td>Residual</td>
<td>517.00</td>
<td>285.00</td>
<td>1.1414</td>
<td>0.159 ± 0.075</td>
</tr>
<tr>
<td>( \log(k_0) )</td>
<td>285.00</td>
<td>141.00</td>
<td>0.5647</td>
<td>0.087 ± 0.046</td>
</tr>
<tr>
<td>( \log(A) )</td>
<td>VA</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Birth year</td>
<td>0.0660</td>
<td>0.0079</td>
<td>0.1374</td>
<td>0.481 ± 0.077</td>
</tr>
<tr>
<td>Residual</td>
<td>0.0416</td>
<td>0.0198</td>
<td>0.0866</td>
<td>0.302 ± 0.102</td>
</tr>
<tr>
<td>( \log(A) )</td>
<td>0.0298</td>
<td>0.0024</td>
<td>0.0620</td>
<td>0.217 ± 0.037</td>
</tr>
</tbody>
</table>

SD, standard deviation; CV, coefficient of variation (calculated as the ratio of the variance due to a given effect over the mean of the response trait); \( V_p \), total phenotypic variance; ns, nonsignificant.

Alternative models compared in the model selection procedure are shown in the Table S2.
that litters growing slowly before nutritional independence compensated afterwards.

**Discussion**

We first investigated the extent to which early growth rate (EGR) affected subsequent growth trajectories in wild meerkats. The phenotypic covariance between pre-independence growth and two of three post-independence growth parameters (mass at independence $m_0$ and transformed asymptotic mass $A$) was positive, which suggests that fast-growing pups often maintain their advantage until adulthood. This advantage may help to understand why fast early growth predicts early breeding success in both sexes (Russell et al., 2007) and chances of acquiring dominance in females (Hodge et al., 2008; English et al., 2013b). However, the strength of the correlation between early growth and adult mass was weak and the distribution of meerkat growth trajectories does not show any bimodal signal distinguishing slow and fast growers as may be expected for alternative developmental paths similar to those observed in the morphological castes of eusocial insects (Wheeler, 1986; Beekman et al., 2006). Instead, the negative covariance between pre- and post-independence growth rate suggests the occurrence of compensatory growth at the population level and may relate to seasonal rhythm, where pups born during the dry lean season often reach independence shortly before or after the first rains, when food availability increases. Future studies may investigate the determinants and consequences of compensatory growth, as studies from a range of organisms suggest that catch-up growth may bear metabolic costs, in the form of increased oxidative stress, that may be associated with fitness costs (Metcalfe & Monaghan, 2001; De Block & Stoks, 2008).

We next investigated the extent of heritable variation in growth trajectories. Significant additive genetic variation was only detected in two growth parameters, mass at independence $m_0$ and transformed asymptotic mass $A$, but not in pre-independence growth rate EGR or transformed post-independence growth rate $log(k_0)$, suggesting that growth rates may be extremely plastic phenotypes. Our estimates of the heritability of mass parameters are consistent with findings from a recent analysis of genetic and environmental sources of variation in morphometric measures around 3, 6 and 18 months of age in the same population (Nielsen, 2013). These values lie in the range reported for the heritability of body mass for age in other natural populations of mammals (e.g. Reale et al., 1999; Wilson et al., 2005, 2006).

Empirical investigations of the heritability of growth curve parameters in domestic vertebrates have sometimes reported high heritability for all growth parameters ($h^2 = 20–50\%$: (Mignon-Grasteau et al., 1999; Grossman & Bohren, 2008; Lewis et al., 2002), whereas others have reported higher heritability for asymptotic mass than for growth rate (Le Rouzic et al., 2008; Aslam et al., 2011). The extent of environmental influence on growth rates by comparison to adult mass in wild birds (Ricklefs & Peters, 1981; Gebhardt-Henrich & van Noordwijk, 1991, 1994) has led some authors to hypothesize that genetic variation would be more important on the asymptotic part of the growth curve than during development (Gebhardt-Henrich, 1992), supporting our observations. Studies of the heritability of growth parameters in wild mammals are rare, making it difficult to place our results in a broad comparative framework. The heritability of prenutritional...
Genetic and developmental effects on meerkat growth

The development of morphological and life-history divergence in cooperative vertebrates may be more contingent on environmental variation affecting later stages of development than in cooperative invertebrates. The causes underlying these profound differences may be multiple and remain to be identified. They may reflect fundamental contrasts in morphology and life history, where invertebrates are more constrained by their exoskeleton and associated fixed developmental steps (metamorphosis, moults, etc.) or a greater need for the longer-lived vertebrates, who may face a greater variety of environments throughout their life, to permanently readjust their development to recent environmental changes. They may also relate to contrasts in social organization, where the queen may exert a greater control over the inheritance of the breeding status, which is determined early, in eusocial insects. In contrast, stochastic factors often play a decisive role in the acquisition of breeding positions in vertebrates, who generally only obtain them when they are fully grown-up and may thus retain their ability to compete as long as possible, rather than specializing early (Clutton-Brock, 2009).

Our results reveal that growth rate prior to nutritional independence contributes to shape lifetime growth trajectories until adulthood, although its effect on adult mass, an important determinant of female breeding success in meerkat societies (Clutton-Brock et al., 2006), is relatively weak. We found no evidence...
for alternative developmental paths leading to breeders vs. helpers that would be characterized by a bimodal distribution of growth parameters, with fast and slow growers. Instead, environmental effects generate most variation in growth trajectories throughout development, which is occasionally mediated by episodes of compensatory growth. The heritability of growth parameters is undetectable to moderate, whereas the weak positive covariance between early growth and adult mass is partly genetic in origin. These results reveal that meerkat growth trajectories remain plastic throughout development, rather than showing early and irreversible environmentally induced divergence. Overall, our findings may reflect profound differences in the development of morphological and life-history variation between cooperative invertebrates and vertebrates, which may be more contingent of environmental variation affecting later stages of development than in cooperative invertebrates. Further investigation of the proximate causes and evolutionary significance of these contrasts represents an important avenue for future research.

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References


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**Supporting information**

Additional Supporting Information may be found in the online version of this article:

**Appendix S1** Parameterization of the monomolecular model.

**Table S1** Summary statistics for the pedigrees used in the analyses.

**Table S2** Model selection for univariate models of growth parameters.

**Table S3** Model selection for bivariate models investigating sources of variance and covariance in early and post-independence growth.

**Table S4** Model selection for bivariate models investigating sources of covariance among post-independence growth parameters.

**Table S5** Sources of phenotypic variance and covariance between early growth and \( m_0 \).

**Table S6** Sources of phenotypic variance and covariance between early growth and \( \log(k_0) \).

**Table S7** Sources of phenotypic variance and covariance between early growth and \( \log(A) \).

**Table S8** Sources of phenotypic variance and covariance between \( m_0 \) and \( \log(k_0) \).

**Table S9** Sources of phenotypic variance and covariance between \( m_0 \) and \( \log(A) \).

**Table S10** Sources of phenotypic variance and covariance between \( \log(k_0) \) and \( \log(A) \).

**Figure S1** Plot of weight by age between 1 and 3 months of age.

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