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Fitness-related patterns of genetic variation in rhesus macaques

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Abstract The patterning of quantitative genetic descriptions of genetic and residual variation for 15 skeletal and six life history traits was explored in a semi-free-ranging group of rhesus macaques (*Macaca mulatta* Zimmerman 1780). I tested theoretical predictions that explain the magnitude of genetic and residual variation as a result of 1. strength of a trait's association with evolutionary fitness, or 2. developmental and physiological relationships among traits. I found skeletal traits had higher heritabilities and lower coefficients of residual variation than more developmentally and physiologically dependent life history traits. Total lifetime fertility had a modest heritability (0.336) in this population, and traits with stronger correlations to fitness had larger amounts of residual variance. Censoring records of poorly-performing individuals on lifetime fertility and lifespan substantially reduced their heritabilities. These results support models for the fitness-related patterning of genetic variation based on developmental and physiological relationships among traits rather than the action of selection eroding variation.

Keywords Cayo Santiago · Censored data · Coefficient of variation · Fundamental theorem of natural selection · Heritability · Life history · *Macaca mulatta* · Rhesus macaque · Morphology · Variance components

Abbreviations

h^2	Heritability
CV_A	Coefficient of additive genetic variation
CV_R	Coefficient of residual variation

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Introduction

Understanding the level of genetic variation in animal behavior, physiology, morphology, and life history is a major goal of evolutionary biology. Knowledge of a trait's genetic variance and covariance with other traits is critical to predicting both short-term responses to selection (Falconer and Mackay 1996), and for inferring longer-term evolutionary patterns of speciation, adaptation, and drift (Schluter 1996; 2000; Marriog and Cheverud 2004; Ackermann and Cheverud 2004; Lande 1979).

Despite the importance of a knowledge of inheritance to understanding evolutionary processes, little is known about the genetic bases of quantitative traits in primate populations (Rogers 2005). In this article I report estimates of the heritability and coefficients of genetic and residual variation for a set of life history and morphological variables in the female members of a population of free-ranging rhesus macaques. In addition to providing basic information on the genetics of these traits, I test several ideas on how genetic variation should be patterned among them. The theoretical predictions themselves are extremely general, and are expected to apply to most animals and plants (Roff 1997), though they have been explored primarily in ungulates and rodents, birds, and insects.

Exploring the genetic architecture of primate life histories is critical because of the unique features that typify the order including long lifespans, low reproductive rates, slow somatic growth rates requiring protracted periods of infant care, large brains and extensive sociality when compared to other mammals (Martin 1990; Leigh 2001). Social interactions in many primate groups also create difficulties for standard methods of quantitative genetics, such as parent-offspring regression or sib analysis (Lynch and Walsh 1998). Female rhesus macaques form strict

dominance hierarchies in which a mother's rank is passed on to her daughters (Missakian 1972; Datta 1983). Individual females remain in their natal group for life and often experience very different availability of food and stress environments according to their rank (Sapolsky 2005; Bercovitch and Strum 1993). This pattern of intergenerational transmission of social rank places female relatives in similar environments and may result in inflated estimates of additive genetic variance when they are based on mother-daughter pairs or sets of sisters (van Tienderen and de Jong 1994; Silk 1984), as is commonly the case in ecological studies. Instead, relying on extended pedigree networks, including paternities, and allocating individuals to rank categories allows proper decomposition of phenotypic variance into genetic and environmental components (Kruuk 2004).

Proposed explanations for fitness-related patterns

The standing level of additive genetic variance for a trait is due to some relationship between input of novel variants from mutation or migration and its elimination by selection and drift. In the ecological literature two hypotheses have been discussed to explain the patterning of genetic variances in traits with fitness. The first, referred to as the *erosion of variance* hypothesis, invokes Fisher's (1930) "fundamental theorem of natural selection"—that the rate of change in fitness is equal to the additive genetic variance in fitness—and Robertson's (1966) "secondary theorem of natural selection"—that the rate of change in a trait under selection is equal to its additive genetic covariance with fitness. Rephrased, these state that, all else being equal, traits with greater correlations with fitness should have less additive genetic variance in populations near an evolutionary equilibrium. Alleles that affect fitness should quickly be driven to fixation or eliminated, and this should occur more rapidly in traits more strongly correlated with fitness. Selection quickly erodes the additive genetic variance in traits closely correlated with fitness. The prevalence of low heritabilities for life history traits, which should be under strong selection, has been argued as evidence in favor of this hypothesis (Gustafsson 1986; Roff 1987; Mouseau and Roff 1987).

A contrasting idea in the ecological literature is that traits with low heritabilities, like life history traits, do *not* have low amounts of additive genetic variance, but instead have elevated amounts of residual variance because they are functionally "downstream" from other morphological variables (Price and Schluter 1991; Houle 1992). For example, age of sexual maturation in many animals is dependent on reaching a critical size threshold. If there is genetic variation for this threshold size and growth rate differences are environmental then the heritability of age of maturation will be considerably lower than the size threshold it depends on (Roff 1997). Age of maturation is downstream of the size threshold and incorporates the environmental variance in growth rate. I will refer to this as the *incorporation of residual variance* hypothesis. Because of this relationship, the phenotypic variance of traits closely associated with fitness contains the sum of residual variance of their "upstream" variables and any independent residual variance of their own. Symbolically, the heritability of an upstream variable (u) is $h^2(u) = \sigma_A^2(u)/[\sigma_A^2(u) + \sigma_E^2(u)]$, while that for the downstream variable (d) is $h^2(d) = \sigma_A^2(u)/[\sigma_A^2(u) + \sigma_E^2(u) + \sigma_E^2(d)]$. Empirical studies of wild birds and mammals demonstrate life history traits do indeed have large amounts of additive genetic variance when compared with morphological traits on a mean-standardized scale as a coefficient of variation $(CV_A = 100 \times \sqrt{\sigma_A^2}/\bar{x})$ (Houle 1992; Kruuk et al. 2000; McLeery et al. 2004; Merilä and Sheldon 2000, 1999).

However, both sorts of mechanisms may act to explain patterns in heritabilities among traits differently correlated with fitness. In contrast to the scheme proposed by Price and Schluter (1991), if a downstream variable, like a life history trait, has some additive genetic variance of its own, then its heritability is instead $h^2(d) = [\sigma_A^2(u) + \sigma_A^2(d)]/[\sigma_A^2(u) + \sigma_E^2(u) + \sigma_E^2(d)]$. With stronger selection on life history traits $\sigma_A^2(d)$ will be reduced faster than $\sigma_A^2(u)$ and the common pattern of low heritabilities of life history traits will still be observed. Some evidence suggests this is a more realistic model for the inheritance of life history traits. Crnokrak and Roff (1995) compared published values for the relative amounts of dominance and additive genetic variance in life history and morphological traits. Under the assumption that life history traits are under stronger selection that will erode additive variance quickly, they predicted and indeed found greater dominance variance in life history traits than morphological traits in wild animal populations. This pattern is not predicted by the incorporation of residual variance model for life history traits which have no independent source of additive genetic variance.

Laboratory experimentalists have refined these ideas, particularly in the details of the genetic architecture of traits. Houle (1998) provides a comprehensive and critical review of *Drosophila* studies on genetic variance. He advocates explaining standing genetic variance in traits through the variety of mutational inputs they may experience. Traits closely related to fitness, and total reproductive output itself, are likely to be influenced by many loci, making them a large "mutational target." Additionally, pleiotropy among fitness-related traits may also maintain genetic variation by involving the traits in trade-offs (Rose 1982). Houle further suggests that traits expressed later in life should have greater variance than those early in life,

Table 1 Hypotheses on heritability (h^2) and coefficients of additive genetic (CV_A) and residual variation (CV_R) of traits based on their association with fitness (r_{fit}), and hypothesized relationships between heritabilities and coefficients of variation

Hypothesis	h^2–r_{fit}	CV_A–r_{fit}	CV_R–r_{fit}	h^2–CV_A	h^2–CV_R
Erosion of additive genetic variance	−	−	?	+	?
Incorporation of residual variance	?[a]	?	+	?	−
Mutational target size[b]	?	+	?	?	?

Positive and negative relationships are indicated where strong predictions are made

[a] A negative relationship would be expected in this case, but it is not an essential prediction. If CV_A happens to increase with r_{fit} along with CV_R the drop in heritabilities would not be observed

[b] Further refinements and predictions of this hypothesis require more detailed information on mutational and epistatic variance (Houle 1998)

provided there are temporally cumulative effects of alleles. Finally, traits more closely related to fitness may be more canalized by epistatic interactions among loci such that variation in locus A does not translate into phenotypic variation because it is masked by a modifier locus B (Stearns and Kawecki 1994; Stearns et al. 1995). However, much of this research remains speculative because of difficulties in clearly defining the size of "mutational targets" and estimating the number of segregating alleles for different traits. Furthermore, some results depend heavily on the life history model used to asses the traits' correlations with fitness. Inferences from such laboratory studies can also be difficult to extrapolate to wild populations with different selective optima and distinct population histories.

Predictions of proposed explanations

There are a number of predictions of these hypotheses that can be tested in wild and free-ranging populations. The erosion of variance hypothesis predicts low heritability of fitness and decreasing heritability of traits as their association with fitness increases. At evolutionary equilibrium additive genetic variance in fitness (σ_A^2 or CV_A) should be approximately 0 (Gustafsson 1986; Roff and Mouseau 1987; Mouseau and Roff 1987). The incorporation of residual variance hypothesis does not require evolutionary equilibrium and does not predict 0 additive genetic variance in fitness or traits closely associated with it. Its important prediction is that traits functionally dependent upon others have higher residual variance (CV_R). If one accepts that such traits are more closely related with fitness, then it also predicts a positive relationship between a trait's association with fitness and its residual variance (Price and Schluter 1991; Merilä and Sheldon 1999). More detailed hypotheses on the genetic architecture of traits are difficult to distill into exclusive predictions. However, one prediction of the mutational target hypothesis is that additive genetic variance (CV_A) should be greater in traits more closely associated with fitness. This requires the assumption that fitness is the ultimate mutational target—the sum total of all allelic effects, and that traits more closely associated with it are subject to greater mutational input (Houle 1998). These predictions are summarized in Table 1.

Materials and methods

I tested these predictions using the demographic database and skeletal collections of the Cayo Santiago rhesus macaques. I focused on females because there are large samples of life history data that can be extracted from the demographic records. Cayo Santiago is a 15.2 ha island located 1 km off the southeast coast of Puerto Rico in the Caribbean Sea. Rhesus macaques ($n = 409$) were introduced in 1938 from diverse sources in India, and have been monitored nearly continuously since 1956 (Rawlins and Kessler 1986; Sade et al. 1985). Animals are fed commercial monkey chow daily, and are provided water *ad libitum*. The population has been managed through the annual cull of randomly selected one and two year olds and periodic removal of social groups. The total size of the population has ranged from about 175 individuals in the mid-1950s to over 1300 in 2001. Monkeys live in naturally formed social groups in which matriline dominance hierarchies are observed to be stable (Stucki et al. 1991; Missakian 1972). Although the founding population of Cayo Santiago was small, blood polymorphism studies indicate little difference in allelic diversity from other rhesus monkey populations and no molecular evidence for high rates inbreeding on the island (Duggleby et al. 1986). A recent investigation of mitochondrial haplotypes indicates low diversity on Cayo Santiago, although all wild Indian rhesus macaque populations appear to have little mitochondrial variation (Smith and McDonough 2005).

A set of 15 morphological measurements and six life history variables were used in this study (Tables 2 and 3). Skeletal measurements were selected for comparisons with previous heritability estimates (Hallgrimsson et al. 2002; Lawler 2006). Data were collected from the skeletons of

Table 2 Measurements collected on the skeletons of Cayo Santiago macaque mothers

Measurement	Abbreviation
Post-Cranium	
Humerus length	humerus
Humerus anterior–posterior diameter at midshaft	h_ap_dim
Radius length	radius
3rd Metacarpal length	mcarp3
Femur length	femur
Femoral bicondylar width	f_bcw
Femoral anterior–posterior diameter at midshaft	f_ap_dim
Tibia length	tibia
3rd Metatarsal length	mtars3
Cranium	
Mesial canine–distal M^2 distance	ctom2
Orbital height	orbht
Glenoid tubercle–endomolare	glenm1
Basion-external auditory meatus	baseam
Lateral infraorbital foramen–external auditory meatus	eamiof
Bizygomatic width	bizyg_w
Cranial length (alveolare–most posterior point)	cranial_l

More detailed explanation of these measurements can be found in published sources (Hallgrimsson et al. 2002; Hallgrimsson 1999; Bass 1995)

individual females born between 1957 and 1990. All individuals in this data set were sexually mature adult females who reproduced at least once and died naturally on Cayo Santiago or were removed and immediately sacrificed. No significant differences were found between removed and naturally dying individuals for any of these morphological traits. Measurements were taken on the left and right side of each individual if possible and these values were averaged for this analysis. All morphological measurements were normally distributed.

Life history variables were used from females born between 1960 and 1990 for all variables except age of first birth for which birth cohorts up to 1999 were accepted. I defined the total number of offspring born to a female as a fitness indicator (# offspring). This was calculated in two ways. First, only females that reproduced were included in the measure, censoring those that died prior to maturity or reached reproductive age but never reproduced. Second, all females who died on Cayo Santiago were included, assigning a 0 for females who did not reproduce. A similar approach was taken to lifespan which was measured once for females that reproduced, and once for all females who died. A more refined indicator of fitness (λ_{ind}) that incorporates the age schedule of reproduction (McGraw and Caswell 1996) was also explored. However, results using λ_{ind} and number of offspring were very similar and they are not reported here. Two other life history variables were used. Age of first reproduction is the cohort age of the female when she gave birth to her first offspring. Birth seasonality at Cayo Santiago ensures that cohorts are all roughly of the same age (Rawlins and Kessler 1985). Females with first births after their sixth year were excluded because of potential pathology. With these restrictions, age of first birth is an ordinal variable taking only integer values between three and six. The final life history variable analyzed is mean interbirth interval (mean IBI). This is the average number of integer years between successive births by a female. Only females reproducing three or more times had this variable calculated. Age of first reproduction and mean IBI are roughly normally distributed. Lifespan and number of offspring are not, but this does not substantially affect the estimates of quantitative genetic statistics. Lifespan and number of offspring have left-truncated distributions and are strongly positively skewed. Their variances are also larger than their means. This departure from normality inflates their *CV*s (Kruuk et al. 2000).

The "animal model," a linear mixed model, was used for for estimating variance components of the morphological and life history traits in the program DFREML 3.1 (Meyer 2000; Kruuk 2004). Fixed effects to be included in the model for each trait were first tested in general linear models in SAS (SAS Institute 2003). For the morphological traits four fixed effects were tested: matriline social rank (a three-level ordinal variable for high, middle, or low ranking), natural death/removal, age at death, and contemporary group. Contemporary group was used to control for temporal changes in colony population size, management, and weather. Contemporary groups were defined as five year intervals of birth cohorts beginning in 1960. Animals born prior to 1960 were assigned to a separate contemporary group. Rank and removal were not significant for any traits. Age at death and contemporary group were used for traits which their *p*-values were less than 0.10. The only fixed effects for the life history variables were matriline social rank and contemporary group. These were significant or nearly significant for all variables except adult lifespan. Analyses with and without this non-significant predictor for adult lifespan were nearly equivalent and only the results including rank are presented. The only random effects in the model were animal identity and the residual (Kruuk 2004). A maternal effect was explored by fitting the additional random effect of maternal identity, but it was not significant for any of the variables. It was estimated to be 0 for all the morphological traits, but small values were estimated for some of the life history variables. Dropping the maternal effect had little effect on the heritabilities of any traits.

Significance tests for the heritabilities are derived from *z*-scores computed by dividing the heritability by its

Table 3 Variance components, heritabilities, and *CV*s for life history and morphological traits in the Cayo Santiago females. Morphological measurements are defined in Table 2

	n	$\bar{x}$	σ^2_P	σ^2_A	σ^2_R	$h^2 \pm SE$	CV_A	CV_R	r_{fit}
Morphological variables									
Baseam	104	32.209	1.6798	0.8677	0.8121	0.5166 ± 0.3304	2.8921	2.7979	0.6103
bizyg_w	102	82.921	11.4253	5.9982	5.4271	0.5250 ± 0.3591	2.9536	2.8094	0.6690
cranial_l	105	117.249	17.8170	3.9615	13.8554	0.2224 ± 0.3145	1.6975	3.1747	0.6180
ctom2	98	31.553	1.0433	0.7780	0.2653	0.7457 ± 0.2602**	2.7954	1.6326	0.0546
eamiof	105	53.932	4.8024	1.4015	3.4009	0.2918 ± 0.2762	2.1951	3.4194	0.4565
femur	104	166.601	41.8044	21.6718	20.1327	0.5184 ± 0.3155*	2.7943	2.6932	0.2523
glenm1	105	58.076	7.8989	0.1356	7.7633	0.0172 ± 0.3207	0.6341	4.7976	0.6020
h_ap_dim	103	10.812	0.4808	0.3461	0.1347	0.7198 ± 0.2827**	5.4410	3.3951	0.5438
humerus	103	142.061	30.6069	9.2577	21.3492	0.3025 ± 0.3748	2.1418	3.2525	0.2116
innom_l	102	146.174	34.7148	23.9331	10.7816	0.6894 ± 0.3899*	3.3468	2.2463	0.4240
mcarp3	102	35.995	2.9341	1.9999	0.9342	0.6816 ± 0.4062*	3.9288	2.6852	0.0192
mtars3	101	48.964	4.7093	3.4420	1.2673	0.7309 ± 0.3582*	3.7890	2.2991	0.0383
orbht	105	29.434	2.8057	1.4836	1.3221	0.5288 ± 0.2547*	4.1382	3.9064	0.4322
radius	103	139.440	30.7092	14.8039	15.9054	0.4821 ± 0.2757*	2.7593	2.8601	0.1743
tibia	103	155.030	29.1571	15.8957	13.2614	0.5452 ± 0.2742*	2.5717	2.3490	0.2976
Life history variables									
Age of first rep.	883	4.224	0.2882	0.0340	0.2542	0.1179 ± 0.0629*	4.3640	11.9359	−0.0441
Mean IBI	148	1.238	0.0605	0.0044	0.0562	0.0722 ± 0.1876	5.3381	19.1375	−0.1441
Lifespan	208	10.798	26.8717	5.6507	21.2211	0.2103 ± 0.1751	22.0142	42.6615	0.9503
Lifespan[a]	377	7.040	29.8902	14.1770	15.7132	0.4743 ± 0.1129***	53.4851	56.3083	0.9524
# Offspring	208	5.861	16.2294	1.4325	14.7969	0.0883 ± 0.1754	20.4222	65.6365	1.0000
# Offspring[a]	377	3.233	15.7151	5.2788	10.4364	0.3359 ± 0.1170**	71.0567	99.9108	1.0000

Age of first reproduction (age of first rep.) and lifespan are given in cohort years. The mean number of years between births for a female is "mean IBI." Total fecundity, a fitness indicator, is given by "# offspring." The phenotypic Pearson's correlation between the trait and # offspring is given in the column r_{fit}. Fixed effects used for the individual traits are noted in section "Materials and Methods"

* $P < .05$, ** $P < .01$, *** $P < .001$ for the heritability

[a] This is for all available females, *not* just those that reproduced

standard error and examining z-tables for p-values (Kruuk et al. 2002; Sokal and Rolf 1994). Dominance and epistatic variance cannot be calculated in this population. The low frequency of full-sibships when paternities are known argues against dominance playing much of a role in phenotypic resemblance in these traits among siblings and should not pollute estimates of additive genetic variance. Accordingly, most dominance and epistatic variance should be included in residual variance.

Animal model estimation of variance components, relying on restricted maximum likelihood (REML), accommodates highly unbalanced sets of related individuals and maximizes use of the genetic information available in a pedigree. For the life history variables a single pedigree of interlocking individuals was used for the quantitative genetic analysis. This pedigree involves 6,543 known individuals, in 17 matrilines connected by paternities. This is 82.43% of the entire demographic database. Morphometric data were only used on individuals belonging to this same pedigree and one other containing 55 individuals. Pedigree membership was identified with PEDSYS (Dyke 1996).

Trait correlations with fitness were assessed with a Pearson's correlation (r) between the trait and the uncensored value for number of offspring. This is the most basic method of measuring this relationship, but the difficulty of relating morphological measurements in any other ways to fitness precludes use of more rigorous techniques such as sensitivity analysis (Houle 1998). Two traits negatively correlated with number of offspring, age of first reproduction and mean IBI, were positivized by taking their absolute value.

The association between these correlations with fitness and trait heritabilities or coefficients of variation was measured with the Spearman rank correlation (r_s). Two modifications of the standard Spearman correlation were made. First, because there was variation in the precision of the quantitative genetic statistics, they were weighted by

the inverse of the heritability standard error ($\frac{1}{SE(h^2)}$). This gives values with smaller standard errors greater influence on the correlation (Chuang-Stein and Agresti 1997). Second, because many of the life history and morphological variables are highly correlated, assumptions of standard hypothesis tests are violated. To correct this, two-tailed *P*-values were obtained from randomizing the pairs of data 50,000 times. The number of randomized trials in which the correlation absolute value exceeded that of the observed correlation is the probability of finding the correlation strictly by chance.

Results

Heritabilities

Heritabilities of morphological traits ranged from 0.017 to 0.731, and 0.072 to 0.474 in life history traits (Table 3, Fig. 1). When trait correlations with fitness were low (age of first reproduction and mean IBI), life history traits had substantially lower heritabilities than morphological traits. As would be expected from the erosion of variance hypothesis, there was a generally weak decline in heritability with increasing correlation with fitness (Fig. 1). This was strongest in the morphological traits ($r_s = -0.495$, $P = 0.066$). However, the opposite pattern was seen in the life history variables. In contrast to predictions of the erosion of variance view, increasing correlation with fitness increased the heritability of life history traits. However, none of these patterns reach statistical significance (Table 4). Including females that died before reproducing more than doubles the heritability of lifespan and number of offspring, suggesting there is a great deal more additive genetic variance or less residual variance when including sub-adult survival in the measures. These two uncensored measures are both statistically significant as is the heritability for age of first reproduction. The heritability of the majority of the morphological traits are statistically significant (9 of 15), and the bulk of those are postcranial (7 of 9).

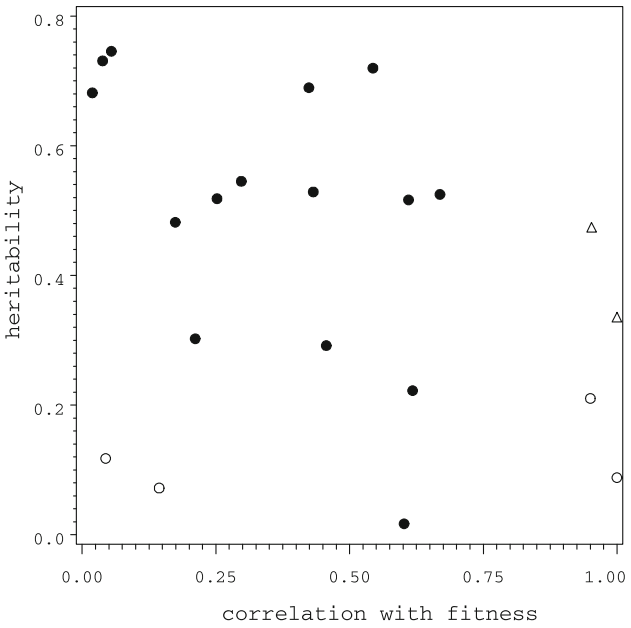

Fig. 1 The relationship of trait heritability and correlation with fitness in the Cayo Santiago females. Morphological traits are the filled dots. Life history traits are the open symbols. Uncensored lifespan and number of offspring are shown with open triangles. Censored values, including only females that reproduced, for these variables are the open circles

Table 4 Spearman correlations (r_s) between quantitative genetic statistics and the trait's correlation with fitness (see the values in Table 3)

	all n=21		Morphological n=15		Life history n=6	
	r_s	P	r_s	P	r_s	P
h^2	0.0595	0.8264	−0.4953	0.0663	0.3691	0.4405
CV_A	0.4715	0.0505	−0.1667	0.5585	0.8700	0.0554
CV_R	0.5773	0.0133	0.5361	0.0455	0.9912	< .0001

These correlations correspond to the scatterplots in Figs. 1–3. Correlations were calculated weighting the quantitative genetic statistic by $\frac{1}{SE(h^2)}$. *P*-values were computed from a null distribution of 50000 randomizations of the data pairs being tested

Coefficients of variation

The patterns in heritabilities are explained, in part, by the coefficients of variation (Figs. 2 and 3). As predicted by the incorporation of residual variance hypothesis, the coefficient of residual variation increases significantly as the trait correlation with fitness increases ($r_s = 0.577$, $P = 0.013$). This pattern holds in both the morphological and life history traits, though it is much stronger in the life history traits.

Coefficients of additive genetic variation show a modest positive overall trend ($r_s = 0.472$, $P = 0.050$), which is due primarily to the life history traits ($r_s = 0.870$, $P = 0.055$). This is because CV_A for age of first reproduction and mean IBI are similar to morphological traits, but those for lifespan and number of offspring are much higher. A positive relationship between CV_A and correlation with fitness was predicted by the mutational target size hypothesis. These nearly significant relationships are weak support for this model.

CV_R for life history traits are always higher than morphological traits, suggesting that they are more responsive to environmental inputs or have larger non-additive genetic components. For lifespan and number of offspring, both

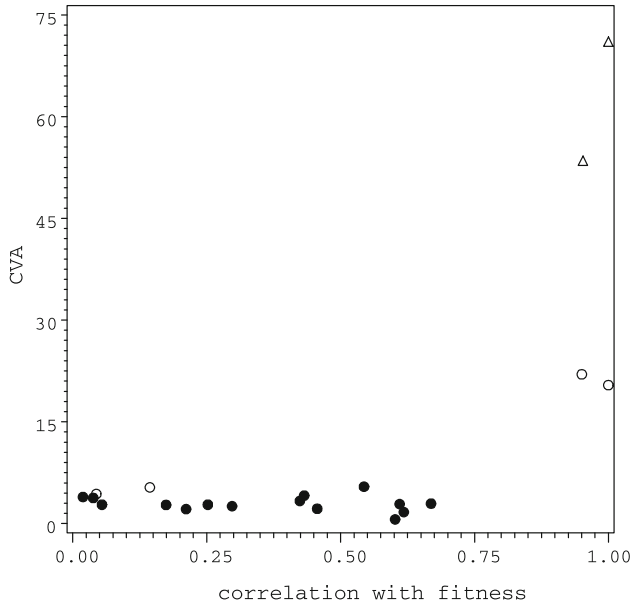

Fig. 2 The relationship of trait additive coefficient of variation (CV_A) and correlation with fitness. See Figure 1 for legend

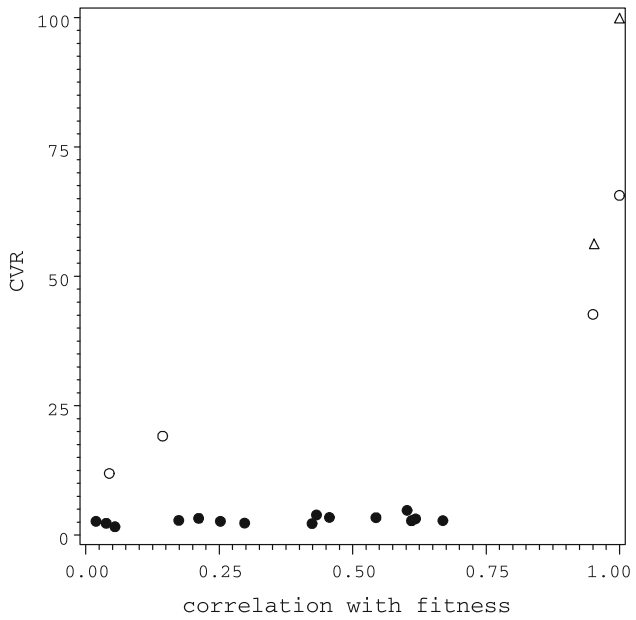

Fig. 3 The relationship of trait residual coefficient of variation (CV_R) with correlation fitness. See Figure 1 for legend

CV_A and CV_R are higher when including females that died before reproducing. Although both *CV*s increase, the increase is much greater in CV_A implying there is relatively more additive genetic variance in these traits when including sub-adult survival. Note that this also causes the elevation in heritability for these traits when all cases are included.

Table 5 Weighted Spearman correlations (r_s) among quantitative genetic statistics for the complete set of traits ($n = 21$), with randomization *p*-values immediately below the correlation

	CV_R	h^2
CV_A	0.8259	−0.1934
	0.0001	0.4955
CV_R		−0.6122
		0.0078

Correlations between h^2 and *CV*s

The quantitative genetic statistics themselves are highly correlated in some respects (Table 5). Importantly, CV_R and heritability are negatively correlated ($r_s = -0.612$, $P = 0.008$), but CV_A is uncorrelated with heritability ($r_s = -0.193$, $P = 0.496$). This agrees with the prediction that heritabilities decline with increasing correlation with fitness because of increased residual variance (incorporation of residual variance), not reduced additive genetic variance (erosion of variance). The correlation between CV_A and CV_R is also significantly positive, indicating that traits with greater genetic variance also have larger residual variance. However, this must be interpreted cautiously as the *CV*s must have some correlation because of division by the same mean.

Discussion

Match with theoretical predictions

A wide range of heritabilities and coefficients of additive genetic and residual variation was identified that reflects differences in genetic structure for traits that are physiologically or developmentally dependent on other traits. These results offer support to the incorporation of residual variance model (Price and Schluter 1991). Traits closely correlated with fitness in this population have lower heritabilities because of increased residual variance, not reduced additive genetic variance as suggested by the erosion of variance model which overly prioritizes the action of selection (Fisher 1930; Roff and Mouseau 1987, Mouseau and Roff 1987). The incorporation of residual variance model is the only hypothesis which predicted any of the important patterns observed.

Little support was found for the mutational target size hypothesis (Houle 1998). Only a weak increase in coefficients of additive genetic variance with increasing correlation with fitness was found overall. The life history variables appear to be the main source of this trend. Life history traits more directly tied to fitness may be larger

mutational targets, but this is not the case for the morphological variables. Furthermore, the negative relationship between coefficients of additive genetic variation and fitness, predicted by the erosion of variance view, was not found nor was the predicted strong decline in heritability with increasing correlation with fitness observed. However, because the Cayo Santiago population is unlikely to be in equilibrium these are weak tests of the erosion of variance hypothesis.

Comparison with previous studies

Heritabilities of morphological traits from the Cayo Santiago population in previous studies are comparable to values reported here. Animal model estimates of heritabilities are often lower than those from parent-offspring regression, but this does not appear to be the case with this study. Cheverud (1982) found a range of values from −.040 to 0.866 with a mean of 0.327 in a set of 56 cranial linear distances. In other analyses, non-metric cranial characters had somewhat higher average heritabilities (Cheverud and Buikstra, 1981) as did cranial capacity and surface features of the brain (Cheverud et al., 1990).

Hallgrimsson et al. (2002) calculated heritabilities on many of the same measurements reported here. Surprisingly, their measurements are essentially uncorrelated with those in Table 3 ($r_s = -0.063$, $P = 0.845$). One pattern they noted was decreasing heritability as one moved distally down the limb. The opposite pattern is reported here. Additionally, the average heritability reported here is higher than their study (0.44 vs. 0.34). Disagreement between animal model and parent-offspring regression or sib analysis heritabilities are well documented, but they tend to be ordered similarly (Kruuk 2004).

At least three factors contributed to differences from the estimates in Hallgrimsson et al. (2002). First, somewhat different data sets were used in each analysis, with only females who reproduced included here and a mixed-sex set of individuals over five years of age analyzed by Hallgrimsson et al. (2002, $n \approx 260$). For the individuals included in both analyses, measurements were all very highly correlated ($r = 0.954$ to 0.998). However, this portion of overlap was only one third of Hallgrimsson et al. (2002) dataset.

The method of estimating heritabilities offers two additional sources departure. First, fixed effects or covariables were included in linear models to eliminate temporal and age-related variation for the heritabilities reported here. Age-effects were particularly strong on many of these skeletal elements (Blomquist, unpublished data) despite limiting the analysis to adult indiviuals. Finally, animal model techniques for estimating heritabilities differ from parent-offspring regression and sib analysis by utilizing the full genealogical information available in a given pedigree rather than relying on a single type of relationship.

An animal model analysis of Hallgrimsson et al.'s full dataset, including fixed effects to control for temporal and age-related variation yields heritability estimates only modestly correlated with their published values ($r_s = 0.315$, $P = 0.31$). This suggests that methodological differences in estimating heritabilities caused some of the difference between studies. However, these animal model estimates from Hallgrimsson et al.'s full dataset are similarly correlated with the values explored in Table 3 ($r_s = 0.259$, $P = 0.41$). This implies the method was not the sole factor—the individuals measured also contributed. If analysis is restricted to the ≈ 70 individuals in both datasets and animal model techniques are applied to estimate heritabilities, they are highly correlated ($r_s = 0.810$, $P = 0.02$). This remaining difference can only be attributed to minor inter-observer variation in measuring the same skeletons.

Based only on the heritabilities reported in their study and the heritabilities and correlations of the traits with fitness shown here, their study does not support the erosion of variance hypothesis while those reported here do. Like Hallgrimsson et al. (2002), Lawler (2006) found descending heritability of limb segment length as one moves down the limb in young sifakas. However, his analysis included selection gradients on these limb elements (Lande and Arnold 1983). This showed that traits under stronger selection also had lower heritabilities. According to both Lawler (2006) and the results reported here, selection may sufficiently erode genetic variance in limb elements to reduce their heritabilities, but which elements are under stronger selection and thus have reduced heritability can vary among taxa or populations. Caution should be exercised in accepting this conclusion, as the erosion of variance hypothesis received no general support in this study, though it is difficult to deploy in the case of the Cayo Santiago population. Furthermore, selection was indexed rather crudely as the bivariate correlation between each trait and lifetime fitness.

Differences in heritabilities of age of first reproduction and censored lifespan with other primate populations are also notable. Age of first reproduction is quite high in captive baboons but low in the Cayo Santiago females (Williams-Blangero and Blangro 1995). In contrast, adult lifespan has a lower heritability in the baboons than in macaques (Martin et al. 2002). Heritability studies on living and historical human populations indicate a wide range of values can be found for these traits, and suggest these are largely population-level rather than interspecific differences (Towne et al. 2005; Pettay et al. 2005; Lee et al. 2004; Madrigal et al. 2003; Mitchell et al. 2001).

A number of studies of wild mammal and bird populations have provided support for the incorporation of

residual variance hypothesis (reviewed in Merilä and Sheldon 1999, 2000), and some limited support for the mutational target hypothesis. The results of this study are quite similar. However, the modest heritability of fitness in the Cayo Santiago females requires further explanation. First, it should be noted that although fitness is predicted to have very low heritability, the results of this study are not unusual. Studies of human populations and wild mammals have calculated large heritability of fitness (e.g. Pettay et al. 2005; Reale and Festa-Bianchet 2000; Kelley 2001). Second, there are a number of processes that could result in modest-high heritability of fitness. One factor that can maintain additive genetic variance in traits closely related to fitness is antagonistic pleiotropy. This cannot suffice as an explanation for fitness itself, but may function for lifespan. If lifespan is negatively genetically correlated with other traits under strong selection, such as early fertility (Blomquist 2006, 2007), additive genetic variance may be preserved (Rose 1982). Additionally, there may be a role for phenotypic plasticity in explaining the modest heritability of lifespan and number of offspring. If the environments rhesus macaques in the wild generally encounter are quite different from Cayo Santiago it is possible that genotypes express different phenotypes in this novel environment. Perhaps there is little additive genetic variance relative to environmental variance in the wild, but at Cayo Santiago non-parallel reaction norms cause an increase in additive genetic variance (see Roff 1997, p. 206). Finally, fluctuating selection pressures based on cycles of rapid evolution of parasite resistance has been suggested as a source of true heritability of fitness (Eshel and Hamilton 1984). Any of these might operate in the Cayo Santiago females.

However, the simplest explanation for modest heritability of fitness is the reduction of residual variance for fitness in the homogeneous, mild environment of Cayo Santiago. While CV_Rs for lifespan and number of offspring are high, they would likely be much higher without provisioning or with greater spatial variation in environments. The difference in heritability between the censored and uncensored h^2 for number of offspring (0.088 vs. 0.336) suggests this effect is largely due to females surviving to reproductive age. Cayo Santiago is a generally benign environment for subadults with little disease and no predation, which—assuming their random action—would drive down the uncensored heritability for total lifespan and thus number of offspring.

Data censoring for lifespan and fitness

These considerations suggest that estimates of heritabilities and other quantitative genetic statistics are sensitive to the censoring of cases, particularly for measures of lifespan and total fitness. There is ample *a priori* justification for including females that never reproduce in lifespan or number of offspring when calculating their heritability. A large amount of information on reproductive success is lost by excluding these females. This can be quantified according to the following expression from Grafen (see Brown 1988)

$$p(\sigma^2_{Pb}) + p(1-p)\bar{x}^2_{Pb} \quad (1)$$

where p is the proportion of females that breed [$p = n_b/(n_b + n_f)$ with n_b as the number that breed and n_f as the number that fail to breed], σ^2_{Pb} is the phenotypic variance in fitness for reproductive females, and $\bar{x}_{Pb}$ is the mean fitness of reproductive females. The terms on the left of the addition are the fraction of the total variance due to reproductive females; those on the right are variance due to non-reproducers. Using the values in Table 3 only 51.3% of the variance in lifetime fitness is due to females that reproduced. The remaining half of the variance is due to non-reproducers. As the opportunity for selection is the total mean-standardized variance in fitness, the best estimate for the variance in total fitness should be used, rather than half of it (Crow 1962, 1958).

Furthermore, simulation studies in animal breeding have demonstrated that censoring observations in this fashion tends to downwardly bias estimates of additive genetic variance (Burns et al. 2006; Vukasinovic et al. 1998). Removing individuals from the analysis who die before a cut-point age, or who never reproduce will yield lower estimates of additive genetic variance, and, depending on the magnitude of residual variance, lower heritability estimates. For example, in the study of Burns et al. (2006), the more data censored (10%–25%) the more depressed the heritability estimate was (11%–31%). As in the case under discussion here, the data censored were not selected at random, but were the poorer performing individuals. While this effect can be seen in the results for the Cayo Santiago females, several studies of wild bird and wild mammal populations and one study of a historical human population have found ≈ 0 heritability of female fitness regardless of censoring (Merilä and Sheldon 2000; Kruuk et al. 2000; McLeery et al. 2004; Gustafsson 1986; Esparza et al. 2006). In these populations which are unmanaged, and probably closer to evolutionary equilibrium, censoring has little effect on the heritability estimates.

Despite these complications, some predictions on the genetic architecture of traits related to fitness in the Cayo Santiago females can be tested. The incorporation of residual variance hypothesis (Price and Schluter 1991) appears to be widely applicable to mammalian and avian populations, whether they are in evolutionary equilibrium or not. Traits closely related to fitness can have large

additive genetic variances, that may get translated into sizable heritabilities when environmental conditions change such that the residual variance is reduced. Additional work is needed to clarify the contents residual variance (σ_R^2 or CV_R). Traits closely associated with fitness are widely thought to have large amounts of dominance and epistatic variance (Merilä and Sheldon 1999; Crnokrak and Roff 1995), with important effects on how they respond to selection. Furthermore, residual variance includes the effects of environmental inputs—such as diet, climate, microhabitat, disease, and injury. The ability of humans, and to some extent other animals including primates, to control their environments highlights behavioral mechanisms, such as dominance hierarchies, that strongly impact fitness, but may not be under direct genetic control.

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