



THE UNIVERSITY *of* EDINBURGH

Edinburgh Research Explorer

Linking genetic merit to behavioral data

Citation for published version:

Regan, C, Pemberton, J, Pilkington, J, Smiseth, PT & Wilson, A 2019, 'Linking genetic merit to behavioral data: Behavior and genetic effects on lamb growth in Soay sheep?', *Behavioral Ecology*.
<https://doi.org/10.1093/beheco/arz166>

Digital Object Identifier (DOI):

[10.1093/beheco/arz166](https://doi.org/10.1093/beheco/arz166)

Link:

[Link to publication record in Edinburgh Research Explorer](#)

Document Version:

Publisher's PDF, also known as Version of record

Published In:

Behavioral Ecology

General rights

Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy

The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.





Original Article

Linking genetic merit to sparse behavioral data: behavior and genetic effects on lamb growth in Soay sheep

Charlotte E. Regan,^{a,*} Josephine M. Pemberton,^a Jill G. Pilkington,^a Per T. Smiseth,^{a,*} and Alastair J. Wilson^b

^aDepartment of Biological Sciences, Institute of Evolutionary Biology, University of Edinburgh, Charlotte Auerbach Road, Edinburgh, EH9 3FL, UK, and ^bCentre for Ecology and Conservation, College of Life and Environmental Sciences, University of Exeter, Treliiever Road, Penryn, Cornwall, TR10 9FE, UK

Received 17 January 2019; revised 14 June 2019; editorial decision 7 August 2019; accepted 28 August 2019.

Wild quantitative genetic studies have focused on a subset of traits (largely morphological and life history), with others, such as behaviors, receiving much less attention. This is because it is challenging to obtain sufficient data, particularly for behaviors involving interactions between individuals. Here, we explore an indirect approach for pilot investigations of the role of genetic differences in generating variation in parental care. Variation in parental genetic effects for offspring performance is expected to arise from among-parent genetic variation in parental care. Therefore, we used the animal model to predict maternal breeding values for lamb growth and used these predictions to select females for field observation, where maternal and lamb behaviors were recorded. Higher predicted maternal breeding value for lamb growth was associated with greater suckling success, but not with any other measures of suckling behavior. Though our work cannot explicitly estimate the genetic basis of the specific traits involved, it does provide a strategy for hypothesis generation and refinement that we hope could be used to justify data collection costs needed for confirmatory studies. Here, results suggest that behavioral genetic variation is involved in generating maternal genetic effects on lamb growth in Soay sheep. Though important caveats and cautions apply, our approach may extend the ability to initiate more genetic investigations of difficult-to-study behaviors and social interactions in natural populations.

Key words: behavior, breeding value, genomic prediction, parental care, quantitative genetics, Soay sheep.

INTRODUCTION

Understanding the evolutionary trajectory of a trait requires information on the strength of selection on the trait, its genetic basis, and the genetic correlations between it and other traits. By developing methodologies to estimate these parameters, quantitative genetics has enabled empirical tests of evolutionary hypotheses (Falconer and Mackay 1996; Lynch and Walsh 1998). The application of quantitative genetic methods to studies of natural populations has extended our understanding of evolutionary processes in numerous areas, including the importance of genetic correlations between traits for determining evolutionary outcomes (Brommer et al. 2007; Charmantier et al. 2006) and the role of indirect genetic effects (IGEs) in generating phenotypic variation (McAdam et al. 2002; Wilson et al. 2011).

IGEs occur when an individual's phenotype is affected by genetically determined trait(s) in a conspecific (Wolf et al. 1998). Maternal

genetic effects are one specific kind of IGE where maternal genotype affects offspring phenotype over and above the genes that offspring directly inherit. Maternal genetic effects are of considerable interest due to their potential to alter evolutionary responses to selection. For example, theoretical models have shown that depending on the covariance between maternal and offspring traits they can dampen or accelerate evolution (Kirkpatrick and Lande 1989; Wolf et al. 1998; Wolf 2003). This growing appreciation of the role of maternal genetic effects in mediating evolutionary outcomes has meant that maternal genetic effects are now widely incorporated into quantitative genetic studies of wild populations. For example, such studies demonstrate that maternal genetic effects can be substantial (e.g., Wilson et al. 2005a, 2005b; Kruuk and Hadfield 2007; Quéméré et al. 2018) and that failing to account for them can lead to erroneous estimates of heritability (Wilson et al. 2005a; Kruuk and Hadfield 2007) and evolvability (McFarlane et al. 2015).

Despite the fact that it is now commonplace to account for maternal genetic effects in quantitative genetic analyses, we often know very little about the candidate traits mediating these effects.

Address correspondence to C.E. Regan. E-mail: charlotte.regan@usask.ca.

Studies on livestock species have revealed significant heritabilities for traits such as milk yield and content (Torres-Vázquez et al. 2009; Aspilcueta-Borquis et al. 2010), but examinations of behavioral traits have produced contrasting results, with some studies reporting substantial heritability for maternal behavior (Hoppe et al. 2008; Brown et al. 2016), while others find little evidence for heritability in behavioral traits (Everett-Hincks et al. 2005; Løvendahl et al. 2005; Gäde et al. 2008). Therefore, the role of genetically derived differences in behavior in mediating maternal genetic effects remains relatively poorly understood.

In general, behavioral traits have received much less attention from quantitative geneticists studying wild systems than morphological and life-history traits (Postma 2014). This is despite the fact that understanding the genetic basis of behavioral traits is vital for understanding how behavioral traits evolve and how they influence the evolution of traits expressed in interacting individuals (Mousseau and Fox 1998; Wolf et al. 1998; Wilson et al. 2011; Bengtson et al. 2018). There are likely many reasons for the relative lack of quantitative genetic studies of behavior. For example, behavior is highly plastic and its repeatability can be hard to demonstrate. Additionally, understanding variation in behaviors involved in interactions between individuals are particularly difficult to investigate because they require the study of more than a single individual. For example, to understand variation in parental care, it is necessary to both quantify parental behaviors and their impact on offspring performance. Furthermore, the lack of behavioral quantitative genetic studies is likely to reflect that quantifying behavior often involves many hours of focal watches on each individual. This limits the number of individuals that can be included, thereby preventing the collection of the high volumes of data necessary to make quantitative genetic approaches tractable. For instance, robust inferences about the role of genetic differences between mothers in generating behavioral variation during maternal care would require the estimation of maternal genetic covariances between offspring performance traits, such as growth, and the measured behavioral traits using a multivariate version of a quantitative genetic approach known as the “animal model.” Such models are notoriously data hungry and are likely to be out of reach even in the most established long-term individual-based studies.

Here, we explore an approach for preliminary investigations of the role of genetic differences between individuals in generating variation in behavioral traits. We advocate this approach cautiously, not as an endpoint in itself, but as a useful way to take data that are often already available to generate hypotheses regarding the genetic basis of behaviors, reducing the set of plausible traits to explore in an exhaustive manner, and thus direct data collection more effectively. For example, although it may not be feasible to measure parental care traits in enough individuals to permit powerful quantitative genetic analysis, we often have large volumes of data on offspring traits, such as growth. These traits are known to determine offspring fitness (e.g., Gaillard et al. 1997; Dantzer et al. 2013), and crucially they are often subject to parental effects (e.g., McAdam and Boutin 2004; Wilson et al. 2007). As mentioned above, using the animal model framework, it is possible to estimate parental effects on offspring phenotypes, and this is now regularly done in studies of wild vertebrates (e.g., Wilson et al. 2005a; McFarlane et al. 2014). Importantly for current purposes, variation in parental genetic effects for offspring performance is expected to arise from among-parent genetic variation in parental care (Cheverud and Moore 1994). We suggest that predicted maternal (or paternal)

genetic merits for offspring performance generated from animal models can be used to select individuals for targeted studies of parental care behaviors to begin to understand the genetic component of behavioral variation. The analysis of predicted genetic (or individual) merits is fraught with statistical issues (Hadfield et al. 2010; Houslay and Wilson 2017) and not all problems are avoided by treating them as predictors rather than responses. Consequently, subsequent inferences about the genetic basis of parental care variation will necessarily be subject to more assumptions and caveats than arise from quantitative genetic analyses of behavioral data (discussed in full later). However, our indirect approach is potentially applicable in situations where large sample sizes are neither available nor readily obtained. Our hope is that it provides a strategy for pilot studies that can ultimately be used to justify allocation of time and funds to the measurement of behavioral traits sufficient for confirmatory studies using more robust quantitative genetic methods.

In this study, we ask whether estimated maternal breeding values for lamb growth predict behavioral variation over the maternal care period in a subset of female Soay sheep selected for targeted observations. This system is well suited as a test case for this approach due to the marked variation in lamb growth (Clutton-Brock et al. 2004), significant maternal genetic effects on early-life traits (Wilson et al. 2005a; Bérénos et al. 2014), availability of high-quality relatedness information, and ability to locate and follow uniquely identifiable individuals in the field. We first fit quantitative genetic models of lamb growth to verify the presence of maternal genetic effects and then used genomic best linear unbiased prediction (gBLUP) to predict maternal breeding values (subsequently MBV_{gBLUP}) from our models. We then used these predicted maternal breeding values to select a subset of females for behavioral phenotyping (in 2014 or 2015). While care is normally viewed as a parental trait (albeit one that is often plastically adjusted in response to offspring phenotype—Royle et al. 2014), we observed both maternal and lamb behaviors here. This is because offspring behaviors can themselves be useful proxies of parental care. For instance, suckling behavior is frequently used as a proxy for care provided by female mammals during lactation (Cameron 1998). We hypothesize that lambs predicted to grow more quickly as a result of maternal (genetic) effects will be provisioned differently by their mothers. Specifically, we predict that mothers with high MBV_{gBLUP} for lamb growth will suckle lambs more frequently or for longer and/or reject fewer suckling attempts. We also hypothesize that any variation in suckling behaviors will influence nonsuckling lamb behaviors, with lambs that suckle less and/or that have their suckling attempts rejected more frequently being predicted to show increased grazing behavior.

MATERIALS AND METHODS

Study population

The Village Bay populations of Soay sheep on the island of Hirta in the St. Kilda archipelago have been studied intensively since 1985. More than 95% of sheep are marked with plastic ear tags making them individually identifiable (Clutton-Brock et al. 2004) and regular mortality checks and censuses enable the monitoring of individual life history on the whole population. Large amounts of phenotypic data, including lamb weights, are obtained through the capture of most lambs shortly after birth and of ~60% of all individuals each August. Samples for genotyping are obtained from all

captured individuals, which enable the additive relatedness matrix among individuals to be determined from high-density single nucleotide polymorphism (SNP) data.

Animal models and female selection

Using ASReml-R (Butler et al. 2007), we built a univariate animal model to partition the variation in lamb growth (treated as a trait of the lamb) into genetic and environmental components. We calculated lamb growth as the change in weight (g/day) between birth and August measurements. We excluded individuals that were more than 5 days old when first weighed to minimize effects due to age at capture. The model contained lamb sex (two-level factor), litter size (two-level factor—singleton or twin), lamb julian birth date (covariate), and maternal age in years (linear and quadratic terms) as fixed effects. We included a series of random effects to partition the variance in lamb growth into a number of environmental and genetic components. As standard, we assumed all random effects were drawn from normal distributions with means of zero and variance to be estimated. We fitted additive genetic merit of the lamb to estimate the additive genetic variance (V_A), and the MBV_{gBLUP} of the mother to estimate the maternal genetic variance (V_{MG}). We also modeled a direct-maternal genetic covariance term (COV_{am}), which was positive but nonsignificant ($COV_{am} = 6.35$, $\chi^2_{(df=1)} = 0.46$, $P = 0.50$). To estimate genetic (co)variance terms, we used SNP-derived maternity identities and relatedness information in the form of a SNP-derived realized genomic relatedness matrix (GRM—see Bérénos et al. 2014 for more details) rather than inferring the (expected) additive relatedness matrix from an explicit pedigree structure. We fitted additional random effects of birth year (V_{yob}), maternal permanent environment (V_{ME}), and maternal identity associated with a matrix containing home range overlap information for all pairs of females. We calculated individual home ranges using lifetime spatial locations for each individual and kernel density estimation methods. We then used Bhattacharyya's affinity to quantify the home range overlap for each pair of females. Individuals have an overlap of one with themselves and zero with an individual whose home range does not overlap at all with their own. We incorporated this information into the model to account for the fact that closely related females often associate spatially as adults and thus to prevent bias in the estimates of genetic components due to spatially derived phenotypic similarity (see Regan et al. 2017).

We initially fitted our animal model in Autumn of 2014 using growth data for 1490 lambs born prior to 2013 and the realized genomic relatedness between these individuals. We found evidence for substantial maternal genetic effects, with the term accounting for 12% (SE = 4%) of the variance in lamb growth (conditional on fixed effects). Dropping the maternal genetic effect resulted in a significantly poorer model fit ($\chi^2_{(df=0,1)} = 22.10$, $P < 0.001$). MBV_{gBLUP} , interpretable as the predicted deviation of a lamb's growth from the fixed-effect mean as a result of maternal genes (over and above additive inheritance) were predicted by $gBLUP$. $gBLUP$ relies on the realized genomic relatedness between individuals rather than their expected relatedness and can therefore provide more accurate predicted breeding values than pedigree-based BLUP (Meuwissen et al. 2016). The use of genomics to predict breeding values, now widespread in animal breeding, has only recently been taken up in quantitative genetics of wild populations (e.g., great tits; Bosse et al. 2017), but holds great promise for the future (Gienapp et al. 2017).

Using these predictions, we compiled a list of 60 females (aged 3–8 years) known to be alive in summer 2014, with the intention of selecting the upper and lower thirds of the MBV_{gBLUP} distribution for behavioral observations in the summer of 2015. In practice, the eventual data structure differed somewhat from this for the following reasons. First, only females surviving over winter and giving birth in the spring were available for selection. Second, because twinning rate was low (12% of litters in 2015), we decided to limit behavioral work to mother–singleton pairs to avoid having to control for litter size effects. Third, we elected to opportunistically increase our sample size by including existing behavioral data collected in 2014 as part of another study (see Regan et al. 2017). For those females observed in 2014, MBV_{gBLUP} were thus predicted after behavioral observation, although we stress the genetic analysis conducted was “blind” with respect to behavioral variation. We observed 64 females and their lambs in either 2014 or 2015, and used data for 33 of these individuals, that were in either the upper or lower quartile of the MBV distribution and therefore represented the extremes (see Supplementary Figure S1), for analysis. These were categorized as either high MBV_{gBLUP} (females with $MBV_{gBLUP} > 2.65$ g day⁻¹) or low MBV_{gBLUP} (females with $MBV_{gBLUP} < 0.29$ g day⁻¹). Analyses using all individuals and treating MBV_{gBLUP} as a covariate produce qualitatively similar results (Supplementary Table S1).

Behavioral observations and trait definition

We conducted 534 observations, each lasting 1 h, on 29 females in 2014 and 35 in 2015, with 286 h of observation on the 33 animals featured in our analysis. Observations were made over three field-work trips per year (April–May, June–July, July–August) to monitor mother and lamb behavior across the maternal care period. Mother–lamb pairs were observed 2–13 times (mean = 8.3). We used binoculars (10x42 - Vortex, USA) and spotting scopes (16-48x - Opticon, UK) to locate individuals and subsequent observations were conducted from a distance of at least 10 m to minimize disturbance. During each observation, we used “Animal behaviour Pro” (Newton-Fisher 2012) to continuously record lamb behavior, noting whether the lamb was suckling, grazing, resting, or playing, while also recording whether the mother was grazing, resting, or moving at 2-min intervals (see Supplementary Table S2 for behavior descriptions). One hour focal observations took place between 08:00 and 19:00 and the observations of each pair were distributed across the day and between observers (two at any one time) to prevent any bias caused by the data collection procedure. Where mothers and lambs separated during an observation, we preferentially kept the lamb in view to accurately record non-suckling behaviors. If either the mother or her lamb entered a cleit (dry-stone structures used for storage by the St. Kildans), we recorded them as “Out of sight,” as in this case, we could be sure that no suckling events were missed. However, we terminated observations when both mother and lamb entered a cleit and excluded the session from further analysis.

From each focal observation, we calculated *suckling frequency* (number of suckling events, whether successful or unsuccessful), *total suckling time* (time in seconds that a lamb spent suckling), *mean suckle duration* (total suckling time divided by suckling frequency), and *suckling success* [proportion of successful suckling events (failed suckles were classified as being shorter than 5 s following Hass 1990; Birgersson and Ekvall 1994; Tollefson et al. 2011)]. Of all failed suckling events, 92% were terminated by the mother and this variable is therefore indicative of the mother rejecting the lamb rather than of lamb satiation.

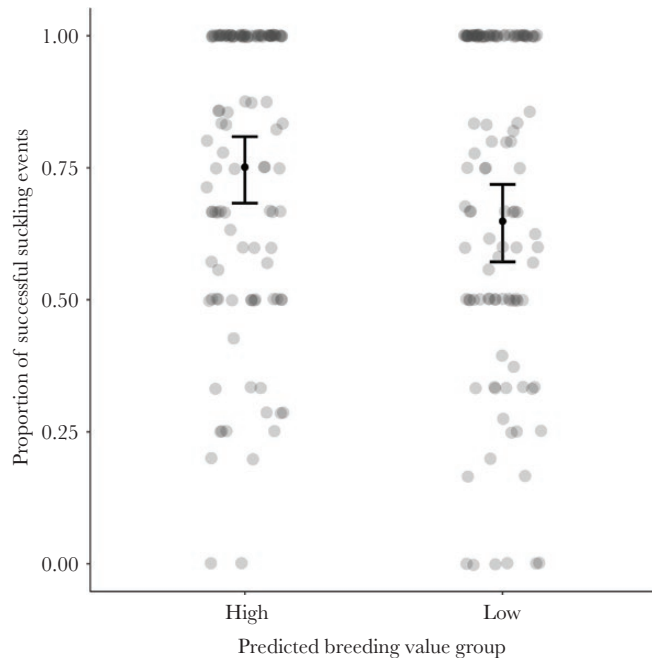


Figure 1

The proportion of successful suckling events was greater for lambs born to females whose predicted breeding value for lamb growth was high. Shown are point estimates and 95% confidence intervals from the best fit generalized linear mixed model using maternal breeding values (MBV_{gBLUP}) predicted with the genomic relatedness matrix. To aid interpretation we plot the relationship for 2015 only.

lambs born to females in the high MBV_{gBLUP} group (Table 2, Figure 1). MBV_{gBLUP} group did not feature in the best fit model for any of the other measures of lamb suckling behavior (Supplementary Tables S3 and S5). Similarly, MBV_{gBLUP} group did not feature in the best fit model for either of the nonsuckling behaviors (Table 2), but when using AICc, it was included in a competitive model for both grazing time ($\Delta AICc = 1.71$) and resting time ($\Delta AICc = 1.38$), indicating that lambs born to females in the high MBV_{gBLUP} group had a tendency to spend more time per hour resting ($MBV_{gBLUP} [low] - Est = -101.38$, $SE = 116.57$) and less time grazing ($MBV_{gBLUP} [low] - Est = 0.1564$, $SE = 0.2412$). See Supplementary Table S3 for AICc values for all lamb behavior models.

Maternal behavior

We found evidence for significant between-pair differences in maternal movement behavior ($\chi^2(1) = 9.79$, $P = 0.002$), but not in maternal grazing or resting frequency (grazing— $\chi^2(1) = 0$, $P = 1$, resting— $\chi^2(1) = 0$, $P = 1$).

As for the lamb behaviors, lamb age was important in explaining variation in the mother's behavior, particularly in the case of *grazing frequency*, which decreased over the maternal care period, and *resting frequency* which increased as lambs approached weaning (Table 3). MBV_{gBLUP} group did not predict grazing frequency, resting frequency, or moving frequency (Table 3). See Supplementary Table S4 for AICc values for all maternal behavior models.

Post hoc analyses

We found that lambs with higher average suckling success tended to have higher growth rates (Supplementary Table S9), and that there was a tendency for females in the high MBV_{gBLUP} group to be

Table 3

Parameter estimates (\pm standard error) and AICc values from the full additive models for all female behaviors when using predicted maternal breeding values (MBV_{gBLUP}) calculated using the genomic relatedness matrix (covering individuals born between 1985 and 2012). $N_{ind} = 33$, $N_{obs} = 286$

Trait	Term	Est (SEM)	t/z*	
Grazing frequency	Intercept	3.10 (0.08)	37.89	
	Lamb Age	-0.17 (0.10)	-1.73	
	Lamb age ²	0.06 (0.10)	0.65	
	Maternal age	-0.01 (0.01)	-0.60	
	Year (2015)	0.006 (0.05)	0.13	
AICc = 1998.52 $w_i = 0.09$	$MBV_{gBLUP} [low]$	0.03 (0.05)	0.67	
	† Intercept	-0.99 (0.44)	-2.23	
	Lamb Age	-0.23 (0.38)	-0.60	
	Lamb age ²	0.31 (0.38)	0.81	
	Maternal age	0.09 (0.07)	1.24	
AICc = 725.53 $w_i = 0.13$	Year (2015)	0.43 (0.26)	1.62	
	$MBV_{gBLUP} [low]$	-0.26 (0.24)	-1.07	
	Resting frequency	Intercept	1.65 (0.45)	3.65
	Lamb Age	0.93 (0.60)	1.55	
	Lamb age ²	-0.49 (0.59)	-0.83	
AICc = 1366.20 $w_i = 0.09$	Maternal age	0.02 (0.08)	0.30	
	Year (2015)	-0.27 (0.27)	-1.01	
	$MBV_{gBLUP} [low]$	-0.15 (0.24)	-0.62	

*t values for linear mixed effects models and z values for generalized linear mixed effects models.

†Date was removed due to convergence problems.

heavier, though this relationship was not statistically significant (β (SE) = -2.06 (1.26), $P = 0.12$).

DISCUSSION

Here, we show that MBV_{gBLUP} for lamb growth predicted variation in behavior associated with maternal care in Soay sheep. This suggests that at least some of the maternal genetic variance in lamb growth is likely to be explained by heritable behavioral traits linked to maternal provisioning. We did so using a novel approach that combines information from the quantitative genetic animal model with targeted behavioral observations that could not logistically be conducted on the whole population. Lambs born to mothers with high predicted breeding values for offspring growth had a greater proportion of successful suckling events, and a tendency to spend greater time resting and less time grazing. These results were consistent whether we used breeding values predicted using the genomic relatedness matrix (using phenotype data for lambs born between 1985 and 2012) or an updated pedigree that included individuals born between 2013 and 2016 (see Supplementary Tables S7 and S8). Maternal performance has been linked to body mass in species including sheep (Réale and Festa-Bianchet 2000) and we did find that females in the high MBV_{gBLUP} group tended to be slightly heavier, though not significantly so. This may suggest that differences in body mass were partially driving the behavioral differences we observed, but given that body mass is not necessarily an accurate measure of condition due to size differences between individuals, differences in body mass may not be entirely responsible for the results found.

We found evidence for a relationship between MBV_{gBLUP} and one behavior: suckling success. This finding could, in part, reflect that this behavioral trait is largely under maternal control, with the majority of suckling events being terminated by the mother. However, we cannot rule out differences between females in the quality or quantity of their milk, and resulting differences in

lamb satiation, as a cause of these differences in suckling success. Indeed, the use of suckling behavior as an indicator of milk intake and maternal investment during lactation has been criticized (summarized in [Cameron 1998](#)). For example, there might be individual differences in nutritional quality of a female's milk, which may influence the level of satiation of her offspring ([Skibiell and Hood 2015](#)), and there may be differences between offspring in the efficiency with which they obtain milk ([Cameron 1998](#)). We must also acknowledge that it is possible that our inability to detect a relationship between MBV_{gBLUP} and the other behaviors may be due to a lack of statistical power, particularly given that variation in any one of these behaviors is likely to come from a vast array of sources.

Relatively little work has examined the role of genetic differences in generating variation in the parental care shown by individuals living under natural conditions, with only a small number of studies demonstrating heritability in traits such as yolk and egg mass ([Tschirren et al. 2009](#)) and the provisioning rate of passerine parents ([MacColl and Hatchwell 2003](#)). Such studies are important for establishing the contribution of genetic effects to variation in parental care that is apparent in natural populations, thereby advancing our understanding of how parental care responds to selection in natural systems. They are also important given the potential environmental dependence of heritability estimates ([Charmanier and Garant 2005](#)) and the need to use empirical data on parental and offspring traits to develop the quantitative genetic models that provide the theoretical basis for studying the evolution of parental care ([Hadfield 2012](#)). Though sample sizes preclude direct estimation of genetic parameters for behaviors observed, our approach provides some indirect and preliminary evidence that genetic differences between female Soay sheep are associated with variation in behavior over the maternal care period. This in turn suggests that behavioral variation is involved in the pathway that generates maternal genetic effects on lamb growth in this population.

The number of long-term individual-based studies of natural populations has been steadily increasing since the first studies on birds began in the 1940s. Although these studies are largely restricted to mammals and birds, they now cover a range of species that vary substantially in the parental care provided, including passerines (e.g., [Verhulst et al. 1997](#)), seabirds (e.g., [Grist et al. 2014](#)), marsupials (e.g., [Gélin et al. 2013](#)), rodents (e.g., [Hayes et al. 2017](#)), and primates (e.g., [Alberts et al. 2003](#)). Many of these studies are likely to have the data necessary to calculate a suitable proxy for parental care, thereby making the approach we have used in this paper tractable in these systems. Offspring growth is likely to be one of the most important and widely available measures of offspring performance for two reasons. First, many long-term studies involve the capture of offspring shortly after birth or hatching and before weaning or fledging, thereby providing data on growth for a large number of individuals. Second, offspring growth in both birds and mammals is closely linked with the investment of parents into care given that offspring of many species are entirely reliant on resources from the parent(s) early in life ([Clutton-Brock 1991](#)). Our approach provides a promising way to begin to study the genetic basis of parental care in the wild, but it may also prove beneficial to use the approach to direct studies when appropriate data for semicaptive populations are available. This may be particularly useful for taxa other than mammals and birds where it is very difficult to establish long-term individual-based studies. In doing so, it may be possible to begin to understand the role of genetics in

generating variation in a more complete range of parental care patterns. Furthermore, our approach is not necessarily restricted to looking at the mediators of genetic sources of trait variation, given that it is entirely possible to use this method to look more broadly at traits that may be driving overall phenotypic differences between individuals (i.e., consisting of both genetic and environmental determinants).

The use of the animal model to direct field sampling on a subset of individuals could provide a starting point for understanding how genetic differences between individuals result in variation in traits other than those associated with parental care. In our case, we started by estimating the maternal genetic effect (a special case of IGEs) on lamb growth. However, by modeling different IGEs, this approach could be used whenever the interest is in how the genotype of a specific individual influences the phenotype of an interacting individual. Indeed, studies on wild populations are beginning to examine how specific traits in an interacting individual influence a focal individual's phenotype ([McGlothlin and Brodie 2009](#)), and incorporate a wider range of IGEs into the animal model, such as IGEs on social dominance ([Wilson et al. 2011](#)) and reproductive traits such as laying date ([Brommer and Rattiste 2008](#)). Thus, given an appropriate pedigree and a suitable proxy for the trait of interest, our approach provides a tractable means for understanding whether focal individual's predicted breeding value for a trait expressed in an interacting individual can be used to predict how it behaves towards the other individual. This could include understanding how the genes carried by a focal individual influences its reproductive investment or the ways in which individual genetics influences competitive behaviors, such as dominance or aggression, or social behaviors, such as cooperative breeding or antipredator behaviors.

Despite the potential utility of the animal model for directing field sampling schemes, such an approach does come with caveats that must be acknowledged. The power to estimate genetic and environmental components within the animal model relies on the ability to parametrize an appropriate model, which itself is dependent on the pedigree and phenotypic data available ([Clément et al. 2001](#); [Kruuk 2004](#); [Kruuk and Hadfield 2007](#); [Wilson et al. 2010](#)). Therefore, we stress that the breeding values we used to select individuals are only predictions (generated by gBLUP), and although genomic estimated breeding values are generally more accurate than breeding values estimated using pedigree data ([Clark et al. 2012](#); [Gienapp et al. 2017](#)), they will necessarily be associated with error and bias ([Postma 2006](#); [Hadfield et al. 2010](#)). Statistical hypothesis testing can be substantially anticonservative when BLUP are treated as response variables and the uncertainty around them is ignored, a practice that has been shown to be problematic in both evolutionary and behavioral studies ([Hadfield et al. 2010](#); [Houslay and Wilson 2017](#)). Here, we use BLUP as a basis for selecting individuals for targeted study, and (analytically) we treat them as predictors rather than response variables. This approach still suffers from the uncertainty around the predicted breeding values and thus violates the assumption of linear models that predictors are measured without error. The result of this failure to propagate error is unclear and is why we strongly advocate this approach not as a general alternative to quantitative genetic modeling of high volume behavioral data where it can be obtained, but very specifically as a necessarily exploratory approach where it cannot.

We reiterate that our results show relationships between predicted, as opposed to true, maternal breeding values and observed behaviors. The accuracy of predicted breeding values is

determined by the information available, for example, the extent to which data are available for individuals of varying degrees of relatedness (Postma 2006), and by the appropriateness of the model used to predict them. However, given that observations on the focal individual and its close relatives contribute most information to the prediction of breeding values, predicted breeding values tend to be more closely correlated with the phenotypic observations than true breeding values (Postma 2006; Hadfield et al. 2010). This means that an individual's predicted breeding value is, at least to some extent, determined by environmental effects on the individual's phenotype. To better understand whether our results were likely to have been somewhat driven by the environmental component of a mother's phenotype, we repeated our analyses using maternal breeding values predicted from an animal model where the growth rates of each mother's lambs were removed in turn. When using AICc, there was some support for the model containing MBV_{gBLUP} group, with this being only 0.33 AICc units from the best model and having a similar AICc weight (0.32) to the best fit model (0.37).

We acknowledge that explicitly estimating the maternal genetic covariance between lamb growth and each of the observed behaviors using a bivariate animal model would be the most appropriate and robust means for understanding whether the maternal genetic effect on lamb growth was mediated by differences in maternal behavior. This is the strategy we advocate for confirmatory studies. However, such an approach is often precluded, as in our case, by the limited availability of behavioral data. Small sample sizes mean that, even where it is possible to use the animal model to estimate these parameters, it is not possible to draw substantive conclusions from the estimates. For example, we estimated the maternal genetic covariance between lamb growth and each of the behavioral traits using a series of bivariate animal models in ASReml-R (see Section 6 in Supplementary Information), but in all cases, our variance or covariance estimates had the boundary condition making them very difficult to interpret (see Supplementary Table S11). This is expected given the low sample size of behaviorally phenotypes mothers, and the low variance in relatedness among them (mean genomic relatedness = 0.009, variance = 0.003). To verify that the data structure precluded meaningful application of the bivariate animal model, we conducted a power analysis using the package “pedantics” (Morrissey and Wilson 2010) to assess our ability to detect variance components given our real data structure (see Section 7 in Supplementary Information for details). Given the mothers and lambs observed, we were unable to recover simulated components (Supplementary Table S12), indicating that it was not possible to use the more appropriate bivariate approach in our case. Therefore, although obtaining precise estimates of these covariances would be a more appropriate approach for determining whether or not maternal genetic effects were mediated by differences in maternal care behavior, using this approach is not possible with the limited data available. Thus, our approach may serve as the starting point and justification for a more exhaustive sampling scheme involving a bivariate animal model approach if predicted breeding values were found to predict variation in the trait(s) measured in the selected subset of individuals.

In summary, by using an animal model of lamb growth to select females whose genotypes were associated with differing lamb growth rates, we show that suckling behavior differed between individuals born to females with different predicted breeding values. Further work is needed to establish the more specific maternal traits underlying the differences in behavior we observed here and to provide better estimates of the genetic basis of maternal care in this

population. The number of long-term studies with the data necessary to make the approach proposed here possible is increasing and the continuing development of genomics tools is likely to make analyses such as ours possible in species where pedigree information is not available (Gienapp et al. 2017). As a result, we believe that using animal model estimates of breeding values to target the collection of phenotypic data from a subset of animals may be a valuable approach for starting to uncover the traits mediating maternal and other IGEs.

SUPPLEMENTARY MATERIAL

Supplementary data are available at *Behavioral Ecology* online.

FUNDING

The Soay Sheep Project is supported by grants from the UK Natural Environment Research Council, the genomic work was supported by the European Research Council, and this work was supported by a BBSRC PhD studentship (BB/J01446X/1) to C.E.R. and BBSRC David Phillips fellowship (BB/G022976/2) to A.J.W.

The authors first wish to thank all project members and many volunteers for their contributions to field work on St. Kilda, and to all those who have contributed to keeping the project running over many years, including T. Clutton-Brock, M. Crawley, S. Albon, T. Coulson, L. Kruuk, and D. Nussey. The authors are also grateful to the National Trust for Scotland and Scottish Natural Heritage for permission to work on St. Kilda, and QinetiQ and Eures for logistics and other support on the island. The authors also wish to extend thanks to Timothee Bonnet and David Fisher for their thorough and constructive reviews that helped to improve this paper, and to Jarrod Hadfield and Ian White for helpful discussions and assistance with the bivariate animal models.

Data accessibility: Analyses reported in this article can be reproduced using the data provided by Regan et al. (2019).

Handling editor: Colette St Mary

REFERENCES

- Alberts SC, Watts HE, Altmann J. 2003. Queuing and queue-jumping: long-term patterns of reproductive skew in male savannah baboons, *Papio cynocephalus*. *Anim Behav*. 65:821–840.
- Aspilcueta-Borquis RR, Araujo Neto FR, Baldi F, Bignardi AB, Albuquerque LG, Tonhati H. 2010. Genetic parameters for buffalo milk yield and milk quality traits using Bayesian inference. *J Dairy Sci*. 93:2195–2201.
- Bates D, Mächler M, Bolker B, Walker S. 2015. Fitting linear mixed-effects models using lme4. *J Stat Softw*. 67:1–48.
- Bengston SE, Dahan RA, Donaldson Z, Phelps SM, van Oers K, Sih A, Bell AM. 2018. Genomic tools for behavioural ecologists to understand repeatable individual differences in behaviour. *Nat Ecol Evol*. 2:944–955.
- Béréanos C, Ellis PA, Pilkington JG, Pemberton JM. 2014. Estimating quantitative genetic parameters in wild populations: a comparison of pedigree and genomic approaches. *Mol Ecol*. 23:3434–3451.
- Birgersson B, Ekvall K. 1994. Suckling time and fawn growth in fallow deer (*Dama dama*). *J Zool*. 232:641–650.
- Bosse M, Spurgin LG, Laine VN, Cole EF, Firth JA, Gienapp P, Gosler AG, McMahon K, Poissant J, Verhagen I, et al. 2017. Recent natural selection causes adaptive evolution of an avian polygenic trait. *Science*. 358:365–368.
- Brommer JE, Kirkpatrick M, Qvarnström A, Gustafsson L. 2007. The intersexual genetic correlation for lifetime fitness in the wild and its implications for sexual selection. *PLoS One*. 2:e744.
- Brommer JE, Rattisti K. 2008. “Hidden” reproductive conflict between mates in a wild bird population. *Evolution*. 62:2326–2333.

- Brown DJ, Fogarty NM, Iker CL, Ferguson DM, Blache D, Gaunt GM. 2016. Genetic evaluation of maternal behaviour and temperament in Australian sheep. *Anim Prod Sci*. 56:767–774.
- Butler DG, Cullis BR, Gilmour AR, Gogel BJ. 2007. Analysis of mixed models for S language environments: ASReml-R reference manual, release 2. Brisbane (Australia): Queensland Department of Primary Industries and Fisheries.
- Cameron EZ. 1998. Is suckling behaviour a useful predictor of milk intake? A review. *Anim Behav*. 56:521–532.
- Charmantier A, Garant D. 2005. Environmental quality and evolutionary potential: lessons from wild populations. *Proc Biol Sci*. 272:1415–1425.
- Charmantier A, Perrins C, McCleery RH, Sheldon BC. 2006. Quantitative genetics of age at reproduction in wild swans: support for antagonistic pleiotropy models of senescence. *Proc Natl Acad Sci USA* 103:6587–6592.
- Cheverud JM, Moore AJ. 1994. Quantitative genetics and the role of the environment provided by relatives in behavioral evolution. In: Boake CRB, editor. *Quantitative genetic studies of behavioral evolution*. Chicago (IL): University of Chicago Press. p. 67–100.
- Clark SA, Hickey JM, Daetwyler HD, van der Werf JH. 2012. The importance of information on relatives for the prediction of genomic breeding values and the implications for the makeup of reference data sets in livestock breeding schemes. *Genet Sel Evol*. 44:4.
- Clément V, Bibé B, Verrier E, Elsen JM, Manfredi E, Bouix J, Hanocq E. 2001. Simulation analysis to test the influence of model adequacy and data structure on the estimation of genetic parameters for traits with direct and maternal effects. *Genet Sel Evol*. 33:369–395.
- Clutton-Brock TH. 1991. *The evolution of parental care*. Princeton (NJ): Princeton University Press.
- Clutton-Brock TH, Pemberton JM, Coulson T, Stevenson IR, MacColl ADC. 2004. The sheep of St Kilda. In: Clutton-Brock TH, Pemberton JM, editors. *Soay sheep: dynamics and selection in an island population*. Cambridge (UK): Cambridge University Press. p. 17–51.
- Dantzer B, Newman AE, Boonstra R, Palme R, Boutin S, Humphries MM, McAdam AG. 2013. Density triggers maternal hormones that increase adaptive offspring growth in a wild mammal. *Science*. 340:1215–1217.
- Everett-Hincks JM, Lopez-Villalobos N, Blair HT, Stafford KJ. 2005. The effect of ewe maternal behaviour score on lamb and litter survival. *Livest Prod Sci*. 93:51–61.
- Falconer D, Mackay TF. 1996. *Introduction to quantitative genetics*. 4th ed. London (UK): Prentice Hall.
- Gade S, Bennewitz J, Kirchner K, Looft H, Knap PW, Thaller G, Kalm E. 2008. Genetic parameters for maternal behaviour traits in sows. *Livest Sci*. 114:31–41.
- Gaillard JM, Boutin JM, Delorme D, Van Laere G, Duncan P, Lebreton JD. 1997. Early survival in roe deer: causes and consequences of cohort variation in two contrasted populations. *Oecologia*. 112:502–513.
- Gélin U, Wilson ME, Coulson GM, Festa-Bianchet M. 2013. Offspring sex, current and previous reproduction affect feeding behaviour in wild eastern grey kangaroos. *Anim Behav*. 86:885–891.
- Gienapp P, Fior S, Guillaume F, Lasky JR, Sork VL, Csilléry K. 2017. Genomic quantitative genetics to study evolution in the wild. *Trends Ecol Evol*. 32:897–908.
- Grist H, Daunt F, Wanless S, Nelson EJ, Harris MP, Newell M, Burthe S, Reid JM. 2014. Site fidelity and individual variation in winter location in partially migratory European shags. *PLoS One*. 9:e98562.
- Hadfield JD. 2012. The quantitative genetic theory of parental effects. In: Royle N, Smiseth PT, Kölliker M, editors. *The evolution of parental care*. Oxford (UK): Oxford University Press. p. 267–280.
- Hadfield JD, Wilson AJ, Garant D, Sheldon BC, Kruuk LE. 2010. The misuse of BLUP in ecology and evolution. *Am Nat*. 175:116–125.
- Hass CC. 1990. Alternative maternal-care patterns in two herds of bighorn sheep. *J Mammal*. 71:24–35.
- Hayes LD, Ebensperger LA, Kelt DA, Meserve PL, Pillay N, Viblanc VA, Schradin C. 2017. Long-term field studies on rodents. *J Mammal*. 98:642–651.
- Hoppe S, Brandt HR, Erhardt G, Gauly M. 2008. Maternal protective behaviour of German Angus and Simmental beef cattle after parturition and its relation to production traits. *Appl Anim Behav Sci*. 114:297–306.
- Houslay TM, Wilson AJ. 2017. Avoiding the misuse of BLUP in behavioural ecology. *Behav Ecol*. 28:948–952.
- Kirkpatrick M, Lande R. 1989. The evolution of maternal characters. *Evolution*. 43:485–503.
- Kruuk LE. 2004. Estimating genetic parameters in natural populations using the “animal model”. *Philos Trans R Soc Lond B Biol Sci*. 359:873–890.
- Kruuk LE, Hadfield JD. 2007. How to separate genetic and environmental causes of similarity between relatives. *J Evol Biol*. 20:1890–1903.
- Løvendahl P, Damgaard LH, Nielsen BL, Thodberg K, Su G, Rydmer L. 2005. Aggressive behaviour of sows at mixing and maternal behaviour are heritable and genetically correlated traits. *Livest Prod Sci*. 93:73–85.
- Lynch M, Walsh B. 1998. *Genetics and analysis of quantitative traits*. Sunderland: Sinauer.
- MacColl AD, Hatchwell BJ. 2003. Sharing of caring: nestling provisioning behaviour of long-tailed tit, *Aegithalos caudatus*, parents and helpers. *Anim Behav*. 66:955–964.
- McAdam AG, Boutin S. 2004. Maternal effects and the response to selection in red squirrels. *Proc Biol Sci*. 271:75–79.
- McAdam AG, Boutin S, Réale D, Berteaux D. 2002. Maternal effects and the potential for evolution in a natural population of animals. *Evolution*. 56:846–851.
- McFarlane SE, Gorrell JC, Coltman DW, Humphries MM, Boutin S, McAdam AG. 2014. Very low levels of direct additive genetic variance in fitness and fitness components in a red squirrel population. *Ecol Evol*. 4:1729–1738.
- McFarlane SE, Gorrell JC, Coltman DW, Humphries MM, Boutin S, McAdam AG. 2015. The nature of nurture in a wild mammal's fitness. *Proc Biol Sci*. 282:20142422.
- McGlothlin JW, Brodie III ED. 2009. How to measure indirect genetic effects: the congruence of trait-based and variance-partitioning approaches. *Evolution*. 63:1785–1795.
- Meuwissen T, Hayes B, Goddard M. 2016. Genomic selection: a paradigm shift in animal breeding. *Anim Front*. 6:6–14.
- Morrissey MB, Wilson AJ. 2010. pedantics: an R package for pedigree-based genetic simulation and pedigree manipulation, characterization and viewing. *Mol Ecol Resour*. 10:711–719.
- Mousseau TA, Fox CW. 1998. The adaptive significance of maternal effects. *Trends Ecol Evol*. 13:403–407.
- Newton-Fisher N. 2012. *Animal behaviour pro (Version 1.0)* [Mobile application software]. Retrieved from <http://itunes.apple.com>
- Postma E. 2006. Implications of the difference between true and predicted breeding values for the study of natural selection and micro-evolution. *J Evol Biol*. 19:309–320.
- Postma E. 2014. Four decades of estimating heritabilities in wild vertebrate populations: improved methods, more data, better estimates? In: Charmantier A, Garant D, Kruuk LEB, editors. *Quantitative genetics in the wild*. Oxford (UK): Oxford University Press. p. 16–33.
- Quéméré E, Gaillard JM, Galan M, Vanpé C, David I, Pellerin M, Kjellander P, Hewison AJM, Pemberton JM. 2018. Between-population differences in the genetic and maternal components of body mass in roe deer. *BMC Evol Biol*. 18:39.
- R Development Core Team. 2008. *R: a language and environment for statistical computing*. Vienna (Austria): R Foundation for Statistical Computing.
- Réale D, Festa-Bianchet M. 2000. Mass-dependent reproductive strategies in wild bighorn ewes: a quantitative genetic approach. *J Evol Biol*. 13:679–688.
- Regan CE, Pemberton JM, Pilkington JG, Smiseth PT, Wilson AJ. 2019. Data from: linking genetic merit to sparse behavioral data: does behavior explain genetic variation for maternal care in Soay sheep? Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.617744v>
- Regan CE, Pilkington JG, Smiseth PT. 2017. Female Soay sheep do not adjust their maternal care behaviour to the quality of their home range. *Behav Ecol*. 118:450–459.
- Royle NJ, Russell AF, Wilson AJ. 2014. The evolution of flexible parenting. *Science*. 345:776–781.
- Self SG, Liang KY. 1987. Asymptotic properties of maximum likelihood estimators and likelihood ratio tests under nonstandard conditions. *J Am Stat Assoc*. 82:605.
- Skaug H, Fournier D, Nielsen A. 2006. *glmmADMB: generalized linear mixed models using AD Model Builder*. Available from: <http://glmmadmb.r-forge.r-project.org/>
- Skibił AL, Hood WR. 2015. Milk matters: offspring survival in Columbian ground squirrels is affected by nutrient composition of mother's milk. *Front Ecol Evol*. 3:111–121.
- Tollefson TN, Shipley LA, Myers WL, Dasgupta N. 2011. Forage quality's influence on mule deer fawns. *J Wildl Manage*. 75:919–928.
- Torres-Vázquez JA, Valencia-Posadas M, Castillo-Juárez H, Montaldo HH. 2009. Genetic and phenotypic parameters of milk yield, milk composition and age at first kidding in Saanen goats from Mexico. *Livest Sci*. 126:147–153.

- Tschirren B, Sendecka J, Groothuis TG, Gustafsson L, Doligez B. 2009. Heritable variation in maternal yolk hormone transfer in a wild bird population. *Am Nat.* 174:557–564.
- Verhulst S, Perrins CM, Riddington R. 1997. Natal dispersal of great tits in a patchy environment. *Ecology.* 78:864–872.
- Wilson AJ, Coltman DW, Pemberton JM, Overall AD, Byrne KA, Kruuk LE. 2005a. Maternal genetic effects set the potential for evolution in a free-living vertebrate population. *J Evol Biol.* 18:405–414.
- Wilson AJ, Kruuk LE, Coltman DW. 2005b. Ontogenetic patterns in heritable variation for body size: using random regression models in a wild ungulate population. *Am Nat.* 166:E177–E192.
- Wilson AJ, Morrissey MB, Adams MJ, Walling CA, Guinness FE, Pemberton JM, Clutton-Brock TH, Kruuk LE. 2011. Indirect genetics effects and evolutionary constraint: an analysis of social dominance in red deer, *Cervus elaphus*. *J Evol Biol.* 24:772–783.
- Wilson AJ, Pemberton JM, Pilkington JG, Clutton-Brock TH, Coltman DW, Kruuk LE. 2007. Quantitative genetics of growth and cryptic evolution of body size in an island population. *Evol Ecol.* 21:337–356.
- Wilson AJ, Réale D, Clements MN, Morrissey MM, Postma E, Walling CA, Kruuk LE, Nussey DH. 2010. An ecologist's guide to the animal model. *J Anim Ecol.* 79:13–26.
- Wolf JB, Brodie III ED, Cheverud JM, Moore AJ, Wade MJ. 1998. Evolutionary consequences of indirect genetic effects. *Trends Ecol Evol.* 13:64–69.
- Wolf JB. 2003. Genetic architecture and evolutionary constraint when the environment contains genes. *Proc Natl Acad Sci USA* 100: 4655–4660.