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On the heritability of blue-green eggshell coloration

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Abstract

Avian blue-green eggshell coloration has been proposed as a female signal of genetic or phenotypic quality to males. However, little is known about the relative importance of additive genetic and environmental effects as sources of eggshell colour variation in natural populations. Using 5 years of data and animal models, we explored these effects in a free-living population of pied flycatchers. Permanent environmental and year effects were negligible, although year environmental variance (V_{Year}) was significant for all but one of the traits. However, we found high-moderate narrow-sense heritabilities for some colour parameters. Within-clutch colour variability showed the highest coefficient of additive genetic variation (i.e. evolvability). Previous evidence suggests that eggshell colour is sexually selected in this species, males enhancing parental effort in clutches with higher colour variability and peak values. Eggshell colour could be driven by good-genes selection in pied flycatchers although further genetic studies should confirm this possibility.

Introduction

Evolutionary change within a population requires a genetic basis of phenotypic variation. Thanks to quantitative genetic approaches, we have gained valuable insight into the genetic variation of fitness and nonfitness traits (see reviews by Merilä & Sheldon, 1999, 2001; Charmantier & Sheldon, 2006; Kruuk et al., 2008). However, empirical knowledge on the heritability of sexually selected traits lags behind that about other traits (Qvarnström, 1999; Kruuk et al., 2002). This is surprising because some influential models of sexual selection such as good-genes or fisherian processes require that sexual ornaments are heritable (Andersson, 1994; Jones & Ratterman, 2009). This relatively poor understanding is even more evident in the case of secondary sexual traits in females. Good examples on the inheritance of female ornaments come from studies on wild bird populations.

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These were initially based on parent–offspring comparisons (Møller, 1993; Potti, 1993), and subsequently, also on cross-fostering manipulations to break environmental correlations between parents and offspring (Roulin et al., 2000, 2001; Roulin & Dijkstra, 2003; Bize et al., 2006; Gasparini et al., 2009; Quesada & Senar, 2009). Still, we need a better empirical understanding of the genetics underlying the evolution of female ornaments and of sexual traits in general (Garant et al., 2004).

The blue-green biliverdin pigment is used by female birds to colour their eggshells green and blue (Kennedy & Vevers, 1976). Blue-green eggshell coloration has been very recently incorporated into the sexual selection framework, as it has been proposed as a signal of female phenotypic or genetic quality to males in species with biparental care (Moreno & Osorno, 2003). The offspring of high-quality females would merit more effort according to the differential allocation hypothesis (Burley, 1986), as applied to female traits. This post-mating character has been shown to mirror some aspects of female quality in most species studied to date (Moreno et al., 2005, 2006a; Morales et al., 2006; Siefferman et al., 2006; Krist & Grim, 2007; Hanley et al., 2008; Hargitai et al., 2008; López-Rull et al., 2008; Soler et al., 2008; Morales et al., 2010; but see Hanley & Doucet, 2009).

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Also, it has received support that males respond to egg colour by enhancing parental contribution to their offspring in some studies (see Moreno et al., 2004, 2006b, 2008; Hanley et al., 2008; Soler et al., 2008) however not in others (Krist & Grim, 2007; Hanley & Doucet, 2009). Besides, blue-green eggshell colour intensity is positively associated with the duration of nestling care period across species (Soler et al., 2005). Apparently, hole-nesting breeders are able to detect experimental variations in eggshell appearance and respond by enhancing parental care (e.g. Moreno et al., 2006b; Soler et al., 2008; Avilés et al., 2009), despite the fact that their retinal dark adaptation has been suggested to be slow (Cassey, 2009).

Investigations into the genetic architecture of eggshell coloration go back to Punnett & Bailey (1920). Subsequent studies, mainly on poultry, have supported that blue-green eggshell coloration was under genetic control (Punnett, 1933; Yang et al., 2003; reviewed by Stevens, 1991 and Washburn, 1990; see also Collias, 1993 on a sub-Saharan passerine). However, most research to date has been restricted to captive populations (but see studies on the inheritance of porphyrins-based pigmentation, e.g. Gosler et al., 2000 and Mahler et al., 2008). The controlled and constant conditions in the laboratory are more homogeneous than natural variation, and this may lead systematically to reduced environmental variance and increased estimates of heritabilities (for a review, see Charmantier & Garant, 2005). Thus, although the existence of a genetic basis seems well established, little is known about the relative importance of additive genetic environmental effects as sources of blue-green and eggshell colour variation in natural populations. Estimating genetic variability in the wild can be tricky, as environmental variation may obscure underlying evolutionary patterns (Kruuk, 2004). Thus, quantitative genetic approaches applied to natural populations should allow the observed phenotypic variation to be separated into genetic and environmental components. Animal models are mixed models that use all information available in a pedigree to estimate additive genetic variance (i.e. covariance across all possible pairs of relatives; Kruuk, 2004) and may include additional variance components for specific environmental effects (Postma, 2006; Wilson et al., 2010).

Here, we explored the heritable variation of blue-green eggshell coloration in a wild population of pied flycatchers (Ficedula hypoleuca), using animal models. Although tests exploring male investment decisions according to egg colour have yielded diverse results (reviewed by Reynolds et al., 2009), some pieces of evidence suggest that egg colour is sexually selected in this species (Moreno et al., 2004, 2006b, 2008). Egg pigmentation in pied flycatchers reflects female immunological quality (Moreno et al., 2005; Morales et al., 2006), is subject to varying environmental conditions, such as food availability (Moreno et al., 2006a) and is costly to produce for laying females (Morales et al., 2008). Furthermore, egg colour predicts fledgling condition (Moreno et al., 2008) and reproductive success (Morales et al., 2006, 2008), which may ultimately affect fitness. We explored the additive genetic, year and permanent environmental (repeated measures) effects on blue-green eggshell colour over a period of 5 years, while controlling for other known sources of variation of egg colour in this species (e.g. manipulated early maternal effects).

Methods

Study species and general procedures

The pied flycatcher is an insectivorous, migratory, holenesting passerine that breeds in European woodlands (Lundberg & Alatalo, 1992). It is a summer visitor that adapts readily to breeding in nestboxes. The study population breeds in a deciduous forest located in Valsaín, central Spain (Segovia, 40°53¢74N, 4°01¢W, 1200 m a.s.l.), where there are 300 nestboxes monitored since 1991 (between 75 and 125 are occupied by pied flycatchers depending on the year). Egg laying typically begins in late May, and clutch size ranges from 4 to 7 eggs with a mode of six eggs. The most common pattern in this species is to start full incubation with the penultimate or last egg in the clutch (Potti, 1998a). Males in the study population visit their nestbox frequently during the laying period, when females have not yet started full incubation, and spend some time inside the nest cavity (Moreno et al., 2005). Hence, males have ample opportunities to observe freshly laid eggs (see a recent study on this male behaviour in another hole-nesting breeder, the blue tit, Cyanistes caeruleus; Holveck et al., 2010).

In all breeding seasons, adults are captured at the nest with nestbox traps when nestlings are about to fledge (day 11 or 12; hatching day = day 0). All birds are individually marked with numbered aluminium rings (Dirección General de Medio Natural, ringing permit by regional authorities), and their reproductive success and local survival between years are known (female local survival probability is very high in this population, reaching 90% at 3-4 years of age; Sanz & Moreno, 2000). We assume for all recruited adult females that were not raised in the study area a minimum age of two (Sanz & Moreno, 2000). We used all data available for eggshell colour, which was measured in 346 pied flycatcher nests of 215 individual females during five consecutive breeding seasons, from 2003 to 2007. In 2003, we experimentally manipulated the size of the sexually selected white forehead patch of males on arrival to the breeding grounds (see Osorno et al., 2006 for a full description). Females laid smaller eggs when paired with less attractive (patch reduced) mates (Osorno et al., 2006). In 2005, females that were supplemented with mealworms before and during laying laid bluer and heavier clutches (Moreno et al., 2006a). To account for

potential maternal effects on eggshell colour derived from these two experiments, we included all nests but controlled for experimental group (see statistical analyses).

Eggshell colour measurement

Eggshell colour was measured with a portable spectrophotometer MINOLTA CM-2600d (Minolta Co. Ltd., Osaka, Japan) on the day eggs were laid or on the following day. Eggs were placed directly with their broad pole on a target mask with a diameter of 8 mm, so that eggs completely filled the space of the mask. Reference calibrations against zero and a white standard tablet (Minolta Co. Ltd.) were performed periodically according to the apparatus instructions. The reflectance spectra are automatically obtained as means of three sequential measures of each egg by changing the position of the egg with respect to the apparatus. The SPECTRAMAGIC software (Minolta Co. Ltd.) was used to obtain the reflectance spectra from 360 nm in intervals of 10 nm. From the reflectance spectra, we calculated blue-green chroma (BGC) as the proportion of total reflectance that is in the blue-green region of the spectrum $(R_{400-570}/R_{360-700})$. This corresponds to the region with least absorbance (and therefore greatest reflectance) of biliverdin (Falchuk et al., 2002) and pied flycatcher eggs reflect maximally in it (Moreno et al., 2005). There is a highly positive significant correlation of BGC values estimated with the MINOLTA spectrophotometer and with an OCEAN OPTICS spectrophotometer covering also the UV range (Moreno et al., 2006a). In 2003, we only recorded Lightness and Chroma in CIELAB colour space (CIEL*a*b*, Commission Internationale de l'Eclairage, 1976) (see Moreno et al., 2004) and not the reflectance spectra of eggs. Measures in CIELAB are highly correlated with BGC, so that higher values of BGC are positively associated with Chroma and negatively with Lightness (Moreno et al., 2006a). Although they may be redundant, these measures describe different aspects of colour, and birds may show different detection rates for different colour attributes (Cazetta et al., 2009). While Lightness represents achromatic properties of an object on a scale from 0 = black to 100 = white, Chroma, often used as a synonym of purity or saturation, characterizes colour by the a* (red to green) and b* (yellow to blue) values. It is calculated according to the formula: Chroma $\frac{1}{4} \int da^{\frac{1}{2}} b b^{\frac{1}{2}}$, which indicates that the further the value is away from zero, the more saturated is the colour. Finally, BGC measures reflectance in the blue-green part of the spectrum and thus includes both chromatic and achromatic aspects. We estimated variance components for the three colour parameters: Lightness, Chroma (n = 346 nests) and BGC (n = 282), which are associated with biliverdin amount in the eggshell (Moreno et al., 2006a). Pied flycatcher males in our population invest more parental effort in clutches more variable in colour and with higher peak

values rather than with higher means (Moreno et al., 2006b, 2008). Therefore, we have used within-clutch means, maxima and standard deviations of Lightness, Chroma and BGC for statistical analyses.

Eggs were weighed on the day of colour measurement with a portable electronic balance (accuracy 0.1 g) in all years except 2003, when eggs were measured with a digital calliper (accuracy 0.01 mm) and their volume estimated in mm³ with the formula volume =)0.042 + 0.4976 (length - (width)²) (Ojanen et al., 1978). Using data from another study population of pied flycatchers (see Morales et al., 2006, for a description), we performed the regression of mass on volume (r = 0.99, P < 0.001, n = 38) and estimated egg mass in 2003 from the resulting equation (egg mass = 0.0819 + 0.001 - egg volume). There are no appreciable differences in egg shape between both populations. After colour measurement, eggs were marked for identification according to their laying order and placed back in the nest.

Statistical analyses

Exploration of fixed effects

Prior to the quantitative genetic analyses using animal models, we first explored the effects of potential covariates on each egg colour trait, using linear mixed effect models (LME) with female identity as a random effect: female age, egg mass and experimental treatment [fourlevel factor: control or unmanipulated nest (i), male's forehead patch either enlarged (ii) or reduced (iii) and nest supplemented with mealworms (iv)]. As we used pooled data from all years, treatment had an unbalanced structure because of a large amount of unmanipulated nests (all nests in 2004, 2006 and 2007) and thus, no clear conclusion can be drawn from its effects on egg colour. Effects of the food supplementation experiment on eggshell colour were already presented and discussed by Moreno et al. (2006a), when they were appropriately tested. Therefore, here we only accounted for them to ensure that at least part of the variation in egg colour because of manipulated early maternal effects is taken into account. Initially, an LME with all explanatory variables as fixed effects and individual identity as random effect was fitted for each egg colour trait using a maximum-likelihood (ML) algorithm (full model). Then nonsignificant terms were dropped sequentially to simplify the model. The significance of the removal of each term was tested using a likelihood ratio test (Crawley, 2007). This model simplification method proceeded until we obtained minimum adequate LMEs that included only terms significant at the $\mathsf{P} < 0.05$ level. The minimum adequate models were then rerun using restricted maximum-likelihood (REML) methods (Crawley, 2007). Although BGC is a proportion, its normal approximation is good (Kolmogorov-Smirnov tests for mean, SD and maximum values of BGC: all P > 0.20). All other colour parameters and laying date

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were normally distributed as well (K–S test; all P > 0.20). None of the variables were thus transformed. Analyses were carried out using R version 2.7.2 (R Development Core Team, 2008).

The relevant fixed effects found for each colour parameter (see Appendix 1) were taken into account in the quantitative genetic analyses (see the following section). Note that laying date was not included as a fixed effect in the univariate models, as this life-history trait is expected to show substantial additive genetic variance (e.g. Sheldon et al., 2003; in the related collared flycatcher, Ficedula albicollis). Instead, we explored the heritability of laying date with another univariate model. In contrast, egg mass, which is expected to be mainly determined by maternal effects and environmental conditions (e.g. Moreno et al., 2006a; Osorno et al., 2006), was included as a fixed effect in subsequent quantitative genetic analyses where significant.

Animal model

Animal model is a form of mixed model that partitions individual phenotypic variations for a quantitative character into different variance components and includes an individual's genetic merit as a random effect (Lynch & Walsh, 1998; Kruuk, 2004). We fitted univariate animal models using a REML procedure. ASReml v2 (VSN International; Gilmour et al., 2006) was used to fit animal models and calculate variance ratios and standard errors (see Lynch & Walsh, 1998).

Univariate animal models were fitted to the pedigree for each egg colour trait and laying date, including the significant fixed effects determined from the LME analyses (see Appendix 1). The pedigree was formed by 242 identities, incorporating 27 fathers and 28 mothers. Note that extra-pair paternity is moderately low in our population (7.5% of nestlings), and intraspecific brood parasitism is extremely rare (Moreno et al., 2010). Thus, our estimates of genetic parameters are conservative. Among the 346 clutches included in the animal models, there were 112 belonging to females with at least one known relative (i.e. with known mother, or at least one known daughter or sister). The rest of the clutches included in the analyses did not belong to females with known relatives, but they contributed to estimating more accurately the total phenotypic variance of eggshell colour in the study population. In the univariate model for each egg colour trait and laying date, we included the additive genetic, year-specific and permanent environmental (individual-specific) effects as random factors. The permanent environmental effect, estimated using repeated measures, includes individual sources of variance that are conserved across repeated records on individuals but are not because of additive genetic effects (Kruuk, 2004). There were 88 females that bred in various years (54 bred twice, 27 bred in 3 years, six in 4 years and one in 5 years) and 127 that bred once. The total phenotypic variance (V_P) is the sum of all the

variance components of each random effect and was calculated as $V_P = V_A + V_{Year} + V_{PE} + V_R$, where V_A is the variance explained by additive genetic effects, V_{Year} is the environmental variance because of year, V_{PE} is the permanent environmental variance (i.e. individual identity), and V_R is the residual variance (Falconer & Mackay, 1996). Narrow-sense heritability ($h^2 = V_A/V_P$), the effects of year $(y^2 = V_{Year}/V_P)$ and permanent environmental effects ($pe^2 = V_{PE}/V_P$) were calculated as the proportion of the relevant variance component to the total phenotypic variance for each trait. We also calculated the coefficient of additive genetic variance as $CV_A = 100 \ JV_A/X$, for which the additive genetic variance was scaled by the trait mean rather than the total variance (Houle, 1992). The statistical significance of each variance component was assessed using likelihood ratio tests that compare models based on -2 times the difference in REML loglikelihood scores distributed as v² where the number of degrees of freedom equalled the number of variance terms removed. The significance of variance ratios (h^2, y^2) and pe^2) was assessed using two-tailed t-tests.

Additionally, we tried to fit a multivariate animal model to explore the heritability of eggshell colour when accounting for potential genetic and environmental correlations between the colour parameters and laying date. Unfortunately, a convergence problem was encountered when attempting to fit the individual-specific effect, possibly because the permanent environmental (co)variances were close to zero in the multivariate model. Note that dropping the permanent environmental effect from this type of model may result in overestimated heritabilities (see Kruuk & Hadfield, 2007) and, therefore, the multivariate model is not shown.

Results

Exploration of fixed effects for colour traits and laying date

Female age did not affect any of the colour traits, but did affect laying date, young breeders laying later in the season (Appendix 1). Egg mass affected maximum Lightness, clutches with smaller eggs showing higher peaks in Lightness (Appendix 1).

Univariate animal models

Estimates of additive genetic variance (V_A) were significant for SD Lightness, maximum Lightness, SD BGC and marginally nonsignificant (P < 0.1) for mean BGC (Table 1). Heritabilities (h^2) of blue-green eggshell colour traits ranged from 0.15 to 0.54 and were significant for the later four parameters and marginally nonsignificant for mean Lightness and maximum Chroma (Table 1). The highest significances (both for V_A and h^2 values) were found for SD BGC and maximum Lightness (Table 1). Coefficients of additive genetic variance

Table 1 Quantitative genetics for egg colour traits and laying date (univariate animal models). Estimates (SE) of variance components, total phenotypic variance (V_P), additive genetic variance (V_A), year environmental variance (V_{Year}), permanent environmental variance (V_{PE}), residual variance (V_R) and the variance ratios, narrow-sense heritability (h^2), year environmental effects (y^2), permanent environmental effects (y^2) and coefficient of additive genetic variance (CV_A). These models included the fixed effects that were relevant for each colour trait (see Appendix 1).

Trait	V _P	V _A	V_{Year}	V _{PE}	V _R	h ²	y ²	pe²	Mean	CVA
Mean Lightness	2.297 (0.375)	0.961 (0.563)	0.457 (0.334)	0.484 (0.531)	0.396 (0.051)	0.42 (0.24)	0.20 (0.12)	0.21 (0.23)	72.27 (0.08)	1.36
		P = 0.111	P < 0.001	P = 0.328		P = 0.088	P = 0.092	P = 0.369		
SD Lightness	0.280 (0.026)	0.043 (0.022)	0.018 (0.016)	0	0.219 (0.025)	0.15 (0.08)	0.06 (0.05)	0	1.41 (0.03)	14.71
		P = 0.035	P = 0.007			P = 0.044	P = 0.243			
Max Lightness	2.527 (0.267)	1.018 (0.213)	0.224 (0.185)	0	1.286 (0.155)	0.40 (0.07)	0.09 (0.07)	0	74.24 (0.09)	1.36
		P < 0.001	P < 0.001			P < 0.001	P = 0.187			
Mean Chroma	3.193 (0.728)	1.150 (0.698)	0.964 (0.699)	0.514 (0.659)	0.565 (0.071)	0.36 (0.23)	0.30 (0.15)	0.16 (0.21)	11.38 (0.09)	9.42
		P = 0.144	P < 0.001	P = 0.431		P = 0.113	P = 0.051	P = 0.443		
SD Chroma	0.228 (0.019)	0.076 (0.060)	0.006 (0.007)	0.013 (0.056)	0.134 (0.016)	0.33 (0.26)	0.03 (0.03)	0.06 (0.25)	1.40 (0.03)	19.69
		P = 0.242	P = 0.090	P = 0.828		P = 0.193	P = 0.363	P = 0.823		
Max Chroma	3.588 (0.748)	1.398 (0.825)	0.973 (0.710)	0.519 (0.774)	0.698 (0.088)	0.39 (0.24)	0.27 (0.15)	0.14 (0.22)	12.82 (0.10)	9.22
		P = 0.155	P < 0.001	P = 0.509		P = 0.099	P = 0.063	P = 0.508		
Mean BGC*	1.062 (0.166)	0.573 (0.295)	0.164 (0.139)	0.130 (0.274)	0.196 (0.029)	0.54 (0.27)	0.15 (0.11)	0.12 (0.26)	0.589 (0.001)	1.29
		P = 0.091	P < 0.001	P = 0.639		P = 0.048	P = 0.168	P = 0.637		
SD BGC*	0.115 (0.014)	0.055 (0.011)	0.010 (0.010)	0	0.050 (0.007)	0.48 (0.08)	0.09 (0.07)	0	0.009 (0.000)	26.06
		P < 0.001	P < 0.001			P < 0.001	P = 0.242			
Max BGC*	1.275 (0.214)	0.481 (0.366)	0.219 (0.186)	0.301 (0.352)	0.274 (0.040)	0.38 (0.29)	0.17 (0.12)	0.24 (0.28)	0.598 (0.001)	1.16
		P = 0.244	P < 0.001	P = 0.383		P = 0.187	P = 0.160	P = 0.398		
Laying date	33.92 (9.83)	3.491 (5.398)	13.47 (9.678)	6.229 (5.502)	10.73 (1.323)	0.10 (0.16)	0.40 (0.17)	0.18 (0.17)	48.12 (0.31)	3.88
		P = 0.497	P < 0.001	P = 0.245		P = 0.525	P = 0.022	P = 0.278	-	

*Variance components and their SEs: e⁾⁴.

BGC, blue-green chroma.

 (CV_A) ranged from 1.16 to 26.06; the highest values were found for parameters describing within-clutch colour variation (SD in Lightness, Chroma and BGC; Table 1). Surprisingly, although year environmental variance (V_{Year}) was significant for most colour parameters, year effects (y²) were nonsignificant for all of them, because of high standard errors; note, however, that they were marginally nonsignificant for within-clutch mean Lightness, mean Chroma and maximum Chroma (Table 1). Also, permanent environmental effects (pe²) were nonsignificant for all colour traits (Table 1). Laying date had nonsignificant V_A and h² but significant y² (Table 1).

Discussion

We found significant additive genetic variance on some eggshell colour parameters in a free-living population of pied flycatchers. The highest coefficients of additive genetic variance (CV_A) were found in traits describing within-clutch colour variation, suggesting that this trait shows the highest evolvability. On the other hand, year and permanent environmental effects did not explain a significant proportion of the variance. However, year environmental variance (V_{Year}) was significant for all but one of the traits.

The exploration of fixed effects indicated that withinclutch maximum Lightness was negatively associated with egg mass, supporting previously observed trends in the relationship between egg colour and size (Moreno et al., 2004). As could be expected, young females laid later in the season, which is a common pattern in this species (Lundberg & Alatalo, 1992).

Our findings support a genetic basis of blue-green eggshell coloration, as suggested in previous studies (e.g. Collias, 1993 and references therein). The univariate animal models estimated high additive genetic variances (V_A), which were significant for maximum Lightness, SD Lightness and SD BGC, and marginally nonsignificant for mean BGC. Narrow-sense heritabilities (h²) were significant for the later four parameters and marginally nonsignificant for another two. Heritabilities for all colour traits were moderately high and explained between 15% and 54% of the total phenotypic variance. Laying date showed very low and nonsignificant heritability $(h^2 = 0.10)$, which may contrast with previous evidence in other avian species. For instance, in the closely related collared flycatcher, Ficedula albicollis, the heritability of laying date estimated with animal models was similarly low $(h^2 = 0.19)$ but significant (Sheldon et al., 2003). Nevertheless, previous pied flycatcher studies using parent-offspring regressions either found substantial heritability on laying date (Lundberg & Alatalo, 1992) or no evidence of additive genetic variation (see Potti, 1998b; in a close Iberian population). Note that there are moderate-low levels of extra-pair paternity in the study population (7.5% of nestlings; Moreno et al.,

2010), which may lead to downward bias of genetic variance and hence heritability (Wilson et al., 2010).

The CV_A may provide a more informative measure of genetic variability than heritability, as it scales the component of additive genetic variance by the trait mean instead of by the total variance, and so it is not confounded by the magnitude of other variance components (Houle, 1992; Kruuk et al., 2000). Interestingly, the three parameters describing within-clutch SD in colour showed the highest CV_A, suggesting that variation in colour within a clutch has the highest potential for evolutionary change under directional selection (Houle, 1992; Roff, 1997). Genetic variance for variation in colour may indicate genetic heterogeneity of environmental variance, which can arise from genetic differences in environmental sensitivity (Falconer & Mackay, 1996; Lynch & Walsh, 1998). The fact that genotypes may differ not only in mean, but also in environmental variance of the traits they affect, has been considered a rare biological phenomenon (discussed by Mulder et al., 2007); yet empirical studies on this idea are scarce.

Previous findings in the study species stressed the role of environmental effects on eggshell colour, as females laid colourful clutches when food availability was experimentally increased (Moreno et al., 2006a). Also in other species, blue-green eggshell colour seems to be influenced by spring environmental conditions (Avilés et al., 2007) and pollution (Jagannath et al., 2008). Accordingly, the variance because of year (V_y) was significant for all but one colour parameters. However, year effects (y²) were nonsignificant (or almost significant) for all of them. One possibility is that the environmental variances because of year were partly confounded by treatment effects; although treatment was included as a fixed factor, the experiments were performed in two of the five study years. This may explain why Vy was significant for most traits, despite very high standard errors. On the other hand, the significance estimated by the likelihood ratio test for the year variance component may be more reliable than that obtained with the t-test for the year variance ratio, if the distribution of year effect estimates is asymmetric. Thus, the interpretation of the year variance component and its ratio should be taken with caution. Permanent environmental variance (V_{PE}) and effects (pe^2) were negligible for all colour parameters, indicating that between-individual differences (for instance because of mate or territory quality) were not persistent over time (Kruuk, 2004). Current environmental conditions could have played a more important role.

Evidence in the study species suggests that males respond to experimentally increased eggshell colour by enhancing parental contribution to their offspring (Moreno et al., 2006b, 2008). Additionally, egg colour reflects important aspects of female condition (e.g. Moreno et al., 2005) or the quality of maternal effects transferred to the eggs (Morales et al., 2006). Furthermore, it can be subject to trade-offs with crucial self-maintenance processes in females (Morales et al., 2008) that may ensure the honesty of the signal. Moreover, egg colour predicts fledgling condition (Moreno et al., 2008) and reproductive success (Morales et al., 2006, 2008), which may ultimately affect fitness. This study shows that egg colour is heritable. Therefore, blue-green egg colour in pied flycatchers may indicate heritable variation in female fitness and could have evolved via a good-genes process, as expected from theory (Kokko, 2001). In this case, it would add to one clear example of a signal of female genetic quality to males in barn owls (see Roulin et al., 2000, 2001). Nonetheless, to evidence selection by good genes in our pied flycatcher population, we still need to demonstrate that there are positive associations between eggshell colour and female lifetime fitness mediated by the mate's response to colour stimulation.

To conclude, our results from univariate animal models showed substantial additive genetic variation in bluegreen eggshell colour in wild pied flycatchers, as predicted by the sexual signalling hypothesis (Moreno & Osorno, 2003). Within-clutch colour variation (SD in colour) showed the highest coefficient of additive genetic variance and thus, the highest potential for evolution. Interestingly, male pied flycatchers in the study population enhance their parental contribution in clutches with higher variation in colour and peak values rather than average values (Moreno et al., 2006b, 2008).

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Appendix 1

Summary of minimum adequate linear mixed effect models (LMEs) using REML (random effect: individual identity), exploring fixed effects for nine egg colour traits and laying date in pied flycatchers. Full model for colour traits: female age + experimental treatment + egg mass. Full model for laying date: female age + experimental treatment. The significance of each fixed term is based on marginal Wald-type statistics.

Term	Coefficient ± SE	Test	Р
(a) Mean lightness	(n = 346)		
Intercept	71.72 ± 0.35		
Treatment			
enlarged patch size	0	$F_{3,127} = 21.60$	< 0.001
reduced patch size	0.38 ± 0.47		
food supplementation)0.67 ± 0.37		
control	0.71 ± 0.35		
(b) SD lightness	(n = 346)		
Intercept	1.48 ± 0.15		
Treatment			
enlarged patch size	0	$F_{3,127} = 5.47$	0.001
reduced patch size	0.22 ± 0.21		
food supplementation	0.18 ± 0.17		
control)0.11 ± 0.15		
(c) Max lightness	(n = 346)		
Intercept	77.92 ± 1.43		
Egg mass	$)2.24 \pm 0.78$	$F_{1,126} = 8.30$	0.005
Treatment	,	1,120	
enlarged patch size	0	$F_{0.400} = 4.70$	0.004
reduced patch size	$0 13 \pm 0.60$	1 3,126 - 4.10	0.004
food supplementation	0.60 ± 0.00		
control	0.16 ± 0.44		
(d) Mean chroma	(n - 346)		
Intercept	(1 - 3+0)		
Treatmont	10.12 ± 0.41		
anlarged patch size	0	E _ 9.55	- 0.001
enlarged patch size	0 10 - 0 50	$\Gamma_{3,127} = 0.55$	< 0.001
feed supplementation	0.16 ± 0.36		
	1.12 ± 0.44		
	1.49 ± 0.41		
	(11 = 346)		
	1.43 ± 0.13		
Treatment	<u>_</u>	F 4.00	0.000
enlarged patch size	0	$F_{3,127} = 4.88$	0.003
reduced patch size	0.15 ± 0.18		
food supplementation	0.19 ± 0.14		
control	0.06 ± 0.13		
(f) Max chroma	(n = 346)		
Intercept	11.66 ± 0.43		
Treatment			
enlarged patch size	0	$F_{3,127} = 3.74$	0.013
reduced patch size	0.82 ± 0.58		
food supplementation	1.36 ± 0.46		
control	1.32 ± 0.43		
(g) Mean BGC	(n = 282)		
Intercept	0.589 ± 0.001		
(h) SD BGC	(n = 282)		
Intercept	0.011 ± 0.0005		
Treatment			
food supplementation	0	$F_{1,93} = 23.20$	< 0.001
control)0.002 ± 0.0005		
(i) Max BGC	(n = 282)		
Intercept	0.598 ± 0.001		
(j) Laying date	(n = 346)		
Intercept	50.41 ± 0.69		
Age	0.80 ± 0.22	$F_{1,129} = 13.32$	< 0.001

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