Validation of a Bayesian approach for maternity identification in abandoned lambs

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ABSTRACT

Abandoned lambs in sheep flocks use to involve few ewes at the same time; this phenomenon prevents the accurate collection of pedigree data and originates a moderate-to-low percentage of lambs with unknown or uncertain ancestors. Given the economic restrictions inherent to the sheep industry, the systematic implementation of laboratory paternity testing technologies to all abandoned lambs is not affordable by stockbreeders; if possible, only a reduced number of lambs can be validated by genotyping, and we need specific tools to elucidate the most relevant individuals (e.g. lambs with the highest chance to be offspring of high genetic merit ewes). We adapted a Bayesian mixed linear model to infer the dam of abandoned lambs by integrating both genetic and environmental sources of information from phenotypic data, and modelling the uncertain dam as an additional unknown parameter. Model performance was evaluated on simulated data and by assuming seven different scenarios where one to four abandoned lambs had to be assigned to two candidate ewes. The average probability of assignment to the correct dam (PACD) was 0.59, although within-scenario average PACD ranged between 0.51 and 0.70, and raw PACD estimates fluctuated between 0.04 and 1.0. Sensitivity varied across simulation scenarios, although most of the cases revealed values larger than 60%. This approach must be viewed as a useful tool for screening abandoned lambs and their candidate mothers, inferring the most plausible dam for each individual. Note that any inference on uncertain dams may reduce further paternity testing expenses.

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Introduction

Abandoned lambs must be viewed as a relevant cause of lamb mortality in current production systems (Dwyer et al. 2016), and originates additional economic losses due to the need of artificial feeding in some cases. In addition to these direct influences on flock performance, abandoned lambs tend to impair genetic selection programmes because individuals with unknown ancestors must be removed from the list of selection candidates. Abandoned lambs cannot be easily assigned to their own dams if two or more ewes gave birth without supervision and at the same time. Little is known about the incidence of abandoned lambs in commercial sheep flocks, although Alexander et al. (1983) reported up to 6.1% for single birth lambs, 45.7% for twin birth lambs and 35.7% for triplet birth lambs in Merino, Dorset and New Zealand Romney breeds. In the Ripollesa sheep breed, the incidence of abandoned lambs is lower than 5% (R. Bach, personal communication). Although both sire and dam can be identified by current genotyping tests, the systematic implementation of these genotyping technologies to all abandoned lambs becomes economically unfordable for sheep breeders. Within this context, alternative approaches for dam assignment must be evaluated.

There are several statistical approaches to infer unknown parental relationships from the genetic background underlying phenotypic traits (Foulley et al. 1987; Im 2003; Cardoso & Tempelman 2003; Sapp et al. 2007). Although all those authors focussed on missing paternities, the analytical models they developed must be viewed as useful statistical tools for inferring first-degree relationships at a low-cost level, and with potential applications within the context of abandoned lambs. The main objective of our research...
was to adapt the model developed by Sapp et al. (2007) for inferring the dam (and sire) of abandoned lambs within the context of the Ripollesa sheep breed. Among the native sheep breeds in Spain, the Ripollesa is the most abundant breed in Catalonia (i.e. the northeastern region of Spain), thus producing lambs with 22–24 kg of live weight at slaughter (~3 months of age). It is a rustic meat-type breed, with a convex profile, white wool and characteristic pigmentation (Casellas et al. 2007b). Both precision and sensitivity of this analytical approach have been evaluated on simulated data sets. This model must provide an economical alternative to assign abandoned lambs to their own mother or, at least, to reduce the list of animals requiring genotyping paternity tests.

Materials and methods

Animal Care and Use Committee approval was not required for this study because all analyses were performed on simulated data sets; the simulation process relied on pedigree and field data from the experimental Ripollesa sheep flock kept in the Universitat Autònoma of Barcelona (Bellaterra, Spain).

Rationale

Abandoned lambs at birth are troublesome for animal breeding programmes in the sheep industry because its status involves complete loss of genealogical information; note that if registered, sire identification typically links to the ewe. Although these lambs could be treated as founders in genetic evaluations by the implementation of appropriate genetic groups (Westell et al. 1988), they are typically removed from data sets and excluded as potential selection candidates. Even when included in genetic evaluation models with genetic groups, their predicted breeding values are low due to the lack of pedigree data contributing information from close relatives. This problem could be solved by genotyping these abandoned lambs and their potential dams by an appropriate panel of genetic markers, although the cost of this kind of genotyping paternity test prevents by far its systematic implementation in the majority of sheep breeding programmes. Even when the percentage of abandoned lambs is moderate-to-low (Alexander et al. 1983), genotyping efforts must be kept to a minimum due to economic restrictions inherent to the sheep industry. Within this context, the model developed by Sapp et al. (2007) for paternity identification in cattle could be adapted to the sheep framework, focussing on the inference of unknown dams. Although final results must be corroborated by genotyping, farmers could concentrate their budget on lambs with the highest probability to be offspring of those ewes with the highest genetic merit, whereas remaining lambs must remain with unknown maternity and dropped off from the data set (or included in the BLUP analysis with appropriate genetic groups).

Bayesian inference for uncertain maternities

Mismothering in sheep sometimes involves the lamb’s stealing; this phenomenon occurs specially under intensive farm conditions in which several ewes are giving birth very close on to the other. This situation is consequence of the expression of prepartum behaviour that is known as attraction to amniotic fluids. This behaviour induces that some ewes are attracted for newborn lambs, lick them, and even steal the lamb from the postparturient ewes. At the end of this situation, the stolen lamb sometimes ends up being abandoned for both ewes (Arnold & Morgan 1975). This involves a very reduced number of ewes that lambed at the same time and without supervision, even in large flocks. Nevertheless, the analytical model outlined below generalised to any number of lambs and ewes. In order to infer the dam of each unassigned lamb, the model by Sapp et al. (2007) for uncertain paternity was adapted by using information from both environmental (i.e. ewe age and birth type) and genetic sources of variation of a given phenotypic quantitative trait (Y).

Assuming a standard hierarchical structure for Y, the analytical model generalised as:

\[ y = Xb + Wp + Za + e, \]

where \( y \) is the vector of phenotypic records, \( b \) is the vector of systematic effects, \( p \) is the vector of permanent environmental effects, \( a \) is the vector of polygenic additive genetic effects, \( e \) is the vector of residuals, and \( X, W \) and \( Z \) are incidence matrices with appropriate dimensions. Let \( \Pi_i = (\pi_{i1}, \pi_{i2}, \ldots, \pi_{in}) \) be a set of \( n \) potential dams for the \( i \)th abandoned lamb with uncertain dam. Following Sapp et al. (2007), information from phenotypic data must discriminate among candidate dams by the likelihood of observing the phenotypic record from the \( i \)th lamb \( (y_i) \) given each one of the possible dams. Within this context, the conditional distribution of \( y_i \) given the relevant parameters of the model generalised to

\[
p(y_i | \delta_i = \pi_{ij}, b, p, a, \sigma_e^2) \\
c \propto \exp\left[ -0.5 (y_i - x_{ij}b - w_{ij}p_{ij} - a_{ij})^2 \right] \\
\sigma_e^{-2} \left[ y_i - x_{ij}b - w_{ij}p_{ij} - a_{ij} \right].
\]
where the dam of the \(i\)th lamb (\(d_i\)) was identified as \(\pi_p\) and \(\sigma^2_e\) was the residual variance. Submatrices \(X_{ij}\) and \(w_{ij}\) linked the phenotype from the \(i\)th lamb to its own fixed and permanent effects, respectively, whereas \(\rho_{ij}\) and \(a_{ij}\) are vectors of permanent environment and additive genetic effects for the \(i\)th lamb given the \(j\)th potential dam. Given that the \textit{a priori} probability for the \(i\)th lamb to be assigned to each of the \(n\) candidate dams was \(1/n\) (Sapp et al. 2007), the conditional distribution of the data is defined as

\[
p(y|\Delta, b, p, a, \sigma^2_e) = \Pi_{i=1,m}p(y_i|d_i = \pi_j, b, p, a, \sigma^2_e)
\]

where \(m\) is the total number of lambs with phenotypic data included in the analysis, and \(\delta_i\) is fixed to the real dam for mothered lambs and treated as an unknown parameter for abandoned lambs. Note that \(\Lambda\) is the vector storing all \(\delta_i\) elements. It is important to highlight that the structure of both \(X_{ij}\) and \(w_{ij}\) vectors can change depending on the dam assigned to each abandoned lamb (e.g. the lamb moved from a 2-yr-old ewe to a 4-yr-old ewe). Under a standard Bayesian development, the \textit{a priori} distribution for permanent environmental and additive genetic effects is defined as multivariate normal, with the only restriction that at least one lamb must be imputed to each candidate dam.

**Illustration with simulated data**

The statistical performance of the model developed above was exemplified on simulated data sets. Although the incidence of abandoned lambs in commercial sheep flocks fluctuates from almost 0–45.7% (Alexander et al. 1983), we restricted our simulations to a broad scenario involving two ewes and one to four abandoned lambs, assuming that all remaining abandoned lambs were excluded from the data set and their maternal assignment was evaluated in further analyses. Although all abandoned lambs and candidate ewes could be tested at the same time by applying the model outlined above, we preferred to restrict simulation scenarios in order to evaluate the statistical performance of the maternal assignment procedure, avoiding those disturbances from other abandoned lambs with a different list of candidate dams.

New data sets were generated by mimicking the pedigree and birth weight records from the experimental Ripollesa flock kept at the Universitat Autònoma of Barcelona (Bellaterra, Spain). The field data set comprised 2443 birth weight records (single, 53.8%; twins, 44.1%; triplets, 1.9%; quadruplets, 0.2%) registered by the staff of the experimental farm of the Universitat Autònoma of Barcelona between 1986 and 2007. All relevant information at the lamb (e.g. identification, sire, dam, sex, year of birth) and ewe levels (e.g. ewe age, type of parturition) was accurately recorded. The full pedigree file included 2,856 individuals (see Casellas et al. (2009) for a detailed description of this data set).

Given the moderate litter size of the Ripollesa sheep breed (1.2–1.7 lambs per litter; Casellas et al. (2007a)), we designed seven different simulation scenarios where one to four lambs from two different litters were (within-simulation) randomly selected as maternally unassigned (i.e. abandoned lambs). We restricted to single and twin births from the last lambing season (i.e. 141 lambs born during the year 2007). In any case, the two litters contributing unassigned lambs (and their corresponding ewes) were assumed to be known for analytical purposes, and our analyses restricted to the inference of the real dam from those two candidate ewes who gave birth to those litters. For the first simulation scenario, two single-born lambs were randomly selected and they were treated as abandoned for the subsequent analysis, whereas the pedigree of the remaining animals was assumed as...
true and known (SS₂; i.e. two single birth lambs and their dams, although it was assumed for the analysis that lamb-dam relationships were unknown and had to be inferred from phenotypic data). One single birth and one twin birth were randomly selected for each simulation under scenarios two to four, and one (ST₁; from the twin birth), two (ST₂) and three lambs (ST₃) from these litters were re-sampled within each population. The last three scenarios relied on two twins births with two (TT₂; one from each litter), three (TT₃) and four lambs (TT₄) selected at random and treated as abandoned. For each simulation scenario, a total of 1000 independent populations were simulated on the basis of the field data set described below, and both litters and lambs within-litter involved in the dam misspecification phenomena were re-sampled within each population.

For each population, birth weight records \( y_s \) were simulated from the following multivariate normal distribution:

\[
y_s \sim N(X_b b_s + Z_s p_s + Z_s a_s, I_s \sigma^2_{s,e})
\]

where \( b_s \) is the vector of simulated systematic effects, \( p_s \) is the vector of permanent environmental deviations characterised by the dam, \( a_s \) is the vector of additive genetic effects, \( X_s \), \( Z_s1 \) and \( Z_s2 \) are incidence matrices with appropriate dimensions, \( I_s \) is an identity matrix with dimensions equal to the number of phenotypic records, and \( \sigma^2_{s,e} \) is the residual variance. Note that \( b_s \) stored four systematic effects in our population, they being (a) the sex of the lamb (male or female), (b) birth type (single, twins, triplets or quadruplets), (c) age of the ewe (1, 2, 3, 4, 5 and more than 5 yrs), and (d) year of lambing (from 1986 to 2007). Values in vector \( b_s \) (Table 1) were preliminarily estimated in the Ripollesa data set by analysing the model outlined above (except for term \( Z_s2Z_s3 \) by the mixed model procedure of SAS v.9.1 (SAS Institute, Inc., Cary, NC) (Table 1). Permanent effects were generated from the following multivariate normal distribution:

\[
p_s \sim N(0, I_s \sigma^2_{s,p})
\]

\( I_s \) being an identity matrix with appropriate dimensions, and \( \sigma^2_{s,p} \) being the permanent environmental variance. Additive genetic effects for founder individuals were generated from \( N(0, \sigma^2_{s,a}) \), where \( \sigma^2_{s,a} \) was the additive genetic variance, whereas additive genetic effects for non-founder individuals were obtained by averaging their parents’ breeding values, and plus a Mendelian sampling term drawn from \( N(0, 0.5(1-f)\sigma^2_{s,a}) \). Note that \( f \) was the average inbreeding coefficient of the sire and dam. Variance components previously reported by Casellas et al. (2009) on the same data set were assumed during the simulation process (Table 1).

Each simulated data set was analysed under the Bayesian linear mixed model developed above. Boundaries of flat priors for \( b \) (−1000 to 1000) and variance components (0 to 1000) were assumed large enough to cover a very wide parametric space. A total of 25,000 Markov chain Monte Carlo (MCMC) cycles were run for the analysis of each simulated population, after a burn-in period of 1,000 cycles. The length of the burn-in period was large enough to ensure convergence. This was checked during preliminary analyses by visual inspection and by the method of Raftery and Lewis (1992) on \( \sigma^2_p \) and \( \delta_r \).

The probability of assignment to the correct dam (PACD) was calculated for each lamb at the end of the MCMC process. Focusing on the \( i \)th lamb, this parameter was defined as \( PACD_i = l_{cd}/l_T \), where \( l_{cd} \) was the number of MCMC iterations choosing the correct dam, and \( l_T \) was the total number of MCMC iterations (i.e. 25,000). Departures from the expected 0.5 PACD under blind assignment to the two candidate dams were evaluated by the CHISQ option implemented in the PROC FREC procedure of SAS v.9.1 (SAS Institute, Inc.). Statistical performance was also evaluated in terms of sensitivity, this parameter being defined as the proportion of dam assignments correctly identified as such. Note that PACD restricts to a given simulation and analysis, whereas sensitivity accounts for the proportion of true positives within a simulation scenario.

| Sex of the lamb | Values |
|-----------------|--------|
| Male            | 2.70   |
| Female          | 2.47   |

| Birth type      | Values |
|-----------------|--------|
| Single          | 1.26   |
| Twins           | 0.52   |
| Triplets        | 0.00   |

| Age of the ewe, yr | Values |
|--------------------|--------|
| 1                  | 0.40   |
| 2                  | 0.48   |
| 3                  | 0.16   |
| 4                  | 0.06   |
| 5                  | −0.03  |
| >5                 | 0.00   |

| Variance components | Values |
|---------------------|--------|
| Additive genetic variance | 0.09   |
| Permanent environmental variance | 0.12   |
| Residual variance    | 0.29   |

**Table 1.** Assumed values for systematic effects (excluding year of lambing) and variance components for the simulation of birth weight data of Ripollesa lambs.
Results

Statistical performance of the methodology outlined above for inferring unknown maternities in lambs has been evaluated by simulation. On average, PACD reached 59.5%, this value being significantly ($p < .01$) greater than the expected 50% under random guessing when only two candidate ewes are involved; a remarkable degree of heterogeneity was observed across simulations scenarios. Indeed, within-scenario average PACD values fluctuated between 52.5% (scenario ST3; $p > .1$) and 69.2% (scenario ST1; $p < .05$), and evidenced non-significant ($p > .1$) departures from random guessing in scenarios ST 3, ST2 and TT4. It is important to highlight that raw PACD estimates obtained from each analysis showed a wider range, they moving from 4.00% to 100% (Table 2).

In order to characterise the relevance of this analytical approach for the sheep industry, sensitivity estimates (i.e. proportion of dam assignments correctly identified as such) from scenarios SS2 and ST1 are shown in Figures 1 and 2, respectively. Sensitivity increased with the probability of dam assignment, although trends showed very different patterns when comparing across simulation scenarios. Two main sensitivity cut-points were assumed, 99% and 80%. The first cut-point required a high PACD, this fluctuating between 67.7% (scenario TT3) and 96.6% (scenario ST1; Table 3). Focusing on a less stringent criterion with a sensitivity of 80%, minimum PACD values drastically reduced up to values of $\sim$50% in some cases (scenarios ST1, ST2S and TT3; Table 3), although they maintained high in other scenarios such as the ST3S (93.7%; Table 3).

Table 2. Probability of assignment to the right dam in the different scenarios (Two lambs from single births with unassigned dams (abandoned; SS2); one single birth and one twin birth with one (ST1) two (ST2) and three (ST3) unassigned lambs; and two twins birth with two (TT2), three (TT3) and four (TT4) four lambs with unassigned dam).

| Scenario | Mean   | SE    | Minimum | Maximum |
|----------|--------|-------|---------|---------|
| SS2      | 0.575ns| 0.006 | 0.048   | 0.999   |
| ST1      | 0.692  | 0.007 | 0.040   | 0.995   |
| ST2      | 0.683* | 0.006 | 0.073   | 0.996   |
| ST3      | 0.525ns| 0.003 | 0.061   | 0.996   |
| TT2      | 0.559ns| 0.004 | 0.125   | 0.984   |
| TT3      | 0.608† | 0.004 | 0.333   | 1.000   |
| TT4      | 0.545ns| 0.003 | 0.232   | 0.954   |
| Overall  | 0.595***| 0.001 | 0.040   | 1.000   |

Means significantly different from 50% with:
* $p < .01$,
* $p < .05$,
† $p < .1$; and not different from 50% with: ns $p > .05$.

Figure 1. Number of right (black columns) and wrong (white columns) dam assignments (left y axis), and their subsequent sensitivity (right y axis), for single-birth abandoned lambs with one single-birth candidate dam and without additional abandoned lambs (scenario SS2). Note that lambs were classified depending on the ewe with highest probability of dam assignment (x axis).

Table 3. Minimum values of assignment probabilities to reach a sensitivity of 99% and 80%, and percentage of assignments agreeing with an 80% sensitivity or larger (Proportion80) under different scenarios (two lambs from single births with unassigned dams (abandoned; SS2); one single birth and one twin birth with one (ST1) two (ST2) and three (ST3) unassigned lambs; and two twins birth with two (TT2), three (TT3) and four (TT4) four lambs with unassigned dam).

| Scenario | 99% sensitivity | 80% sensitivity | Proportion80 (%) |
|----------|-----------------|-----------------|-------------------|
| SS2      | 0.952           | 0.660           | 34.8              |
| ST1      | 0.999           | 0.509           | 100.0             |
| ST1S     | 0.895           | 0.503           | 100.0             |
| ST1T     | 0.966           | 0.692           | 59.7              |
| ST2S     | 0.941           | 0.937           | 16.9              |
| ST2T     | 0.944           | 0.894           | 2.0               |
| TT2      | 0.881           | 0.627           | 33.9              |
| TT3S     | 0.677           | 0.510           | 100.0             |
| TT3T     | 0.780           | 0.536           | 49.9              |

*There are no $p$-values linked to these results.
Discussion

Parental uncertainty and abandoned lambs are troublesome phenomena for modern sheep industry, with low-to-moderate percentages of abandoned lambs in commercial flocks (Stevens et al. 1982; Alexander et al. 1983; Knight et al. 1989). As the lack of sire and dam identification can be linked to two different main causes (i.e. multiple matings and abandoned lambs, respectively), they both rely on missing pedigree data (Sapp et al. 2007), with harmful consequences on genetic evaluation methods (Casellas & Piedrafita 2015) and breeding programmes (Van Vleck 1970a,b; Banos et al. 2001). Several analytical approaches were developed to account for sire uncertainty (Cardoso & Tempelman 2003; Sapp et al. 2007) although there is a shortage of specific and low-cost methodologies to infer missing dams from available phenotypic and pedigree data. This second kind of pedigree data loss (i.e. abandoned lambs) can only be confirmed by genotyping paternity tests, although this solution is too expensive for most sheep breeders, and can only be applied to a few individuals per year. Alternative low-cost approaches such as the naive modelling of missing pedigree data (i.e. genetic groups; Westell et al. 1988) must be considered as an incomplete solution of the problem, whereas discarding all the abandoned lambs for breeding purposes would imply the removal of potential selection candidates. The mixed linear model for dam assignment developed in this manuscript provides a useful solution, reducing the list of candidates to be genotyped. Under economic restrictions, genotyping efforts could be directed to those lambs assigned to elite ewes.

On the basis of the model developed by Sapp et al. (2007) for paternity identification using phenotypic and pedigree data, we developed a specific parametric approach for dam identification, using a mixed linear model which included additional sources of information (i.e. systematic and permanent environmental effects). It is important to note that Sapp et al.’s (2007) model relied on the additive genetic background transmitted from the sire to the offspring, whereas systematic and permanent environmental effects were not relevant for paternity identification. In our case, the dam must be viewed as a link involving not only half of its genetic background, but also other systematic (e.g. ewe age) and permanent environmental (e.g. maternal ability) sources of variation accounted for by the model. The statistical performance of our analytical approach was evaluated on simulated data sets mimicking the pedigree and the birth weight data set of the experimental Ripollesa flock kept in the Universitat Autònoma of Barcelona experimental farm. We observed a wide range of average PACD values (14–100%), they suggesting that this statistical tool could be really useful for the sheep industry under several scenarios, and less useful in others. Our average PACD values were larger than those reported by Cardoso and Tempelman (2003; 52%) and Sapp et al. (2007; 51–54%), despite these authors focussed on paternity identification under higher heritabilities. This may be due to the inclusion of alternative sources of information in our analytical approach, given that different candidate dams involved different additive genetic, permanent environmental, and systematic background. Although our analyses suggested higher PACD values, this performance cannot be uniquely attributed to the benefit of including additional sources of information during dam assignment (i.e. fixed and permanent environmental effects), but also to both the size and structure of the data set; note that each analysis focussed only on a couple troublesome litters, assuming that all remaining individuals were correctly assigned to their parents, and all information was available.

The proportion of lambs with correctly identified dams classified depending on the ewe with the highest probability of dam assignment, and its trend, was straightforwardly characterised by plotting sensitivity against the probability of dam assignment (see Figures 1 and 2 as example). The minimum PACD value for reaching a level of sensitivity of 99% ranged from 67.7% (scenario TT3) to 96.6% (scenario ST1; Table 3). A less stringent criterion (80% sensitivity) revealed lower boundaries of PACD, they ranging from ~50% (scenarios ST1, ST25 and TT3; Figure 2) up to 93.7% (scenario ST35; Table 3). It is important to highlight the remarkable performance of our analytical approach under scenarios ST1, ST25 and TT3; all tests reached sensitivities equal to or larger than 80%. The percentage of analyses matching this 80% sensitivity was close to 50% under scenarios ST2T and TT4, and to 34% for scenarios SS2 and TT2 (Table 3). In any case, results from those scenarios revealed a very appealing performance where more than one-third of the analyses reached high sensitivity and contributed useful information for future genotyping decisions. Unfortunately, scenarios ST35 and TT3T suffered the worse statistical performances and low sensitivity.

In this research, we focussed all simulations on a single comparison in order to clarify the contribution of the different factors involved in the test, i.e. number of abandoned lambs and litter size. Nevertheless, the model could easily be extended to compare all the abandoned newborn lambs at the same time,
like the model developed by Sapp et al. (2007) within
the context of beef cattle herds. Our simulations
showed that uncertain maternities could be appro-
priately modelled under a Bayesian approach by taking
advantage of systematic (e.g. age of the dam and type
of birth), permanent environmental (e.g. maternal abil-
ity of the sheep), and genetic (e.g. breeding value)
sources of information. This method may help stock-
breeders to prevent information loss and enhance the
accuracy of ascertaining maternity in livestock popula-
tions. Current development must not be viewed as a
statistical tool for the massive reconstruction of pedi-
grees (the percentage of unknown maternities in the
current extensive sheep industry is moderate to low),
but to pinpoint abandoned lambs. This approach pro-
vides a statistical tool for inferring unknown materni-
ties at a very low-cost, this being useful as a
preliminary step for identifying those replacement can-
didates to be confirmed by laboratory paternity tests;
moreover, these analyses must discard those lambs
with a low chance to be offspring of elite dams and,
as a consequence, with poor breeding values. Although any result must be corroborated by geneti-
com data, their potential parents, a prelimin-
ary screening for unknown maternities would discard
several candidates from selection, thus reducing
unnecessary genotyping costs and the consequent
economic wastage.

Conclusions
The implementation of appropriate mixed linear mod-
el models allowed inferring unknown maternities in sheep
when a reduced number of abandoned lambs were
involved. This must be viewed as a useful and cost-
effective approach for inferring lost information from
the phenotypic data, and providing relevant data to
the stockbreeders.

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