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Equivalent effective population size mating as a useful tool in the genetic management of the Ibicenco rabbit breed (Conill Pages d'Eivissa)

A.J. Martín de la Rosa, I. Cervantes, J.P. Gutiérrez

Department of Animal Production, Faculty of Veterinary, Complutense University of Madrid, Madrid, Spain

ABSTRACT: The Ibicenco rabbit (Conill Pages D'Eivissa) is a rare breed mainly located on Ibiza Island, in rural areas. Today breeders are looking for a sustainable use and alternative routes for profitability of the population to avoid its extinction. The breed presents some variety in coat colour (brown, black, orange, and grey), and breeders would like to maintain these characteristics. The objectives of this study were to develop a method to design matings in a population with unbalanced pedigree depth in a scenario of maintaining the variety of coat colours, and to analyze the genealogical information of the Ibicenco rabbit to ascertain the genetic structure of the population. Equivalent effective population size mating was developed as a useful parameter to design the mating in this particular scenario. Results obtained by the initial application showed that this population was properly managed for maintaining the maximum genetic variability. This mating method is recommended to manage the genetic variability of this small rabbit population in a scenario of partial permanent colour structure. For the pedigree analysis, a reference population formed by 143 animals available for reproduction was used. A demographic study, a probability gene origin analysis, computation of inbreeding and effective size, and an analysis of genetic structure were done. The generation interval was approximately one year (11.8 months). The average number of equivalent generations was 3.4. The effective numbers of founders and ancestors were 10 and 11, respectively, and the founder genome equivalent was 6. The average inbreeding was 10.8%, but the mean inbreeding seems to have stopped increasing as a consequence of deeper monitoring in the mating design. The realized effective size was 9.6 (via inbreeding) and 17.5 (via coancestry). Regarding the genetic structure, the orange and black groups are the most distant genetically while grey and blacks are closer.

Keywords: diversity; genetic structure; pedigree; small populations

INTRODUCTION

The need to prevent the disappearance of endangered breeds has been an objective of national and international scientific organisations and enthusiasts of native breeds (Ryder 1976).

The Ibicenco rabbit (Conill Pages D'Eivissa) is a regional breed of uncertain origin, inhabiting the Island of Ibiza, and is basically found in rural areas (Anguera 2005). Its main coat characteristic is the *Dutch* gene fixed: white collar, and head profile, muzzle and end of legs in white. The rest of the coat can be coloured black, grey, orange or reddish-brown, with nuances of intensity. Breeders today are looking for a sustainable use and alternative routes for profitability of the population to avoid its extinction. In this context, preservation could be achieved by making this rabbit's meat available for use. Despite the huge use of selected commercial rabbit breeds, local farmers have kept individuals of Ibicenco for personal consumption, arguing their excellent carcass quality and meat and trying to

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exploit the extra value of an ecological production linked to rural areas. Therefore, the breed has been recently boosted in order to recover its maximum genetic diversity to guarantee its future. Aided by its short generation interval, the registering, analysis and designing of mating strategies to prevent extinction have been very successful.

On the other hand, the preservation of maximum genetic diversity is one of the main objectives in small populations. There is a consensus that the best strategy to manage genetic diversity when the pedigree of the population is available is to optimize the contributions of parents by minimizing their global coancestry weighted by their contributions (Ballou and Lacy 1995; Caballero and Toro 2000; Fernandez et al. 2003). This strategy would be feasible if health conditions were under control and fresh or frozen semen was available in a cryobank. However, the use of these methods often ignores the possibility that the pedigree content can be strongly unbalanced among individuals thus giving advantage to those animals with lack of information, such as the case of the Ibicenco rabbit breed. Moreover, in the case of the breed under study, an optimal mating solution cannot be blindly accepted because of the need to maintain, as much as possible, a balance of the coat colours of the animals. A different tool seems to be needed for this particular population.

The objectives of this study were to develop a method to design the mating in a population with unbalanced pedigree depth in a scenario of maintaining the coat colour variety, and to analyze the genealogical information of the Ibicenco rabbit breed to ascertain the genetic structure of the population.

MATERIAL AND METHODS

The pedigree information of a small population of Ibicenco rabbit was analyzed. The herd book for this breed was founded in 2009 by the breeders' association and the information contained animals born between December 2009 and April 2014 and originated from two main farms. The figures presented in this study refer to a whole population of 277 animals. The population is structured as shown in Supplementary Table S1 (for the supplementary material see the electronic version).

It is important to observe that this population is roughly structured according to the base coat colours. The genes involved for the base coat colour of this rabbit breed are the *Agouti* (*A*), *Chinchilla* (*C*), and *Extension* (*E*) genes (Kerns et al. 2004; Fontanesi et al. 2006). We hypothesized that alleles *A* and *a* are present, thus the allele *A* (dominant) produces a pheomelanin banding into the black eumelanin (banding on hair shaft). The recessive allele determines only the production of eumelanin, the hair lacks the banding and has black colour. Regarding gene *C*, in this population we hypothesized the presence of phaeomelanic dilution, due to a recessive allele c^{ch}. In this way, the presence of a homozygote recessive in gene *C*, with the presence of *A* allele-banding on hair shaft, produces phaeomelanic dilution into white colour and gives the so called grey colour (chinchilla). Finally, in the *Extension* gene, the recessive allele in homozygosis (genotype *ee*) causes the disappearance of black eumelanin band making brown rabbits appear orange (Table 4).

In order to study the actual Ibicenco rabbit population, a reference population of 143 animals born between 2013 and 2014 that were expected to reproduce was defined. Since there was an interest in keeping the different coat varieties, some parameters were computed separately for four different subpopulations according to the base coat colour: brown, grey, black, and orange (Supplementary Figure S1 – for the supplementary material see the electronic version).

Demographic parameters. The evolution of the registered population was assessed by counting the number of animals registered per year. This evolution does not necessarily mean an evolution in the population census, given that registration has only been recently opened and breeders are being encouraged to join the association.

Pedigree completeness, proportion of ancestors known per generation for each offspring, was computed (Gutierrez et al. 2003). And the number of equivalent generations (g_e) in the pedigree was assessed, too (Boichard et al. 1997).

The generation interval was calculated in the four different pathways: mother–daughter, mother–son, father–daughter, and father–son (James 1977).

Probability of gene origin. The genetic representation of the founder population was assessed using the following parameters: the effective number of founders f_e (Lacy 1989) computed from the genetic contribution of founders to the descendant gene pool of the population (James 1972), the effective

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number of ancestors f_a (Boichard et al. 1997), and the number of founder genome equivalents (f_g) (Ballou and Lacy 1995), computed as the inverse of twice the average coancestry of the individuals within the population (Caballero and Toro 2000).

Inbreeding and coancestry coefficients, and effective population sizes. Inbreeding coefficient (F) (Malecot 1948) and the coefficient of coancestry between two individuals (c) (Falconer and Mackay 1996) were computed.

Effective population size (N_e) was assessed via the realized effective population size given that it is currently considered one of the main methods of choice (Leroy et al. 2013) because it reflects all the events that occurred to the pedigree of each individual in the population, such as the generational overlapping, selection, and subdivision that may appear. This parameter, therefore, shows the possible consequences of the mating policy, possible bottlenecks, and founder population size. The realized effective population size was computed using the individual increase in inbreeding ΔF_i (Gutierrez et al. 2009). This is currently the method that performs best when computing N_e in permanent partially subdivided populations since it focuses on the final result in terms of inbreeding. However, if mixing becomes a usual practice, then another related approach would be the computation of realized effective population size using the increase in coancestry (Cervantes et al. 2011) between any pair of individuals.

By averaging the respective individual increases in inbreeding and in pairwise coancestry for all pairs of individuals in a reference subpopulation, the realized effective population size can be ascertained either based on inbreeding $\overline{N_e} = 1/(2\overline{\Delta F})$ or in coancestries $\overline{N_{ec}} = 1/(2\overline{\Delta C})$.

Genetic structure. The mean coancestry and inbreeding coefficient of the entire metapopulation and the mean coancestry of subpopulations were used to obtain Wright's (1978) F-statistics. F-statistics were computed following Caballero and Toro (2000, 2002).

Equivalent effective population size mating. This new concept is introduced here as an interesting tool in populations with unbalanced pedigree depth in the individuals to be mated. Under such scenario, coancestry coefficients depend on the pedigree knowledge so standardization would be indicated.

The increase in coancestry (Cervantes et al. 2011) between any pair of individuals j and k to be mated enables the standardization of the coancestry coefficients regarding pedigree depth. This coefficient can then be transformed to its equivalent effective population size mating (Ne_m), as a useful tool to interpret the diversity provided by a particular mating:

$$Ne_m = \frac{1}{2\Delta c_{jk}} = \frac{1}{2\left(1 - \frac{g_j+g_k}{2}\sqrt{1 - c_{jk}}\right)}$$

where:

c_{jk} = inbreeding of a descendent from j and k

g_j, g_k = equivalent complete generations for j and k

The equivalent effective population size mating (Ne_m) would be defined as the size of an idealized population in which the mean inbreeding would be equivalent to that obtained by this particular mating.

In the very particular scenario of this breed, with unbalanced pedigree depth, and with the permanent interest of the breeders in keeping the variability of layers, optimizing methodologies would not have been appropriate. On the other hand, simple methods available for breeders to minimize inbreeding (for example choosing individuals equally from all families) would not account for the inbreeding arising by certain matings. In fact, that approach would enforce the present unbalancing representation of founders (Gutierrez et al. 2003). With the methodology proposed here, matings would be designed in the way the effective population size of individual offspring would be maximized, and minimizing risks of inbreeding depression.

All the analyses were carried out using ENDOG v4.8 (Gutierrez and Goyache 2005).

RESULTS AND DISCUSSION

This is the first time that a genetic structure has been addressed from pedigrees in a small census rabbit breed, and this is also the first time that equivalent effective population size mating method was essayed. Initially a brief description of the demographic information provided by the herd book was carried out, analyzing its genetic foundation and discussing the current situation of the effective population size. Finally, the method that was being introduced was described as a useful mating strategy for this low census rabbit breed with unbalanced pedigree depth and under the desired condition of maintaining the four base coat colour variants associated with this breed.

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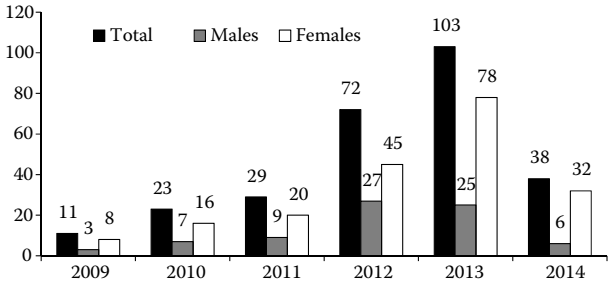

Figure 1. Evolution of males, females and total registration of animals in the herd book of Ibicenco rabbit breed

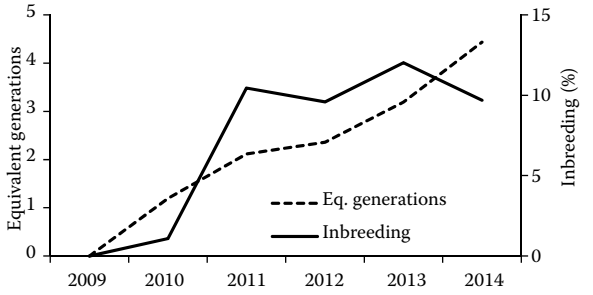

Figure 2. Evolution of mean inbreeding coefficients (%) and the equivalent complete generations across years

Demographic parameters. The evolution of animal registration is shown in Figure 1. It has to be taken into account that only three months of records were included in 2014. Supplementary Figure S2 (for the supplementary material see the electronic version) shows an evolution of the four coat colour subpopulations between 2009 and 2014. Today, the orange colour represents 34% of the population, brown represents 29%, grey 24%, and black colour represents 13%.

Concerning the pedigree depth for the reference population (animals born in 2013 and 2014) until the fifth generation back, the completeness level was 97% for the parent generations, 86% for the grandparents generation, 76% for the great-grandparents generation, and 49% for the great-great-grandparents generation. The unbalanced knowledge of the pedigree in the reference populations with animals appearing as founders and others with ancestral knowledge up to seven generations back is worth pointing out. This makes the mating management based on coancestry coefficients of little use because it would give a preference to animals with scarce pedigree.

Since the loss of genetic variability is accumulated by generation, genetic parameters that measure it must always be referred to the amount of existing genealogical information (Boichard et al. 1997; Gutierrez et al. 2003). The pedigree depth is important because it plays a significant part for the rest of the parameters that require genealogical data for their calculation, since the deeper the pedigree is, the more reliable will be the results. In the Ibicenco rabbit breed, the mean number of equivalent generations was 3.4 for the reference population. This value is enough but not great and the results should be interpreted with caution.

The generation intervals are shown in Supplementary Table S2 (for the supplementary material see the electronic version). This parameter was calculated for four different pathways parent–offspring. For the reference population, the generation interval was around one year (11.8 months). No significant differences seemed to exist between sexes both in parental and offspring generations. This short generation interval could also be reduced if needed, thus favouring the accumulation of genealogical information, taking into account that decreasing generation interval would also result in increasing inbreeding rate over time. Anyway, it is possible that with the entry of other farmers in the herd book, these values could be significantly altered, since the current results are based on data from two farms. Nevertheless, this generation interval is similar to that obtained in a commercial breed, the Pannon White rabbit in Hungary (1.2 years) (Nagy et al. 2010).

Table 1. Parameters related to probability of genes origin in the four base coat colours and in the whole reference population

Colours	Founders/effective number of founders	Ancestors/effective number of ancestors	Founder genome equivalents
Brown	21/9	19/10	5.3
Grey	19/7	17/7	4.0
Black	15/6	14/4	3.0
Orange	19/10	16/8	4.6
Whole	26/10	25/11	5.8

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Probability of gene origin. The analyses regarding probability of gene origin are of great concern when analyzing small census populations since all the genetic stock, excepting migration and mutation, comes from the founder animals. The management of this initial stock is key for the future of the population. Table 1 includes the founders, ancestors, effective number of founders and ancestors, the founder genome equivalents within these subpopulations and for the total population. In the Ibicenco rabbit breed the total number of founders for the reference population was 26 animals, thus a clear evidence that the herd book needs to include breeders who are not yet registered. This is particularly disturbing given that breeders want to keep the four different base coat colour subpopulations. On the other hand, the imbalance in the representation of this set of founders leads to an effective number of founders of 10. The reduction of the initial genetic stock attributed to bottlenecks was absent given that the number of ancestors was only 25. In addition, the effective number of ancestors was 11, showing that the new mating strategy avoided the bottlenecks in this shallow pedigree unlike one year before when the effective number of founders and ancestors had the same value of 9. When compared to the results one year before (Martin de la Rosa et al. 2013), rebalancing the representation was, however, possible by mating preferably those less represented animals (Goyache et al. 2003; Gutierrez et al. 2003). The unbalanced representation of these ancestors caused the initial genetic diversity to be reduced to 38% (f_e/f) or to 44% (f_a/a). The good news was that, within this low genetic variability frame, the preferable use of some ancestors was not really important. Thus, the minimum number of ancestors explaining 50% of the genetic diversity was 4.

These values of effective number of founders and ancestors are very low if we compare them with values attained with other commercial breeds such as the Pannon White in Hungary (Nagy et al. 2010), with 52 and 26 for f_e and f_a, respectively. But these comparisons should be made with caution because of the differences in the census and information about pedigree content.

On the other hand, even when matings are optimally designed to maintain genetic variability, there is an unavoidable genetic loss by genetic drift. Founder genome equivalents provide the information of the equivalent number of independent founders that are represented in the reference population. This parameter decreased to almost 6, but it was higher than 5 one year before (Martin de la Rosa et al. 2013). Even though this number is very low, a bigger population such as the Pannon White rabbit, had a value of 7 for this parameter (Nagy et al. 2010), but with a much deeper pedigree depth of about 11 equivalent generations. The genetic diversity that remained from the foundation was 60% (f_g/f_e), and the reasons, other than unbalancing of founders or ancestors, were additional random losses of genes during the segregations, and also others besides bottlenecks such as drift.

An additional concern of the present small rabbit population is the need to keep animals with different base coat colours because this low genetic variability is still considered lower within base coat colours. Colour varieties are demanded and skins could be an additional income for breeders. The highest value was found for brown colour followed by black and grey colour. These figures could explain why the total gene loss had been higher for the grey and black colour, as a consequence of the particular determination of the colour genes, some of them only appearing under homozigosity, thus enforcing animals to mate within coat colour if no segregation is desired. Note that the global parameters are much lower than the sum of these parameters across coat colours and very slightly higher than the maximum given that the four subpopulations share many ancestors. Special attention was paid, therefore, when designing mating strategies of these two particular colour variants as explained later.

Inbreeding and effective population size. Mean inbreeding coefficient for the reference population was 10.8%. This value is higher than the 6.4% found in Pannon White rabbit (Nagy et al. 2010). The evolution of mean inbreeding coefficients jointly with those of the equivalent generations across years is shown in Figure 2. While pedigree knowledge has considerably augmented from 2009, the mean inbreeding seems to have stopped increasing in 2011 as a consequence of new measures in the mating design.

Given that increase in inbreeding is a logical consequence of knowing more ancestral generations, the usual parameter used to study inbreeding is the effective population size (N_e). Thus, effective population size has become one of the most important issues in population genetics, given its usefulness

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as a measure of the long-term performance of the population regarding both diversity and inbreeding and, therefore, to characterize the risk status of livestock breeds (FAO 1998; Duchev et al. 2006).

At present, one of the methods of choice to compute N_e is $\overline{N_e}$, i.e. the realized effective population size (Leroy et al. 2013). The estimates of N_e based on the individual increase in inbreeding would accurately reflect the genetic history of the populations, namely the size of their founder population, their mating policy or bottlenecks due to abusive use of reproductive individuals for the period in which the genealogies are known (under these conditions 5 generations). All these phenomena influence the pedigree of the individual and are therefore reflected in the individual increase in inbreeding (Cervantes et al. 2008; Gutierrez et al. 2008, 2009). Furthermore, the use of the individual increase in inbreeding has shown that a pedigree with at least 2 generations can be enough to achieve reliable results (Gutierrez et al. 2009).

On the other hand, another effective population size based on the increase in coancestry complements the information given by the realized effective population size to provide information on the effective population size of a population under random mating. Furthermore, it has been shown that the comparison between this $\overline{N_{ec}}$ parameter and that from the individual increase in inbreeding gives information on the degree of population structure (Cervantes et al. 2011). The realized effective population size computed via the individual increase in inbreeding for the reference population of the Ibicenco rabbit breed resulted in 9.6, and the effective population size obtained via the individual increase in coancestry was clearly superior, 17.5. The former ($\overline{N_e}$) refers to the effective population size assuming that the partial genetic structure of the population conditioning the mating design will be kept in the future, while the latter ($\overline{N_{ec}}$) assumes that random mating will occur in the near future. Given that the difference between both effective population sizes is narrow, it shows how the different colours are actually fairly mixed. In fact taking into account the almost geographical isolation of the two farms involved with very little genetic material interchanged by artificial insemination, the ratio of both effective population sizes ($\overline{N_{ec}}/\overline{N_e}$) gave a result of 1.81 equivalent subpopulations, which only indicates a certain trend to practice inbred mating, focused on maintaining the four different colours of the breed. However, the subdivision index produced as a result of this practice is not too high today.

For the Ibicenco rabbit, we started with an extremely reduced number of founders that were geographically isolated, and together with the low census lead us to think that the trend of the population size was going to decline, if no action was taken to prevent the increase of inbreeding. When we carried out a brief review of N_e in other populations, this parameter indicated that the Ibicenco rabbit breed is currently under the danger of extinction. Both effective sizes gave values far below 50–100 which is the recommended value for this parameter to maintain a viable population in the long-term (Meuwissen 2009). For example, the realized N_e via the increase in inbreeding was 78 in Pannon White rabbit (Nagy et al. 2010). On the other hand, other populations not considered in danger of extinction maintained the N_e values around 50 (Cervantes et al. 2008). As a consequence, these threshold values of 50–100 have been criticized and should be revised (Leroy et al. 2013).

When effective population size was compared with the effective number of founders (10), with the effective number of ancestors (11), and with the founder genome equivalents (6), N_e values became higher, showing that the population is being properly managed from the point of view of maintaining the maximum genetic variability.

Table 2. Wright's *F*-statistics (F_{IS}–F_{ST}) and mean coancestry (f_{ij}), within (diagonal) and between subpopulations (off diagonals), defined by the base coat colour for the reference population

F_{IS}–F_{ST}	Grey	Brown	Black	Orange	f_{ij}	Grey (%)	Brown (%)	Black (%)	Orange (%)
Grey	–0.0462	0.0372	0.0219	0.0523	Grey	17	6	11	3
Brown	0.0372	–0.0304	0.0353	0.0236	Brown	6	9	4	4
Black	0.0219	0.0353	–0.0404	0.0376	Black	11	4	13	4
Orange	0.0523	0.0236	0.0376	–0.0168	Orange	3	4	4	11
Mean	0.0163	0.0164	0.0136	0.0242	Mean	9	6	8	5

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Genetic structure. The particular structure of the Ibicenco rabbit breed makes a deeper analysis worthwhile given the difficulties in managing the reduction of variability under these conditions. In Table 2, Wright's *F*-statistics (F_{IS} for each colour group and all F_{ST} coefficients between colour groups) and mean coancestry (Caballero and Toro 2002) within and between colour groups are given. Both parameters, *F*-statistics and mean coancestry, show that orange and grey groups are the most distant genetically while grey and blacks are closer. Also, in accordance with the results from inbreeding and probabilities of gene origin, the grey group is the most inbred.

The F_{IS} negative values indicate the existence of more coancestry than inbreeding within all the subpopulations, which, in theory, would reflect mating between rabbits within the same colour is being designed to avoid close relatives. However, this circumstance has to be interpreted with caution when Wright's *F*-statistics are addressed from coancestries given that in the within mean coancetry, self coancestries (½ + ½* inbreeding) have a high weighting.

Mating strategy. The danger of this small rabbit breed becoming extinct has been demonstrated in the present study. It is also well documented that the best strategy for managed breeding programs to retain gene diversity and limit inbreeding is to select breeding pairs that minimize a population's average kinship (Ivy and Lacy 2012). However, given that measured coancestry strongly depends on the pedigree depth, this might not be the best solution when animals have unbalanced pedigree knowledge. Under this scenario, the genetic contributions of the animals involved are also dependent on the pedigree depth. And finally, the intention of the breeders to keep the colour structure of the population in the case of the Ibicenco rabbit breed adds complexity to the mating management. In fact, if only coancestries were taken into account when designing matings, the population would evolve towards the disappearance of the different coat colours other than brown. And if coancestries are not managed with caution, minor animals with minor colours, such as black and grey, would increase their inbreeding to dangerous levels.

In the present study the use of a new tool helping designing the matings is proposed. In the left core of Table 3, a real scenario is shown with the coancestry coefficients between two males and three females represented as an example. In the right core of the same table, those coancestry coefficients were standardized and transformed to their equivalent effective population sizes mating (N_{em}). It should be noted here that without this transformation, for example, F1 and F2 females could be mated either to M1 and M2 females, given that the coancestry coefficients between them are equivalent. Also F3 can be either mated to M1 or M2 for the same reasons. However, differences in the pedigree depth of all the cited individuals show that for all the cases matings involving M2 would be preferable. The method is developed enough for the case of the Ibicenco rabbit breed with consideration for coat colour which requires special attention in mating. However, this method could be studied for applications in matings minimizing global increase in coancestry instead of those minimizing absolute coancestry coefficients (Toro et al. 1988; Fernandez et al. 2003). Note also that, even when N_{em} is the most useful information in the case of this rabbit breed, it would not be advisable to optimize by maximizing this parameter because very low increases in coancestry would be transformed into too high equivalent effective population sizes. Instead, as mentioned before, optimization would be indicated by minimizing the global increase in coancestry.

In the case of the Ibicenco rabbit breed, as noted in Table 3, other information regarding animals to be mated have to be accounted for as well. In this

Table 3. Coancestry coefficients (*c*) between males and females of an example scenario (left core), average relatedness coefficient (AR) for each reproductive individual, and individual effective population size (N_{em}) for a hypothetic descendant (right core)

c		♂	Grey		*Ne*$_m$		♂	Grey	
♀		AR	M1 20%	M2 21%	♀		AR	M1 20%	M2 21%
Black	F1	14%	9%	9%	Black	F1	14%	9.8	12.6
Black	F2	19%	13%	13%	Black	F2	19%	10.5	12.7
Brown	F3	19%	10%	10%	Brown	F3	19%	13.7	16.0

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Table 4. Segregation hypothesis of coat colour inheritance in Ibicenco rabbit breed.

Alleles	*ACE*	*ACe*	*Ac^{ch}E*	*Ac^{ch}e*	*aCE*	*aCe*	*ac^{ch}E*	*ac^{ch}e*
ACE	*AACCEE*	*AACCEe*	*AACc^{ch}EE*	*AACc^{ch}Ee*	*AaCCEE*	*AaCCEe*	*AaCc^{ch}EE*	*AaCc^{ch}Ee*
ACe	*AACCEe*	*AACCee*	*AACc^{ch}Ee*	*AACc^{ch}ee*	*AaCCEe*	*AaCCee*	*AaCc^{ch}Ee*	*AaCc^{ch}ee*
Ac^{ch}E	*AACc^{ch}EE*	*AACc^{ch}Ee*	*AAc^{ch}c^{ch}EE*	*AAc^{ch}c^{ch}Ee*	*AaCc^{ch}EE*	*AaCc^{ch}Ee*	*Aac^{ch}c^{ch}EE*	*Aac^{ch}c^{ch}Ee*
Ac^{ch}e	*AACc^{ch}Ee*	*AACc^{ch}ee*	*AAc^{ch}c^{ch}Ee*	*AAc^{ch}c^{ch}ee*	*AaCc^{ch}Ee*	*AaCc^{ch}ee*	*Aac^{ch}c^{ch}Ee*	*Aac^{ch}c^{ch}ee*
aCE	*AaCCEE*	*AaCCEe*	*AaCc^{ch}EE*	*AaCc^{ch}Ee*	*aaCCEE*	*aaCCEe*	*aaCc^{ch}EE*	*aaCc^{ch}Ee*
aCe	*AaCCEe*	*AaCCee*	*AaCc^{ch}Ee*	*AaCc^{ch}ee*	*aaCCEe*	*aaCCee*	*aaCc^{ch}Ee*	*aaCc^{ch}ee*
ac^{ch}E	*AaCc^{ch}EE*	*AaCc^{ch}Ee*	*Aac^{ch}c^{ch}EE*	*Aac^{ch}c^{ch}Ee*	*aaCc^{ch}EE*	*aaCc^{ch}Ee*	*aac^{ch}c^{ch}EE*	*aac^{ch}c^{ch}Ee*
ac^{ch}e	*AaCc^{ch}Ee*	*AaCc^{ch}ee*	*Aac^{ch}c^{ch}Ee*	*Aac^{ch}c^{ch}ee*	*aaCc^{ch}Ee*	*aaCc^{ch}ee*	*aac^{ch}c^{ch}Ee*	*aac^{ch}c^{ch}ee*
	Chinchilla		Agouti		Orange		Black	

case, representation of each animal in the pedigree of the breed is included through the average relatedness coefficient, defined as the probability that an allele randomly chosen from the whole population in the pedigree belongs to the animal (Goyache et al. 2003; Gutierrez et al. 2003). Also the coat colour or probable genotypes for the genes involved with them can be added to the table to decide the definitive mating. Monitoring this way, all matings are recommended to manage the genetic variability of this small population in a scenario of partial permanent colour structure. In fact this has been applied in the last 18 months leading to some improved parameters such for example $\overline{N_{ec}}$ from 11.8 to 17.5 or f_a from 9 to 11 (Martin de la Rosa et al. 2013).

CONCLUSION

The genetic structure of the Ibicenco rabbit breed was addressed here from the pedigree information perspective, and a new mating strategy was developed *ad hoc*. This methodology has been demonstrated as potentially very useful for other populations. However, much more research is required. Strategies to put into action may be related with the promotion of the valorisation of Ibicenco rabbit meat, through the adoption of quality labels and studies of some quality characteristics of the meat of this breed. Besides, by keeping the colour variety it will bring additional income for breeders.

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Corresponding Author

Prof. Isabel Cervantes, Ph.D., Complutense University of Madrid, Faculty of Veterinary, Department of Animal Production, Avenida Puerta de Hierro s/n, E-28040 Madrid, Spain
Phone: +34 913 943 773, e-mail: icervantes@vet.ucm.es

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Equivalent effective population size mating as a useful tool in the genetic management of the Ibicenco rabbit breed (Conill Pages d'Eivissa)

A.J. Martín de la Rosa, I. Cervantes, J.P. Gutiérrez

Department of Animal Production, Faculty of Veterinary, Complutense University of Madrid, Madrid, Spain

Supplementary Online Material (SOM)

Table S1. Distribution of the number of dead and live animals, males and females, and by colours, in the database of the herd book of the breed

	Dead/Alive **Total**		
	males	females	total
Brown	20/9 29	43/35 78	**63/44** **107**
Black	13/4 17	21/27 48	**34/31** **65**
Grey	13/8 21	23/28 51	**36/36** **72**
Orange	1/10 11	3/19 22	**4/29** **33**
Total	47/31 78	90/109 199	137/140 277

Table S2. Generation intervals (in years), standard deviations (SD), and mean standard errors (SE) for the four pathways parent–offspring. *n* is the number of computations in the four different pathways

Type	*n*	Interval ± SE	SD
Father–son	8	1.26 ± 0.254	0.720
Father–daughter	14	0.896 ± 0.250	0.708
Mother–son	8	1.049 ± 0.223	0.631
Mother–daughter	14	0.996 ± 0.236	0.669
Average	44	0.979 ± 0.100	0.663

Figure S1. Four different base coat colours in Ibicenco rabbit: brown, grey, orange, and black

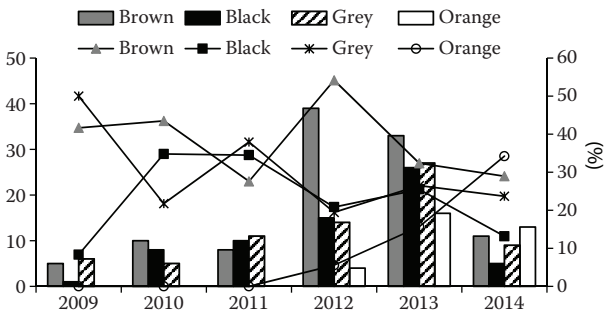

Figure S2. Evolution of coat colour subpopulation across the years in total numbers (bars) and in percentage (lines) per year (M = brown, N = black, G = grey, O = orange)