Genetic determination of selected reproduction traits in raccoon dog (*Nyctereutes procyonoides*)*

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The study aimed at analysing the reproduction merit, including its genetic variation, in raccoon dog. Input data covered records on 837 brood females maintained on a single farm over the years 1997-1999. Animals were divided into three groups according to whether they delivered and raised a litter (group 1), delivered and destroyed a litter (group 2) or failed to deliver a litter (group 3). Variance components for the probabilities of assigning an animal to particular group were estimated with the REML/animal model approach. The statistical model accounted for fixed effects of years of birth and delivery of the female, her litter-of-origin size, parity, regression on age at delivery within parity, and random effects of female's permanent environment and additive genetics. Over the years 1997-1999 as much as 72.8% of the females were assigned to group 1, 16.0% to group 2, and 11.2% to group 3. Heritability coefficients of particular probabilities were 0.37, 0.32, 0.08 and repeatabilities 0.54, 0.45, 0.13 for delivering, destroying, and failing to have a litter, respectively. Moderate heritabilities and repeatabilities of the traits studied indicate that effective improvement of the reproduction merit in the analysed raccoon dog population is feasible.

KEY WORDS: genetic parametres / inbreeding / raccoon dog / reproduction

Raccoon dog has only been bred in Poland for some thirty years, now. It has, therefore, been difficult to estimate the variance components of economically important traits as the population studies require adequate numbers of balanced data to end up with reliable estimates. On the other hand reliable estimates of the variance components are required upon defining the breeding objective, which usually combines several economically important traits. The reproduction complex has been found to be one of the most important factors affecting the economics of a breeding enterprise.

According to different authors, degree of inbreeding within a herd is one of the features, which can have fundamental impact on results of reproduction of the different species of animals. Wildt *et al.* [1982], Laikre and Ryman [1991], Laikre *et al.* [1993], Nordrum [1994], Laikre [1999], Holt *et al.* [2005] demonstrated a negative effect of inbreeding upon fecundity of different animal populations.

Fertility and fecundity are important elements of the reproductive ability of a species. While the ability to conceive and to deliver many offspring within a unit of time has generally been described in fur animals [Frafjord 1993; Wierzbicki 2004], the problem of maternal ability component has not been given proper attention [Axenovich, 2006]. Possibility of genetic recognition of superior females (BLUPs) can facilitate culling decisions in a herd. The purpose of the present study was to partition the phenotypic variance of chosen reproduction traits into its components in the raccoon dog as a contribution to the process of defining an overall breeding objective for this species.

Material and methods

Reproduction records were statistically processed of 837 females of raccoon dog (*Nystereutes procyonoides*) maintained in a single farm in the years of 1997-1999. Feeding and maintaining of animals followed the standard recommendations for the species. For statistical processing the females' records were divided into three groups according to whether they delivered and raised a litter (group 1), delivered but destroyed a litter (group 2), or failed to deliver a litter (group 3). Group 2 included also females which aborted their litters or the litters were stillborn.

Three genetic parametres, *i.e.* heritability (h^2), genetic correlation (r_G), and repeatability (r^2) coefficients were estimated with the VCE restricted maximum likelihood (REML) software [Groeneveld 1998]. The following statistical classification was employed:

$$y_{ijklm'n} = \mu + YB_i + YD_j + LO_k + P_l + a_{im} + p_{im'} + \beta_l(ww_{ijklm'n} - \overline{ww_l}) + e_{ijklm'n}$$

where:

$y_{ijklm'n}$ – vector of three traits for n^{th} observation on im'^{th} animal of age $ww_{ijklm'n}$ at l^{th} parity delivering in j^{th} year;

μ – vector of constants;

YB_i – vector of fixed effects for 3 traits for each of i=1,...,13 years of birth;

YD_j – vector of fixed effects for 3 traits for each of j=1,...,3 years of delivery;

LO_k – vector of fixed effects for 3 traits and k=1,...,15 sizes of mother's litter of origin;

P_l – vector of fixed effects for 3 traits for each of l=1,...,7 parities;

a_{im} – vector of random additive effects for 3 traits for each of 1069 animals in i^{th} year of birth;

$p_{im'}$ – vector of random permanent environment effects for 3 traits for each of 837 animals;

β_l – vector of three regression coefficients on age for each of l=1...7 parities;

$(ww_{ijklm'n} - \overline{ww_l})$ – deviation of m'^{th} animal's age at parity k from average age at that parity;

$e_{ijklm'n}$ – vector of random error terms.

Since the phenotypic expression of the traits studied was discrete the resulting heritabilities and repeatabilities were transformed to the continuous scale with the probit transformation [Żuk 1989].

Results and discussion

Table 1 gives numbers and percentage of females within the three reproduction groups considered during the analysed period. The proportion of dams successfully delivering and raising litters (group 1) exceeded 70% each year. However, the decrease was observed in its per cent value over successive years.

Table 1. Farm reproduction record during the investigated years

Year	Females						
	delivering litters		delivering but destroying litters		not delivering litters		year total
	number	%	number	%	number	%	number
1997	445	74.92	87	14.65	62	10.44	594
1998	432	72.61	102	17.14	61	10.25	595
1999	288	70.07	67	16.30	56	13.63	411
Class total	1165	72.81	256	16.00	179	11.19	1600

The genetic parametres of the examined reproduction traits are shown in Table 2. Heritability coefficient (h^2) of the no-trouble deliveries and of destroying a litter were moderately high (0.37 and 0.32). On the other hand heritability of failing to deliver was low (0.08). The magnitudes of repeatability were about one and a half times higher.

Table 2. Heritabilities (diagonal), genetic correlations (above diagonal) and repeatability (r^2) of probabilities of studied reproduction events (*standard errors*)

Trait	Delivery and raising litters	Delivery but destroying litters	Failing to deliver litters	r^2
Delivery and raising	0.37 (*0.03*)	-0.98 (*0.07*)	-0.94 (*0.04*)	0.54 (*0.07*)
Destroying of litter	-0.71	0.32 (*0.04*)	0.81 (*0.07*)	0.45 (*0.07*)
Failing to deliver	-0.49	-0.26	0.08 (*0.03*)	0.13 (*0.05*)

Negative genetic correlations were found between the probability of successful delivery and both probability of destroying the litter (-0.98) and probability of failing to deliver (-0.94). The failure traits correlated with each other at 0.81.

There were only 0.5% of inbred animals (such, which coefficient of inbreeding was larger than zero) of all the animals in the pedigree. Magnitudes of the coefficient of inbreeding of these animals ranged from 0.0313 to 0.1250; however, mean value for the whole population only reached 0.0005 (figures not tabulated).

In the present study the proportion of females raising litters, appeared to be a little higher than that reported for the Polish conditions by Jeżewska *et al*. [1991] and Lorek and Gugołek [1993]. Still, relatively high proportion of females loosing or failing to have litters leaves some space for effective breeding work in the examined herd. The improvement of reproduction would even be easier as the failure traits appear highly genetically correlated.

It is difficult to refer to the results on reproduction traits variance components' estimates reported for the raccoon dogs, as there is a lack of available bibliography. Genetic background of functional traits in mink, was the subject of studies by Rozempolska-Rucińska [2004]. Heritability coefficients estimated by her were slightly higher than those estimated in the present study (h^2 ranged from 0.241 for probability of destroying a litter to 0.593 for probability of infertility). Yet, when compared to the estimates obtained in other species for litter size (h^2 from 0.08 to 0.31) described by a number of authors [Saarenmaa 1990, Jeżewska *et al*. 1996, Przysiecki *et al*. 2000, Peura *et al*. 2003; Wierzbicki 2004, Wierzbicki and Jagusiak 2006] seem to be a little higher. However, the results of the studies that have, so far, been carried out on raccoon dog [Ślaska 2002] demonstrate low heritability of litter size (h^2=0.068). Those results also show that reproduction traits in fur-bearing animals are generally of comparatively low heritability.

Axenovich *et al*. [2006] demonstrated that inheritance of litter size in the arctic fox population bred at the Pushkinsky Fur Farm (Russia) can be described within the framework of a major gene model. The model was based upon the results of complex segregation analysis and was also supported by the pattern of its familial segregation and by the comparison of observed and expected distributions of the trait in the population. The heritability of litter size estimated in the mentioned study appeared similar to the estimates obtained in farmed populations of the arctic fox in Poland [Wierzbicki 2004]. Apparently, such polymorphism is also present in other farmed populations of arctic fox.

Heritability of destroying a litter was found to be moderately high (Tab. 2), and that is why females originating from a litter, where mother destroyed part of pups in it, should not be further used for breeding. Getting rid of females destroying a litter, or born in a litter that was partially destroyed, ought to be routinely practiced to limit the failure traits in the farm.

The repeatability of destroying a litter was also relatively high. This is an optimistic phenomenon as optimizing the environmental conditions may appear a very effective way of improving the efficiency of reproduction. The more so, quite high heritability of successful delivery and raising (0.37) accompanied by high negative genetic correlations with the failure traits (-0.98 and -0.94) – Table 2 – add to the probability of improving the reproduction complex.

Low value of the coefficient of inbreeding of the studied raccoon dog herd results from the plan of mating. Thus, it can be assumed that the estimates of genetic parametres are not burdened with the possible inbreeding depression. Laikre and Ryman [1991] and Laikre [1999] presented results of genetic studies of Nordic *carnivora* populations bred in captivity. Inbreeding depression has been shown in the brown bear *(Ursus arctos),* wolf *(Canis lupus),* and lynx *(Lynx lynx)* populations held in Nordic Zoos. The characters negatively affected by inbreeding included litter size (brown bear and wolf) and female reproduction (wolf). Wildt *et al*. [1982] observed that litter size at birth, number of pups born alive, and litter size at weaning decreased with inbreeding rate in foxhound dog (*Canis familiaris*). In arctic fox (*Alopex lagopus*) female reproduction and litter size was reduced by 0.71 and 0.47 pups with each 10% increase of inbreeding [Nordrum 1994]. Holt *et al*. [2005] demonstrated in mice that inbreeding reduced the mean litter size by 0.72 pups per each 10% increase in inbreeding.

Judging upon the present results it can be concluded that the reproduction performance of the raccoon dogs can be successfully improved both genetically and environmentally. Nevertheless, combining production and reproduction traits within an overall breeding goal require further genetic and economic analyses. The raccoon dog herd considered in this report was virtually not inbred at all and the described outcome should not be ascribed to inbreeding.

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Genetyczne uwarunkowania wybranych cech rozrodu jenotów (*Nyctereutes procyonoides*)

S t r e s z c z e n i e

Celem badań była analiza wskaźników zdolności rozpłodowej samic jenotów, oraz określenie parametrów zmienności genetycznej wybranych cech ich rozrodu. Wykorzystano dane z lat 1997, 1998 i 1999 zawarte w dokumentacji hodowlanej pojedyńczej fermy jenotów i dotyczące 837 samic stada podstawowego. Zwierzęta podzielono na trzy grupy: samice, które rodziły i skutecznie odchowywały mioty (1), samice, które rodziły, ale zabijały urodzone mioty (2) i samice jałowe (3). Do oszacowania parametrów genetycznych cech rozpłodowych zastosowano metodę REML według wielocechowego modelu osobniczego. Udział samic rodzących i odchowujących mioty (grupa 1) wyniósł średnio za trzy badane lata 72.8% wszystkich samic. Samice rodzące, ale niszczące urodzone mioty (grupa 2) stanowiły w badanych latach średnio 16.00% wszystkich samic objętych obserwacjami. Udział samic jałowych (grupa 3) wyniósł 11.2%. Wskaźniki odziedziczalności urodzenia i odchowania młodych, urodzenia, ale zniszczenia młodych przez samice oraz jałowości samic wyniosły odpowiednio 0,37, 0,32 i 0,08, a wskaźniki powtarzalności tych cech odpowiednio 0,54, 0,45 i 0,13. Stosunkowo wysokie wskaźniki odziedziczalności i powtarzalności niszczenia miotów świadczą o możliwości prowadzenia efektywnej pracy hodowlanej w kierunku zmniejszenia liczby samic niszczących mioty.