

Early selection of leg conformation in Finnish blue fox (*Vulpes lagopus*)

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Summary

The main aim of this research was to investigate the early selection, genetic associations and suitability of two leg conformation traits, carpal hyperlaxity (LAXITY) and valgus deformity (VALGUS), for introduction into the breeding scheme. Results showed that LAXITY1 occurred at an early age (5-14 weeks) in 44% of blue fox puppies. LAXITY1 had moderate heritability (0.20 ± 0.06) and positive genetic correlation (0.40 ± 0.28) with LAXITY2, which was assessed at the end of growth. The frequency of VALGUS was quite low, 6 to 7%, in the data. Also, the heritability was low, close to zero in VALGUS1 and 0.11 ± 0.04 in VALGUS2. Genetic correlation between the two VALGUS traits was positive, even though the standard error was high (0.29 ± 0.68). Obtained genetic parameters indicated that early selection has potential to improve carpal hyperlaxity of blue foxes. However, ideal evaluation and selection time point of valgus deformity is at later growth phase. Selection against VALGUS and LAXITY is highly recommended in order to maintain blue fox's ability to move about. Animals with poor leg conformation should not be used for breeding. If more efficient selection is needed, the selection index and multiple-trait animal models can be applied in breeding for better leg conformation.

Key words: Alopex lagopus, blue fox, correlation, genetics, heritability, leg conformation

Introduction

Carpal deformities are a common problem among Finnish blue foxes (Kempe 2018). The condition involves excessive hyperflexion at the carpus, sometimes with valgus deformity. Flexural leg deformity may occur already at an early age (1.7-3 months), but is most common at the end of growth period on Oct/Nov (Korhonen et al. 2005, Kempe 2018). Recent WelFur results show no improvement in leg conformation (n=4688 on 81 farms), reporting a high frequency of mild or clear laxity of carpus in production animals: 56.5% and 30%, respectively (Ahola et al. 2014). Carpal laxity is moderately heritable trait in blue foxes (Kempe 2018). Other predisposing factors are fast growth rate, high body weight and fatness.

It seems that flexural leg deformity is not the only conformation problem in the Finnish blue fox population. Preliminary studies on orthopaedic abnormalities in blue foxes indicate that juvenile individuals may suffer from incipient and mild skeletal problems (Korhonen et al. 2005, Mustonen et al. 2017, Svenns 2018). The prevalence, severity and genetics of these problems have not been studied. According to Svenns (2018) abnormal conformation and rotation of a blue fox's legs (angular limb deformities, radius curvus) occur when the growth plates close prematurely and radius and ulna are not grown in a synchronized manner. Also nutritional imbalances, trauma or inflammatory process can damage cartilage cells, which are very sensitive to pressure changes, and cause early closure of growth plates (Knapp et al. 2016). This cause the radius to deform in the cranial-caudal plane (radius curvus), external rotation and ultimately to a valgus deformity of the carpus (Knapp et al. 2016).

The objectives of this research were to develop practical evaluation method for on-farm measurement of the carpal laxity and valgus deformity, to determine statistical models for the estimation of (co)variance components and genetic variation in the leg conformation traits, to understand the co-responses among the studied traits and to determine the suitability and feasibility of the new traits for the blue fox breeding programme.

Material and methods

The experiment was carried out on five commercial fur farms in Finland. Data were collected during growth period in 2018 from altogether 3290 blue foxes. The pedigree was obtained from Saga Furs Oyj. The pedigree structure in the data was monitored using RelaX2 (Strandén and Vuori, 2006). Original pedigree was pruned to have only informative animals (n=11 423) in variance component estimation.

The offspring of preselected dams were born between May 18 and June 26 in 2018. Blue foxes were classified into four classes by their time of birth: 104-129, 130-144, 145-160 or 161-180 days from the beginning of the year (Table 2). Litters of more than four pups were selected for the experiment. Pups from the same litter were divided into full-sib pairs as follows: male-male, male-female, or female-female pairs. Uneven animals (70) were housed alone/single in the cage. One percent of the animals were selected for breeding animals and rest were pelted as production animals. Breeding animals are subjected to a restricted feeding regime after weaning, because this improves fertility through longer-term control of BCS (fatness) and body weight (Kempe 2018). The foxes were evaluated twice; first at the time of weaning and for the second time at grading. There were 5 evaluators, who assessed always the same foxes. Age at the time of evaluation was classified into six classes (Table 2).

The studied traits are presented in Table 2. LAXITY, VALGUS, MOVE and BCS were evaluated 1st time on days July 28 to August 23 in 2018 and on days October 29 to November 19 in 2018. The thickness of subcutaneous fat was assessed by a subjective body condition scoring method (Kempe 2018) on a scale of 1 to 5, where 1=very thin and 5=extremely fat. LEG was evaluated on a scale of 1 to 5 (best) (Kempe 2018) and VALGUS on a three-point scale based on the poorer of the forelegs, where VALGUS scores were: 1=toes pointing straight ahead, 2 = toes slightly (0-45°) rotated outwards and 3=toes strongly (>45°) rotated outwards. Four point scoring system of MOVE, where score 4 was the best, was modified from the five point scoring system published by Kempe (2018) (Welfur 2014).

Statistical analysis

Preliminary analyses were performed using PROC GLM in the SAS Studio 5.1 software (SAS Institute Inc., Cary, NC, USA). (Co)variance components for the different traits were estimated using the restricted maximum likelihood (REML) method in the DMU program (Madsen and Jensen 2012). Both single- and multiple-trait analyses were carried out. The following linear animal model was used for variance component estimation:

$\mathbf{y} = \mathbf{Xb} + \mathbf{Wc} + \mathbf{Za} + \mathbf{e}$, where \mathbf{y} is a vector of observations, \mathbf{b} is a vector of fixed effects, \mathbf{c} , \mathbf{a} and \mathbf{e} are vectors of random litter, animal and residual effects, respectively. Matrices \mathbf{X} , \mathbf{W} ja \mathbf{Z} are the corresponding incidence matrices. In the single-trait analyses, the litter (\mathbf{c}), animal (\mathbf{a}) and residual (\mathbf{e}) effects were assumed to be independent, normally distributed random effects with mean zero and $\text{var}(\mathbf{c}) = \mathbf{I}_q \sigma_c^2$, $\text{var}(\mathbf{a}) = \mathbf{A} \sigma_a^2$ and $\text{var}(\mathbf{e}) = \mathbf{I}_n \sigma_e^2$, where \mathbf{I}_n is the identity matrix of size n , n is the number of animals with an observation, \mathbf{I}_q is the identity matrix of size q , q is the number of litter effects, \mathbf{A} is the additive genetic relationship matrix, σ_c^2 is the common litter environment variance, σ_a^2 is the additive genetic variance and σ_e^2 is the residual variance. Genetic correlations between traits were estimated with the multiple- trait animal model for all the analysed traits, three traits at a time. In the multiple-trait animal model, the litter, animal, and residual effects were assumed to be

independent, normally distributed random effects with zero mean and $\text{var}(\mathbf{c})=\mathbf{C} \otimes \mathbf{I}_q$, $\text{var}(\mathbf{a})=\mathbf{G} \otimes \mathbf{A}$ and $\text{var}(\mathbf{e})=\mathbf{R} \otimes \mathbf{I}_n$, where \otimes is the Kronecker product, \mathbf{C} is the variance-covariance matrix for litter effects among traits, \mathbf{G} is the genetic variance-covariance matrix among traits and \mathbf{R} is the variance-covariance matrix for residual effects among traits.

Table 1. Fixed effects in single and multiple trait analyses by trait.

	Farm	Sex	Assessor	Age at EVA	Time of birth	Pair type	Status
LAXITY1	x	x	x	x			
LAXITY2	x	x	x	x		x	x
MOVE1	x	x	x				
MOVE2	x	x	x		x		
VALGUS1	x	x	x	x	x	x	
VALGUS2	x	x	x	x	x	x	
BCS1	x	x		x	x		
BCS2	x	x		x	x	x	

1=evaluation at weaning, 2=evaluation at the end of growth period

EVA=evaluation, Status =breeding or production animal, LAXITY=carpal hyperlaxity, MOVE=ability to move, VALGUS=valgus deformity, BCS=body condition score.

Results and discussion

Carpal hyperlaxity is common, but valgus deformity quite rare (6-7% in the data) among the farmed Finnish blue fox population. In the first evaluation 56% of puppies had sufficient to very good LEG1 and most of them had no valgus deformity. Situation changed quite drastically during growth period. In the second evaluation, most of the blue foxes (97.4%) were evaluated as heavy or extremely fat, and 96.9% of them had carpal laxity. Despite the foxes' poor foreleg structure, MOVE1 and MOVE2 were estimated to be fairly good.

Table 2. Number of observations (n), mean, standard deviation (SD), minimum and maximum values followed by estimated phenotypic variance (σ_p^2), proportion of litter variance (c^2) and heritability (h^2) with standard errors (SE) for the studied traits.

	n	Mean	SD	Min	Max	σ_p^2	$c^2 \pm SE$	$h^2 \pm SE$
LAXITY1	3288	2.56	0.69	1	5	0.40	0.10 \pm 0.03	0.20 \pm 0.06
LAXITY2	3226	1.36	0.56	1	4	0.25	0.10 \pm 0.02	0.06 \pm 0.04
MOVE1	3276	3.99	0.08	2	4	0.01	0.00 \pm 0.02	0.03 \pm 0.02
MOVE2	3227	3.93	0.30	1	4	0.09	0.06 \pm 0.02	0.00 \pm 0.03
VALGUS1	3288	1.07	0.25	1	3	0.06	0.08 \pm 0.02	0.01 \pm 0.02
VALGUS2	3227	1.07	0.26	1	3	0.06	0.03 \pm 0.02	0.11 \pm 0.04
BCS1	3287	1.46	0.50	1	2	0.01	0.29 \pm 0.04	0.20 \pm 0.08
BCS2	3227	4.43	0.55	3	5	0.24	0.104 \pm 0.03	0.23 \pm 0.07

The genetic parameters estimated for LAXITY and VALGUS in this study indicate that genetic improvement through selection may allow to reduce leg weakness in the blue fox and improves the foxes' ability to move.

The heritability estimate of LAXITY at weaning was higher than at the end of growth period, which makes early selection of LAXITY more effective (Table 2). The two traits have favorable genetic correlation with each other, thus a good leg conformation at weaning seems to be linked to better leg conformation later in growth. (Table 3). In the case of carpal hyperlaxity, breeding evaluation and culling can be done already at weaning time.

The valgus posture of forelegs can either improve or worsen as growth progresses. Therefore, valgus deformity needs to be followed carefully during the growth period and assessed preferably twice: at weaning and at the end of growth. Results indicate that environmental factors are main cause behind VALGUS1 as the heritability was close to zero (Table 2). Yet, VALGUS2, which develops during the fast growth period, have genetic background. Although the heritability estimate is low, selection against VALGUS2 is possible.

Table 3. Estimated genetic correlations with their standard errors (upper triangle) and phenotypic correlations (lower triangle) between the studied traits in the Finnish blue fox^a.

	BCS1	BCS2	LAXITY1	LAXITY2	MOVE1	VALGUS1	VALGUS2
BCS1		0.33±.23	0.05±.24	0.27±.36	-0.06±.36	-0.81±.40	0.01±.28
BCS2	0.00		0.57±.19	-0.02±.31	0.66±.35	0.83±.47	-0.50±.22
LAXITY1	0.01	-0.02		0.42±.28	0.93±.30	-0.52±.64	-0.11±.23
LAXITY2	-0.02	-0.33	0.21		0.06±.52	0.00±.83	0.32±.36
MOVE1	0.00	0.01	0.06	0.01		0.04±.73	0.48±1.44
VALGUS1	0.01	0.04	-0.15	-0.02	-0.03		0.29±.68
VALGUS2	0.06	0.00	-0.02	-0.03	0.00	0.05	

^a Genetic correlations differing more than $1.96 \times \text{S.E.}$ from zero are in bold.

The genetic correlation between VALGUS1 and VALGUS2 didn't differ from zero meaning that they seem to have similar phenotypes, but their etiology and genetic background may be different (Table 3). Surprisingly, VALGUS was associated with lower BCS (slimmer) in both weaning and end-of-growth measurements. The reasons behind this negative correlation requires a more extensive set of data and further studies, e.g. the effect of body weight and growth rate on the development of valgus posture.

Lack of genetic variation in MOVE may be due to problems in phenotypic evaluation of the trait (Table 3). In the previous studies, blue fox's ability to move about was rated on a five-grade scale and the heritability was moderate (0.22) (Kempe 2018). If blue fox is selected for breeding, its ability to move should be good and tested properly, because they are kept longer in a cage. Walking test outside the cage, on the ground could be one option to test breeding animals.

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