Genetic trends in hunting behaviour in the Finnish Hound

Anna-Elisa Liinamo

Wageningen University, Animal Breeding and Genetics Group
P.O. Box 338, 6700 AH Wageningen, The Netherlands
anna-elisa.liinamo@wur.nl

Finnish Hound is the most popular dog breed in Finland, with 2 000 – 3 000 pups registered annually in the last years. The great majority of the Finnish Hounds are still used actively as working dogs, so the main breeding goal of the breed is to improve its behavioural abilities with respect to hunting traits. Hunting ability of individual dogs is judged in field trials, and selection of breeding animals is based mainly on dogs' own test results or those of their progeny. From 1996 onwards the breed club has also estimated BLUP breeding values for the most important hunting traits based on the field trial results.

This paper studied the genetic trends in the most important traits evaluated in the hare hunting trials of the Finnish Hounds in the past 30 years. The data included 92 164 trial records from 13 641 dogs collected between 1987 and 2003. The studied traits included measures related to search, pursuit, tongue and ghost trailing. The heritabilities of field trial scores of the Finnish Hounds were low, and environment had a large influence on the trial results. However, substantial positive genetic trends could nonetheless be observed in search, pursuit and tongue scores. The results show that it is possible to achieve genetic progress when selecting for behavioural traits in a general dog population, provided that enough information is available for accurate selection of best breeding animals and the breeding goal is consistent.

Introduction

The Finnish Hound is a solo hunting hound breed developed in Finland during the last 100 years. The major prey of the Finnish Hounds are Arctic hare (*Lepus timidus*) and European hare (*Lepus europaeus*), but some dogs specialise to hunt fox (*Vulpes vulpes*). The Finnish Hounds are highly specialised to the difficult hunting conditions in the northern coniferous forests of Finland, and many consider them to be possibly the best hound breed of its kind in the world.

The Finnish Hound (FH) population has several features that make it interesting for animal breeding studies. First, the FH is the most popular dog breed in Finland, with annual registrations ranging between 2 000 and 5 000 puppies in the past 20 years. However, more than 80% of the world population of the FH are registered within the Finnish Kennel Club, with the only sizeable FH populations outside Finland in the neighbouring countries Sweden and Norway. Third, the FH is today an almost unique dog breed in that virtually 100% of the dogs are still active working animals. Further, approximately 20% of the population participate annually in field trials, where the hunting capability of the dogs is evaluated with standardised measures.

Despite of being 'professional' dogs, the FH are still only a hobby to their owners. There is currently no central breeding programme for the FH, and the breeders are free to select their own breeding material and design the matings. However, Suomen Ajokoirajärjestö (SAJ), the Finnish breed organisation of the FH, provides much information to help making breeding decisions. SAJ has published since early 1980s annually all field trial, show and health disorder records for all dogs, as well as different progeny statistics for the most popular sires. In addition, breeding values have been estimated for the most important hunting traits in the FH population using Best Linear Unbiased Prediction method since 1996.

The breeding value estimation was instigated by SAJ in early 1990s with a study to estimate genetic parameters for the traits evaluated in the field trials of the FH (main results are summarised in Liinamo et al., 1997). Estimates of heritabilities were low for most of the 28 measures, but SAJ nonetheless thought it worthwhile to start estimating breeding values routinely for four main traits: search, pursuit, tongue, and ghost trailing. The EBVs are now published annually with the other statistical information on the dogs, but it is not known how widely they have been used to assist decision making by the FH breeders in addition to the older well-established information sources.

The object of this study was to estimate the genetic trends in the major hunting traits of the Finnish Hound in the past 30 years. More particularly, the aim was 1) to see if genetic progress has occurred in the population, and 2) to evaluate the usefulness of the different forms of information provided by the SAJ for the FH breeders over the years.

Materials and methods

Materials

The data consisted of field trial records for Finnish Hounds between the years 1987 and 2003 from all hare-hunting trials in Finland. Altogether 92 164 trial records were obtained by 13 641 dogs in this period. More than 20 different measures of various aspects of dogs' hunting performance were available from the trial data, but in this study only the four measures for which EBVs are currently estimated in the FH population were considered: search score, pursuit score, tongue score, and binomial ghost trailing score (for descriptions of the traits see Liinamo et al., 1997). Because all measures were not necessarily evaluated in every test situation, the actual numbers of observations varied between the measures (Table 1).

Table 1. Measures of hunting performance and their numbers of observations, means, standard deviations and minimum and maximum values.

Trait	# rec.	avg.	std.	min.	max.
Search	91 457	7.14	2.11	1	10
Pursuit	69 208	39.73	16.91	1	70
Tongue	85 719	6.48	1.00	1	10
Ghost tr.	92 164	1.17	0.37	1	2

Pedigree information used in the analyses was obtained from the register of FH maintained by the Finnish Kennel Club from 1960s onwards. There were 114 411 FH in the register by the end of year 2003, 21 465 of which had some connections with the field trial data set (= competing dogs or their relatives).

Methods

Variance and covariance components for the measures of hunting performance were estimated with multivariate analyses in VCE4.2.4 using Restricted Maximum Likelihood (REML) method (Groeneveld, 1997). Best Linear Unbiased Prediction (BLUP) breeding values were estimated for the animals with multivariate analysis in PEST (Groeneveld, 1994).

The following linear model was assumed in the analyses of the field trial records:

$$y_{ijklmn} = \mu + f + sex_i + age_j + snow_k + \text{area-year-month}_l + pe_m + animal_m + \varepsilon_{ijklmn}$$

where y_{ijklmn} = record for a measure of hunting performance; μ = overall mean; f = regression on inbreeding coefficient of the animal m (0 – 32%); sex_i = fixed effect of i^{th} sex (male or female); age_j = fixed effect of j^{th} age class (1 to ≥ 9 years); $snow_k$ = fixed effect of k^{th} snow class (bare ground or snow cover); area-year-month_l = fixed effect of l^{th} area-year-month subclass (5 geographical areas * 17 years * 3 two-month subclasses from September to February); $animal_m$ = random additive genetic effect of the m^{th} animal; pe_m = random permanent environmental effect associated with the m^{th} animal, and ε_{ijklmn} = random residual effect.

The genetic trends were studied by comparing the means of the predicted breeding values of the dogs born in different years. Dogs born between 1972 and 2001 were included in the comparison. The largest age class (dogs born in 1987) included 1004 dogs, and the smallest age class (dogs born in 2001) included 213 dogs.

Results and discussion

Genetic parameters

The estimates of genetic parameters of the studied traits were very similar to those estimated earlier from a smaller subset of the data used in this study (Table 2; Liinamo et al., 1997). All heritability and repeatability estimates were low, indicating that random environmental effects have a large effect on the scores evaluated at field trials. Trials are held under "wild" conditions that simulate real hunting situations as closely as possible, and although several environmental effects such as snow cover vs. bare ground are recorded at each trial, they are still subject to several unrecorded variations in for example weather, local geography, numbers of game animals in the trial areas etc.

The estimates of phenotypic and genetic correlations were likewise close to earlier estimates from the smaller data subset (Table 2; Liinamo et al., 1997). Correlations between all scores were positive and low to moderate. It is noteworthy that also the genetic correlation between pursuit score (which the most important positive trait) and ghost trailing score (which is the most important negative trait) was moderate and positive. This connection is probably strong enough to cause some problems when trying to lessen ghost trailing and at the same time improve pursuit scores.

Table 2. Heritabilities/repeatabilities (on diagonal), phenotypic correlations (above diagonal) and genetic correlations (below diagonal) of the studied measures.

	Search	*Pursuit*	*Tongue*	*Ghost*
Search	0.07/0.09	0.43	0.10	-0.05
Pursuit	0.60	0.11/0.20	0.21	0.13
Tongue	0.21	0.20	0.16/0.33	0.01
Ghost	0.06	0.44	0.05	0.15/0.29

Genetic trends

Despite the low heritability estimates, substantial genetic progress had occurred in the FH population in search and pursuit scores, and to lesser extent also in tongue score (Figures 1 to 3). However, in ghost trailing score no obvious genetic trend could be perceived (Figure 4).

The average genetic level of the FH population with respect of search score had increased 0.63 points from dogs born in 1972 to dogs born 30 years later (Figure 1). This increase is 1.2 times the genetic standard deviation of the trait (σ_a = 0.53 points). In pursuit score an even larger increase in the average genetic level of the FH population could be observed in the 30 years, with dogs born in 2001 having 6.89 points, or 1.3 times the genetic standard deviation (σ_a = 5.26 points), higher genetic level than dogs born in 1972 (Figure 2). The shapes of the genetic trends of search and pursuit scores were remarkably similar, most likely due to the relatively high positive genetic correlation between the two traits. This connection also probably explains why so much genetic progress could have been obtained in search score that is notoriously difficult to evaluate and has a very low heritability. Pursuit score is considered the most important measure of hunting ability, so obviously most selection pressure has been placed on it over the years.

Although tongue score shows most genetic variation and is the most reliably evaluated of the studied measures, the genetic progress in it from 1972 to 2001 was only 0.38 points, or less than one genetic standard deviation (σ_a = 0.40 points) (Figure 3). Obviously tongue score has only been considered of moderate interest in the breeding goal compared to other traits. It also has quite low genetic correlations with the other traits, so it has not received similar “lift” from selection on pursuit score as for example search score.

In contrast to the other studied traits, the changes in the average genetic level of the FH population with respect of ghost trailing seem more random over the 30-year period (Figure 4). In the first period, before 1982, some genetic progress was achieved in reducing ghost trailing tendency, but from 1982 onwards no clear genetic trend can be observed. The moderate positive genetic correlation between ghost trailing and pursuit score has probably been one reason behind the lack of success in reducing ghost trailing in the FH population, since pursuit score is the most important trait in the breeding goal of the FH. This conclusion is further supported by the slight genetic progress in ghost trailing before 1982, during which time no genetic progress and consequently no selection pressure was observed in the pursuit score (Figure 2). On the other hand, the FH population has no generally accepted breeding goal for ghost trailing, since part of the FH hunters actually like the dog to give some tongue during search although officially ghost trailing is regarded as a fault. Consequently, many FH breeders probably consider ghost trailing as an optimum trait, and therefore aim to keep it around an accepted mean value.

The beginning of the positive genetic trends in search, pursuit and tongue scores in this study coincides with the beginning of the annual publication of all field trial results by SAJ in 1982 (Figures 1 to 3). Further, some additional increase can be observed in the genetic trends of search and pursuit scores from 1996 onwards, when the annual estimation of EBVs for these measures was begun. Thus, it would seem that the information provided by SAJ during the past 20 years has been indeed utilised successfully by the FH breeders to make informed choices when selecting their breeding animals.

Discussion

Selection responses on behavioural traits of canines have mostly been studied in foxes before. The most famous long-term selection experiment on canine behaviour is no doubt in silver fox (*Vulpes vulpes*) for confidence towards humans, which was initiated in then Soviet Union in 1959 (Belyaev, 1979). In this selection experiment 40 years of strict selection on confident behaviour has produced by now a silver fox population as tame as domestic dogs (Trut, 1999). Also in another canid, blue fox (*Alopex lagopus*), selection experiments have been able to demonstrate considerable genetic progress when selecting for improved confidence towards humans (Kenttämies et al., 2002). It should be noted though that the fox selection experiments have been conducted in controlled populations unlike the general dog breed populations such as FH, and the selection has mostly been only on one, simply defined behavioural trait.

Genetic trends or selection responses for behavioural traits in domestic dogs have been reported only rarely in literature thus far. According to Willis (1995), Vangen and Klemetsdal (1988) reported genetic progress per year ranging between +0.04% and -0.3% of the average score for the trait for three measures of hunting performance in the Norwegian Finnish Spitz population. It is difficult to compare these reported responses with this study without knowing more about the population in question. However, in this study the genetic progress per year in the FH population between 1982 and 2001 has been on the average +0.4% of the annual average score for search, +1.1% for pursuit, +0.3% for tongue and +0.06% for ghost trailing. It would thus seem that the genetic progress in the FH population has been considerably superior to that reported in the Norwegian Finnish Spitz population.

Conclusions

The heritabilities of field trial scores of the Finnish Hounds are low, and environment has a large influence on the results. However, substantial positive genetic trends can nonetheless be observed in search, pursuit and tongue scores over the past 30 years. A clear trigger for accelerating the genetic progress in these traits was the beginning of annual publication of all field trial results in sire progeny test format from 1982 onwards. Some additional gain has further been achieved after starting to publish BLUP EBVs for the most important scores from 1996 onwards. The results show that it is possible to achieve genetic progress when selecting for behavioural traits in a general dog population, provided that enough information is available for accurate selection of best breeding animals and the breeding goal is consistent.

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Figure 1. Average EBVs in trait units for search score by birth year.

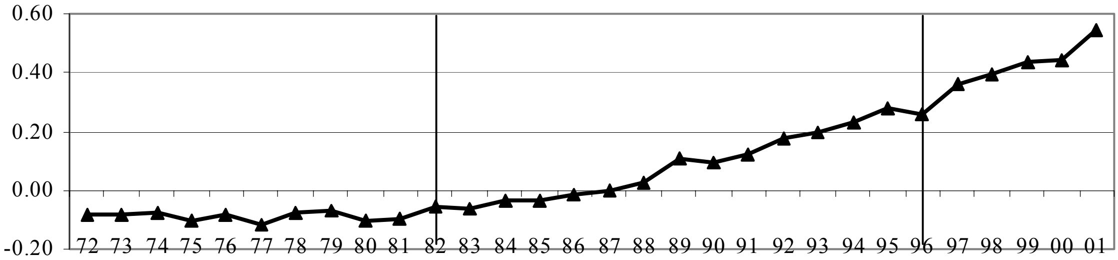


Figure 2. Average EBVs in trait units for pursuit score by birth year.

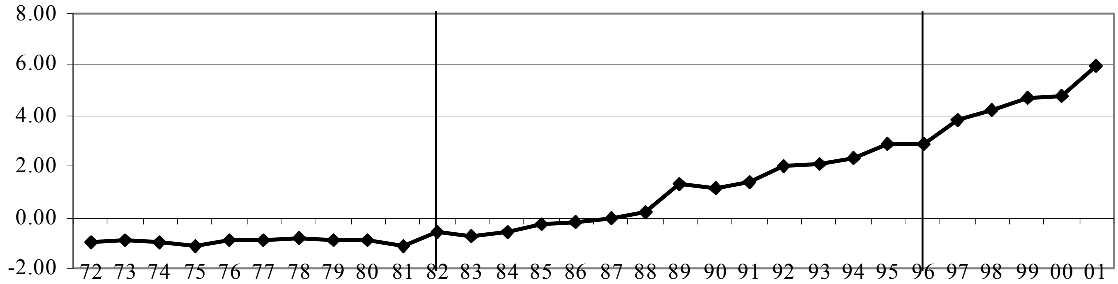


Figure 3. Average EBVs in trait units for tongue score by birth year.

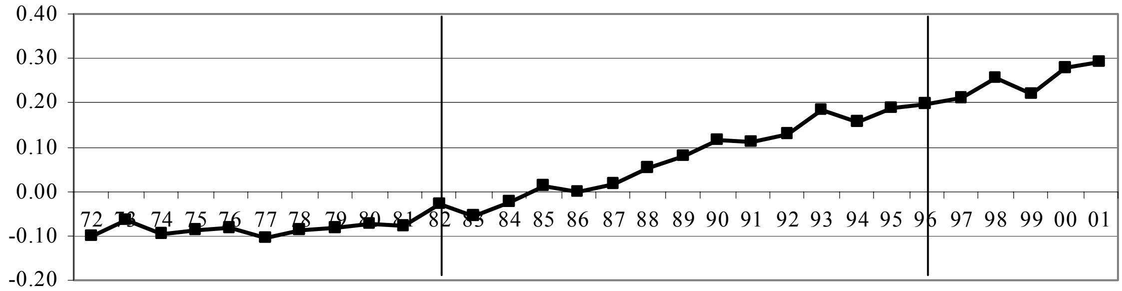
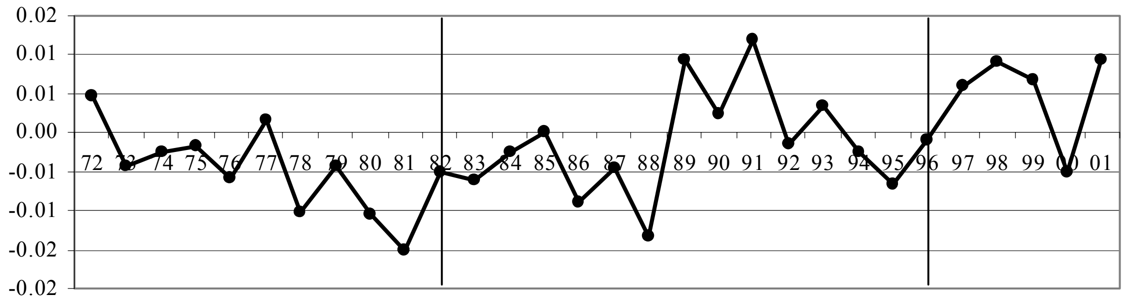


Figure 4. Average EBVs in trait units for ghost trailing score by birth year.



1982: beginning of annual publication of field trial results for all animals
1996: beginning of annual publication of EBVs for most important field trial scores