

## ESTIMATING EFFECTIVE POPULATION SIZE USING PEDIGREE DATA

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### Abstract

*Determining the sample size is the most important factor to effect of reliability of all scientific studies. The reliability of genetic parameter estimations obtained from phenotypic data with using pedigree depends on sufficiency of sample size. In this study was aimed to determine the effective population size for cattle, sheep and goat breeds. For this aim, methods depend on sex ratio, variance of progeny size and inbreeding rate were compared. Results indicated that the methods depends on variance of progeny size was suggestible for interested breeds.*

**Key words:** effective population size, sample size, breeding.

### INTRODUCTION

Easy coverage of the animal-derived proteins share in protein consumption is closely related to the supply of cheap animal protein source. Hence the importance of enhancing the country food of animal origin are included in the strategic planning (Inci et al., 2015; Isik and Ipcak, 2015).

Animal breeding is the effort to increase the proportion of the animals which are economic in appropriate environment in the population in next generation. The main purpose of animal breeding is to raise the yield obtained from animals to economic level (Duzgunes et al., 2012; Onder et al., 2015).

Achieving the aims on animal breeding is depends on the reliability of estimating the genetic parameters such as heritability and breeding value. Adequacy of sampling size is the basic rule of statistics for reliability (Sahin et al., 2003; Yamane, 1967).

In this study we aimed to compare the methods (sex ratio, variance of progeny size and inbreeding rate between two successive generations) to estimate the effective population size for cattle, sheep and goat species (Leroy et al., 2013).

### MATERIALS AND METHODS

The data were obtained from private farms for Holstein Frisian and Jersey breeds for cattle,

Saaenen and Turkish Hair Goat breeds for goat and Dorper sheep breed. Data of Karayaka sheep breeds was obtained from Ondokuz Mayıs University.

### Methods used to estimate effective population size $N_e$

#### Method based on sex ratio: $N_{es}$

Wright's model for estimating  $N_{es}$  is based on sex ratio. This very simple method is supposed to reflect the increased effects of both inbreeding and variance of progeny size under several assumptions, including random mating, no selection and random variation of progeny size across parents. Computation of  $N_{es}$  only requires the estimated numbers of breeding males (M) and females (F) in the reference population and follows equation (1):

$$N_{es} = \frac{4MF}{M + F} \quad (1)$$

#### Method based on the variance of progeny size: $N_{ev}$

This method is more sophisticated than the previous one since it directly takes into account the observed variance of progeny size. Parents of the reference population are considered as a group of useful offspring. In each pathway (mm = sire-sire, mf = sire-dam, fm = dam-sire

or  $ff = \text{dam-dam}$ ), observed variance ( $\sigma^2$ ) and covariance ( $\sigma$ ) of progeny size are computed considering those individuals and their own parents (i.e. the grandparents of the reference population).  $N_{ev}$  is then computed using equation (2) in which  $M_r$  and  $F_r$  are the numbers of new male and female parents beginning to reproduce each year averaged over the 10 years before the reference year:

$$\frac{1}{N_{ev}} = \frac{1}{16M_r T} \left[ 2 + \sigma_{mm}^2 + 2 \frac{M_r}{F_r} \sigma_{mm,ff} + \left( \frac{M_r}{F_r} \right)^2 \sigma_{mf}^2 \right] + \frac{1}{16F_r T} \left[ 2 + \sigma_{ff}^2 + 2 \frac{F_r}{M_r} \sigma_{ff,mm} + \left( \frac{F_r}{M_r} \right)^2 \sigma_{fm}^2 \right]. \quad (2)$$

### Method based on inbreeding rate between two successive generations: NeFt

Considering two successive generations  $t$  and  $t-1$ , inbreeding rate ( $\Delta F_t$ ) can be computed using equation (3), in which  $F_{t+1}$  is the average coefficient of inbreeding of the reference population, and  $F_t$  the average coefficient of inbreeding of their parents:

$$\Delta F_t = \frac{F_{t+1} - F_t}{1 - F_t} \quad (3)$$

The effective population size can then be computed using the formula  $N_{eFt} = 1/2\Delta F_t$ .

## RESULTS AND DISCUSSIONS

The estimated effective population size for the methods based on sex ratio, variance of progeny size and inbreeding rate between two successive generations were given in Table 1.

Table 1. Estimated effective population sizes

	NeFt	Nes	Nev
Holstein Frizian	697	445	56
Jersey	894	564	102
Saanen	347	26	75
Turkish Hair Goat	497	60	178
Dorper	1035	66	204
Karayaka	894	68	185

Spearman rank correlations estimated among the methods were given in Table 2.

Table 2. Estimated Spearman rank correlations

	NeFt	Nes
Nes	0.740	-
Nev	0.890	0.434

To compare the methods regression analysis was used. Estimated population size was used as response variable and breed was used as explanatory variable. Obtained comparison criteria from regression models were given in Table 3.

Table 3. Comparison criteria obtained from regression

	$R_d^2$	MSE	Sig.
NeFt	0.566	2.2E7	<0.001
Nes	0.204	7.9E6	<0.001
Nev	0.523	9.1E5	<0.001

When the criteria examined, the method based on inbreeding rate between two successive generations (NeFt) was more reliable than the others because its determination coefficient was the highest and mean square error was the lowest. However, all the methods were found statistically significant so, all three methods can be used to estimate effective population sizes.

## CONCLUSIONS

The three methods, sex ratio, variance of progeny size and inbreeding rate between two successive generations, can be successfully used to estimate effective population sizes for cattle, sheep and goat species. The method based on inbreeding rate between two successive generations was found as the best method for this aim.

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