RESEARCHES CONCERNING THE AVERAGE RELATEDNESS OF FURIOSO NORTH STAR POPULATION FROM BECLEAN PE SOMES STUD FARM

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Abstract

Average relatedness is a very important parameter in animal genetic resources management because it is related with inbreeding and effective population size. The purpose of the work is average relatedness and its components evaluation in Furioso North Star population from Beclean pe Somes stud farm. Biological material used is represented by the entire livestock of the stud farm Beclean pe Someş (transferred in October of 2011 from the Slatina stud farm), belonging to the Furioso-North Star (and not just evidence of it), existing at the time of analysis (30.11.2011). To determine the average relatedness, have used The Numerator Relationship Matrix method, proposed by Henderson and Cunningham in 1971 and presented for the first time in Romania by Grosu in 1997. The results reflect the existence of a population with an average relatedness by 0.2079 ± 0.0096, and researches underline the existence of some errors in mating, not allowed for a population subject to permanent danger of inbreeding.

Key words: animal breeding, average relationship, horse

INTRODUCTION

As a definition, the averarage relatedness is the genetic relation between all individuals in the population, existing at a given time [1] [2] [3].

Knowing the average relatedness existing at a given time, it can determinate possible inbreeding of the population subject to analysis. This represents the average gain of inbreeding on the generation that would occur if the lack of managing of mate (in the case of panmictic reproduction). The issue is important since, especially in the case of small populations subject to permanent danger of inbreeding, abandoning the system of matching pairs has adverse consequences of population evolutionary way, but predictable.

MATERIAL AND METHOD

Biological material used is represented by the entire livestock of the stud farm Beclean pe Someş (transferred in October of 2011 from the Slatina stud farm), belonging to the Furioso-North Star (and not just evidence of it), existing at the time of analysis (30.11.2011).

To determine the average relatedness, have used The Numerator Relationship Matrix method, proposed by Henderson and Cunningham in 1971 and presented for the first time in Romania by Grosu in 1997 [4].

To test the significance of differences, Fisher's test was used and the limit difference [5].

RESULTS AND DISCUSSIONS

The matrix of relatedness coefficients of stallions and mares that constitute the population of Furioso North Star from Beclean pe Someş stud farm, Bistriţa Năsăud (in the analysis time), allowed the determination of the population average relatedness, at a value of 0.2079 ± 0.0096.

Genetic diversity (variability) can be set by determining the value of relatedness between stallions and mares grouping by birth years of age structure and batch born in different years, with overall heterogeneity testing using Fisher test (F = 29.1429 **), which highlighted the existence of very significant differences between the values of the coefficients of relatedness – table 1.

Table 1 The genetic relation between stallions and mares grouped by birth years of age structure and by batches born in different years

Mares \ Stallions	1992 NS XLIII	1999 F LXVIII	2001 NS XLIV	2007 F LXIX F LXX
1995	0.2827 1 comb.	0.1504 1 comb.	0.0913 1 comb.	0.1399 2 comb.
1999	0.3454 4 comb.	0.1668 4 comb.	0.1721 4 comb.	0.2146 8 comb.
2000	0.0633 2 comb.	0.4299 2 comb.	0.1657 2 comb.	0.1177 4 comb.
2001	0.1553 11 comb.	0.2168 11 comb.	0.2132 11 comb.	0.1978 22 comb.
2002	0.1951 4 comb.	0.1780 4 comb.	0.3211 4 comb.	0.2507 8 comb.
2003	0.2563 3 comb.	0.3497 3 comb.	0.1375 3 comb.	0.1581 6 comb.
2004	0.3614 2 comb.	0.1498 2 comb.	0.1455 2 comb.	0.1777 4 comb.
2005	0.2419 5 comb.	0.2808 5 comb.	0.2425 5 comb.	0.1758 10 comb.
2006	0.0734 1 comb.	0.1682 1 comb.	0.2040 1 comb.	0.2276 2 comb.
$F = 29.1429^{***}$				

To highlight more clearly the important moments in the evolution of the population, it is necessary to determine the difference between stallions and mares relatedness in different years of age structure and population average relatedness. The differences which are statistical significant highlights the action either the cross, or inbreeding. The statistical significance of differences is tested using the limit difference (table 2).

Due to overlapping generations, the population is fragmented into three distinct groups, in which the evolution factors acting in different proportions: a group where acting cross, another with inbreeding and a third unfolds a reproduction process in endogamy without "disrupting" the genetic structure.

Times in which the difference between stallions – mares genetic relation and population average relatedness has no statistical significance, ie times of inbreeding or crossbreeding with weak intensity, represented reproducing of population under endogamy, or population return after between families crossing, ie after applying specific stud farm mating system in order to avoid increasing the inbreeding.

Note that if the difference between stallions-mares average relatedness on the 1992-1995 years and population average relatedness of +0.0748, although limit difference indicates inbreeding existence, we tend to believe that this result is caused by a sample error. This statement is based on the analysis results shown in Table 2, where in similar situations used statistical indicator revealed significant positive difference to the population average.

First situation, inbreeding, is generated by the year groups combination 1992 for stallions (NS XLIII) and 1995 for mares (NS XLI 67), the year groups combination 1999 to stallions (F LXVIII) and 2000 for mares (F LXVI 8 and F LXVI 11), and the combination of 1999 group for stallions (F LXVIII) and 2003 for mares (F LXVI 26, F LXVI 28 and NS XLIII 34).

Table 2 Difference between stallions-mares genetic relation and population average relatedness

Stallions-mares genetic relationship				Difference: $r_{A-I}/ani - r_{pop}$		Limit difference $DL = t_{0.05} \cdot s_d$	Limit difference $DL = t_{0.01} \cdot s_d$	Limit difference $DL = t_{0.001} \cdot s_d$
Year		No of comb.	r_{A-I}/ani	$r_{pop.} = 0.2079$ 165 combinations	Observations			
♂	♀							
1992-1995		1	0.2827	+ 0.0748***	inbreeding	0.0188	0.0247	0.0316
1992-1999		4	0.3454	+ 0.1375^NS	Reproduction in endogamy without "disrupting" the genetic structure	0.2577	0.3380	0.4326
1992-2000		2	0.0633	- 0.1446***	cross	0.0195	0.0256	0.0327
1992-2001		11	0.1553	- 0.0526^NS	Reproduction in endogamy without "disrupting" the genetic structure	0.0838	0.1099	0.1407
1992-2002		4	0.1951	- 0.0128^NS		0.2353	0.3086	0.3950
1992-2003		3	0.2563	+ 0.0484^NS		0.2762	0.3622	0.4636
1992-2004		2	0.3614	+ 0.1535^NS		0.3893	0.5104	0.6534
1992-2005		5	0.2419	+ 0.0340^NS		0.1669	0.2189	0.2802
1992-2006		1	0.0734	- 0.1345***	cross	0.0188	0.0247	0.0316
1999-1995		1	0.1504	- 0.0575***		0.0188	0.0247	0.0316
1999-1999		4	0.1668	- 0.0411*		0.0342	0.0449	0.0574
1999-2000		2	0.4299	+ 0.2220***	inbreeding	0.0335	0.0439	0.0562
1999-2001		11	0.2168	+ 0.0089^NS	Reproduction in endogamy without "disrupting" the genetic structure	0.0722	0.0946	0.1211
1999-2002		4	0.1780	- 0.0299*	cross	0.0250	0.0327	0.0419
1999-2003		3	0.3497	+ 0.1418***	inbreeding	0.0191	0.0250	0.0321
1999-2004		2	0.1498	- 0.0581***	cross	0.0246	0.0322	0.0412
1999-2005		5	0.2808	+ 0.0729^NS	Reproduction in endogamy without "disrupting" the genetic structure	0.1625	0.213	0.2727
1999-2006		1	0.1682	- 0.0397***	cross	0.0188	0.0247	0.0316
2001-1995		1	0.0913	- 0.1166***		0.0188	0.0247	0.0316
2001-1999		4	0.1721	- 0.0358^NS	Reproduction in endogamy without "disrupting" the genetic structure	0.1040	0.1364	0.1746
2001-2000		2	0.1657	- 0.0422***	cross	0.0188	0.0247	0.0316
2001-2001		11	0.2132	+ 0.0053^NS	Reproduction in endogamy without "disrupting" the genetic structure	0.0669	0.0877	0.1123
2001-2002		4	0.3211	+ 0.1132^NS		0.1588	0.2083	0.2666
2001-2003		3	0.1375	- 0.0704***	cross	0.0215	0.0282	0.0362

Table 2 Difference between stallions-mares genetic relation and population average relatedness (continuation)

Stallions-mares genetic relationship			Difference: $r_{A-I} / ani - r_{pop.}$		Limit difference $DL = t_{0.05} \cdot s_d$	Limit difference $DL = t_{0.01} \cdot s_d$	Limit difference $DL = t_{0.001} \cdot s_d$
Year		No of comb.	r_{A-I} / ani	$r_{pop.} = 0.2079$ 165 combinations			
♂	♀			Observations			
2001-2004		2	0.1455	- 0.0624[NS]	Reproduction in endogamy without "disrupting" the genetic structure	0.0677	0.0887	0.1136
2001-2005		5	0.2425	+ 0.0346[NS]		0.1213	0.1591	0.2037
2001-2006		1	0.2040	- 0.0039[NS]		0.0188	0.0247	0.0316
2007-1995		2	0.1399	- 0.0680[NS]		0.1017	0.1333	0.1707
2007-1999		8	0.2146	+ 0.0067[NS]		0.0728	0.0955	0.1222
2007-2000		4	0.1177	- 0.0902[**]	cross	0.0192	0.0252	0.0322
2007-2001		2	0.1978	- 0.0101[NS]	Reproduction in endogamy without "disrupting" the genetic structure	0.1199	0.1572	0.2013
2007-2002		8	0.2507	+ 0.0428[NS]		0.0621	0.0815	0.1043
2007-2003		6	0.1581	- 0.0498[**]	cross	0.0307	0.0403	0.0515
2007-2004		4	0.1777	- 0.0302[NS]	Reproduction in endogamy without "disrupting" the genetic structure	0.0757	0.0993	0.1271
2007-2005		10	0.1758	- 0.0321[NS]		0.0465	0.0609	0.0780
2007-2006		2	0.2276	+ 0.0197[NS]		0.2115	0.2773	0.3550

Inbreeding is definitely caused by errors in matching pairs whereas structural pedigree analysis, a clear result matings between half sibs practice, unacceptable to a stud farm, no matter what caused them (deliberately or not). Analysis of these errors in matching mating is shown in table 3. Because of these errors by matching mating and where the mistake is still, a small part of the population Furioso North Star in Beclean pe Somes stud farm will turn to genetic drift.

Large share held by cross (table 2) is generated by matching pairs compliance system based on the principle of rotation, the only way to reduce inbreeding in small populations by doubling the effective size. For Furioso North Star population in Beclean pe Somes stud farm, the data presented in Table 2 reveals a gratifying fact, the principle of rotating crossing, ensuring its normal evolutionary way without danger of genetic drift. The share of cross definitely can not be attributed to immigration whereas the tests made clear its inefficiency (by analysing important ancestors and population genetic relation with immigrants).

Table 3 Errors in mating plan which generate inbreeding

Specification	Stallion	Mare	Common father	Genetic relationship
1992 - 1995	NS XLIII	NS XLI 67	NS XLI	0.2827
1999 - 2000	F LXVIII	F LXVI 8	F LXVI	0.4158
		F LXVI 11		0.4441
1999 - 2003	F LXVIII	F LXVI 26	F LXVI	0.3506
		F LXVI 28		0.3521
		NS XLIII 34	-	0.3464

Between individual average relatedness values of stallions with mares without statistically significant differences are found, a fact highlighted by the global test of homogeneity ($F = 1.46^{NS}$) – table 4.

Analysis of individual average relatedness between stallions and mares (table 4) reveals several problems. These occur where the average relatedness between stallions and mares is greater than average relatedness in the population, causing inbreeding (which is not valuable for F LXX).

Table 4 Individual relationship between stallions and mares

No	Stallions (cod)	Individual relationship with mares	$\hat{F}$
1	NS XLIII (205)	0.2138	
2	NS XLIV (209)	0.2079	
3	F LXVIII (232)	0.2332	1.46^{NS}
4	F LXIX (235)	0.2199	
5	F LXX (236)	0.1648	

CONCLUSIONS

Appears imperative to respect strictly the principle of mating in stud farm (par excellence small populations, under continuous inbreeding danger): selection within family followed rotational crossing, the only way to reduce inbreeding in small populations by doubling the effective size. Because of mating errors and where it persists in error, a small part of the population Furioso North Star in the Beclean pe Somes stud farm can turn to genetic drift.

REFERENCES
[1] Drăgănescu C., 1970: Researches concerning the method used in animal breeding in Romania, PhD thesis, IANB Bucharest.
[2] Drăgănescu C., 1979: Animal breeding, Ed. Ceres, Bucharest.
[3] Drăgănescu C., Sandu Gh., 1987: Elementary quantitative methods in animal breeding, IANB Bucharest.
[4] Grosu H. et al, 1997: Linear models in animal breeding, Ed. Coral Sanivet, Bucharest.
[5] Sandu Gh., 1995: Experimental models in animal science, Ed. Coral Sanivet, Bucharest.