The Role of Genetic Drift and Selection Intensity on Small Populations

H.D. Blackburn[1], C. S. Wilson[1], B. Krehbiel[1], S. R. Paiva[2]

[1]National Animal Germplasm Program ARS-USDA, Ft. Collins, CO USA
[2]EMBRAPA Genetic Resources & Biotechnology, Brasilia, BR

Summary

Impacts of genetic drift (GD) were evaluated and the ability of breeders to achieve selection goals for small populations. The sensitivity analysis demonstrated the difficulty breeders with small populations or rare breeds will have in achieving selection goals. However, with high selection intensities progress toward selection goals can be made but at slower rates of genetic gain.
Key words: Genetic drift, Small populations, Genetic resources

Introduction

Genetic drift (GD) is not taken into account in developing and implementing livestock breeding programs, even though most of the variance in breeding value is due to genetic drift (Hill, 1977). While GD is dampened in large populations, it can create large and substantial changes in small populations (Blackburn et al. 2014), making it an important factor for breeders to consider with relatively small herds and especially breeders involved in raising rare breeds of livestock. Across livestock species average herd size for major and minor breeds tend to be relatively small (< 100 animals), suggesting the impact of GD is relatively large for the industry. To reduce the loss of genetic diversity among rare breeds there are efforts to increase their utilization in niche markets but for such growth to happen productivity and profitability needs to be increased. But because most minor/rare breeds lag behind industry averages in performance compared to major breeds this suggests minor/rare breeds must undergo selection for higher levels of productivity or traits where they may hold a competitive advantage. Under these types of conditions, GD can come into play in either exceeding or diminishing the expectation of genetic gain. We assess how GD affects obtaining selection goals under different levels of selection intensity, provide potential approaches for breeders and breed association to consider.

Materials and methods

Nicholas (1980) developed an equation to estimate the number of animals needed to achieve selection goal with varying probabilities of success. Dynamic factors of the equation include: selection intensity, heritability, and the number of generations the population is to be selected.

Number of Animals =

Where: Z = standard normal deviate; α = probability of success; β = Proportion of expected response; h = square root of heritability; and t = number of generations.

Using the above equation the impact of GD was evaluated for a population undergoing selection, where magnitude/impact was determined by a sensitivity analysis considering population size needed to achieve an acceptable probability of success in the selection program (Table 1). All of these parameters were used in a factorial combination.

After deriving population sizes needed to achieve a selection goal we consider other aspects of small population breeding programs needed to successfully advance the competitiveness of small populations. There are 17 breeds classified as "Threatened" (annual registrations are < 1,000 animals and the estimated breed population in the US is < 5,000 animals) in the US. Among these breeds phenotypic, pedigree, and genomic information is lacking making the immediate implementation of a standardized breeding program difficult. In addition, herd sizes for these breeds are small with breeders having 10 to 30 females. From limited registration data, we estimate that the female to male ratio is approximately 10:1. Breeder longevity also affects a breed's ability to employ selection strategies and genetic change. In the US breeders raising rare/minor breeds for more than 7 years ranges from 3.6% to 27% (Maiwashe et al. 2004; Welsh et al., 2010); suggesting there is a limited number of breeders to engage about multi-generational breeding programs. That said breeders that have raised a breed for +7 years also tend to have relatively larger herds/flocks. Using this information, we consider the implementation of a breeding program.

Results and Discussion

Figure 1 shows four scenarios which differ by selection intensity. Lower selection intensities (0.50, 1.09, 1.27) required large numbers of animals (from 950 to 6,500) to achieve a high probability of obtaining the selection goal over five generations. Practicing intense selection (1.76) decreased the number of animals needed to have a high probability of meeting the selection goal.

The computed number of animals needed to meet selection goals with a high probability of success are larger than the herd sizes of most livestock producers. This would seem the case for rare/minor breeds in OECD countries and developing countries. To better assess the options available to breeders with small herds or breeders raising rare/minor breeds it may be more informative to evaluate the lower ends of selection response for the various selection intensities. At the highest selection intensities of 1.76 or 1.27 when α is decreased to 0.8 or 0.9 and β to 0.9 herd size required decreases to 37 or 100 and 75 or 150 animals, respectively.

Based on needed population size (Figure 1) and estimated male and female ratios the rate of inbreeding was computed using the two highest selection intensities and varying α and β (Table 2). If $Ne \geq 50$ is the target (FAO recommendations) combinations resulting in a $\Delta F > 0.01$ should not be used. Based upon inbreeding rate estimates $\alpha \geq 0.9$ and $\beta \geq 0.9$ could be used with a selection intensity of 1.27 and $\alpha \geq 0.95$ and $\beta \geq 0.95$ with a selection intensity of 1.76.

With the minimum number of animals ($\geq$ 150) needed to control genetic drift and make selection progress determined we propose an approach for breeders to employ a selection program. Five to 10 breeders with a record of longevity (> 5 years) will need to be identified to reach the minimum number of animals required for the selection program which should be feasible (Mawashe et al., 2004); Welsh et al., 2010). Initially, estimated breeding values will be based upon individual phenotypes and transition over time to combining individual performance with ½ sib progeny (10 per sire) records should have accuracies of 0.50 and 0.77, respectively. Eventually pedigree information will be added to the effort as that data becomes more complete. Breeding circles could be formed to encourage cross herd or flock ties among selected herds.

Many Threatened breeds have a breed association that might maintain pedigree records but performance data is almost non-existent. It will be important that such associations be willing to strengthen capacities in data acquisition and encourage data utilization. Assembled breeders will need to identify selection criteria and how they might exchange genetic resources to facilitate cross herd ties. Once engaged in the selection program breeders will need to see progress after two or three generations to remain interested in the effort.

The results and process defined above represents a major paradigm for breeds in the Threatened category. However, we believe once such an approach is initiated and shown to be successful with one or two breeds other breeders will join in the transformation that will serve to increase the competitive position of this group of breeds.

Conclusion

GD among small populations can have large and substantial affects. By increasing selection intensity GD can be harnessed mitigating negative effects and enhancing positive aspects. But for breeders of Threatened livestock breeds to achieve such a goal requires a paradigm shift about information use, cooperation and making selection decisions.

List of References

Blackburn, H. D., Y. Plante, G. Rohrer, E. Welsh, S. Paiva. 2014. J. Anim. Sci. 92:1405-1411.
FAO. 2013. FAO Animal Production and Health Guidelines. No. 14.
Hill, W. G. 1977. Proc. Intl. Conf. Quant. Genetics.343-365
Maiwashe, A. N., and H. D. Blackburn. 2004. J. Anim. Sci. 82:2900–2905.
Nicholas, F. W. 1980. Genet. Res. 35:85-105.
Welsh, C. S., T. S. Stewart, C. Schwab, H. D. Blackburn. J. Anim. Sci. 2010. 88:1610–1618

Table 1. Parameters used to calculate number of animals needed to meet selection goals.

Standard normal deviate, Z (probability, α)	.0316 (0.9)	0.288 (0.8)	0.258 (0.7)	0.225 (0.6)
Intensity, i (proportion saved)	0.5 (0.70)	1.09 (0.35)	1.27 (0.25)	1.76 (0.10)
Proportion of expected response, β	0.95	0.90	0.80	0.75
Square root heritability, h	0.529	0.529	0.529	0.529
Number of generations, t	5	5	5	5

Table 2. Rate of inbreeding under different selection intensities, standard normal deviate, and proportion of expected response.

Standard normal deviate	Proportion of expected response	Selection intensity	Animal number (males:females)	Rate of inbreeding ΔF*
0.80	0.90	1.27	100 (9:91)	0.015
0.80	0.90	1.76	37 (3:34)	0.045
0.90	0.90	1.27	150 (14:136)	0.010
0.90	0.90	1.76	75 (7:68)	0.020
0.95	0.95	1.27	950 (88:862)	0.002
0.95	0.95	1.76	500 (45:455)	0.003

* $\Delta F = 1/(8Nm) + 1/(8Nf)$

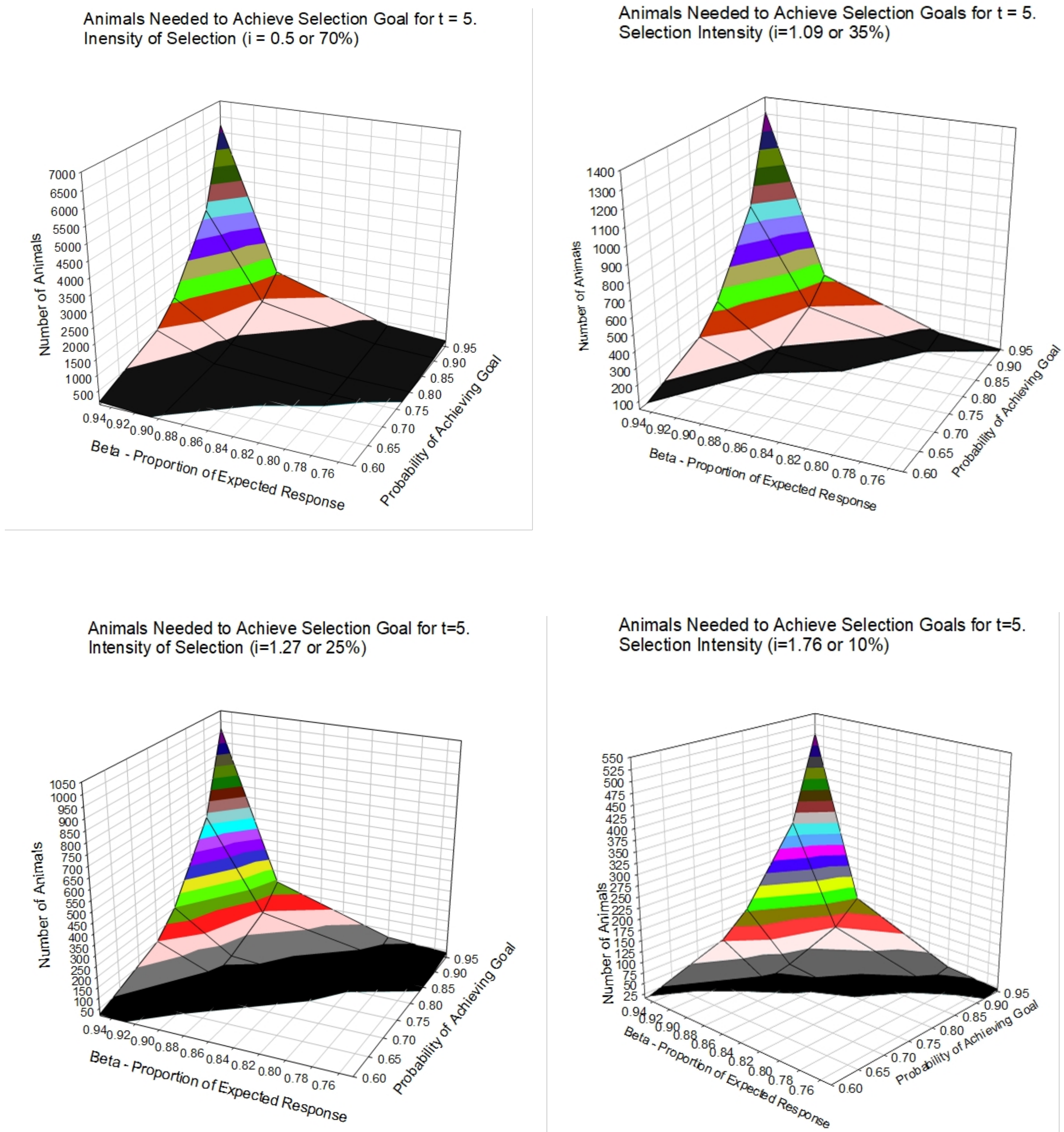

Figure 1. Projected number of animals needed to achieve varying levels of a selection goal and proportion of the expected response.