DIRECT AND MATERNAL ADDITIVE EFFECTS AND HETEROSIS IN PROLIFICACY WEANING TRAITS IN RABBITS

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ABSTRACT

Evaluation of F_1 combinations in an environment with hot climate and nutritional limitations was required in order to establish an objective genetic improvement program. Three complete diallel crossbreeding trials were performed between 1968 and 2005 involving 5915 weaning records of four rabbit breeds (California, C; Chinchilla, Ch, New Zealand, N and Semigiant White, S) to determine direct (as an indicative of higher paternal breed) and maternal (best maternal breed) additive effects and heterosis in prolificacy traits at weaning in rabbits: proportion of litters weaned, number weaned and viability. A generalized linear mixed model (macro for GLIMMIX of SAS) was applied which considered the fixed effects of genotype (16 classes) and experiment (3 trials) and the random effect of parity (5 levels). Genetic effect estimations were done applying linear contrasts between means of the genetic groups after Dickerson (1969) model. Maternal additive effects were more important (significant in all traits analyzed) than direct effects and demonstrate the superiority of New Zealand over Chinchilla and Californian breeds. Direct additive effects were favorable for the Chinchilla breeds. Heterosis averaged 10.0, 8.8, and 13.0% for the three traits resp. and was significant and positive in 61% of the analysis. Maximum heterosis (13-17%) was found for the reciprocal pair of crosses: NS, CCh, ChS and CS. Results support simple crossing as a rapid and effective way of genetic improvement for suboptimal conditions.

Keywords: rabbits, prolificacy, genetics parameters, diallel cross

Introduction

Crossbreeding is utilized in tropical countries and suboptimal environments in order to exploit additive and dominance effects to increase production levels. The knowledge of the genetic parameters of crossbreding allows adjusting the use of different mating systems (Dickerson 1969). In Cuba, the unique studies in this subject were realized by Ponce de Leon (1977), but the performance of pure breeds and crosses is expected to vary according to environmental factors (Rojas and Sprague 1952) making necessary to reevaluate them periodically. An analysis of three complete diallel crosses developed over a period of 30 years was realized to determine genetic parameters of crossbreeding in order to optimize the use of rabbit breeds for commercial crossbreeding schemes.

Material and methods

Data. Three complete diallel crossbreeding trials involve 5915 weaning records of four rabbit breeds: California (C), Chinchilla (Ch), New Zealand (N) and Semigiant White (S). The first two experiments were developed between july/1968 and november/1970 in the rabbitry "8 de octubre", while the third was realized between may/2003 and april/2004 in the rabbitry "26 de Julio", both located at San Jose de Las Lajas, Mayabeque province. The mating design accomplished the assumptions of a complete diallel cross (4*4). The animals were allocated in open sided buildings following a completely random design. Male and female breeders were selected from the genetic population and fulfilled the phenotypic characteristics of each breed.

Statistical analysis. Crossbreeding genetic parameters were determined for the following litter weaning traits: proportion of litters weaned (0=not weaned litter, 1=weaned, PLW), number weaned (kids weaned from a litter with at least one born alive, NW) and viability (No. weaned/no.born*100, VIAB). A generalized linear mixed model (macro for GLIMMIX of SAS (2007) was applied which considered the fixed effects of genotype (16 classes) and experiment (3 trials) and the random effect of parity (5 levels). The same model was used for the three traits, except for the link function in correspondence to the error ascribed to each one (PWL and VIAB log y NW logit). Dickerson's (1969) model was used to estimate the genetic parameters of crossbreeding: direct (g^I) and maternal (g^m) additive effects and the individual heterosis (h^I).

Linear contrasts between means of the genetic groups were used to estimate the genetic parameters.

Results and discussion

Genetic parameters of crossbreeding. **Additive effects**. Significant differences were found among breeds for maternal additive effects in all studied traits, while direct additive effects were only encountered for NW and VIAB (Table 1). These results are in line with those of Ponce de Leon (1988) that encountered pronounced maternal effects relative to minor effects due to the litter genes. Ch breed had favorable additive effects for NW and VIAB over the S. Significant differences between breeds were similar for the maternal effects in all three traits, where N excelled Ch and C breeds without differences with S. It was found that the unique source of genetic variation in the PLW was the additive maternal effect, where the N exhibited 22% more litters weaned than Ch and C. The range for direct and for maternal effects was of 1.3 kids between extreme breeds for NW in the present work. These values are similar to those determined by Khalil (1999) and Al-Saef *et al*. (2008) as climate conditions are comparable and as no highly selected lines are used. These reasons are also valid to explain the scarce number of papers that report significant additive effects in NW in suboptimal conditions. However, for VIAB the range for breed differences was slightly higher for maternal (22.6%) than for direct effects (17%).

		PLW, %			NW, No.			VIAB, %		
		Estimator		SE±	Estimator		SE±	Estimator		SE±
Direct additive effects	$\bar{g}^{I}_{C}$	-0.06	(-2.31)	0.33	0.01^{ab}	(0.08)	0.09	-0.09^{ab}	(-2.31)	0.20
	$\bar{g}^{I}_{CH}$	0.60	(12.31)	0.39	0.20^{a}	(0.57)	0.10	0.56^{a}	(13.73)	0.23
	$\bar{g}^{I}_{N}$	0.03	(1.66)	0.36	0.02^{ab}	(0.03)	0.10	-0.14^{ab}	(-3.38)	0.21
	$\bar{g}^{I}_{S}$	-0.57	(-11.66)	0.35	-0.22^{b}	(-0.68)	0.09	-0.32^{b}	(-8.04)	0.21
Maternal additive effects	$\bar{g}^{M}_{C}$	-0.48^{b}	(-9.19)	0.31	-0.21^{b}	(-0.69)	0.08	-0.26^{b}	(-6.53)	0.18
	$\bar{g}^{M}_{CH}$	-0.49^{b}	(-9.54)	0.33	-0.09^{b}	(-0.27)	0.09	-0.38^{b}	(-9.44)	0.19
	$\bar{g}^{M}_{N}$	0.66^{a}	(12.58)	0.33	0.19^{a}	(0.62)	0.09	0.54^{a}	(13.20)	0.19
	$\bar{g}^{M}_{S}$	0.31^{ab}	(-6.55)	0.33	0.11^{ab}	(0.34)	0.08	0.11^{ab}	(2.77)	0.19
Individual Heterosis	h^{I}_{CCH}	0.58^{***}	(11.26)	0.21	0.15^{**}	(0.45)	0.05	0.31^{*}	(7.76)	0.12
	(%)	16.64			15.26			16.73		
	h^{I}_{CN}	0.18	(4.03)	0.20	0.03	(0.07)	0.06	0.18	(5.97)	0.12
	(%)	5.72			2.31			12.87		
	h^{I}_{CS}	0.35	(6.89)	0.18	0.13^{*}	(0.41)	0.05	0.27^{*}	(6.68)	0.11
	(%)	10.48			14.70			15.19		
	h^{I}_{CHN}	-0.08	(-2.43)	0.20	-0.08	(-0.22)	0.06	-0.11	(-2.66)	0.12
	(%)	-3.28			-6.75			-5.21		
	h^{I}_{CHS}	0.53^{*}	(10.01)	0.22	0.12*	(0.38)	0.05	0.35^{**}	(8.69)	0.13
	(%)	15.26			12.63			18.38		
	h^{I}_{NS}	0.64^{**}	(11.07)	0.22	0.14**	(0.45)	0.05	0.40^{***}	(9.83)	0.12
	(%)	15.37			14.52			20.21		

Table 1. Direct and maternal additive effects and heterosis for prolificacy traits at weaning in diallel crosses. ^{ab}Parameters with different letters in the same column difffer at P<0,05. *P<0,05 *P<0,05 ** P<0,01 *** P<0,001 (Kramer 1956). () Retransformed estimators.

Heterosis. The estimates are presented in the lower part of table 1. The average heterosis for the three traits are 10, 8.8 and 13% resp. Excluding the ChN and CN crosses, where the excellence of the pure N breed affected the heterosis estimation, the mean heterosis for these traits was 14.5, 14.3 and 17.6%. The estimates for heterosis were significant in a 61% of the cases. The pairs of reciprocal crosses with higher values of heterosis for the average of the three traits were NS-SN (17%), CCh-ChC (16%), ChS-SCh (15%) and CS-SC (13%). Is a relevant result that despite the presence of N in the NS-SN crosses they have obtain the highest heterosis estimates showing a strong non additive gene action in this combination. These results vary in different cuban papers referring the same breeds in individual trials (Ponce de Leon 1977 y Garcia et al. 2005). When considering all three diallel experiments with a different statistical analysis, higher heterosis values and the appearance of more significant heterosis estimates were obtained.

Conclusions

The genetic parameters of crossbreeding estimated to ratify the superiority of the maternal additive effects of the N over Ch and C breeds encountered in the first studies and additionally, a superior direct additive effect of Ch over the S breed was determined. High heterosis averaging 13- 17% exhibited for four of the six pairs of reciprocal crosses support simple crossing as a rapid and effective way of genetic improvement for suboptimal conditions.

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