

## Direct and maternal additive effects and heterosis in prolificacy weaning traits in rabbits.

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**ABSTRACT:** Three complete diallel crossbreeding trials were realized between 1968 and 2005 involving 5915 weaning records of four rabbit breeds (California, Chinchilla, New Zealand and Semigiant White) to determine direct and maternal additive effects and heterosis in prolificacy traits at weaning in rabbits: proportion of litters weaned, number weaned and viability. Genetic effect estimations were done applying linear contrasts after Dickerson (1969) model. Maternal additive effects were more important than direct effects and ratify the superiority of New Zealand breed. Direct additive effects were favorable for the Californian and 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 avail simple crossing as a rapid and effective way of genetic improvement for suboptimal conditions.

Keywords:

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prolificacy

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diallel cross

### Introduction

Crossbreeding is an important genetic improvement alternative generally 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 (direct and maternal additive effects and heterosis) allows adjusting the use of different mating systems (Dickerson (1969)). In Cuba, the first and unique studies in this subject were realized in the 70's (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, PWL), 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 ( $g^l$ ) and maternal ( $g^m$ ) additive effects and the individual heterosis ( $h^l$ ). Linear contrasts between means of the genetic groups were used to estimate the genetic parameters. The contrasts were constructed following the definition of each parameter and the coefficient determined by the same author for each type of cross.

### Results and discussion

**Differences between genotypes.** Significant differences were detected ( $P<0.001$ ) between genotypes for all traits, where the SN cross and the New Zealand purebreds showed superiority over pure Californians. The rest of the genotypes did not differ from the extremes. However, some genotypes as CS, CCh, ChN, ChS and SCh exhibited excellent performances, but with high SE.

**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 number weaned and viability (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. Chinchilla breed had favorable additive effects for number weaned and viability over the Semigiants. Significant differences between breeds were similar for the maternal effects in all three traits, where New Zealand excelled Chinchilla and California breeds without differences with Semigiants. It was found that the unique source of genetic variation in the proportion of litters weaned was the additive maternal effect, where the New Zealand exhibited 22% more litters weaned than

Chinchilla and California. Literature mostly deals with the number of weaned rabbits as representative trait of prolificacy up to weaning. The range for direct and for maternal effects was of 1.3 kids between extreme breeds for number weaned in the present work. These values are similar to those determined by Khalil (1999), Asaef et al. (2008) and Youssef 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 number weaned in suboptimal conditions. However, for viability the range for breed differences was slightly higher for maternal (22.6%) than for direct effects (17%).

**Heterosis.** Heterosis estimates express the non additive variability and 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 New Zealand 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%). Contrarily, negative heterosis was detected for ChN-NCh averaging -5% for the three traits. Is a relevant result that despite the presence of New Zealands 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), 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 from a set of three diallel crosses performed during a period of 30 years allowed to ratify the superiority of the maternal additive effects of the New Zealand over Chinchilla and Californian breeds encountered in the first studies and additionally, a superior direct additive effect of Chinchilla over the Semigiant breed was determined. High heterosis averaging 13- 17% exhibited for four of the six pairs of reciprocal crosses avails simple crossing as a rapid and effective way of genetic improvement for suboptimal conditions.

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**Table 1. Direct and maternal additive effects and heterosis for prolificacy traits at weaning in diallel crosses.**

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

<sup>ab</sup>Parameters with different letters in the same column differ at P<0,05. \*P<0,05 \*P<0,05 \*\* P<0,01 \*\*\* P<0,001 (Kramer 1956).

() Estimator retransformados.