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Genetic Effects on Dairy Cattle Production under Different Life Zones in Panama

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ABSTRACT

Background: In Panama, the sustained increase in milk consumption has revealed a growing dependence on external sources to meet national demand. This situation has highlighted a limitation in the productive capacity of the dairy sector, leading authorities to promote strengthening strategies through genetic improvement programs. **Aim:** To evaluate the additive genetic effects of heterosis and gene recombination on milk production in Holstein, Brown Swiss, and their crossbred cattle, considering the interaction across five life zones. **Methods:** A generalized linear model with repeated measures over time (GLM-R) was used, incorporating fixed effects of contemporary groups. **Results:** Heterosis varied across the life zones, indicating a benefit from its use, with the effect being more pronounced in the Lower Montane Rain Forest, while in the other zones it was less marked. Recombination showed negative effects in most life zones, suggesting that gene segregation could reduce productive efficiency. Overall, crossbreds outperformed purebred animals in most life zones, except in the Tropical Very Humid Forest. **Conclusions:** The findings reinforce the importance of implementing genetic improvement strategies tailored to the life zones, given that additivity and recombination effects vary accordingly.

Keywords: crossbreeding; lactation; breed; heterosis (*Source: AGROVOC*)

INTRODUCTION

In Panama, per capita milk consumption has increased considerably, reaching approximately 120 liters per year. However, more than half of this consumption comes from imports, revealing a gap in national dairy production. In response, authorities have promoted genetic improvement, incorporating Holstein, Brown Swiss, and their crossbreds, which have shown favorable performance in the country's productive zones (Guerra-Montenegro & Menéndez-Buxadera, 2020).

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Crossbreeding dairy cattle in tropical production systems can increase productivity through heterosis and additive genetic effects. However, its benefits may vary depending on environmental factors, so targeted analyses are required to maximize performance in each setting. Such studies enable optimized breed selection and reproductive strategies tailored to the conditions in which production takes place—here identified as life zones—to strengthen the sustainability of the activity in Panama. Evidence shows that crossbred cows can achieve considerable increases in production compared with local breeds, demonstrating the effectiveness of crossbreeding as a genetic tool under challenging environmental conditions (Direba *et al.*, 2024).

Currently, there is no study in Panama that compares the interaction between productive factors, dairy cattle, and life zones. Such a study could provide valuable information on which breed or breed combination best fits the production system depending on the life zone in which it operates. The purpose of this work is to analyze the influence of additive genetic effects, heterosis, and gene recombination on the production of Holstein, Brown Swiss, and their crosses, evaluating their interaction with the life zones.

MATERIALS AND METHODS

The database was obtained from the VAMMP software (Romero-Zúñiga *et al.*, 2019), which is applied across multiple herds in Panama and was developed at the School of Veterinary Medicine of the National University of Costa Rica by the Regional Center for Informatics for Sustainable Animal Production (CRIPAS). A total of 951,170 periodic records—internationally known as Test Day (TD)—were collected between January 1990 and December 2023 in Chiriquí Province, Panama, across 20 farms (8,736 cows), each of which included more than one breed type.

Holstein, Brown Swiss, and their crossbred cows with at least one recorded lactation between January 1990 and December 2023 were included, from farms with more than five years of continuous records in the VAMPP software and located according to the life zone classification in Panama (Romero-Zúñiga *et al.*, 2019).

Additionally, other inclusion and exclusion criteria were applied to ensure the quality and homogeneity of the analyzed data. Only lactations with a minimum of 5 days in milking and a cumulative yield equal to or greater than 300 kg of milk were included, consistent with methodological recommendations used in genetic evaluation studies of dairy cattle (Hernández *et al.*, 2011). Duplicate or inconsistent records were excluded, as well as animals lacking sufficient information on herd, calving date, genotype, or with more than five lactations. After data cleaning, a robust database suitable for subsequent genetic evaluation was obtained (Table 1).

Under the conditions of this study, the environmental framework used was the system described by Holdridge (1977), which defines “life zones” based on ecological variables such as total annual precipitation, mean annual biotemperature, and altitude, and is applied by Panama’s Ministry of Environment (2019). This enabled comparison of dairy productivity across the country’s different ecological conditions. The study sites were located within the following life zones: Tropical Humid Forest (T-**hf**), Tropical Very Humid Forest (T-**vhf**), Premontane Very Humid Forest (P-**vhf**),

Lower Montane Pluvial Forest (**LM-pf**), and Premontane Pluvial Forest (**P-pf**) (Ministry of Environment, 2019).

Table 1. Distribution of Brown Swiss, Holstein, and their crossbreds across the different life zones

Live Zones	Holstein	50 Holstein x 50 Brown Swiss	75 Holstein x 25 Brown Swiss	50 Brown Swiss	Brown Swiss x 50 Holstein	75 Brown Swiss x 25 Holstein	Total
Tropical humid forest (T-hf)	60 365	15 392	21 012	12 960	1 635	9195	120 559
Tropical very humid forest (T-vhf)	209 433	11 298	19 959	114 282	53	10 442	365 467
Tropical very humid premontane forest (T-vhp)	33 718	3 694	1 667	37 995	308	1 673	79 055
Lower montane pluvial forest (LM-pf)	41 033	6 291	5 764	1 399	NA	162	54 649
Premontane pluvial forest (P-pf)	295 375	10 358	10 284	14 336	361	726	331 440
Total	639 924	47 033	58 686	180 972	2 357	22 198	951 170

NA Not available (the model accounted for the imbalance in the data).

TD results were analyzed using a generalized linear model with repeated measures.

The MLGR was implemented using the Echidna software (Gilmour, 2018) with fixed effects for contemporary groups (herd–year of calving–natural quarter; 979 levels), lactation number (four classes), life zone (lz; five levels), and the cow’s genotype at the time of the TD (geno; six classes). Lactation length was represented by days in milk grouped in 7-day classes (DIM7; 53 levels representing one year). Interactions among lz, geno, and DIM7 were evaluated to assess their effects on TD level, and final analyses were produced using SAS (SAS Institute Inc., 2021). This MLGR follows the same specification previously presented by Guerra-Montenegro and Menéndez-Buxadera (2020), whose solution procedure yields estimated TD curves for each DIM7 and annual production.

Heterosis was estimated using the following formula previously employed by Vargas-Leitón and Romero-Zúñiga (2010), $\text{Het \%} = \frac{\text{LS}_{F1} - \text{LS}_{\text{Pure}}}{\text{LS}_{\text{Pure}}} \times 100$ where LS_{F1} and LS_{Pure} correspond to the least-squares means from the MLGR model for F1 and purebreds, respectively. For the estimation of heterosis, only data from the two pure parental breeds and their F1 cross were used.

RESULTS AND DISCUSSION

This study analyzed 951,170 TD records from Holstein, Brown Swiss, and their crossbreds, distributed across five life zones in Chiriquí Province, Panama. All results were highly significant, particularly the interactions among life zone, genotype, and DIM7. The production trajectories for each life zone are shown in Figure 1.

The least-squares means displayed a characteristic lactation-curve pattern, with a maximum peak between weeks four and eight, followed by a progressive decline until the end of the period. This

behavior has been widely documented and represents the typical shape of the lactation curve in dairy cattle, which can be modeled with functions to estimate peak and persistency (Pangmao *et al.*, 2022).

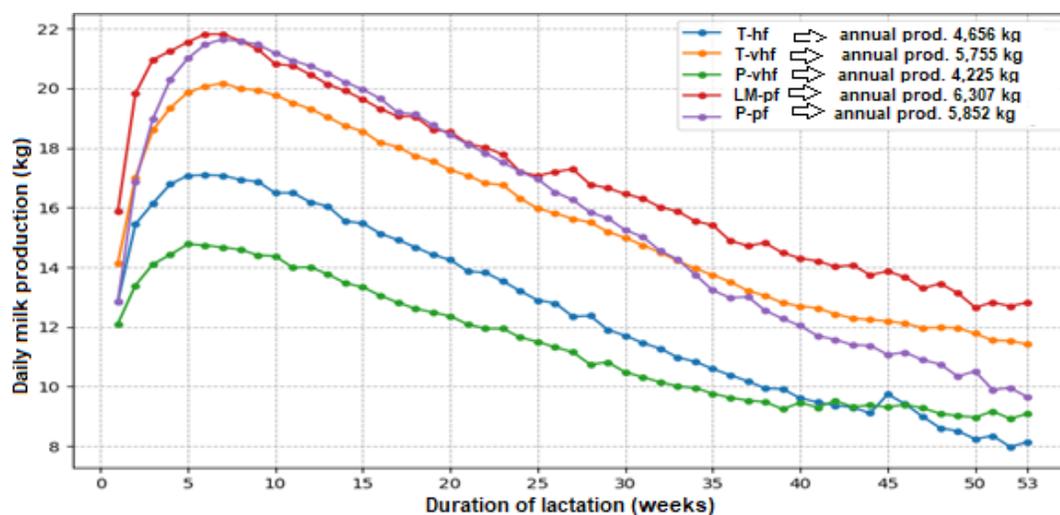


Figure 1. Least-squares means of daily production in each life zone.

The difference in annual production between the best life zone for dairy activity, LM-pf (6,307 kg), and the worst, P-vhf (4,225 kg), amounted to 2,072 kg. These results agree with Vargas and Ulloa (2008) in Costa Rica, who found significant differences in milk yield across agroecological zones, with the highest in LM-pf (6,586 kg) and the lowest in T-hf (3,522 kg). Likewise, the difference in productive persistence (Figure 1) is consistent with reviews conducted in tropical systems, which have found that phenotypic expressions are directly related to the local environment (Osei-Amponsah *et al.*, 2020).

The lactation curve varied among life zones. In P-pf and T-vhf production remained stable, whereas in P-vhf it declined rapidly after the peak. These differences may be related to environmental factors that define the life zones (temperature, precipitation, and humidity index). Sánchez *et al.* (2020) also highlighted this relationship, reporting that certain life zones such as P-vhf and T-vhf exhibit considerable variation in milk yield due to the unique characteristics of each zone influencing the performance of the dairy breeds under study.

Both pure breeds and their F1 cross show a similar pattern, with the well-known ascending phase during the first 7–8 weeks followed by a gradual decline throughout lactation (Figure 2).

Holstein animals reached the highest peak and higher values in the first weeks postpartum; however, this does not imply superior annual production by life zone. The interaction among breed, life zone, and days in milk was highly significant.

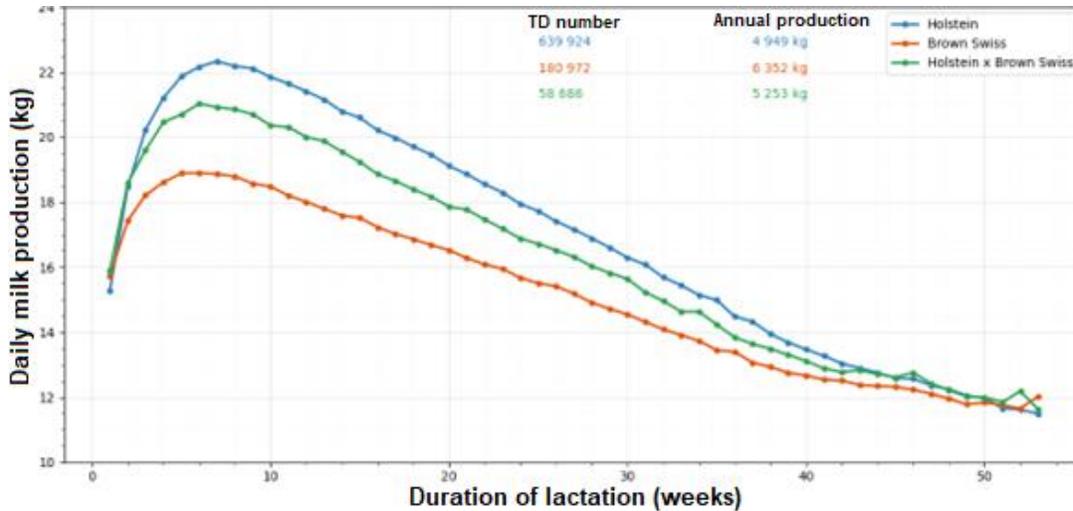


Figure 2. Lactation curve for Holstein, Brown Swiss, and their cross (F1)

A total of 639,924, 180,972 and 58,686 TD records were obtained for Holstein, Brown Swiss and their cross, respectively (Figure 2). Milk yield tended to increase during the first weeks, reaching its highest point between weeks five and seven, and then gradually declining across all breed groups analyzed. Overall annual production was 6,352 kg for Holstein, followed by 5,253 kg for the F1 cross. Brown Swiss produced 4,949 kg. These results suggest that the Holstein \times Brown Swiss cross increases production compared with Brown Swiss alone, although it does not reach the level of pure Holsteins.

Holstein cattle showed the highest production, with a peak of 22 kg/day between weeks five and seven. F1 animals reached intermediate production between Holstein and Brown Swiss, with a maximum peak of 21 kg/day, while pure Brown Swiss recorded the lowest production, peaking at 19 kg/day. These findings agree with Hernández-Zamudio *et al.* (2022), who reported that lactation curves in subtropical regions show similar production patterns between Holsteins and their crosses with Brown Swiss, although Holstein animals tend to reach higher production peaks. In terms of lactation persistency, crosses may represent an advantage under the environmental conditions of these regions.

Figure 2 also reveals notable differences in production stability among the genotypes evaluated. In contrast, Holstein shows a pronounced decline after the production peak. The Brown Swiss curve is more stable, while the F1 remained intermediate between the two parental breeds throughout the evaluation period.

Table 2. Additive, heterosis, and recombination effects in Holstein × Brown Swiss crosses across different life zones

Live Zones	Activity	Heterosis	Recombination	Mean in pure animals	Mean in Holstein x Brown Swiss	Heterosis %
Tropical humid forest (T-hf)	14.32	5.39	-6.7	13.14	12.77	2.8
Tropical very humid forest (T-vhf)	19.24	6.03	-12.14	16.48	16.7	1.03
Tropical very humid premontane forest (T-vhp)	13.51	3.94	-2.46	10.59	11.09	4.7
Premontane pluvial forest (P-pf)	20.42	7.39	9.16	17.06	19.53	14.4
Lower premontane pluvial forest (LM-pf)	16.79	8.63	-0.36	16.8	16.92	0.07
Total	14.81	5.9	-4.3	14.81	15.4	4.01

Notable differences were found in additivity, heterosis, and recombination for milk production. These results underscore the importance of considering not only the lactation peak but also its persistency as a relevant criterion for genetic selection in warm environments. As Hernández-Zamudio *et al.* (2022) highlight in their study of Holstein, Brown Swiss, and their crosses, lactation curve models reflect differences in stability and shape among genotypes.

Additive effects showed their highest values in P-pf and T-vhf, at 20.42 kg/day and 19.24 kg/day, respectively. This suggests that these zones favor the expression of dairy productive potential. Positive results were also found for LM-pf and T-hf, at 16.79 kg/day and 14.32 kg/day, respectively, although to a lesser extent.

In contrast, the P-vhf zone showed the lowest additive effect (13.51 kg/day). These results reinforce the importance of including the genetic component in improvement programs for milk production across the different life zones analyzed. Similar findings were reported by García-Bravo *et al.* (2023), who found that additive genetic effects were relevant in humid subtropical environments and suggested that total genetic differences between breeds can be strategically exploited in proportional balance with the life zone.

Heterosis also varied according to life zone, with 3.94 kg/day in P-vhf and 8.63 kg/day in LM-pf. The highest relative heterosis was observed in P-pf at 14.40%, indicating that in these zones crossbreds may gain a greater production advantage compared with purebreds. These results suggest that in certain life zones the use of crosses can be a beneficial strategy to increase milk yield. This agrees with Hernández-Zamudio *et al.* (2022), who noted that heterozygous effects may be better expressed in challenging environments where purebreds do not reach their full potential. In zones such as P-pf, the F1 cross represents a strategic alternative to improve productivity.

Recombination effects were mostly negative in T-vhf and P-vhf, at -12.14 kg/day and -2.46 kg/day, respectively. This indicates that genetic segregation can negatively affect milk production in these zones. However, a positive effect of 9.16 kg/day was observed in P-pf. Similar results were

reported by Dos Santos *et al.* (2021), who, when evaluating Girolando cows, found that recombination effects were mostly negative, especially at production peaks.

Other studies, such as Singhal *et al.* (2019), indicate that recombination can impose fitness costs on animals when beneficial parental allele combinations are broken, a phenomenon known as recombination load. Likewise, Butlin (2005) emphasizes that recombination can be beneficial by eliminating unfavorable or harmful combinations when coadapted gene complexes are broken, and also beneficial by generating new combinations in variable environments. Similarly, Shen *et al.* (2021) reported that recombination rate in cattle is modulated by environmental factors such as maternal age and temperature, which helps explain why negative effects were observed in some zones and positive effects in others.

When comparing average production of purebred and crossbred animals, crossbreds outperformed purebreds in 4 of 5 zones (T-vhf, P-vhf, P-pf, and LM-pf), while in T-hf the purebreds had higher values. However, in T-vhf the production of the purebreds (16.48 kg/day) was slightly lower than that of the crossbreds (16.70 kg/day).

In certain zones, genetic combination does not guarantee higher production; adaptation to the environment is decisive for performance. The success of crossbreeding depends on selecting the appropriate breed combination according to the environment (Goh *et al.*, 2022). These results confirm that the Holstein breed contributes greater additivity across all evaluated zones, with P-pf and T-vhf being the most favorable for its expression. Likewise, heterosis showed variable values, with LM-pf being the zone where crossing produced the largest increase in yield. However, recombination showed negative effects in some zones, underscoring the need to evaluate environmental conditions before implementing genetic improvement strategies in dairy production systems.

Overall, the results show that the highest production peak occurred in the Holstein breed, Brown Swiss had the most stable persistency, and F1 animals obtained the advantages in average production in four of the five zones evaluated, which suggests that the response depends both on the shape of the curve and on environmental conditions.

CONCLUSIONS

The Holstein breed consistently showed the highest milk production peaks, while the crosses exhibited greater persistency and, in certain life zones, comparable or higher annual yields.

Heterosis was especially favorable in zones such as LM-pf and P-pf, highlighting the potential of crossbreeding as a strategic tool for less restrictive environments. Recombination effects were negative in very humid zones, suggesting that in environments with greater climatic stress complex crossbreeding should be avoided. Conversely, in more stable zones they can be exploited to diversify the genetic base.

Genetic improvement programs must be adapted to life zones. The Holstein breed should be prioritized in herds aiming to maximize production peaks, while controlled crossbreeding is recommended to increase persistency and resilience in adverse environments.

REFERENCES

- Butlin, R. K. (2005). Recombination and speciation. *Molecular Ecology*, *14*(9), 2621–2635. <https://doi.org/10.1111/j.1365-294X.2005.02617.x>
- Direba, A., Tulu, D., & Habte, G. (2024). Genetic improvement of dairy cattle in tropical smallholder systems: A review. *Frontiers in Genetics*, *13*, 1106709. <https://doi.org/10.3389/fgene.2024.1106709>
- Dos Santos, D., Padilha, A. H., Gama, L. T., Silva, M. V. G. B., & Cobuci, J. A. (2021). Breed, heterosis, and recombination effects for lactation curves in Brazilian cattle. *Revista Brasileira de Zootecnia*, *50*, e20200085. <https://doi.org/10.37496/rbz5020200085>
- García-Bravo, L. A., Vega-Murillo, V. E., Villagómez-Cortés, J. A., Zárate-Martínez, J. P., Leyva-Ovalle, O. R., Calderón Robles, R. C., Ríos-Utrera, Á., Montaña Bermúdez, M., & Martínez-Velázquez, G. (2023). Efectos genéticos aditivos y no aditivos para características reproductivas en dialelo Holstein-Suizo Pardo en clima subtropical húmedo. *Revista Mexicana de Ciencias Pecuarias*, *14*(3), 556–571. <https://doi.org/10.22319/rmcp.v14i3.6247>
- Gilmour, A. R. (2018). Echidna mixed models software. In *Proceedings of the World Congress on Genetics Applied to Livestock Production* (p. 995). Auckland, New Zealand. <https://www.echidnamms.org/>
- Goh, Y. M., Tay, T. S., & Lim, K. H. (2022). The potential of using temperate–tropical crossbreds and agro-industrial by-products to alleviate heat stress in tropical dairy production. *Animals*, *12*(1), 1. <https://doi.org/10.3390/ani12010001>
- Guerra Montenegro, R., & Menéndez-Buxadera, A. (2020). Análisis comparativo de la repetibilidad para producción de leche en ganado Holstein puro o cruzado con Brown Swiss y Jersey en la cuenca lechera de Chiriquí. *Revista Investigaciones Agropecuarias*, *3*(1), 12–29. <https://doi.org/10.48204/j.ia.v3n1a2>
- Hernández, A., Ponce de León, R., García, S. M., García, R., Mora, M., Gutiérrez, M., & Guzmán, G. (2011). Parámetros genéticos en rasgos de la producción lechera y la longevidad de vacas Mambí de Cuba. *Archivos de Zootecnia*, *60*(231), 513–520. <https://doi.org/10.4321/S0004-05922011000300040>
- Hernández-Zamudio, J. A., Villagómez-Cortés, J. A., Vega-Murillo, V. E., Leyva-Ovalle, O. R., Vicente-Martínez, J. G., & Ríos-Utrera, Á. (2022). Comparison of models for lactation curves of Holstein, Brown Swiss, and F1 crossbred cows under subtropical conditions.

Sánchez, A., Guerra, R., Mojica, K., Menéndez-Buxadera, A.

Tropical Animal Health and Production, 54, Article 92. <https://doi.org/10.1007/s11250-022-03144-4>

Holdridge, L. R. (1977). *Ecología basada en zonas de vida* (4.^a reimp.). Instituto Interamericano de Cooperación para la Agricultura (IICA). <https://hdl.handle.net/11324/20468>

Ministerio de Ambiente. (2019). *Estrategia Nacional Forestal 2018–2050*. Gaceta Oficial Digital de la República de Panamá, No. 28745-A. Recuperado de <https://www.gacetaoficial.gob.pa>

Osei-Amponsah, R., Asem, E. K., & Obese, F. Y. (2020). Cattle crossbreeding for sustainable milk production in the tropics. *International Journal of Livestock Production*, 11(4), 108–113. <https://doi.org/10.5897/IJLP2020.0717>

Pangmao, S., Thomson, P. C., & Khatkar, M. S. (2022). Genetic parameters of milk and lactation curve traits of dairy cattle from research farms in Thailand. *Animal Bioscience*, 35(10), 1499–1511. <https://doi.org/10.5713/ab.21.0559>

Romero-Zúñiga, J. J., Rojas Campos, J., Bolaños Segura, M., Castillo Badilla, G., Vargas Leitón, B., & Estrada König, S. (2019). Software VAMPP Bovino como instrumento de mediación dialógica entre el sector productivo bovino y la academia. *Universidad en Diálogo: Revista de Extensión*, 9(2), 99–116. <https://doi.org/10.15359/udre.9-2.5>

SAS Institute Inc. (2021). *SAS/STAT® 14.3 User's Guide*. SAS Institute Inc. <https://www.sas.com>

Sánchez, V., Zúñiga, J., Romero, J. R., & Vargas-Leitón, B. (2020). Sistemas de información para el manejo de hatos en apoyo a la investigación de poblaciones bovinas: el caso de VAMPP en las zonas de vida bosque muy húmedo montano, bosque muy húmedo premontano y bosque muy húmedo tropical de Costa Rica (1987–2018). *Agronomía Mesoamericana*, 31(1), 141–156. <https://doi.org/10.15517/am.v31i1.37062>

Shen, X., Li, C., Chen, Y., & Zhang, S. (2021). Effect of temperature and maternal age on recombination rate in cattle. *Frontiers in Genetics*, 12, 682718. <https://doi.org/10.3389/fgene.2021.682718>

Singhal, S., Gomez, S. M., & Burch, C. L. (2019). Recombination drives the evolution of mutational robustness. *Current Opinion in Systems Biology*, 13, 142–149. <https://doi.org/10.1016/j.coisb.2018.12.003>

Vargas-Leitón, B., & Romero-Zúñiga, J. J. (2010). Efectos genéticos aditivos y no aditivos en cruces rotacionales Holstein×Jersey y Holstein×Pardo suizo. *Agronomía Mesoamericana*, 21(2), 223–234. <https://doi.org/10.15517/am.v21i2.4885>

Vargas, B., & Ulloa, J. (2008). Relación entre crecimiento y curvas de lactancia en grupos raciales lecheros de distintas zonas agroecológicas de Costa Rica. *Livestock Research for Rural Development*, 20(8), Article #122. <http://www.utaoundation.org/lrrd2008/varg20122.htm>

AUTHOR CONTRIBUTION STATEMENT

Research conception and design: AS, AMB; data analysis and interpretation: AS, AMB, RG, KM; manuscript writing: AS, AMB, KM, RG.

CONFLICT OF INTEREST STATEMENT

The authors state there are no conflicts of interest whatsoever.