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Population Parameters for Trypanotolerance Traits in an N'Dama x Boran Crossbreeding Population

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Introduction

Cattle are infected with trypanosomosis through the bite of tsetse flies carrying the pathogenic protozoa, causing anaemia, weight loss, pyrexia, abortion, reduced milk yield and, in the absence of treatment, death inter alia (Eisler et al., 2004). With an estimated number of 46 million cattle to be at risk of contracting the disease in tropical Africa (Kristjanson et al., 1999), trypanosomosis is ranked among the ten most severe cattle diseases affecting the poor in Sub-Saharan Africa (Thornton et al., 2002). Tolerant livestock shows the heritable ability to survive, reproduce and gain weight under natural trypanosome challenge without the aid of trypanocidal drug treatment (Murray et al., 1982). The heritable component of any phenotype is very important because it is the only or one of the major genetic parameters that determines how much improvement we can make regardless of environmental or non-genetic input. Genetic components of phenotypic variations also function as sustainable animal breeding tools since genetic superiority once achieved is inheritable and can be maintained over generations. Together with heritability as a predictor of response to selection (Dolan, 1987), genetic correlations give evidence for indirect selection response in correlated traits (Lynch and Walsh, 1998). Hence estimated heritability and genetic correlations are important population parameters to decide which of the targeted traits promise the best results in a selection process.
The present study on phenotypic and genetic population parameters is based on the defined trypanotolerance criteria and dataset from a crossbreeding experiment with N'Dama and Boran cattle used by Hanotte et al. (2003) for the purpose of mapping quantitative trait loci (QTL).

Material and Methods

Population background

In 1983 the crossbreeding between trypanotolerant N'Dama (*Bos Taurus*) and trypanosusceptible Boran (*Bos Indicus*) cattle was initiated at the International Livestock Institute (ILRI) in Kenya to construct a population with a pedigree structure fit to detect quantitative trait loci (QTL) for trypanotolerance. Phenotypic data for the analyzed traits have been recorded on a second generation (F_2) crossbred cattle from seven families. Using multiple ovulation and embryo

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transfer, 176 offspring with complete data-set in families of size ranging from 21 to 39 animals were born between November 1992 and September 1996. A detailed description of the experiment can be found in Hanotte et al. (2003) and Van der Waaij (2001).

Data collection and trait definition

The naïve F_2-offspring were challenged with the bite of a tsetse fly (*Glossina morsitans centralis*) infected with a *Trypanosoma congolense* clone at the age of 12 months mimicking a medium natural challenge level. Phenotypic recording started 3 weeks prior to challenge and continued over a period of 150 days after challenge, monitoring packed red blood cell volume (PCV), level of parasitaemia (estimated by the dark-ground/phase contrast buffy coat method (Paris et al., 1982)) and body weight (BW). Records were taken at least once a week. When PCV declined from an average of 37 to ≤ 12 %, animals were treated, removed from the experiment and their last record before treatment was taken as the value of the trait for the remainder of the challenge period (Hanotte et al., 2003).

Standardized trait definitions to characterize trypanotolerance do not exist. The definition of the 16 phenotypic traits used in this study correspond to the traits that were analyzed for mapping QTL by Hanotte et al. (2003):

Prechallenge (nontrypanotolerance) traits

- PCVI = Initial PCV (mean PCV days 21-0) before challenge
- BWI = Initial BW (mean BW days 21-0) before challenge

Ambiguous (trypanotolerance or nontrypanotolerance) trait

- BWA = Average BW after challenge (days 0-150)

Postchallenge (trypanotolerance) traits

- PCVF = Finale PCV (day 150 or day before treatment)
- PCVM = Minimum PCV recorded during the postchallenge period (days 0-150)
- PCVI minus PCVF (PCVIF) = PCVI (day 0) minus PCVF
- PCVI minus PCVM (PCVIM) = PCVI (day 0) minus PCVM
- PCVFM = PCVF (day 150 or last day before treatment) minus PCVM
- PCV variance (PCVV) = Variance of the PCV values postchallenge (days 0-150)
- PCVD150 = Percentage decrease in PCV up to day 150 after challenge
  [(Mean PCV days 0-11) - (mean PCV days 13-150)]/(mean PCV days 0-11)
- PCVD100 = Percentage decrease in PCV up to day 100 after challenge
- BWF/BWI = Finale BW scaled by BWI
- BWD150 = Percentage decrease in BW up to day 150 after challenge
- PARMLn = Mean of natural logarithm (ni + 1), ni = number of parasites at day i after challenge (days 11-150)
- PARLnM = Natural log. of the mean number of parasites after challenge (days 11-150)
- Detection rate (DR) = No. of times an individual is detected to be infected (days 60-150)

Statistical model and analysis

Each of the defined traits was analyzed separately with a single trait linear mixed animal model using the following model:

$$Y_{jk} = \mu + g_j + a_k + e_{jk}$$

where Y_{jk} was one of the 16 trait variables, μ was the overall mean, g_j was the fixed effect of group j with 23 levels, a_k was the random additive genetic component of animal k, and e_{jk} was the random error term. Only significant effects ($p < 0.05$) were fitted thus excluding group effect for the analysis of DR and PARLnM. It was assumed that dominance variance and variance due to common environment do not exist as well as maternal effects within offspring of one pair of F_1 parents because embryos were randomly assigned to recipient dams. Fixed group effect was fitted to adjust for seasonal changes and differences in challenge level that may have occurred over time as groups combined calves with similar birth date.

Phenotypic and genetic correlations between all traits were estimated with bivariate mixed models, with each trait having the model terms used in single trait analysis. Variance components were estimated in ASREML (Gilmour et al., 2002) that uses residual maximum likelihood techniques.

Results and Discussion

The phenotypic variances (Var(P)), genetic variances (Var(G)) and heritabilities (h^2) with their standard errors (SE) from univariate analysis for all traits are presented in the table below. Heritability estimates range from 0.11 to 0.45 suggesting opportunities for genetic improvement in these trypanotolerance traits. SE are high for Var(G) and heritabilities and Var(G) could not be estimated for PCVV and DR due to limited data size.

Table. Phenotypic variances (Var(P)), genetic variances (Var(G)) and heritabilities, (h^2) with their standard error (SE) estimates for all traits* on 176 F_2 offspring

Traits*	Var(P)	SE	Var(G)	SE	h^2	SE
PCVI	7.95	1.15	1.53	1.76	0.19	0.20
BWI	396.90	65.00	115.39	109.98	0.29	0.24
BWA	445.20	64.78	87.03	99.46	0.20	0.20
PCVM	8.78	1.68	3.66	3.06	0.42	0.28
PCVF	37.78	6.53	13.25	11.31	0.35	0.25
PCVIF	35.94	4.59	3.80	5.48	0.11	0.15
PCVIM	10.35	1.18	0.00	0.00	0.00	0.00
PCVFM	16.83	2.79	5.55	4.71	0.33	0.24
PCVV	24.59	2.81	0.00	0.00	0.00	0.00
PCVD150	68.78	9.60	10.56	14.16	0.15	0.19
PCVD100	45.96	7.36	11.90	12.36	0.26	0.24
BWF/BWI	0.01	0.00	0.00	0.00	0.16	0.18
BWD150	0.24	0.04	0.11	0.08	0.45	0.25
PARMLn	0.47	0.07	0.09	0.10	0.20	0.19
PARLnM	0.22	0.03	0.06	0.05	0.28	0.21
DR	0.03	0.00	0.00	0.00	0.00	0.00

* See text for definitions of the traits.

The starting value for PCV (PCVI) showed only small genetic correlation with any of the trypanotolerance traits, the strongest of which were estimated between PCVI and PCVM, PCVF, PCVIF and BWD150 with values of 0.27 ± 0.07, 0.26 ± 0.07, 0.22 ± 0.07 and -0.19 ± 0.07 respectively, suggesting that an increase in the general PCV-level which is not related to trypanotolerance because it is measured on healthy animals prior to infection cannot be expected to have a major impact on the tolerance level. Body weight at the age of twelve months before challenge (BWI) showed no genetic correlation with the two trypanotolerance traits BWF/BWI and BWD150 and only small to moderate genetic correlation with PCV and parasitaemia traits along with large standard errors making concrete interpretation impossible.

Overall, the limited correlations between the pre- and post-challenge traits clearly demonstrate that selection for trypanotolerance depends on traits that require data from infected animals unless marker information (e.g. QTL) could be used instead. To minimize negative effects of trypanosome infection on animal performance and wellbeing, the test period has to be short and the emphasize of selection is therefore likely to be put on PCV and parasitaemia traits because "over a shortened test period PCV values can be much more accurately measured than can animal performance" (Trail et al., 1991) and blood samples for PCV recording can be used for parasite count at the same time (Eisler et al., 2004).

Minimum PCV (PCVM) was recorded at day 72 post infection (Van der Waaij, 2001) which was earliest compared to all other PCV traits and consequently presents a desirable trypanotolerance parameter. The sizable variation, genetic variance and strong correlation of PCVM with PCVD150 and PCVD100 make PCVM which predicted 42 %, 26 %, 69 % and 61 % of variation in PCVIF, PCVFM, PCVD150 and PCVD100 respectively a favorable measure to describe trypanotolerance in place of other PCV traits in this study. Confirming results from other studies about the favorable relationship between control of anaemia and course of BW during infection (Trail et al., 1991; Naessens et al., 2003), genetic correlations with the BW traits were moderate to high, suggesting that selection on PCVM would indirectly improve production performance under challenge.

As the development of BW under trypanosomosis challenge is economically most important (Kristjanson et al., 1999), it seems reasonable to use a BW criterion to measure trypanotolerance in animals. Genetic variance, heritability and genetic correlation estimates as well as results from QTL analysis (Hanotte et al., 2003) favor BWD150 or BWA as criterion to describe trypanotolerance because BWD150 was associated with three QTL for trypanotolerance compared to BWF/BWI which was associated with only one QTL for trypanotolerance and BWA was associated with an isolate high-BW effect in addition to also three QTL for trypanotolerance (Hanotte et al., 2003). Genetic correlations of BWD150 with BWA, PCVM, PCVF, PCVIF, PCVFM, PCVD150, PCVD100, PWF/BWI, PARMLn and PARLnM were -0.28 ± 0.11, -0.59 ± 0.09, -0.68 ± 0.05, 0.59 ± 0.06, -0.57 ± 0.06, 0.56 ± 0.08, 0.40 ± 0.11, -0.93 ± 0.01, 0.00 ± 0.61 and -0.24 ± 0.51 respectively and for BWA with PCVM, PCVF, PCVIF, PCVFM, PCVD150, PCVD100, PWF/BWI, BWD150, PARMLn and PARLnM were 0.34 ± 0.60, 0.12 ± 0.66, -0.50 ± 0.82, -0.04 ± 0.67, -0.62 ± 0.61, -0.62 ± 0.59, 0.30 ± 0.08, -0.28 ± 0.11, 0.34 ± 0.79 and -0.03 ± 0.68 respectively. QTL results suggest that the use of BWA in a selection scheme is likely to improve trypanotolerance and BW simultaneously.

Besides PCV and body weight traits, the animal's ability to control, reduce or even eliminate the parasites is an important trypanotolerance feature (Murray et al., 1982) as the parasite causes the disease. Genetic correlation between PARMLn and PARLnM was estimated to be 0.44 ± 0.06. All other estimates were either negligible small or accompanied by such huge standard errors that the estimate cannot verify a correlation between the traits. This result confirmed earlier evidence from a chimera experiment where limitation of anaemia and control of parasitaemia were suggested to be based on two separate mechanisms that linked control of anaemia to the influence of haemopoietic tissue genotype while parasite control was independent of the genetic origin of the haemopoietic tissue (Naessens et al., 2003). It is therefore important to select for criteria from both trypanotolerance characteristics to gain the best result in the level of tolerance.

Conclusion and Outlook

Most of the analyzed traits were moderately heritable with a range of 0.11 to 0.45 and sufficient genetic variance to present feasible selection criteria for a breeding program though emphasize should be put on early measures such as minimum PCV (PCVM) and economically important traits like mean body weight (BWA). Because the correlation results confirmed earlier suggestions that control of parasitaemia and limitation of anaemia are functionally independent and based on different mechanisms, it would be reasonable to select on both evolutionary developed traits to maximize the overall disease tolerance and PCVM for anaemia and the number of parasites (PARMLn) after challenge for parasitaemia control seem to be feasible measures. Overall several estimates were accompanied by high SE due to limited data-size and would therefore need to be validated with a larger number of records.

With the estimated population parameters, it is now possible to evaluate genetic merit for trypanotolerance traits in simulated breeding schemes and from there develop a breeding program for cattle with special focus on trypanotolerance to address locations where alternative control

strategies would be difficult to implement or maintain due to lack of resources and infrastructure. Finally, successful breeding and selection on trypanotolerance criteria should give rise to productivity gains through minimizing the deleterious effects of trypanosome infection in cattle.

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References

Dolan, R. B. 1987. Genetics and trypanotolerance. Parasitology Today 3: 137-143.

Eisler, M. C., R. H. Dwinger, P. A. O. Majiwa, and K. Picozzi. 2004. Diagnosis and epidemiology of african animal trypanosomiasis. In: I. Maudlin, P. H. Holmes and M. A. Miles (eds.) The trypanosomiases. p 253-268. CAB International 2004.

Gilmour, A. R., B. J. Gogel, B. R. Cullis, S. J. Welham, and R. Thompson. 2002. Asreml user guide release 1.0. VSN International Ltd, Hemel Hempstead, HP1 1ES, UK.

Hanotte, O., Y. Ronin, M. Agaba, P. Nilsson, A. Gelhaus, R. Horstmann, Y. Sugimoto, S. Kemp, J. Gibson, A. Korol, M. Soller, and A. Teale. 2003. Mapping of quantitative trait loci controlling trypanotolerance in a cross of tolerant west african n'dama and susceptible east african boran cattle. Proceedings of The National Academy of Sciences of The United States of America 100: 7443-7448.

Kristjanson, P. M., B. M. Swallow, G. J. Rowlands, R. L. Kruska, and P. N. de Leeuw. 1999. Measuring the costs of african animal trypanosomosis, the potential benefits of control and returns to research. Agricultural Systems 59: 79-98.

Lynch, M., and B. Walsh. 1998. Genetics and analysis of quantitative traits. Sinauer Associates, Sunderland, Massachusettes, 01375 U.S.A.

Murray, M., W. I. Morrison, and D. D. Whitelaw. 1982. Host susceptibility to african trypanosomiasis - trypanotolerance. Advances in Parasitology 21: 1-68.

Naessens, J., S. G. A. Leak, D. J. Kennedy, S. J. Kemp, and A. J. Teale. 2003. Responses of bovine chimaeras combining trypanosomosis resistant and susceptible genotypes to experimental infection with trypanosoma congolense. Veterinary Parasitology 111: 125-142.

Paris, J., M. Murray, and F. McOdimba. 1982. A comparative-evaluation of the parasitological techniques currently available for the diagnosis of african trypanosomiasis in cattle. Acta Tropica 39: 307-316.

Thornton, P., R. Kruska, N. Henninger, P. Kristjanson, R. Reid, F. Atieno, A. Odero, and T. Ndegwa. 2002. Maping poverty and livestock in the developing world. ILRI (International Research Institute), Nairobi, Kenya. 124 pp.

Trail, J. C. M., G. D. M. d'Ieteren, J. C. Maille, and G. Yangari. 1991. Genetic aspects of control of anaemia development in trypanotolerant n'dama cattle. Acta Tropica 48: 285-291.

Van der Waaij, E. H. 2001. Breeding for trypanotolerance in african cattle. Ph.D. thesis, Wageningen University, Wageningen, The Netherlands.