Evidence of a Major Gene for Tick- and Worm resistance in Tropical Beef Cattle via Complex segregation analyses

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BACKGROUND and OBJECTIVES

Background:

- TICK infestation with *Boophilus microplus* is the major environmental stressor in Tropical North Australia, affecting productivity and welfare of cattle
- Endoparasites or intestinal worms (*Haemonchus, Oesophagostomum, Trichostrongylus and Cooperia*) causes substantial losses in the beef industry and is also of welfare issue in Tropical North Australia
- In extensive pastures of Northern Australia it is often hard and not feasible to use chemicals for controlling parasites ; in addition public awareness of chemical residues in animal products be addressed.
- No study has so far investigated mode of inheritance of tick and worm (whether it is fully polygenic or a mixture of polygenes and a major gene) in Brahman and zebu cross bred cattle.
- The knowledge of genetic properties of tick and worm resistance is essential to develop breeding / selection programs in tropical cattle.

Main objectives:

- Estimate genetic and phenotypic parameters of tick and worm estimates using records from cross breeding experiments conducted at CSIRO Livestock industries Rockhampton Australia.
- Apply Bayesian segregation analysis (BSA) methods using Monte carlo Markov Chain (MCMC) techniques.

MATERIALS

- A crossbreeding experiment was conducted between 1992 and 1997 at the Australian National Cattle Breeding Station 'Belmont' near Rockhampton, Queensland.
- There were 3 crossbred types: *Bos taurus* derived Tropically adapted British (BB) ; *Bos inducus* derived Zebu (ZZ) and Sanga derived (SS) crosses
- Tick counts (TICK) and faecal worm egg counts (EPG) were recorded on all weaned animals from these breeds over a 9-week period at 3 weekly intervals before commencement of the tick and worm treatment (dipping & drenching).
- Data structure used in the analyses are given in Table 1 and is the same as used by Prayaga et al (2003) for estimation of polygenic heritability (h^2) for TICK and EPG from REML analysis.

Fig 1. TICK count in BB cattle; Tick (insert)

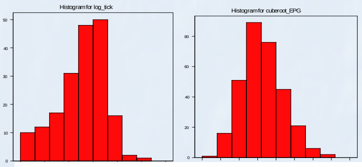

Fig 2.Histogram of log TICK and cube-root EPG counts in BB cattle

METHODS

- Descriptive, exploratory analysis and ANOVA analyses were done prior to full BSA. As data was highly skewed, TICK data was log transformed and EPG data was cube root transformed (Fig 2).
- Segregation Analysis was based on the method of *Kadarmideen and Janss (2005)* which shows detection of major gene for binary traits using MCMC methods and estimation of Mendelian transmission probabilities to distinguish environmental and genetic transmission.
- These routines are available in a software called ***iBay*** (*Janss* 2006).

RESULTS

- there were 6 different datasets (3 breeds x 2 traits)but results are shown only for BB breed in Table 2 below.

Table 1. Dataset used in estimating major gene parameters for tick counts (TICK) and faecal worm egg counts (EPG) in three cattle breed types (BB, SS and ZZ)

	# of animals in TICK-data	# of animals in EPG-data
Breed BB		
Animals	187	307
Sires	29	31
Dams	124	146
# of missing sires	0	5
Breed SS		
Animal	147	224
Sires	31	33
Dams	102	126
# of missing sires	7	8
Breed ZZ		
Animals	178	270
Sires	38	46
Dams	144	182
# of missing sires	5	7

Table 2. Posterior mean and SD of parameters of segregation analysis of TICK count (log transformed) and worm egg count (EPG) cube-root transformed. Confirmation of Mendelian segregation by estimation of transmission probabilities[1]

Major gene Parameters	*TICK in BB breed*		*EPG in BB breed*	
	Posterior Mean	Posterior SD	Posterior Mean	Posterior SD
Additive effect	0.73	0.54	1.72	1.22
Additive variance	0.43	0.38	2.32	2.11
Pr(A|AA)	0.75	0.20	0.81	0.17
Pr(A|AB)	0.45	0.21	0.54	0.19
Pr(A|BB)	0.18	0.11	0.24	0.18

[1] Results indicate that these probabilities are close to those expected by Mendelian segregation

DISCUSSION

Bayesian segregation analysis

- Used a simple model and results are only exploratory
- However, preliminary investigations show large major gene effects for TICK-BB, EPG-BB, EPG-SS and EPG-ZZ

Estimation of Mendelian Transmission Probabilities

- Mendelian segregation was confirmed by estimation of transmission prob. by setting variances, allele effect and frequency at the fitted BSA model.
- The results reported here will be useful in breeding programs aimed at improving tick and worm resistance
- it also provides a basis for more molecular investigations such as whole genome association studies.

REFERENCE

Janss (2006). iBay Reference. http://www.lucjanss.com/
Kadarmideen & Janss (2005). Genetics 171:1195-1206
Prayaga, K.C. 2003. Australian J. Agric. Research, 54: 1027-1038.

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