Genetic and Phenotypic Characteristics of Infectious Keratinoconjunctivitis in Tropical Cattle

A.A. Ali[*†], H.N. Kadarmideen[*], P.C. Thomson[†] and C.J. O'Neill[*]

Introduction

Infectious bovine keratinoconjunctivitis (IBK) is also known as pinkeye and is one of the most economically important diseases in cattle worldwide. An Australian postal survey recorded that 81% of participating cattle owners reported the occurrence of IBK, and 75% observed a reduction in the weight gain of the affected cattle (Slatter *et al*. (1982)). Although this survey is outdated, the IBK is still considered as problematic to livestock industries. The most common bacterial pathogen to cause IBK is *Moraxella bovis* (Brown *et al*. (1998)). Transmission of *Moraxella bov*is is through direct contact, nasal and ocular discharges, and most commonly by the face fly. Breed differences exist in incidences of IBK; generally, *Bos taurus* are more susceptible than *Bos indicus* but within *B. taurus*, animals with Hereford inheritance were reported to be most susceptible (Snowder *et al.* (2005)). Casa and Stones (2006) demonstrated initial evidence of a QTL (quantitative trait loci) on BTA 20 for susceptibility to IBK infection in a composite of Hereford and Shorthorn line adapted to Australian tropical regions. The genetic basis of the tropical or tropically adapted cattle's ocular defense against IBK remains to be investigated. The extent to which genetic selection and breeding programs targeting IBK will decrease the incidence of the disease is unknown. Estimations of heritability and genetic variance of IBK are limited in the literature and confined to temperate regions. The objective of this study was to estimate genetic parameters in a tropical herd of interbred Hereford – Shorthorns (now known as *Adaptaur*) where outbreak of IBK was recorded.

Material and methods

Animals. A detailed history of the Hereford and Shorthorn (HS) line can be found in (Frisch *et al*. (2000)). Briefly, the herd was first introduced to the CSIRO 'Belmont' Research Station in the 1950s at Rockhampton, north-eastern Australia, with a nominal composition of 50% Hereford and 50% Shorthorn. A repeated herd selection was primarily undertaken for high growth rate and high tick resistance. A detailed description of the herd management and environment of 'Belmont' can be found in Frisch (1981). The present study estimates genetic parameters for IBK using a total of 1583 animals, born during 1960 to 1999 and recorded for IBK occurrence. Pedigree of these animals was traced back 3-4 generations and contained 3312 animals.

Phenotype. The incidence and severity of IBK was recorded using the grading system. Briefly, each eye of each animal was recorded on a scale from 1 = clear to 6 = complete corneal opacity, including blindness. Animals were repeatedly assessed of IBK infection

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[*] CSIRO Livestock Industries, Davies Laboratory, University Drive, Townsville, QLD 4810, Australia
[†] Faculty of Veterinary Science, The University of Sydney, Private Bag 4003, Narellan NSW 2567, Australia

status at three life stages: pre-weaning calves (up to three occasions, 3 – 6 months of age), post-weaning calves (up to 5 occasions, 6 – 18 months of age) and females once they joined the breeding herd (up to 4 occasions, 2 – 12 years of age). For each animal, the ordinal scores of both eyes were summed to be a single score resulting in a total score per animal per time point of 2 to 12.

Statistical Analysis.
Variance components were estimated using ASReml version 3.0, (Gilmour *et al.* (2009)) to fit an animal model: $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e}$, where $\mathbf{y}$ is an $n \times 1$ vector of observed IBK scores. In the ordinal raw data, y is an average of individual IBK scores across 3 time points during pre-weaning, across 5 time points during post-weaning and across 4 time points in mature animal, $\boldsymbol{\beta}$ is the $p \times 1$ vector representing coefficients of the fixed effects, $\mathbf{X}$ is an n x p design matrix associated with the fixed effects (animal's birth year, sex and treatment), $\mathbf{u}$ is the $q \times 1$ vector of random animal effects, $\mathbf{Z}$ is the $n \times q$ design matrix associated with random animal effects, and $\mathbf{e}$ is the $n \times 1$ vector of residual errors, assumed to have $N(0, \sigma_\varepsilon^2)$. The same IBK scores were also log transformed across time points and averaged within three life stages and analyzed using the above model. Thus, there were 3 untransformed and 3 log transformed traits for variance component estimation.

Results and Discussion

Descriptive Statistics. Figure 1 shows the distribution of IBK scores in pre-weaning, post-weaning and mature animals. Post-weaning calves had the highest scores for clear eyes (count = 3737), and mature animals had the lowest (count = 711).

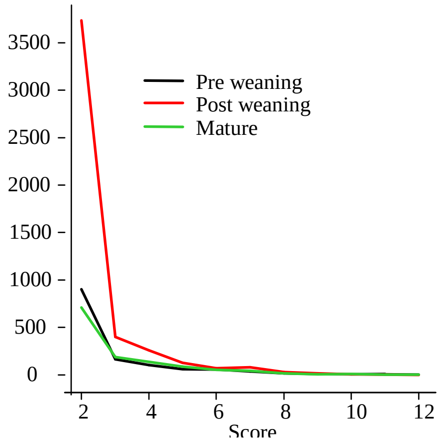

Figure 1. Distribution of IBK scores in beef cattle recorded at 3 life stages

Mean IBK score with complete bilateral and lateral blindness was 3.00±1.16 and 59.67±4.72, respectively, in pre-weaning and mature animals. In the original (untransformed) data, the three animal life stages demonstrated positively skewed distribution. Log transformation decreased the skewness for pre and post-weaning considerably, but not in data for mature animals. In the model, fixed effects of animal's birth year, sex and treatment were all highly significant in the three life stages. Based on the direction of the regression coefficients, the mean IBK score increases as age increases: heifers were more resistant (lower scores) than mature animals.

Distributions of estimated breeding values are shown in Figure 2. This shows that there is a large variability in animals' resistance or susceptibility to IBK and there is a scope for genetic selection. In a breeding program to improve genetic resistance to IBK, individuals with lowest EBV (i.e. extreme left of the BLUP histogram would be desirable selection candidates).

Genetic parameters.

Variance components, standard error (se), *z*-ratio and heritability are shown in Table 1. It demonstrates that estimated parameters are appreciably different between raw ordinal scores and the log transformed data. This difference is partly explained by the effect of skewed data on estimated parameters. In mature animals, the data remained much skewed despite the transformation. This may be due the sample size (n =181) in the mature age animal category.

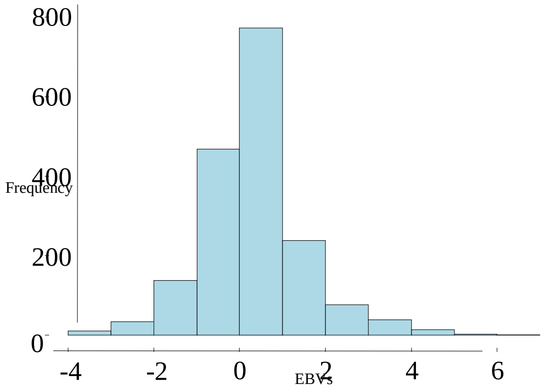

Figure 2. EBVs for IBK scored in Hereford and Shorthorn line

Estimates of heritability for IBK ranged from 0.01 to 0.15 in the three animal life stages we examined (Table 1) where h^2 tended to be slightly higher for raw than log transformed scores. A large scale study of IBK infection involving 41,986 animals from nine pure and three composite breeds of cattle, (Snowder *et al*. (2005)) reported heritability ranged between 0.00 ± 0.02 in Charolais to 0.28 ± 0.05 in Hereford. Our estimate in the HS line was within this range.

Table 1. Comparison of genetic parameters estimates for raw and transformed ordinal scores using linear model analysis in pre-weaning, post-weaning and mature ages. σ_g^2 and σ_e^2 are estimates of the animal and environmental variances respectively.

Data	n	σ_g^2 (se)	z-ratio	σ_e^2 (se)	z-ratio	h^2
Raw data						
Pre-weaning	458	1.07(0.57)	1.88	16.18(0.75)	21.69	0.06
Post-weaning	944	5.06(2.19)	2.32	48.42(2.45)	19.80	0.10
Mature	181	5.57(1.59)	3.51	30.56(1.61)	19.04	0.15
Log$_{10}$-transformed data						
Pre-weaning	458	0.28(0.53)	0.52	27.61(1.10)	25.01	0.01
Post-weaning	944	17.96(10.55)	1.70	319.62(14.46)	22.10	0.05
Mature	181	5.57(1.59)	3.51	30.56(1.61)	19.04	0.15
Total	1583	-	-	-	-	-

It should be also noted that we fitted a cross-sectional linear mixed model on longitudinal ordinal categorical data but a more statistically appropriate model would be a longitudinal or random regression threshold mixed model for ordinal data (Kadarmideen *et al*. (2001)). Threshold models usually provide higher heritability estimates than linear models as the estimation is based on liability scales rather than the observed categorical data (Kadarmideen *et al*. (2001)). However, using linear mixed and multi-threshold models, previous study showed that log transformed ordinal scores resulted in heritability estimates more similar to those obtained when ordinal logistic regression model was used, (Wilson *et al*. (2009)). Further work is currently underway to assess the accuracy of genetic parameter estimates for ordinal traits by implementing multi-threshold models and genetic correlations of IBK with other production and reproduction traits.

Conclusion

Analysis of this IBK data suggests a low heritability ranging from 0.01 to 0.15 at different stages of lifetime performance of beef cattle in the tropics. This suggests that a genetic selection against this disease is possible although the response to selection would only be moderate due to low heritabilities in general. However, estimated heritability increases with animal's age indicating that selection is more effective at later than early stages.

Acknowledgments

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