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Genetic relationships of breech cover, wrinkle and wool coverage scores with key production traits in Australian Merino sheep

S. Hatcher^{a,b,*}, J.W.V Preston^{a,b}^a CRC for Sheep Industry Innovation, Homestead Building, University of New England, Armidale, New South Wales 2350, Australia^b NSW Department of Primary Industries, Orange Agricultural Institute, 1447 Forest Road, Orange, New South Wales 2800, Australia

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ABSTRACT

Merino breeding programs seeking a genetic solution to reduce the incidence of flystrike require estimates of genetic correlations between both flystrike itself and its indicator traits with wool production and quality traits that affect the profitability of a Merino enterprise. This will enable Merino producers to predict the outcome of selection strategies and genetic improvement programs that include reducing flystrike on flock productivity and profitability. Genetic correlations of breech cover, wrinkle (breech, body and neck) and wool coverage with liveweight, wool production, wool quality and visual wool traits were estimated from a Merino genetic resource flock. Breech cover had favourable genetic correlations with liveweight that increased in magnitude with age at scoring (−0.34 to −0.66). However, the magnitude and direction of the genetic correlations of breech cover traits with wool production traits differed with the age of assessment and were mostly negligible. The genetic correlations between breech cover and the measured wool quality traits, where significant, tended to increase in magnitude with the age of assessment. Apart from a favourable genetic association with the severity of fleece rot (0.22–0.26) the genetic correlations between breech cover and the visual wool quality scores were all antagonistic. The wrinkle traits (breech, neck and body) each tended to have similar genetic relationships with the key Merino production traits. These were favourable with liveweight (−0.27 to −0.50), antagonistic with wool production, fibre diameter and most visual wool quality scores but favourable with staple length, fibre diameter variability and midbreaks. Wool coverage however, had few significant genetic relationships with key production traits and these were highly variable between age expressions. These genetic correlations of breech cover and wrinkle scores with key Merino enterprise profitability traits, together with the previously published phenotypic variances, covariances and phenotypic correlations, can now be used to predict the outcomes of multi-trait breeding programs seeking to reduce the incidence of flystrike with minimal impact on wool production or quality.

1. Introduction

Since 1999, when Australian Merino ram breeders became more aware of the need to breed sheep that do not have to be mulesed, there has been a slight downward genetic trend of about −0.1 units over 10 years for breech wrinkle (Brown et al., 2010), a trait which is commonly used as an alternative selection criterion to reduce the incidence of breech strike. Breech strike is the major form of flystrike throughout Australia in most years (James 2006; Reeve and Walkden-Brown 2014), as well as internationally (Heath and Bishop 1995; Scholtz et al., 2010a; Pickering et al., 2015). However, due to the effectiveness of mulesing in controlling the incidence of flystrike, most past research and breeding programs have focussed on breeding for resistance to body strike (James, 2006; Scholtz et al., 2010b). The heightened focus by the

Australian sheep industry on a genetic solution to reduce wrinkling, particularly around the breech, is in response to changing public values that are increasingly questioning the animal welfare aspects of mulesing (Scholtz et al., 2010b; Greeff et al., 2014) in which the excess caudal skin folds are surgically removed (Beveridge, 1984). However, breech wrinkle is just one indicator trait of breech strike resistance. Others include breech cover, dag score, wool colour and urine stain (Greeff and Karlsson, 2009; Scobie and O'Connell 2010; Scobie et al., 2011; Scobie et al., 2012), with the relative importance of the indicator traits under Australian conditions varying between winter rainfall Mediterranean (Greeff et al., 2014), summer rainfall (Smith et al., 2009) and non-seasonal rainfall environments (Bird-Gardiner et al., 2014). Hatcher and Preston (2015) have estimated genetic parameters for breech cover and breech wrinkle traits assessed at various ages.

* Corresponding author at: Makin Outcomes Pty Ltd, PO Box 8358 Orange East, New South Wales 2800, Australia.
E-mail address: sue@makinoutcomes.com.au (S. Hatcher).

They concluded that a single assessment of either breech cover or breech wrinkle, preferably at the yearling stage of assessment (10–13 months of age), would be sufficient for genetic improvement programs to achieve correlated improvements in either trait. MERINOSELECT, the national genetic evaluation system for Australian Merino sheep (Brown et al., 2007), currently publishes Australian Sheep Breeding Values (ASBVs) for breech cover and breech wrinkle at two ages, ‘early’ assessed at either marking or weaning and ‘late’ assessed at yearling, hogget or adult ages (Brown et al., 2010).

However, estimating genetic parameters and ASBVs for breech cover and breech wrinkle is only part of the story. Breeding objectives for Merino sheep can be complex and a wide range of traits are usually considered for inclusion (Brown and Swan, 2016) including liveweight, carcass traits, reproduction and wool production, together with objectively measured wool quality traits and visual sheep scores (Mortimer et al., 2009). MERINOSELECT now includes a range of indexes for fibre production (for enterprises with wethers kept for wool production), Merino production (for enterprises with a balance of wool and surplus sheep sales) and dual purpose (for enterprises with the majority of income from sheep sales) enterprises (Sheep Genetics, 2014). Quantifying the genetic relationships between the breech cover and wrinkle traits with key production and wool quality characters will provide some of the information required to evaluate the impact of including the former into Merino breeding objectives.

Previous research has identified significant relationships, both favourable and antagonistic, of the various breech cover (Hebart et al., 2006; Edwards et al., 2009; Greeff and Karlsson, 2009; Brown et al., 2010; Scholtz et al., 2011; Scobie et al., 2011; Scobie et al., 2012; Pickering et al., 2013), breech wrinkle (Jackson and James, 1970; Lewer et al., 1995; Greeff and Karlsson, 2009; Brown et al., 2010; Scholtz et al., 2011; Scobie et al., 2011; Scobie et al., 2012), neck and body wrinkle (Beattie, 1962; Jackson and James, 1970; Mortimer and Atkins, 1993; Lewer et al., 1995; Hatcher et al., 2009; Mortimer et al., 2009; Brown et al., 2010) traits with liveweight, wool production, measured wool quality and some visual wool quality scores. However, the majority of modern Merino sheep are relatively free of wrinkles in comparison to the strains that prevailed when most of the previous studies were conducted (James, 2006). Furthermore, there has been significant and increasing admixture between Merino strains since the late 1980s, particularly in ram breeding flocks participating in MERINOSELECT (Swan et al., 2016), although there is still a large range in genetic group differences for some traits.

This study provides estimates of genetic correlations of breech cover, breech, body and neck wrinkle and wool coverage traits with liveweight, wool production, measured wool quality and visual wool quality scores in a contemporary Merino population. Together with the phenotypic variances and covariances among the selection criteria traits (Hatcher and Preston, 2015), these correlations, and the corresponding phenotypic correlations (Hatcher and Preston 2017), can then be used to predict the outcomes of multi-trait breeding programs seeking to improve wool production and wool quality as well as reducing the incidence of flystrike.

2. Materials and methods

2.1. Data

As described by Hatcher and Preston (2015), data for this study were obtained from the Sheep Cooperative Research Centre (Sheep CRC) Information Nucleus (IN) (Fogarty et al., 2007; van der Werf et al., 2010). The IN consisted of eight flocks managed by Sheep CRC partner organisations located in the major sheep growing areas of Australia (Hatcher and Preston, 2015). Each IN site was responsible for the research activities at their location and all data collection activities were approved by each organisation’s Animal Ethics Committee.

Data were collected from Merino progeny born into the IN program

between 2007 and 2011. Breech cover (BCOV), breech wrinkle (BRWR), body wrinkle (BDWR) and neck wrinkle (NKWR) were assessed using the industry approved standards for these traits (Australian Wool Innovation Limited and Meat & Livestock Australia Limited, 2013) and wool coverage (COV) was assessed according to Casey et al. (2009) at various ages (marking M, 7–42 days; yearling Y, 300–400 days and; adult A, > 540 days), as described by Hatcher and Preston (2015).

Prior to shearing at approximately 11 (yearling) and 23 (adult) months of age, a suite of visual wool quality scores that included fleece rot (FLROT), greasy colour (COL), character (CHAR), dust penetration (DUST), weathering (WEATH) and staple structure (SSTRC) were assessed according to the Visual Sheep Scores guide (Australian Wool Innovation Limited and Meat & Livestock Australia Limited, 2013). Fleece density (DENS) and nourishment (NOUR) were assessed according to the Australian Merino Sire Evaluation Association (AMSEA) protocol (Casey et al., 2009), while textural greasy wool handle (HAND) was assessed according to the protocol devised by Casey and Cousins (2010). Briefly, the fleece was parted at the midside where a single staple was chosen at random and stroked with a single finger in a base to tip direction. Effort was made to ignore any part of the staple covered with dust and a score allocated based on the relative textural softness of the fibre. Each of the visual assessments was made using a five-point system with low scores representing desirable attributes.

A sample of approximately 70–80 g of wool was then taken from the midside of each sheep. The samples were sent to a commercial laboratory (AWTA Limited, Melbourne), where they were measured for a range of wool traits. A random sub-sample of 10 wool staples from each greasy midside sample was initially taken for measurement of staple length (SL), staple strength (SS) and the percentage of midbreaks (MID) using the Automatic Tester of Length and Strength (ATLAS, Australian Wool Testing Authority Limited, 2000). The remainder of the sample was scoured in hot water and detergent, rinsed in cold water twice, spun and oven dried at 105 °C with the clean washing yield (YIELD) calculated using a 16% regain. The samples were then passed through a Shirley Analyser, conditioned at 20 °C and 65% relative humidity and minicored to provide 2 mm snippets for Sirolan™ Laserscan (AWTA Ltd, Melbourne) measurement of fibre diameter (FD), fibre diameter standard deviation (FDSD), fibre diameter coefficient of variation (FDCV) and fibre curvature (CURVE). The carded sample was further sub-sampled and measured for resistance to compression (RTOC). All AWTA measurements were conducted using IWTO test methods or Australian standards (RTOC).

The greasy fleece weight (GFW) of each unskirted fleece, belly wool included, was recorded at shearing with clean fleece weight (CFW) calculated as the product of GFW and YIELD. GFW and CFW were corrected to 365-day growth equivalents by dividing fleece weight by the number of days between birth and the initial shearing of each sheep for the yearling measurement or by the number of days between the yearling and adult shearing for the adult measurement, and then multiplying the result by 365. Following the yearling and adult shearing, the liveweight (LWT) of each sheep was recorded with all sheep held off feed for approximately 2 h prior to being weighed. Summary statistics detailing the number of records, mean and standard deviation of each of the liveweight, wool production and measured wool quality traits as well as the visual wool quality scores are presented in Table 1.

2.2. Statistical analyses

Genetic parameters were estimated with the statistical package ASReml (Gilmour et al., 2009) using general linear mixed models and residual maximum likelihood methods. The analysis included data from a maximum of 6469 Merino female and male progeny representing 183 different Merino sires as described by Hatcher and Preston (2015), with between 4 and 79 progeny per sire (average 36). Young sires were selected for use in the IN based on high within breed ASBVs for traits of

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