Genetic parameters for breech cover, wrinkle and wool coverage scores and their implications for Merino sheep breeding programs and flock management

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ABSTRACT

There is an increased impetus within the Australian sheep industry to pursue a genetic solution to increase the bare area around the breech and reduce the degree of breech wrinkles in order to reduce the incidence of flystrike and the need for surgical mulesing. Breeding programs seeking either a genetic increase in bare skin area around the breech or a decrease in wrinkling require accurate estimates of genetic parameters for breech cover, wrinkle and wool coverage traits as well as the phenotypic and genetic correlations between these traits. Genetic parameters for breech cover, breech wrinkle, body wrinkle, neck wrinkle and wool coverage were estimated from a Merino genetic resource flock at various ages from marking (breech cover and breech wrinkle), to yearling and adult (all traits). The breech cover and wool coverage traits were lowly heritable ($h^2 < 0.16$), while the various wrinkle traits were moderately heritable (h^2 range 0.26–0.34). While all traits will respond to selection, genetic improvement of breech cover and wool coverage are likely to be slower and potentially more difficult due to their low heritability estimates. The various breech cover and wrinkle traits are moderately correlated, phenotypically and genetically, both across age assessments (marking, yearling and adult) and with each other. The phenotypic and genetic correlations were medium to high, particularly between the yearling and adult expressions of these traits. It is likely that selection at yearling age, 10–13 months, may be sufficient for genetic improvement programs seeking to decrease the extent of wool coverage around the breech or the degree of wrinkling on the breech or body of sheep. Such genetic improvement programs would have no impact on wool coverage due to negligible phenotypic and genetic correlations between this trait and the breech cover and wrinkle traits. There is potential for the phenotypic variation in breech cover and wrinkle traits to be exploited by commercial sheep producers to support various on-farm decisions including truncation selection to keep or cull individuals with high breech cover or wrinkle scores, mating allocation as well as potential flock segmentation into 'easy care' versus normal management mobs.

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1. Introduction

Historically, wool producers were encouraged to increase the degree of wrinkling in their sheep in an effort to achieve greater wool cuts (Roberts, 1959). However, increasing the degree of wrinkling not only resulted in increased wool cuts (Beattie, 1962; Lewer et al., 1995; Hatcher et al., 2009), but a greater susceptibility to and incidence of flystrike (Donnelly, 1978; Scholtz et al., 2010), fleece rot (Raadsma et al., 1988) and wool yellowing (Crook and James, 1991). These changes resulted in sheep that required an increased level of management (Roberts, 1959; Baillie, 1978) including

surgical mulesing, regular crutching, jetting with insecticides and treating individually fly struck sheep with chemicals (Greeff et al., 2014). Other correlated effects associated with increased wrinkling included a higher number of dry ewes (Baillie, 1978) and higher birth weights (Dun and Wall, 1962) which were associated with an increased incidence of dystocia (Dun and Wall, 1962; Donnelly, 1978). In addition, the more highly wrinkled sheep take longer to shear (Baillie, 1978; Donnelly, 1978; McGuirk et al., 1981; Scobie et al., 2005; Smith et al., 2010) and produced a greater amount of second cuts during shearing (Carter, 1943). These associated responses were contrary to the sheep producer's objective of breeding a Merino that not only improved economic returns but required low maintenance (Baillie, 1978). Producers have since taken heed of the problems of the past, and as a result there has been a reduction in the degree of wrinkling in the modern Australian Merino

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Table 1
Geographical and climatic conditions of the Information Nucleus flock sites.

Site	Sheep CRC partner organisation[a]	Location	Coordinates	Rainfall (mm)	Rainfall dominance
IN01	UNE	Armidale NSW	30.50°S 151.66⁰E	786 mm	Summer
IN02	NSW DPI	Trangie NSW	31.99°S 147.95E	501 mm	Non seasonal
IN03	NSW DPI	Cowra NSW	33.82°S 148.68°E	623 mm	Winter
IN04	DPI VIC	Rutherglen VIC	36.06°S 146.46°E	588 mm	Winter
IN05	DPI VIC	Hamilton VIC	37.74°S 142.02°E	621 mm	Winter
IN06	SARDI	Struan SA	37.09°S 140.79°E	549 mm	Winter
IN07	SARDI	Turretfield SA	34.56°S 138.83°E	467 mm	Winter
IN08	DAFWA	Katanning WA	33.69°S 117.58°E	456 mm	Winter

[a] UNE The University of New England; NSW DPI New South Wales Department of Primary Industries, DPI VIC Department of Primary Industries Victoria, SARDI South Australian Research and Development Institute and; DAFWA Department of Agriculture and Food Western Australia.

(Roberts, 1959; Baillie, 1978; Donnelly, 1978; Hatcher et al., 2009), particularly since 1999 when ram breeders became more aware of the need to breed sheep that do not have to be mulesed (Brown et al., 2010) due to increased public awareness that questioned the animal welfare aspects of surgical mulesing (Greeff et al., 2014).

As a result, there has been a renewed focus in the Australian sheep industry to develop a genetic solution to reduce wrinkling, particularly around the breech, in an effort to reduce the incidence of flystrike and the need for mulesing (James, 2006). Implementing a genetic reduction in wrinkles requires accurate estimation of genetic parameters for a range of breech, wrinkle and wool coverage traits and knowledge of the correlations between these traits. Previous studies have shown that breech wrinkle is a highly heritable trait (Brown et al., 2010; Bird-Gardiner et al., 2014; Greeff et al., 2014), neck and body wrinkle scores are moderately (Beattie, 1962; Mortimer and Atkins, 1993; Lewer et al., 1995) to highly heritable (Hatcher et al., 2009; Mortimer et al., 2009; Brown et al., 2010; Bird-Gardiner et al., 2014; Greeff et al., 2014) and estimates for breech cover vary from moderate to high (Bird-Gardiner et al., 2014; Greeff et al., 2014). However, the earlier reports used various non-standard scoring systems, selection can change the genetic relationships within a population (Turner and Young, 1969) and there are no published reports on phenotypic and genetic correlations between breech cover, breech-, body- and neck-wrinkle or wool coverage at various ages. It is therefore, necessary to estimate genetic parameters for these traits in a contemporary population of Merino sheep using a standard industry scoring system.

This study provides a current summation of the phenotypes and genetic diversity within the Australian Merino flock with respect to breech cover, breech-, body- and neck wrinkle and wool coverage. Estimates of genetic parameters for each of these traits at various stages of assessment from marking to adult are presented together with phenotypic and genetic correlations among them. These parameters are essential foundation information for Merino breeders seeking to breed plainer bodied sheep as part of a genetic alternative to surgical mulesing.

2. Materials and methods

2.1. Data

Data was obtained from the Cooperative Research Centre for Sheep Industry Innovation (Sheep CRC) Information Nucleus (IN) flock (Fogarty et al., 2007; van der Werf et al., 2010). The IN consisted of eight flocks located in each of the major sheep growing areas of Australia managed by Sheep CRC partner organisations (Table 1). Each IN site was responsible for the research activities at their site and all data collection activities were approved by their respective Animal Ethics Committee.

This paper reports on data collected from Merino progeny born into the IN between 2007 and 2011 and assessed at marking (7–43 days), yearling (300–400 days) or adult (>540 days) ages for breech cover (BCOV) and breech wrinkle (BRWR) and at both the yearling and adult ages for body wrinkle (BDWR) and neck wrinkle (NKWR) as per the Visual Sheep Scores book (Australian Wool Innovation Limited and Meat & Livestock Australia Limited, 2013). Assessment of breech-, body- and neck- wrinkle was undertaken within one month post shearing and was assessed relative to a 1 to 5 diagrammatic scale which depicts various degrees of wrinkling over the entire breech, neck or body. For each trait, a score of 1 depicts the least expression and score 5 the most expression of each trait. Wool coverage (COV) was assessed according to the Australian Merino Sire Evaluation Association (AMSEA) Central Test Sire Evaluation (CTSE) protocol (Casey et al., 2009) at both the yearling and adult ages. COV refers to the amount of wool growing skin surface area including the extent and amount of wool on the body points and belly from 1 (very little coverage) to 5 (very large amount of coverage). A number of different assessors, both within a site across years and between sites, were involved in assessing the suite of breech, wrinkle and wool coverage scores.

A total of 6469 Merino progeny were included in the analysis from 183 different Merino sires (depending on the trait) (Table 2). The average number of progeny per sire was 36 (ranging from 4 to 79). All Merino progeny included in the analysis were not mulesed, but were tail docked at marking age (7–43 days). Males were castrated and either slaughtered at yearling stage to measure individual meat carcass data or kept in the program until the completion of their adult wool assessment (Table 2).

2.2. Statistical analyses

Fixed effects, variance components and genetic parameters were estimated using general linear mixed model and residual maximum likelihood methods with ASReml (Gilmour et al., 2009). An initial univariate sire and dam analysis was conducted to estimate the following fixed effects: flock (eight levels: IN01, IN02, IN03, IN04, IN05, IN06, IN07 and IN08), drop (five levels: 2007, 2008, 2009, 2010 and 2011), sex (two levels: ewe or wether), dam age (seven levels: 2, 3, 4, 5, 6, 7 and 8 years of age) and birth rearing rank (BRR) (four levels: born single raised single (SS), born as a multiple and raised as a single (MS), born as a twin and raised as a twin (TT) and born as multiple raised as a multiple (MM)). Sire group (three levels: ultra/superfine, fine/fine medium and medium/strong) was included in the initial fixed effects model along with appropriate 2-way interactions. Age at shearing (days) was included as a covariate for the analysis of yearling COV to take account of the varying ages of animals across the eight IN flocks between birth and the initial assessment of COV at approximately 11 months of age.

A series of univariate animal models were subsequently fitted for each trait with random effects including genetic group, sire × flock and a maternal environmental effect to estimate genetic parameters. The genetic group effect represents the proportion of genes from various Merino strains of each animal derived from its