

MANAGING DELETERIOUS GENETIC CONDITIONS AT THE HERD LEVEL

J.M. Allen¹, P.F. Parnell² and C.F. Teseling²

¹ Agricultural Business Research Institute, University of New England, Armidale, NSW 2351

² The Angus Society of Australia, 86 Glen Innes Road, Armidale, NSW, 2350

SUMMARY

A simple herd model was developed to show the potential impact of a sire which is the carrier of a deleterious, recessive genetic condition. Through typical replacement strategies, Carrier females would remain in the herd for 13-23 years if no further introductions occurred. Introduction of another Carrier sire would lead to Affected calves. Random matings would give only low incidence (< 1 calf per year) that might not be readily identified. Selected matings and/or further introductions of Carrier sires increase the incidence of Affected animals significantly. No Affected calves will be produced if the herd only uses sires that are free of the genetic condition, even with Carrier females still in the breeding herd.

INTRODUCTION

Deleterious genetic conditions have been observed in cattle populations and many of these are caused by recessive genes where Carrier animals have one copy of the deleterious gene and one copy of the normal gene. Carriers seem to be normal and productive animals while Affected animals (two copies of the deleterious gene) show clinical signs of the disorder making them unsuited for breeding. DNA based diagnostic tests have been developed to identify Carrier animals for many conditions.

The frequency of genes resulting in deleterious genetic conditions is generally low in natural mating population. In modern animal breeding situations, a genetic condition could become a problem if it occurs in animals that have some superior benefit that breeders' desire. Even then, it is likely to take several generations before the gene frequency increases to a level that the condition becomes fully evident, as cattle breeders tend to be averse to inbreeding. A recent example of this is Arthrogryposis Multiplex (AM) in the Australian Angus population (Allen and Teseling 2011).

Seedstock producers that belong to breed associations can value-add the benefits of DNA testing on animals linked (even remotely) through pedigree. Tools like GeneProb (Kerr and Kinghorn 1996, Kinghorn 1997) can be used on these extensive pedigree data bases to estimate the probability of untested animals being Carriers (Teseling and Parnell 2011). Commercial herds do not have access to this technology, but simple strategies can be employed to manage genetic conditions in the herd.

HERD DYNAMICS

Consider a self-replacing herd of 200 breeding females, where:

- 90% of females mated produce progeny to yearling age (available for selection)
- Females that do not produce a calf are culled
- A further 3% of female breeders are culled/died for other reasons
- Replacement heifers are sourced within the herd and mated as yearlings to calve at 2 years
- Cows are cast for age as 10 year olds
- Sires are purchased from outside the herd, are randomly mated to 50 (non-daughter) females for four years and then replaced.

Cattle II

Under this Standard scenario, 37% of heifers produced each year are required as replacements to maintain the size of the breeding herd. On average, each replacement heifer will produce around 5.4 calves in her lifetime – but the range will be 0 to 9 calves.

This Standard herd structure was modelled for random matings (excluding daughters) and a gene flow approach used to estimate the average influence of a gene moving through the breeding herd per year and per generation. This approach was taken to simulate a herd that was unaware of the existence of a deleterious gene. The model allowed for 5 generations of descendants spanning 53 years with variables for cow-herd size, cows per sire, percentage of yearling progeny per cow mated, percentage of extra culls/deaths in the cow herd, average selection percentage of heifers and selection percentage of heifers from the candidate sire.

The model was used to consider the purchase of a bull that is a Carrier for a genetic condition. If the first progeny of the Carrier sire (CS1) are considered to be born in year 1, then the average time for that deleterious genetic condition to be naturally removed from the herd under random mating conditions is around 16 years (Figure 1), assuming no further use of Carrier sires.

One limitation of the model is the influence of chance on how many heifers from a Carrier sire are available for selection, how many of these heifers were Carriers themselves and whether they were subsequently randomly selected as replacement females. The Standard scenario was altered so that 2000 breeding cows were in the herd and CS1 was mated to 500 cows. Hence, the proportion of genes in the population is the same, but the results were less influenced by the relatively small sample size. The 2000 breeding cow results were calculated and then divided by 10 to give yearly counts of Carrier females in the herd (Std2000) on a 200 cow equivalent basis. This strategy was used to demonstrate how unfavourable chance effects may extend the time to 26 years that carrier females may still remain in the breeding herd.

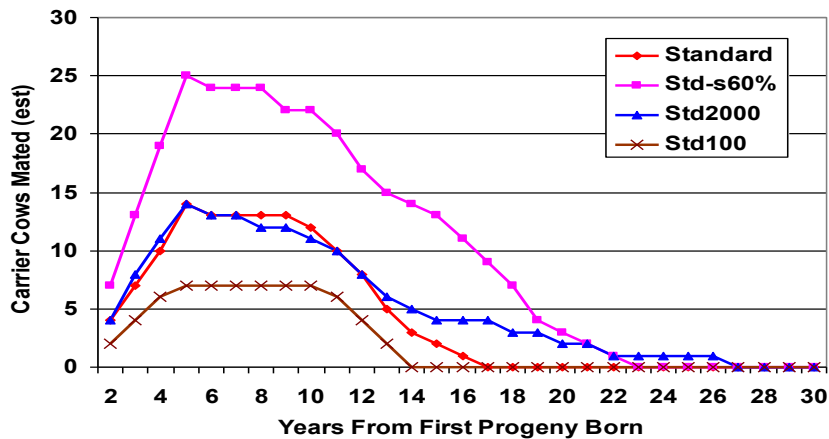


Figure 1. Years of influence of Carrier cows under different mating, selection and herd structures. Standard: 200 cow herd, 50 cows/sire, 37% heifers retained; Std2000: 2000 cow herd, 500 cows/sire and result divided by 10; Std100: 100 cow herd, 25 cows/sire; Std-s60% is Standard with 60% heifers retained.

Conversely, when a 100 cow herd was modelled with 25 cows per sire (Std100), the estimated time for Carrier females to stay in the herd was reduced to 13 years.

The modelling showed that higher fertility rates and/or lower culling meant that selected animals stayed in the herd longer and this extended the time frame that the Carrier breeding females remained in the herd. Conversely, lower fertility and/or higher culling increased the change over of breeding females and reduced the time frame that Carrier females were in the herd.

Where retention of CS1 heifers was higher than herd average (say 60% rather than 37%), the average time to natural removal of the deleterious gene was extended to 22 years (Std-s60%). This example was included to simulate the herd's preference for heifers from a particular sire line.

If the herd does not introduce another Carrier sire and it does not sell bulls or heifers to other breeders, then the cost of using one Carrier sire in the herd is zero (as only Affected calves reduce the profitability of the herd directly) – assuming the sire is not mated to his own daughters.

However, if a relatively unrelated Carrier sire (CS2) is randomly mated in the Standard herd while Carrier cows are already present, then the cost of the genetic condition becomes real. Consider where a new Carrier bull (CS2) replaces the original Carrier sire (CS1). CS2's daughters will start to appear in the herd in year 6. Figure 2 shows the number of Carrier females likely to be in the cow herd each year (year 1 is the first calves born sired by CS1) for the Standard scenario (CS1 only), Standard with CS2 introduced (2sire-Std), Std-s60% and Std-s60% with CS2 introduced (2sire-s60%). As expected, the number of Carrier females in the cow herd increases and they remain in the cow herd for a longer period.

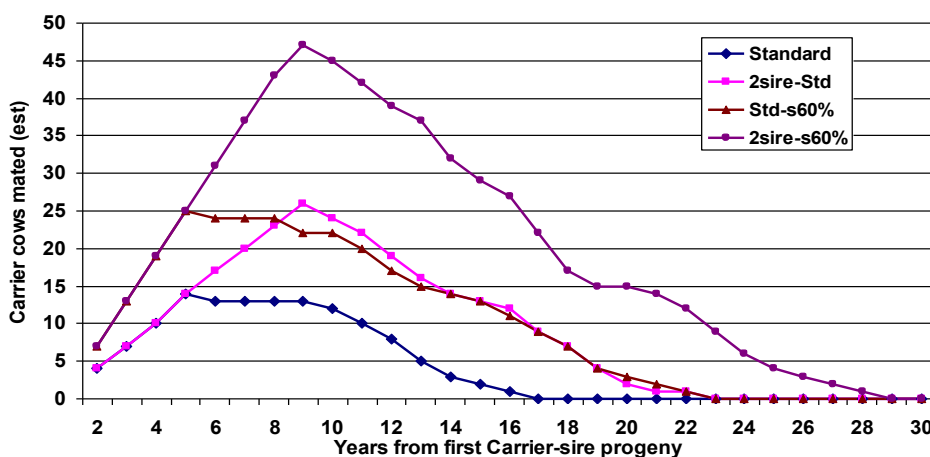


Figure 2. Influence on number of Carrier cows from using a single Carrier sire or two successive Carrier sires. Standard: 200 cow herd, 50 cows/sire, 37% heifers retained, 1 Carrier sire; 2sire-Std: Standard with 2 successive Carrier sires; Std-s60% is Standard with 60% heifers retained; 2sire-s60% is Std-s60% with two successive Carrier sires.

If CS2 is randomly mated, then on average there will be 0.8 Affected progeny born per year for 4 years (Table 1). This is based on 14 Carrier cows from the previous sire among 200 female breeders per year (Standard in Figure 1); on average there will be 3.5 Carrier females per 50 females/sire (ie 14/200) and one in four Carrier to Carrier matings produce an Affected calf (Mendelian theory). However, if 60% of the daughters are retained (rather than 30%), then Affected progeny per year is around 1.4. If a third Carrier sire (CS3) replaces CS2, then the number of Affected progeny almost doubles in the following 4 years.

Cattle II

The herd cost for using CS2 in the Standard scenario would be about one calf in every 180 calves per year for each of four years (years 5-8). At this level of incidence, any Affected calves born may not cause initial concern – especially if foxes, dogs, crows, etc had mauled the calf before it was observed. Keeping 60% of the heifers from CS1 (2sire-s60% in Figure 2 and Table 1) rather than 30% will produce 1.4 Affected progeny per year for 4 years. Hence, in many cases, the herd may only realise they have a problem once CS3 progeny start being born (2-3 Affected progeny per year).

Table 1. Estimated number of Affected calves when a second and third Carrier sire introduced successively into the herd in year 4 and year 8. Standard is one sire mated to 50 cows for 4 years with 30% selection of daughters. 2sire-Std is Standard with a second and third Carrier sire introduced into the herd in year 4 and year 8 respectively. 2sire-s60% is where 60% of Carrier daughters are selected.

Year (first calf)	First Carrier Sire				Second Carrier Sire				Third Carrier Sire				
	1	2	3	4	5	6	7	8	9	10	11	12	13
Standard	0	0	0	0	0	0	0	0	0	0	0	0	0
2sire-Std	0	0	0	0	0.8	0.8	0.8	0.8	1.5	1.5	1.5	1.5	0
2sire-s60%	0	0	0	0	1.4	1.4	1.4	1.4	2.6	2.6	2.6	2.6	0

If the herd selectively mated CS2 to all the daughters from CS1 in the Standard scenario, then the number of Carrier to Carrier matings increases to 13-14 per year with the expectation of 3-4 Affected calves observed each year. This could be as high as six Affected calves per year if 60% of CS1 heifers were selected as replacements (Std-s60%). Such selection may also indicate a higher acceptance of inbreeding or designed line breeding within the herd.

Note that without testing any animals, the breeder can immediately stop any further Affected calves being born by simply using Sires that are known to be free of the genetic condition (Year 13 in Table 1). As such, the deleterious gene will eventually be bred out of the herd through normal cow replacement strategies. Of course this strategy relies on having a diagnostic test available for the genetic condition.

The herd's existing Carrier cows will produce Carrier progeny 50% of the time. If the herd sells cows or bulls back into the industry for breeding purposes, the herd should strategically test animals for the genetic condition.

CONCLUSION

The incidence of Affected animals in a random mating herd using occasional Carrier sires can be quite low (less than 1% in the example). However, non-random selection and mating decisions can increase this significantly. Carrier females are likely to remain in the herd for around 20 years after a single introduction of a deleterious gene. However, commercial herds that have Carrier females can manage deleterious genetic conditions by ensuring they only use tested free sires. DNA testing on strategic animals will enable herds and their clients to effectively manage deleterious genetic conditions.

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