

INFORMATION EMPOWERS – ARTHROGRYPOSIS MULTIPLEX IN ANGUS AUSTRALIA

J.M. Allen¹ 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

Arthrogryposis Multiplex (AM) is a deleterious recessive genetic condition found in Angus cattle. In 2008 a DNA test was developed in USA to identify Carrier animals. The Angus Society of Australia (AA) adopted a system to calculate genotype probabilities for untested animals. These probability results are available to AA members and the public on the AA web site. Armed with this information, AA members have made significant progress in reducing the incidence of AM in the current calf drops.

INTRODUCTION

Arthrogryposis Multiplex (AM) is a deleterious recessive genetic condition found in Angus cattle where affected animals die before or soon after birth while carrier animals are not negatively impacted. Research has shown the mutation originated in 1979 in the American Angus population. Unbeknown at the time, genetics of Carrier animals were subsequently exported to other Countries, including Australia.

A DNA test to identify Carrier animals was developed in the USA in 2008 which became available in Australia in early 2009 (Beever 2008).

GeneProb (Kerr and Kinghorn 1996: Kinghorn 1997) is software which calculates genotype probabilities using segregation analysis on large animal populations. The Agricultural Business Research Institute (ABRI), in collaboration with Dr Brian Kinghorn from the University of New England and Angus Society of Australia (AA), has integrated GeneProb into the suite of software available to ABRI clients for use with their pedigree and performance databases. There are currently six ABRI clients (Breed Associations) using GeneProb on 8 different recessive genes.

AA members have collected pedigree information for many years. GeneProb uses the pedigree information combined with the results from the DNA tests for AM to estimate probabilities for non-tested animals being AM Carriers. Results are displayed as probabilities for each allele combination plus an index that indicates the amount of information available to estimate the probability (Kinghorn, 1997). These results are interpreted and made public, generally through the AA website, as tested Free (AMF), tested Carrier (AMC), free untested (AMFU and is < 1 probability) or as a probability of being a Carrier (eg AM23). GeneProb analyses are run regularly to update the probabilities as new animals and DNA test results are added to the database. Each herd is also supplied with an updated list of probabilities for their animals in a data file uploaded to a secure web site with password access. In this way, AA members get the updated information quickly and efficiently, maximising the benefit obtained from each DNA test result and GeneProb analysis. This has been complemented by a proactive education program by AA in supporting their members to identify and manage animals that may be AM Carriers (Teseling and Parnell 2011).

There has been strong global cooperation in sharing DNA test results between the different Angus Associations across many countries. This cooperation has significantly reduced testing costs, increased the speed of dissemination of the information and allowed test results to be available on animals that may only appear in a pedigree on another Association's database.

Cattle II

ARTHROGRYPOSIS MULTIPLEX IN THE AUSTRALIAN ANGUS POPULATION

The AA data base in January 2011 comprised nearly 1.3M animals with 16,247 animals DNA tested for AM (Table 1). The vast majority of animals are AMF and AMFU (92.7). The majority of AM1 to AM99 animals and AMC animals are born between 2000 and 2010. Affected animals (AMA) are not tested and any “observed” animals are not recorded as they may be associated with other unrelated factors. There are 4,944 AMC and 11,303 AMF, reflecting an industry testing cost at \$35 per head of AU\$568,645.

Table 1. Summary statistics of January 2011 GeneProb analysis of AM in Angus Australia

AM Result	All Animals	()	Born 2000 - 2010	()	AMCU*
Tested Free (AMF)	11,303	(0.9)	10,756	(1.8)	
Free Untested (AMFU)	1,191,133	(91.8)	488,092	(83.4)	
AM 1 to 14	28,401	(2.2)	22,907	(3.9)	1,580
AM 15 to 34	25,702	(2.0)	23,925	(4.1)	6,035
AM 35 to 64	35,306	(2.7)	33,966	(5.8)	16,959
AM 65 to 94	399	(0.0)	387	(0.1)	271
AM 95 to 99	617	(0.0)	535	(0.1)	530
Tested Carrier (AMC)	4,944	(0.4)	4,864	(0.8)	
Total Animals	1,297,805		585,432		25,375

*AMCU is estimated number of untested Carriers based on probabilities

Progeny of AMC animals have a 50 probability of being a Carrier (AM50). Similarly, an AM10 animal has 10 chance of being a Carrier. By multiplying the number of animals by their probability, we can estimate that there are approximately 25,375 (4.3) untested Carriers (AMCU) in the 2000 to 2010 born animals.

DNA testing was generally done on a “sires first” basis with AA ensuring that AI sires were tested early. Members also focused on sale animals for quality assurance reasons. DNA testing can raise pedigree inconsistency issues which are being resolved using DNA parent verification.

Animals tested by birth year (Table2) shows that Angus breeders utilised the AM DNA test as soon as it became available. This coincided with the 2007 and 2008 drop calves going into the sales and being considered for within herd selection decisions. Many of the 2009 drop calves will only become available for sale in the first half of 2011, so it is presumed that more 2009 drop tests will be done in the near future. Tests done on pre-2007 drop animals followed the “sires first” and “significant animals” principles.

Table 2. Angus Society of Australia AM DNA test results by birth year of animal

Result	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
AMF	104	227	313	264	640	837	1078	2949	3204	1134	6
AMC	27	117	180	104	192	409	555	1071	1588	617	4

Breeders have had little opportunity to effect change since testing began and it is difficult and costly to change the cow herd structure. Selection decisions based on AM could only come into effect for late 2009 and 2010 drop calves and be largely driven by sire selection. To determine if AA

members are effecting change based on AM results, animals were counted by birth year and sire’s AM category (Table 3). The majority of calves are from AMF and AMFU sires in all years, with a noticeable 8 increase in progeny of AMF sires in last 2 years. Progeny from AMC sires peaked in 2006-2008, but halved in 2009 with DNA testing and AM results. Similarly, the use of AM sires decreased in the last 2 years. The 2010 figures are incomplete but look extremely encouraging.

Table 3. Percentage of calves born each year categorised by AM status of sire

AM Status of sire	Birth year of calf										
	2000	01	02	03	04	05	06	07	08	09	10
AMC	0.9	5.5	6.3	2.7	4.3	6.9	9.1	7.1	7.7	4.4	0.7
AM95+	0.2	0.2	0.2	0.3	0.5	0.5	0.6	0.7	0.4	0.0	0.0
AM65-94	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AM35-64	0.0	0.3	0.4	1.5	2.5	3.1	2.5	1.7	1.5	1.1	1.0
AM15-34	0.3	0.3	0.5	0.5	1.3	1.1	1.6	1.2	1.1	1.2	0.8
AM1-14	0.8	1.1	1.1	1.4	1.2	1.4	1.3	1.7	1.7	1.4	1.1
AMFU	77	74	69	69	60	55	52	51	49	45	50
AMF	21	19	22	25	30	32	33	37	39	47	47

Research conducted by Beever (2008) has tracked the source of the AM genetic mutation back to the bull “Rito 9J9 of B156 7T26” (USA9J9 ident in AA). All AA tested Carrier animals also have USA9J9 as an ancestor. USA9J9 was born in 1979 with first progeny recorded on AA database born in 1982. In 1990, 1 of the calves born were descendents of USA9J9 increasing to 64 in 2009. Two AMC descendants have significantly contributed to this increase. GAR Precision 1680 (USA1680) is a grandson born in 1990, and CA Future Direction 5321 (USA5321) born in 1995 is a son of USA1680. Their influence in the AA pedigrees is shown in Figure 1. The influence of each animal has been partitioned and compared to unrelated animals.

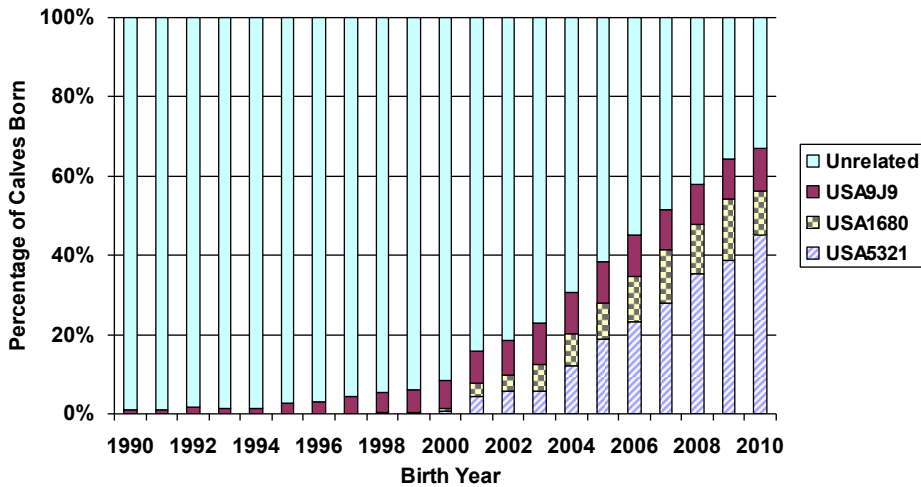


Figure 1. Percentage of USA9J9 descendants in Angus Australia database by birth year.

The increase in USA9J9 descendants since 1999 is reflected by the increase in animals with AM probabilities > 1 (Table 1). However, AA members are cognitive of inbreeding issues and average inbreeding levels have only moved from 1.9 in 2000 to 3.1 in 2009 (J. Allen unpublished data).

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The rapid increase in USA9J9 descendants and their spread of the AM genetic condition is explained by reviewing the genetic merit of sires as reflected in the AA Long Fed CAAB Selection Index (Figure 2). This Index has a high weighting on marbling and these USA9J9 descendants are generally good for marbling. The average Index is only marginally lower for AMF sires compared to AMC sires indicating that herds can source high performing AMF sires without sacrificing much genetic progress. The decline in estimated frequency of the deleterious allele in the sires (based on their AM estimates) indicates that breeders have recognised this and selected sires accordingly.

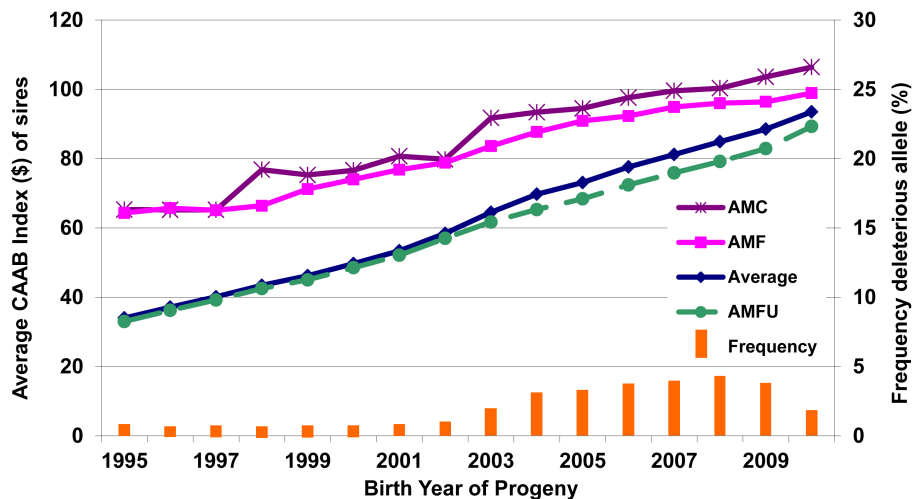


Figure 2. Average CAAB Index and deleterious allele frequency for sires by progeny birth year

CONCLUSION

Over 90 of calves recorded on the AA database are AMF and AMFU despite 60 being descendants of the source animal (USA9J9). DNA testing combined with GeneProb since 2009 has enabled AA members to actively and efficiently select against using Carrier and high probability sires in their breeding programme. Herds that have Carrier females can manage AM by ensuring that they only use AMF sires. Strategic DNA testing combined with GeneProb will enable herds and their clients to effectively manage AM. Similar outcomes could reasonably be expected for other genetic conditions and/or breeds where DNA tests are available.

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