

# final report

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Limited  
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Development of a fully automated  
procedure of analysing DNA test  
results

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## **PROJECT No. P.PSH.0478**

### **DEVELOPMENT OF A FULLY AUTOMATED PROCEDURE OF ANALYSING DNA TEST RESULTS**

#### **Milestones, Objectives and Outcomes**

##### **1. Initial gene probability analysis**

Two versions of the GeneProb software were delivered by Prof Brian Kinghorn, UNE and have been successfully installed and tested at ABRI on both the ILR1 and ILR2 society database platforms that are deployed by ABRI with its breed association clients.

One version of GeneProb is aimed at lethal recessive markers (like AM - Arthrogyrosis Multiplex) where the probability estimates allow for the expectation that live animals cannot be homozygous for the lethal recessive. The other (standard) version assumes that all forms of the gene are viable in the population (eg GeneStar Tenderness markers).

##### **2. Integrate GeneProb software with ABRI's production software.**

Custom software was written to run either version of the GeneProb software and get probabilities into data formats that suited the Society integrated pedigree and performance systems in ILR1 and ILR2.

The software was written so that multiple DNA markers could be analysed, stored and reported independently of each other. This flexibility allows Society technical staff to work on one gene at a time – particularly where tests are being done at different DNA laboratories.

##### **3. Software to allow updating of AM DNA tests from multiple labs to Angus database, extract of both Angus and Brahman pedigrees and provide to Geneprob, software to pick up probabilities file from Geneprob and update to Angus and Brahman databases, populate Internet Solutions with results.**

DNA test results for multiple genes and from multiple labs can be stored on any animal recorded in the Society database. There is no effective limit to the number of DNA results that can be stored for any particular animal and new markers can be added as these become available. Where available, as well as storing the DNA marker and its result, information on the test date, laboratory and unique laboratory reference for the DNA sample are also stored. This allows better liaison between the DNA laboratory and the Society where anomalies are encountered.

Software has been written for both ILR1 and ILR2 database systems to extract full database pedigrees and gene test results for the nominated gene, run the appropriate

version of the GeneProb software (lethal recessive or standard), run diagnostic reports (see milestone 4) and load the results into the Preliminary Results table.

Once the Preliminary results have been checked, then the results are quickly released to the Production database and subsequently updated to the web based enquiry system for the Society if the Society has requested this. The following example is from the Angus Society of Australia website ([www.angusaustralia.com.au](http://www.angusaustralia.com.au)).

### Angus Animal Details

## PRIME YOUR DIRECTION Y37 (AI) (ET)

<b>Identifier:</b>	CXBY37
<b>Sex:</b>	Male
<b>Tattoo:</b>	P RAISED LEFT OF A Y37 (F)
<b>Birth Date:</b>	19/03/2003
<b>Calving Year:</b>	2003
<b>Status:</b>	Active
<b>Register:</b>	HBR
<b>Gene Tests / Probs:</b>	<a href="#">[View]</a>
<b>Sire:</b>	<a href="#">C A FUTURE DIRECTION 5321</a>
<b>Dam:</b>	<a href="#">MERRIC RIVERS EVE V139 (AI)</a>

When you click on [View] next to “Gene Tests / Probs” the codes derived from the GeneProb results for the animal are displayed as shown in the example below.

### Angus Animal Additional Details

## PRIME YOUR DIRECTION Y37 (AI) (ET) CXBY37

Click [here](#) for a description of genetic test codes

<b>Genetic Test Codes:</b>	AM2% NH50%
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The GeneProb calculations are run as necessary – usually once per week, but more often if results are available and sales catalogues are required.

**4. Software to use Geneprob in a what if scenario plus diagnostic reports to help identify suspect test results and/or pedigrees.**

The GeneProb results are loaded into a Preliminary Results table which allows them to be reviewed and reported on. These preliminary results can be updated into the Production database or discarded. This approach allows for multiple GeneProb analyses without affecting the results in the Production Society system.

Preliminary and Production results are both available for reporting from. Diagnostic reports have been developed to compare preliminary results against the Production version as a way of assessing the impact of recent results on the probabilities calculated for the un-tested population.

Diagnostic reports developed are:

- Compare new DNA test results against previously calculated GeneProb probabilities and report where there are significant differences between these
- List inconsistencies in the GeneProb analysis between tested animals and their probability estimates
- List animals that have at least 27% increase in their carrier status from production (previous) results to Preliminary (new) analysis
- Overall summary of status differences for Production results compared to Preliminary results
- For calves born in the last three years, list untested sires and maternal grand sires (MGS) if sire/MGS are from high AM status parents themselves
- List Sires and MGS of current calves if the Sires/MGS have a low gene probability index (GPI) – that is, effectively low accuracy estimate of their GeneProb probability estimate
- List untested animals with high probability (>52%) of being a carrier of the recessive gene
- Estimate source animal(s) in database for original carrier of recessive gene (ie oldest animal in pedigree that is a tested carrier)
- List five generation pedigree showing nominated gene GeneProb and DNA test results for each animal in the pedigree
- List nominated animal, its parents and progeny along with the nominated gene GeneProb results and DNA tests. Progeny selection can optionally be trimmed to only include progeny above a nominated probability of being a carrier.

In ILR2, some of these diagnostics are also available as screen displays.

Trends of the influence of the gene in the population over years are also available for calves, their sires and current dams and heifers.

Comma delimited, ASCII files of all DNA tested animals for the nominated gene are created at each GeneProb analysis. This is specifically aimed at sharing of information of deleterious genetic conditions with other societies.

Each active herd in the Society also has a comma delimited ASCII file created for all its animals. The information includes DNA test results and GeneProb probabilities on the animal and its parents. These data files are made available on the web after each GeneProb run for download by the herd (password protected area accessible only by

the nominated herd). Restricted printed reports are also available for herds that do not have PC and web access.


## 5. Undertake test run to see that system is working correctly.

Multiple test GeneProb analyses have been run to ensure the system is robust and to look at the impact of:

- The different GeneProb versions (standard and lethal recessive)
- Different genes and gene frequency in the tested population
- Different breeds and societies
- Different database systems (ILR1 and ILR2)

GeneProb is currently running in production mode on three Society databases across both ILR1 and ILR2 platforms.

Following is an example of the web based information on the AM gene available on the Angus Australia website. (<http://www.angusaustralia.com.au/DNATests.htm>)



**Description of genetic test codes**

Index of description of codes:

- [Arthrogyposis Multiplex \(AM\)](#)
- [Neuropathic Hydrocephalus \(NH\)](#)

Genetic test results are based on samples provided by breeders. Angus Australia makes no statements, representations or warranties about the accuracy or completeness of, any information relating to the status of a particular animal; and, disclaims all responsibility for information and all liability (including without limitation, liability in negligence) for all expenses, losses, damages, and costs you may incur as a result of information being inaccurate or incomplete in any way for any reason.

### Arthrogyposis Multiplex (AM) status

<b>AMF</b>	Indicates that the sample submitted for this animal <b>has been tested</b> and found to be <b>free</b> of the causative mutation responsible for Arthrogyposis Multiplex (AM). This animal is homozygous free, meaning that it has two copies of the normal variant (or allele) of the gene.
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<b>AMC</b>	Indicates that the sample submitted for this animal <b>has been tested</b> and found to be <b>a carrier</b> of the causative mutation responsible for Arthrogyrosis Multiplex (AM). This animal is heterozygous for the mutation, meaning that it has one mutant allele and one normal allele. This animal could pass the AM mutation to approximately half of its progeny.
<b>AM __%</b>	Indicates that, based on pedigree information supplied by the breeder of the animal, the animal <b>has a chance to be a carrier</b> of the mutation responsible for Arthrogyrosis Multiplex (AM) but <b>has not been tested</b> . The higher the indicated percentage, the larger the chance the animal may be a carrier. To verify the status of this animal, Angus Australia recommends that AM testing be undertaken prior to using this animal for breeding purposes.
<b>AMFU</b>	Indicates that, based on pedigree information supplied by the breeder of the animal, the animal is <b>expected to be free</b> of the mutation responsible for Arthrogyrosis Multiplex (AM), but has not been tested. However, this animal <b>has not been tested</b> for the causative mutation and Angus Australia gives no guarantee as to the animal's "free" status.
<b>AMA</b>	Although AM <b>affected calves</b> will be dead at birth and are rarely tested, they would be homozygous for the mutation responsible for Arthrogyrosis Multiplex (AM) and have two copies of the mutant variant of the gene.

GeneProb is also running on Brahman, but the results are not being included on the web as it is unclear whether individual tenderness markers will be made available to the Society on an ongoing basis. Discussions with Pfizer are still to determine whether they are prepared to give individual marker results as well as MVPs for animals tested for tenderness.

## 6. Enhance GeneProb with module to help identify candidate animals for DNA testing and conducting trial runs. Create user friendly output and explanations of the results.

In most cases, a herd is interested in identifying the potential impact of the gene on current calves. These are considered the “Target” animals and have been defined in these discussions to calves born in the herd in the last 3 years.

The enhanced module to GeneProb that looks at the relative influence animals have on the overall current population of animals has been implemented. The module looks at pedigree relationships within the herd (average NRM element across the Target animals) and combines this relationship value with the GeneProb output.

Candidates for DNA testing are the Target animals themselves, their parents and grand-parents. Including ancestors of Target animals beyond grand parents runs the high risk of nominating animals that cannot have DNA collected. Most herds have inter-related pedigrees and multiple generations present at any one time. That is, an animal can be a parent and a grand-parent in the same calving year. In such cases, the effective depth of pedigree for DNA candidates is great-grand-parent.

Relating the output to individual herd requirements is complex and needs to address the type of gene and where the herd is in relation to its testing program. Obviously this is dynamic as more animals are tested within the population (both in the herd under consideration and in the breed as a whole) and how these DNA results impact through the pedigree relationships.

For herds that have little or no information on a gene, testing the sires of the Target animals will give best value for DNA testing dollars as a scoping exercise. This accounts for 50% of the potential gene expression in the Target animals. A further 25% of the potential gene expression can be identified by testing maternal grand sires of the Target animals. However, grand sires can be a larger sample of sires if dams have been sourced from a range of blood lines – usually through the use of a broad range of AI sires.

Following is a sample (reduced) report of the sires used in a typical herd that has recorded 195 calves in the last three years from 115 dams. There are 28 sires that only have progeny and another 12 that have both progeny and are also the sire of at least one dam (ie maternal grand sire). Hence for this high AI use herd, there were 40 sires to test (although many would have already been tested as part of the initial program to define the impact of the gene in the Australian Angus population. To also test the maternal grand sires, there are another 55 sires.

ANCS - Sires and Maternal Grand Sires  
 For calves born in 2007 and onwards for Herd

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Sire-Ident	Prog	Dtrs	AM-res	AMI	NH-res	NHI	Sire-Name
USA416	0	4	AMF	100	NHF	100	ALBERDA TRAVELER 416
CGKB31	3	0	AMFU	99	NHFU	99	ALPINE BRADMAN B31
NAQ2	6	0	AMF	100	NHF	100	ARDROSSAN ADMIRAL A2
NAQX15	0	1	AMC	100	NHF	100	ARDROSSAN CONNECTION X15
NAQW109	0	1	AMF	100	NHC	100	ARDROSSAN DIRECTION W109
NAQX3	1	1	AMF	100	NHC	100	ARDROSSAN DIRECTION X3
USA14575589	12	0	AMF	100	NHF	100	B A F LIMITED EDITION 372
USA41-93	0	2	AMF	100	NHF	100	B C C BUSHWACKER 41-93
USA297E	0	1	AMF	100	NHF	100	B T ULTRAVOX 297E
USA14188956	2	0	AMF	100	NHF	100	B/R AMBUSH 28
USA036	1	2	AMF	100	NHF	100	B/R NEW DESIGN 036
USA323	0	2	AMFU	99	NHFU	99	B/R NEW DESIGN 323
USA095	0	1	AMF	100	NHF	100	B/R NEW FRONTIER 095
VGIT18	0	2	AMFU	99	NHFU	98	BEARTOOTH TANK ENGINE T18
VGIV34	5	1	AMFU	95	NHFU	69	BEARTOOTH V34
USA1407	0	3	AMF	100	NHF	100	BCN VIEW NEW DESIGN 1407
USA7047	0	2	AMF	100	NHF	100	BOYD BLUEGRASS 7047
USA14237157	5	0	AMF	100	NHF	100	BT EQUATOR 395M
USA24J	2	0	AMF	100	NHF	100	BT RIGHT TIME 24J
USA14N	1	0	AMF	100	NHC	100	BT TOUCHDOWN 14N
USA756	12	4	AMF	100	NHF	100	BUSHS STRUT 756
USA3130	0	1	AMF	100	NHF	100	BUTCHS MAXIMUM 3130
USA5321	0	2	AMC	100	NHC	100	C A FUTURE DIRECTION 5321
USA15148659	7	0	AMF	100	NHF	100	CONNELLY THUNDER
USA4192	0	1	AMF	100	NHF	100	G A R BINGO 4192
USA12548568	0	1	AMF	100	NHF	100	G A R EXPECTATION 4915
USA1680	0	1	AMC	100	NHC	100	G A R PRECISION 1680
USA1422615	4	0	AMC	100	NHF	100	G A R SOLUTION
USA13708459	0	1	AMF	100	NHC	100	G T ECHO
USA88	0	1	AMF	100	NHF	100	G T MAXIMUM
QBGM16	0	1	AMFU	99	NHFU	99	GLENOCH MEGAFORCE
USA13992383	0	2	AMF	100	NHF	100	H A POWER ALLIANCE 1025
USA15313140	4	0	AMF	100	NHF	100	HARB PENDLETON 765 J H
USA14219388	2	0	AMF	100	NHFU	55	HOFF FIRST EDITION 058 242
USA13119152	0	10	AMF	100	NHFU	95	HOFF LIMITED EDITION S C 594
USA43	0	1	AMFU	99	NHFU	92	HOFF VALEDICTORIAN S C 925
USA14037894	5	0	AMF	100	NHF	100	HYLINE RIGHT WAY 781
USA13320150	0	1	AMF	100	NHF	100	IRONWOOD NEW LEVEL
USA14885809	1	0	AMF	100	NHF	100	K C F BENNETT PERFORMER
NENZ181	3	0	AMF	100	NHF	100	KAROO W109 DIRECTION Z181
NDIZ101	3	0	AMF	100	NHF	100	KENNY'S CREEK WHITWORTH Z101
VLYA754	2	0	AMFU	99	NHFU	88	LAWSONS ROMEO A754
USAG689L	0	1	AMF	100	NHC	100	LCC DILLON G689L
USA14570934	3	1	AMF	100	NHF	100	LCC NEW CHAPTER G831N
USAG041	0	1	AMF	100	NHF	100	LCC SULTAN G041
USA3025E	0	1	AMF	100	NHF	100	LEACHMEN CONVEYOR 3025E
USA8618	0	1	AMF	100	NHFU	80	LEACHMEN NEW ERA
VPLA94	14	0	AMFU	99	NHFU	99	LLANDARLO DESIGN DOUBLE A94
VPLB72	8	0	AMFU	97	NHFU	90	LLANDARLO DESIGNER GENES B72
VPLZ86	11	1	AMFU	99	NHFU	99	LLANDARLO DESIGNER Z86
VPLA33	10	0	AMFU	99	NHFU	97	LLANDARLO LIMITED EDITION A33
VPLA89	8	0	AMFU	99	NHFU	96	LLANDARLO SECOND EDITION A89
VPLC221	2	0	AMFU	99	NHFU	99	LLANDARLO STRUT C221
VPLV29	0	1	AMFU	99	NHFU	93	LLANDARLO V29
VPLW33	0	1	AMFU	99	NHFU	93	LLANDARLO W33
VPLZ15	11	0	AMFU	99	NHFU	95	LLANDARLO Z15
CAN12E	0	1	AMFU	61	NHFU	33	YOUNG DALE MONARCH 12E
VLYU28	0	3	AMF	100	NHF	100	YTHANERAE PRECISION U28
VLYW129	0	1	AMFU	99	NHFU	77	YTHANERAE ROCKN D AMBUSH W129

Total of 95 Sires: 191 115  
 28 sires with only progeny.  
 55 sires with only daughters.  
 12 sires with both progeny and daughters.

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Higher AMI & NHI indicates more information available on AM and NH results



Despite most of the sires having good information on AM status, a profile of the AM results for the herd shows that there are 34 Target animals that have a > 5% chance of being AM carriers, with 12 of these around the 50% level:

17/11/09 ANGS Herd - Animals by Year Born, Sex, Rego-Status and AM category page 1

Year	Reg	Sex	AMPU?	Animals	AMP	AMFU	AMS<5%	AMS10%	AMS20%	AMS30%	AMS40%	AMS50%	AMS60%	AMS70%	AMS80%	AMS90%	AMS95+	AMC	AMA	
2007	H	F	0	34	0	24	1	1	0	3	0	5	0	0	0	0	0	0	0	0
	H	M	0	46	0	37	0	0	2	2	0	7	0	0	0	0	0	0	0	0
2007	all		0	80	0	61	1	1	0	5	0	12	0	0	0	0	0	0	0	0
2008	H	F	0	38	0	31	1	2	0	4	0	0	0	0	0	0	0	0	0	0
	H	M	0	35	0	30	0	1	0	4	0	0	0	0	0	0	0	0	0	0
	H	S	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2008	all		0	75	0	63	1	3	0	8	0	0	0	0	0	0	0	0	0	0
2009	H	F	0	17	0	16	0	1	0	0	0	0	0	0	0	0	0	0	0	0
	H	M	0	19	0	15	0	3	0	1	0	0	0	0	0	0	0	0	0	0
2009	all		0	36	0	31	0	4	0	1	0	0	0	0	0	0	0	0	0	0
All Years			0	191	0	155	2	8	0	14	0	12	0	0	0	0	0	0	0	0

Lower % categories are more desirable; AMFU? animals have AMFU status but < 2.1% index

A review of the animals in the herd indicates there are potential savings by testing selected animals rather than just DNA testing target animals. An index (ic2) was developed that combined the connectedness (CONN) of DNA candidate animals and the GeneProb index (GPI) which is an indicator of the amount of information available to estimate gene probabilities.

$$ic2 = (CONN + (100 - GPI)) / 2 \quad \text{with an expected range in values between 0 and 100 (0 indicates no DNA test required)}$$

where CONN is connectedness where zero means no pedigree connectedness (reported with a range from 0-100)  
 GPI is GeneProb index reported as a value between 0-100 where zero means no information available

The index highlights animals that are well connected but have only a small amount of information to calculate the gene probabilities. The ic2 index is used to identify significant animals within the herd and then their close relatives are identified that are also DNA candidate animals. A report is then generated that lists significant animals in their related pedigree lines as follows.

ANCS - Herd Candidate animals for gene AM INA testing  
 Selection: ic2 >= 20.0 GPI <= 98.0

Dam Ident	P	D-ic2	S-ic2	P	Sire Ident	Animals	Sex	ic2	CONN	GPI	p11	Tprg	GTPROG	SELN
NZE240317	-	0.0	0.0	-	NZE37738	NZE33885	F	39.8	0.0	20.3	78.9	2	7	140.6
NZE33885	-	39.8	0.0	F	USA416	+-- VPLX6	F	50.3	10.4	9.7	89.4	5	2	316.3
VPLX6	-	50.3	0.0	-	VPLV29	+++ VPLZ41	F	54.3	12.9	4.3	94.7	1	0	109.8
VPLZ41	-	54.3	6.3	-	VPLZ15	+++ VPLC91	F	55.5	12.8	1.7	97.3	0	0	55.5
VPLX6	-	50.3	0.0	F	USA756	+++ VPLB29	F	53.3	10.9	4.3	94.7	1	0	109.7
VPLB29	-	53.3	8.9	-	VPLA94	+++ VPLD26	F	56.4	14.5	1.7	97.3	0	0	56.4
VPLX6	-	50.3	0.0	F	USA14575589	+++ VPLD13	M	52.0	8.3	4.3	94.7	0	0	52.0
VPLX6	-	50.3	5.8	-	VPLA33	+++ VPLE38	M	53.4	11.1	4.3	94.7	0	0	53.4
VPLX6	-	50.3	5.8	-	VPLA33	+++ VPLE39	M	53.4	11.1	4.3	94.7	0	0	53.4
NZE33885	-	39.8	0.0	F	USA416	-- VPLX5	F	50.6	10.2	8.9	90.1	2	0	157.2
VPLX5	-	50.6	0.0	F	USA756	+++ VPLB18	M	53.3	10.7	4.0	95.0	0	0	53.3
VPLX5	-	50.6	0.0	F	USA756	+++ VPLD57	F	53.3	10.7	4.0	95.0	0	0	53.3
VSN53	-	0.1	0.0	C	USA5321	VPLA3	F	32.6	14.8	49.5	50.0	5	1	250.1
VPLA3	-	32.6	5.5	-	VPLZ86	+-- VPLC45	F	44.4	13.1	24.2	75.0	1	0	95.2
VPLC45	-	44.4	7.8	-	VPLB72	+++ VPLE27	M	50.8	13.2	11.6	87.4	0	0	50.8
VPLA3	-	32.6	0.0	F	USA14575589	+-- VPLD27	F	43.2	10.6	24.2	75.0	0	0	43.2
VPLA3	-	32.6	0.0	F	USA14575589	+-- VPLD28	F	43.2	10.6	24.2	75.0	0	0	43.2
VPLA3	-	32.6	0.0	F	USA14575589	+-- VPLD30	M	43.2	10.6	24.2	75.0	0	0	43.2
VPLA3	-	32.6	0.0	F	USA14037894	+-- VPLD53	M	43.7	11.7	24.2	75.0	0	0	43.7

ic2=(conn + (100 - gpi))/2 CONN is connectedness to target animals; GPI is acc; p11 is probability of non-carrier

**P** is the DNA result for the sire and dam (C is tested carrier, F is tested free, - is untested)

**D-ic2** is the dams ic2 value; **S-ic2** is the sires ic2 value; zero ic2 indicates animal is not a candidate for DNA testing.

**p11** is the probability of being a non-carrier animals;

**Tprg** is the number of Target progeny for this animal,

**GTPROG** is number of Target grand progeny

**SELN** is the sum of the animals own ic2 plus the ic2 values of its progeny. Used as an indicator for determining significant animals.

The example report shows two animals that should be considered for DNA testing.

- **NZEG3885** has two daughters (VPLX6 and VPLX5), 7 grand progeny and 2 great grand progeny that are DNA candidates. If DNA can not be obtained from NZEG3885, then VPLX6 would be the next best alternative in this pedigree line. Note that there are tested free animals in this pedigree tree, but no tested carriers. Tested free animals are not definitive tests for their parents whereas tested carriers do help describe a parent.
- **VPLA3** is the progeny of a tested carrier. It has 5 progeny and 1 grand progeny that are DNA candidate animals. If VPLA3 is tested free, then all these animals and get high GPIs (particularly as will be considered free by descent most of the progeny are by tested free sires). If VPLA3 tests as a carrier, then each of the progeny will need to be tested.

These examples from a reasonably typical Angus herd demonstrate the potential for using these diagnostics to help breeders maximise the results from their DNA testing investments. With the additional benefit of GeneProb recalculating gene probabilities across the entire database as new DNA test results are added to the database, financial benefits to the breeders as a whole can potentially be value added beyond just the herd that submitted the test – the value of the whole is greater than the sum of the parts.

## **7. Release of project results at Beef Australia, 2009.**

Results of the AM testing on Angus have been released on the Web as seen in the example in Milestone 3.

In April, 2009 ABRI released 5,000 copies of BREEDPLAN News to industry. This included the following 1 ½ page report on the project acknowledging MLA's participation.

# GeneProb - Maximising the use of DNA test results

GeneProb is a new product that has recently been offered by ABRI. GeneProb was developed by Prof Brian Kinghorn and Dr Richard Kerr at the University of New England and utilises the basic principles of inheritance to estimate the probabilities of specific genes being present in a wider, related population than the DNA tested animals. Hence it is ideally suited to Breed Society databases where pedigree relationships have been collected over many generations.

GeneProb can be used to track lethal recessive genes like Arthrogyposis Multiplex (AM) and also for genes of interest like the red/black gene, genes for horn/poll, etc. In addition, Angus Australia, the Australian Brahman Breeders Association, ABRI and Meat and Livestock Australia also have undertaken a joint project to look at using GeneProb on production markers (eg Tenderness genes) while developing protocols to maximise DNA test information.

## GeneProb: The Angus Australia Experience

DNA test results are never cheap – especially when you run them one at a time as the Angus Australia (AA) was forced to do when the DNA test for Arthrogyposis Multiplex (AM), a lethal recessive gene, became available in Australia. As Carel Teseling, Breed Development Manager of AA commented: "When you consider that we have over 1.2 million animals in our database and we started with only a couple of hundred animals with DNA test results, we needed something to help us focus on the animals that needed testing – rather than just blindly testing all animals. We needed something to maximise



*Prof Brian Kinghorn and Carel Teseling discuss the use of GeneProb by Angus Australia*

the usefulness of the DNA test results we had. Fortunately for us, Prof. Brian Kinghorn, Dept Animal Science at the University of New England, had already developed GeneProb - an application that uses the known test results to calculate the probability of untested animals being carriers." Not only was GeneProb developed, but ABRI and the UNE quickly organised a world wide licence agreement for ABRI to run GeneProb. It was quickly implemented into ABRI's pedigree recording system with the results automatically updating onto the Internet Solutions Animal Enquiry system, as well as making each herd's results available as a download from the web. Several reports have been developed in conjunction with AA to monitor new results loaded onto the database since the previous analysis. Monitoring new results is critical to ensure the integrity of sample collection and accuracy of pedigree information used

for the GeneProb analysis. "This quick response to the AM problem has meant that both bull sellers and bull buyers can go into the next bull selling season with the confidence of having the latest AM status on all animals up for sale – and this information is updated on the web on a weekly basis as new test results come in". "We were very pleased with ABRI and UNE's exceptionally quick response to AA's request for the development of the software and are convinced that the software will, in future, benefit many other organisations through ABRI's international presence." Angus has tackled the AM problem head on – and Angus Australia is leading the way with having an AM Status on all 1.2M animals in the database.

For more information on GeneProb, contact Jack Allen, Technical Director, ABRI on 02 6773 3555 or email jack.allen@abri.une.edu.au.

## Technically Speaking

The concept of tracking a gene through a population is reasonably straight forward. Genes occur in pairs and generally have 2 forms (lets call them A1 and A2). These are called alleles. Where available, a DNA test will specify which alleles an animal actually has. When an embryo is formed, it gets one allele of the gene from its father and one from its mother. Where both alleles are the same (eg A1A1 or A2A2), they are called homozygous. In this case, the animal will always pass on this allele to the next generation. Where the alleles are different (ie A1A2 or A2A1), they are called heterozygous and there is an equal chance of passing on either allele to the next generation.

GeneProb uses a segregation analysis to calculate probabilities of which alleles an untested animal will have. The complex analysis allows for pedigree relationships, gene frequencies within the populations and makes allowance for unequal effects of the genes (for example, the A2A2 form of the AM gene causes the animal to die at birth). GeneProb also calculates a Gene Probability Index (GPI) which indicates how much information was available to estimate the probability (much like an accuracy of an EBV). All animals in the target database get gene probabilities and GPIs.

ABRI and Angus Australia manned 5 booths in total at Beef 2009 – ABRI providing 4 BREEDPLAN Staff and Angus Australia 4 of its representatives with technical skills. This team handled many enquiries from breeders about the project.



One of the ABRI booths at Beef 2009

## Conclusion

The GeneProb system has been integrated into both ILR1 and ILR2 platforms and is running in production mode on a routine basis for three Societies. Two recessive genes and four production genes have been run to date. Further recessive and production genes are envisaged to be run in the next few months. Where applicable, results are available on the Web and individual herd files are available for download for each current herd.