Polled Genetics and Simple Inheritance Explained

Background

The ability to confidently apply selection pressure and increase the frequency of the polled trait in tropical breeds has positive implications for animal welfare, productivity, labour requirements and safety of station staff. The frequency of the polled gene in Brahman cattle is generally low compared to some other breeds. In the past, breeding polled *Bos. indicus* cattle has been complicated, due a complex interaction of the polled, scurred and African horn gene. However the recent release of a gene marker test for the trait has allowed us to distinguish a homozygote ('true poll') polled animals with a high level of confidence in Brahman cattle. Homozygote polled sires provide a more rapid rate of infusion of the polled gene into a Brahman herd, with 100% polled/scurred progeny when mated with horned cows compared to just 50% polled/scurred progeny from the same matings using a sire with only one copy of the polled allele (heterozygote). This article aims to provide the background required to understand the mating outcomes from different polled/horn genotypes, which can now be determined using a gene marker test.

Genetics in a nutshell

There are a few terms that it can be useful to become familiar with when understanding simple inheritance in relation to the poll/horn trait.

Genotype: The genetic makeup of an animal (ie. can't be seen, but can be determined with genomic technology such as gene marker tests.

Phenotype: The observed performance or trait, as a result of gene expression (eg. coat colour, horn status, 200d weight)

Chromosome: A long strand of DNA/genes (BIG)

Gene: A DNA sequence which sits at a specific location on a chromosome, which controls or contributes to a phenotypic outcome (SMALL)

Allele: Two alleles make up a gene, one allele has come from each parent (SMALLER)

Homozygous: Gene is made up of two identical alleles

Heterozygous: Gene is made up of two different alleles (ie. a 'carrier')

T*his is easy to remember if you think of 'Homo' as meaning 'same, 'Hetero' as meaning different.*

Simple inheritance in simple terms

An animal has two copies of all genes. When the animal produces its own sperm or egg (gametes) the gamete will have only one of these genes randomly selected, so it ultimately only has half the genes required for an animal. When an embro is formed, it will again have a full set of genes, but one of each gene from each parent. So an animal's genes a mix of 50% randomly selected from the female parent and 50% randomly selected from the male parent.

Dominance – how it works

With simple inheritance, there can be two forms of a gene and one can be dominant over the other. For example, say we have the genotype **BW** in sheep (heterozygous), where **B**=black colour and **W**=white colour, but black is dominant over white. The phenotype of the sheep would be black. If it was **BB** (homozygous), it would still be black, but if it was **WW** (homozygous) it would be white (as there is no **B** gene to dominate). This works the same for Pompes disease in cattle. Say if the **tt** gene causes pompes, and **TT** doesn't, and **TT** is dominant. An animal that is **tt tt** would have pompes. A **TT tt** animal would not have pompes disease even though it is carrying the disease gene, as the TT is dominant. This animal can be called a 'carrier'. In some cases, one gene is not completely dominant over another, and the resulting phenotype can be a mix of both. For example, if **B** in sheep wasn't completely dominant over **W**, then the **BW** sheep may show black and white spots.

Mating outcomes – how it works

Lets go back to the **TT tt (**heterozygous) pompes animal or pompes 'carrier'. This animal's sperm or egg will have a copy of either **TT** or **tt**, which will be purely random. The **TT TT** homozygous animal can only produce a sperm/egg that has the gene **TT**, as there is no **tt** to pass on. This is where we come to predicting mating outcomes.

Say we mate a **TT TT** animal with a **TT tt** animal. The progeny has equal chance of having either one of each parent's genes. We can easily sketch this out with a punnet square (below), which helps us calculate all possible combinations. We can see that this cross would result in 50% of progeny being **TT TT** and 50% being **TT tt**. If **TT** was dominant, then 50% of progeny would be carriers of **tt**, but none would show signs of the **tt** trait.

Parent 1

Parent 2		**TT**	**TT**
	TT	***TT TT***	***TT TT***
	tt	***TT tt***	***TT tt***

Progeny likelihood
50% **TT TT**
50% **TT tt**

Deciphering the polled gene in Bos indicus cattle using gene marker test results

The polled gene in Bos indicus cattle is not entirely simple, as it is controlled by more than one gene. Also, the dominance is not simple, rather there is the intermediate phenotype 'scurrs'. That is, rather than either the poll or horn gene being dominant over each, the heterozygote animal is more likely to be scurred. But this isn't always the case, and that is why it is difficult to tell an animal's genotype on phenotype alone. The use of the gene marker test tells us, to a high level of confidence, whether an animal is a homozygous poll (**PP**). An animal that carries no copy of the poll gene is a homozygote **HH**, while an animal that carries one copy of the polled gene is a heterozygote **PH**. Validation of the test results have shown that in most cases (98%) **PP** animals are polled. **PH** animals are most often (50%) scurred, but can be polled (40%) and in few cases horned (10%). **HH** animals are mostly horned (93%), although few can be scurred (6%). This is summarised in Table 1. Without knowing the genotype, it would be difficult to tell whether an animal which appears polled does or does not carry a copy of the horn gene.

Table 1: Poll/Horn genotype and resulting phenotype from validation animals (simplified)

Genotype	Phenotype		
	Polled	Scurred	Horned
PP	**98 %**	1 %	1 %
PH	**40 %**	**50 %**	10 %
HH	1.6 %	6 %	**93 %**

Mating outcomes using polled/horn genotypes

The same process can be used for predicting mating outcomes as where simple inheritance is at work.

Let's cross a homozygote polled animal (**PP**) with a homozygote horned animal (**HH**). All progeny from this mating would have the genotype **PH**, which from the validation we know have a high possibility of being scurred or polled, and only a small chance of being horned.

Parent 1

Parent 2		**P**	**P**
	H	***PH***	***PH***
	H	***PH***	***PH***

Progeny likelihood
100% **PH**

Let's cross a homozygote **PP** animal with a heterozygote **PH** animal. 50% of progeny from this mating would be genotype **PP** and 50% **PH**. If you were to mate these animals only once, it would be random to which progeny outcome would result. But if you mate a **PP** bull to 100 **PH** cows, then you would expect to see the ratio of **PP**:**PH** calves approach 50:50. Table 2 shows the progeny likelihood for all possible matings of poll/horn genotypes.

Parent 1

Parent 2

	P	**P**
P	***PP***	***PP***
H	***PH***	***PH***

Progeny likelihood
50% **PP**
50% **PH**

Table 2: Progeny likelihood for all potential combinations of sire/dam genotypes.

Parent 1	Parent 2	Progeny genotype
PP	PP	100% PP
PP	PH	50% PP, 50% PH
PP	HH	100% PH
PH	PH	75% PH, 25% HH
PH	HH	50% PH, 50% HH
HH	HH	100% HH

Disclaimer

This article has been written with the purpose of simplifying the poll gene marker test results and mating predictions. It is acknowledged that an ambiguous allele associated with the poll and horn gene appears to occur, which means that the phenotypic outcomes of the genotypes are not 100% probable. However, the validations so far indicate that the ambiguous outcomes are uncommon in Brahman cattle, therefore for the purpose of simplifying the concepts the ambiguous allele has been ignored. For updated results of validation, go to http://www.beefcrc.com.au/PolledGeneMarkerTest. Article written 24/06/2011.