GeneProb

GeneProb amplifies the use of DNA test results to create breed wide benefits and management solutions for genetic conditions and simple qualitative traits.

GeneProb utilises the basic principles of inheritance to estimate the probabilities of specific genes being present in a wider, related population than the animals with DNA test results available. It allows registered breeders to focus on animals that need testing, instead of blindly testing all animals.

The most common use of GeneProb is to track recessive genetic conditions but it can also be used to track genes of interest such as the genes for coat colour or polledness. The GeneProb software was developed by Prof Brian Kinghorn and Dr Richard Kerr at the University of New England in Armidale, Australia and is licensed for commercialisation to the Agricultural Business Research Institute (ABRI).

What does GeneProb do?

GeneProb uses known DNA test results for a nominated gene and combines this with pedigree information stored on Breed Society databases to calculate the probability of alleles (different forms of the gene) being present in untested animals. GeneProb is commonly used to:

- Track recessive genetic conditions such as Osteopetrosis (OS), Alpha Mannosidosis (MA), Arthogryposis Multiplex (AM), Contractural Arachnodactyly (CA) and Neuropathic Hydrocephalus (NH).

- Track genes of interest like the genes for coat colour or polledness.

- Report the probability of the animal being a carrier of the nominated gene mutation.

Display of GeneProb Results

GeneProb results can be provided to both Breed Societies and individual seedstock herds in a number of paper and electronic forms. Many Breed Societies currently using GeneProb software display results for each animal on their online database facility while providing members with specific csv files that contain the results for all animals owned or bred within their herd.

Figure 1. Example GeneProb Results for an Individual Animal

Genetic Test Codes: (MAFU) (OS50%) (NH1%)(AMFU)

The figure above indicates that based on the DNA results for the relatives of the animal, this animal has a 50% probability of being an OS carrier, 1% probability of being an NH carrier and is expected to be free but has not been directly tested for MA and AM.

What benefits does GeneProb have for Individual Herds?

GeneProb allows individual herds to:

- Better identify animals within their herd that need testing, instead of blindly testing all animals.

- Manage the spread of undesirable or desirable genes within their herd.

What benefits does GeneProb have for Individual Breed Societies?

GeneProb enables each Breed Society to:

- Monitor the prevalence of genetic conditions within their breed.

- Maximise the usefulness of the DNA test results stored on Breed Society databases, whilst minimising the number of extra animals that need testing.

Explanation of GeneProb Results

_ _F	Indicates that the sample submitted for this animal has been tested and found to be free of the causative mutation responsible for the indicated genetic condition. This animal is homozygous free, meaning that it has two copies of the normal variant (or allele) of the gene. Eg. AMF
_ _C	Indicates that the sample submitted for this animal has been tested and found to be a carrier of the causative mutation responsible for the indicated genetic condition. This animal is heterozygous for the mutation, meaning that it has one mutant allele and one normal allele. This animal could pass the mutation to approximately half of its progeny. Eg. AMC
_ _ _%	Indicates that, based on pedigree information supplied by the breeder of the animal, the animal has a chance to be a carrier of the mutation responsible for the indicated genetic condition but has not been tested. The higher the indicated percentage, the larger the chance the animal may be a carrier. Breeders are recommended to test this animal for the genetic condition prior to using this animal in a breeding program. Eg. AM45%
_ _FU	Indicates that, based on pedigree information supplied by the breeder of the animal, the animal is expected to be free of the mutation responsible for the indicated genetic condition but has not been tested. Eg. AMFU
_ _A	Indicates that the sample submitted for this animal has been tested and found to be affected by the genetic condition. This animal is homozygous for the mutation responsible for the indicated genetic condition and have two copies of the mutant variant of the gene. Eg. AMA