

## Equine DNA Profiling

### **What is 'DNA Typing'?**

DNA profiling or 'typing' establishes a unique genetic profile. Since an individual inherits one of its two sets of genes from each parent, its profile is a combination of the genetic makeup of both parents.

### **What is 'Parentage Testing'?**

Parentage testing establishes whether there is a genetic relationship between a dam, foal and possible sire. DNA parentage verification can determine who is/is not, the possible sire or dam of a foal. It is the most precise and accurate method for determining the sire of any foal. There is no charge for parentage verification as long as the sire, dam and foal have been DNA typed or profiled.

### **What samples can be submitted?**

DNA is present in almost every cell. For equine testing, DNA is extracted from follicles found in the hair samples (mane). Do not cut off hair samples as it is critical that hair is attached with the root (follicle) intact.

### **How accurate is the testing?**

Genetic Technologies is a member of the International Society of Animal Genetics (ISAG). All our tests and profiles use the 17-plex genetic equine markers, thereby ensuring the most accurate and reliable results. These markers are used and developed in the Stockmarks for Horses Genotyping Kit - Equine (Applied Biosystems).

### **How does the testing work?**

The principle behind parentage testing in humans and animals is based on 'exclusion'. An individual inherits one copy of each of their genes from each parent. When assessing parentage, a foal's DNA profile (genotype) is compared with that of the dam and potential sire(s). Any alleles (fragments of DNA) present in the foal, which are not present in the dam's DNA, are concluded to have come from the sire.

A panel of seventeen equine-specific markers allow for a DNA profile unique to that individual horse. Each marker generates two alleles (bands) of a particular size (base pairs). When the alleles are the same size, the individual is considered **homozygous** i.e. the foal has inherited two identical-sized bands from each parent. Where the two bands appear as different sizes, the individual is considered **heterozygous**, i.e. the foal has inherited one specific sized allele from each parent.

Results are shown as *Sire Confirmed* or *Sire Excluded*. In cases of exclusion, results are shown with the markers determining the point/s of exclusion. Where the results are confirmed, they are interpreted as an inclusion – enough markers are considered to have a high probability of having come from the sire.

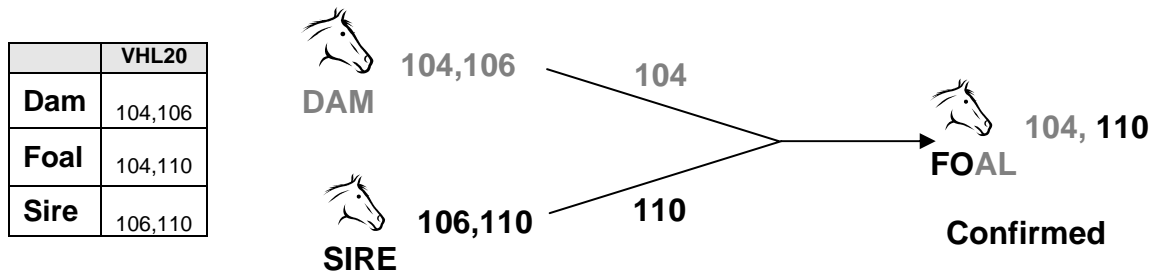
### **Nomenclature**

The nomenclature for the reporting of all profiles using the equine STR markers is based on the actual size (base pairs) observed. These observed fragment lengths of amplified

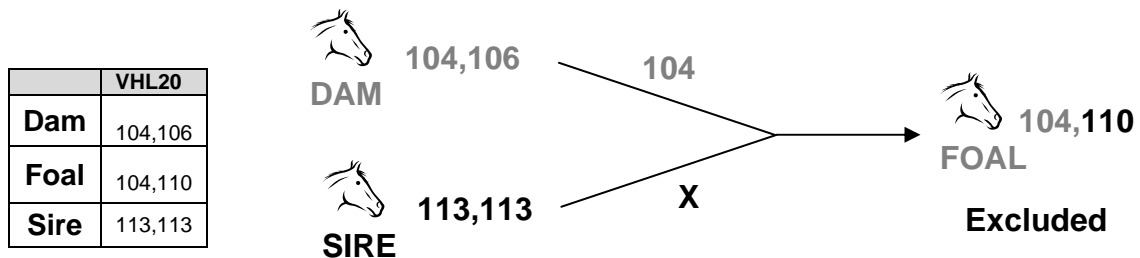
products are grouped into categories according to their size using allelic bins of 1 base pair.

### Example of Parentage Analysis

Parentage is verified by comparing the profile of the dam, foal and sire at all 17 markers. In some cases, letters are used as a representation of the real size data or number. All Genetic Technologies results are shown as real data (base pair numbers). The example below shows the results at one marker:



The above example shows confirmation of Sire. All alleles (numbers) in Foal can be verified in the Dam's and possible Sire's profile.



The above example shows exclusion of 'Sire 2' at marker VHL20. Foal allele 110 is not present in Sire 2.

### EXAMPLE OF EQUINE DNA PROFILING REPORT

**Name of Horse:** GENETIC SCIENCE  
**Identity Number:** 912567000000867  
**Sire:** GENETIC TECHNOLOGIES  
**Sire Code:** 652125466945869  
**Dam:** SILBASE  
**Dam Code:** 124875875236694  
**Sex:** FEMALE  
**Breed:** PURA RAZA ESPANOLA  
**Colour:** GREY

Date of Birth: 01/01/2004  
 Laboratory Number: EQU001

**DNA Results Table**

<b>LOCUS</b>	<b>GENETIC SCIENCE Lab ID: EQU001</b>
VHL20	104, 104
HTG4	126, 130
AHT4	144, 144
HMS7	170, 178
HTG6	85, 85
AHT5	137, 137
HMS6	157, 161
ASB23	188, 190
ASB2	234, 242
HTG10	NR
HTG7	125, 125
HMS3	165, 167
HMS2	222, 235
ASB17	119, 119
LEX3	155, 157
HMS1	181, 181
CA425	239, 239

NR: No Result

**EQUINE DNA PARENTAGE EVALUATION**

<b>LOCUS</b>	<b>DAM</b>	<b>FOAL</b>	<b>SIRE</b>
	<b>Serenilla Technoliga</b>	<b>Mayica Genetica</b>	<b>Escala Sciencia</b>
<b>VHL20</b>	<b>92, 104</b>	<b>92, 96</b>	<b>96, 104</b>
<b>HTG4</b>	<b>130, 130</b>	<b>130, 130</b>	<b>130, 130</b>
<b>AHT4</b>	<b>150, 150</b>	<b>150, 150</b>	<b>150, 150</b>

SAMPLE ONLY

<b>HMS7</b>	<b>180, 180</b>	<b>180, 180</b>	<b>180, 180</b>
<b>HTG6</b>	<b>85, 95</b>	<b>85, 95</b>	<b>85, 95</b>
<b>AHT5</b>	<b>131, 140</b>	<b>131, 140</b>	<b>131, 140</b>
<b>HMS6</b>	<b>157, 168</b>	<b>157, 168</b>	<b>157, 157</b>
<b>ASB23</b>	<b>188, 190</b>	<b>190, 192</b>	<b>190, 192</b>
<b>ASB2</b>	<b>242, 246</b>	<b>242, 250</b>	<b>234, 250</b>
<b>HTG10</b>	<b>NR</b>	<b>100, 104</b>	<b>NR</b>
<b>HTG7</b>	<b>125, 125</b>	<b>125, 125</b>	<b>125, 125</b>
<b>HMS3</b>	<b>163*</b>	<b>*167</b>	<b>165, 167</b>
<b>HMS2</b>	<b>216, 222</b>	<b>222, 222</b>	<b>222, 222</b>
<b>ASB17</b>	<b>105, 109</b>	<b>94, 105</b>	<b>94, 98</b>
<b>LEX3</b>	<b>153, 153</b>	<b>153, 157</b>	<b>157, 157</b>
<b>HMS1</b>	<b>181, 183</b>	<b>175, 181</b>	<b>175, 181</b>
<b>CA425</b>	<b>229, 239</b>	<b>229, 239</b>	<b>239, 239</b>

\*Null allele

**Confirmed**

SAMPLE ONLY