



## CONFERENCE 2010, Edinburgh, Scotland

### Equine Genetics and Parentage Analysis Workshop

The workshop was Chaired by Alan Guthrie (OPVGL, South Africa)

#### 1 Current ISAG Equine Standing Committee: 2006-2010

Alan Guthrie - Chair (OPVGL, South Africa)  
Hitoshi Gawahara (LRC, Japan)  
Sofia Mikko (SLU, Sweden)  
Romy Morrin-O'Donnell (Weatherbys, Ireland)  
Lee Millon (VGL-UCD, USA)  
Ann Trezise (AEGRC-UQ, Australia)

#### 2 Welcome

Alan Guthrie welcomed all participants to the 2010 workshop.

#### 3 ISAG Horse Comparison Test 2009-2010

ISAG – 110 Institutional Members in 2010  
Horse CT 2007-2008 – 75 Participants reported HCT Results  
Horse CT 2009-2010 – 82 Participants reported HCT Results (10% increase)

75% of ISAG Institutional Members reported results in the 2010 Horse CT  
This is the largest Comparison Test run under the auspices of ISAG.

New Numerical Laboratory Codes – 5 digit number – must be used in future  
All old codes are Obsolete

##### 3.1 Report from Duty Laboratory – Ann Trezise, AEGRC-UQ Australia

2009-2010 ISAG HCT Duty Laboratory was the Australian Equine Genetics Research Centre at the University of Queensland.

- 91 Laboratories requested HCT samples
- 82 Laboratories reported HCT Results

##### 3.1.1 2009-2010 HCT Problems

- Late Requests for HCT Samples
- Only 40% HCT Requests received by the Deadline .
  - Only 80% HCT Requests received by 31 Oct 2009
  - Last Samples sent 15 Dec 2009

Incomplete Consignment Forms  
Incomplete Import Documentation  
Incomplete Courier Account Information

### 3.1.2 Suggested Solutions for 2011-2012 HCT

Late requests for HCT Samples can NOT be accepted  
Re-designed HCT Consignment Request Form  
HCT Requests via ISAG web site will help  
Submission not accepted until essential information complete  
**Current** ISAG Institutional Membership  
Pre-pay or *Valid* Courier account number only  
Large, international courier companies only  
Eg. Fedex, DHL, TNT  
*ALL* import documents, *correctly completed* and provided/requested with original Consignment Request

## 3.2 Report from HCT Results Analysis Laboratory – Lee V. Millon, VGL-UC Davis USA

2009-2010 ISAG HCT Results Analysis Laboratory was VGL at UC Davis  
HCT Results were compiled and analysed by Lee V. Millon and presented by Alan Guthrie

### 3.2.1 2009-2010 HCT Problems

Results not formatted according to provided instructions  
Multiple submissions from the one laboratory, often from different senders  
Use of an old/incorrect Laboratory ID

### 3.2.2 Suggested Solutions for 2011-2012 HCT

1. Obtain or secure correct Lab ID.
2. Write "ISAG 2012 HCT" in the email Subject field followed by your Lab ID.  
Example: ISAG 2012 HCT 84414
3. Follow submission instructions exactly, especially the format and arrangement of the file.
4. It would be best submit only one HCT results file, unless an updated version is absolutely necessary.
5. If you must submit another version of your HCT results, then include that information to the email subject field. Example: ISAG 2012 HCT 84414 version2
6. Comments were provided in a variety of ways and are very time consuming to compile. If you must include comments, then put all comments written in a single cell and a single row in the same sheet as the results.

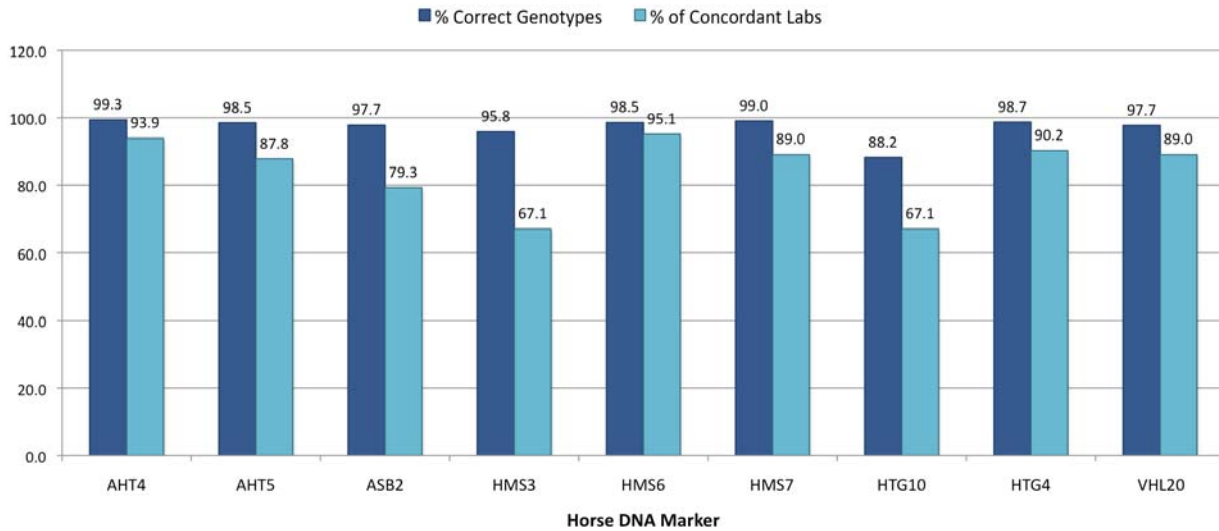
### 3.2.3 Analysis of the Results of the 2009-2010 ISAG Horse Comparison Test

This analysis considers the HCT Results for the nine Horse STR DNA Markers recommended by ISAG at the time laboratories were genotyping the 2009-2010 HCT Samples.

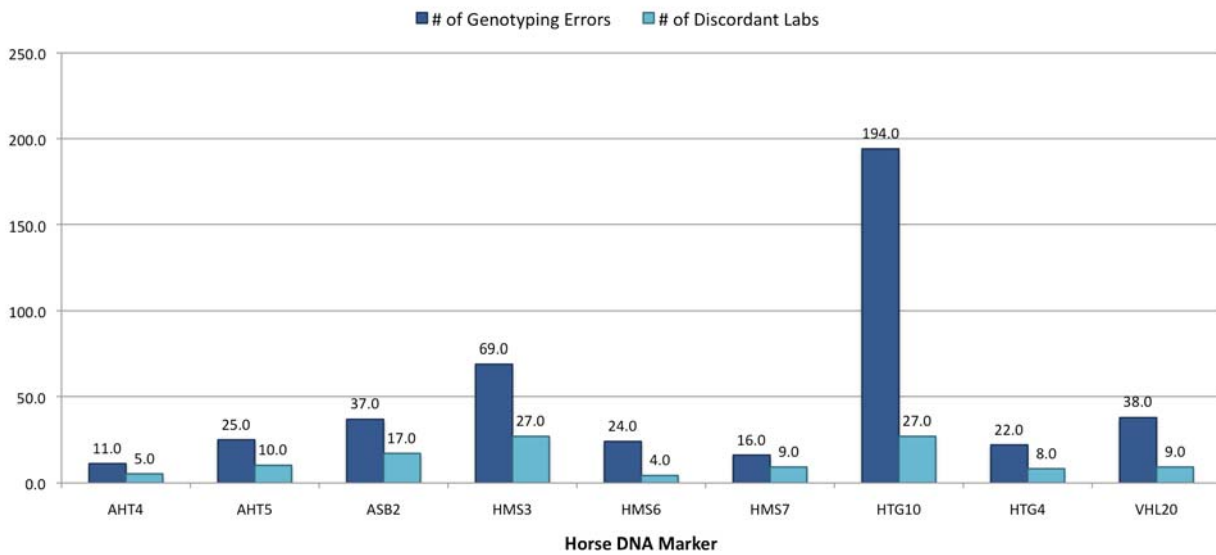
In this analysis a genotyping error is counted if one or both alleles are incorrectly reported or not reported.

The ISAG recommended Horse STR DNA Markers for the 2009-2010 HCT are: AHT4, AHT5, ASB2, HMS3, HMS6, HMS7, HTG10, HTG4, VHL20.

**2010 HCT: Percentage Genotyping Accuracy**



**2010 HCT: Number Genotyping Errors**



Participating laboratories had most difficulty accurately genotyping the HMS3 and HGT10 Horse STR DNA Markers. For each of these DNA Markers, one third of the laboratories participating in the 2010 HCT made genotyping errors.

#### 4 Certificates of Participation and Performance in the 2009-2010 ISAG Horse Comparison Test

Workshop members discussed the paper released by ISAG regarding a rating system for laboratories participating in the horse comparison test (INTERNATIONAL IFAG-ISAG COMPARISON TEST, 2009-2010 - Suggestions for implementing a rating of the CT results).

The workshop endorsed the proposed five-level rating system and the percentage correct genotypes associated with each rating. Rating 1 being the highest, and Rating 5 the lowest. The following Table shows the level of genotyping accuracy associated with Ratings 1 to 5.

Rating	% Correct Genotypes
1	98-100%
2	95-98%
3	90-95%
4	80-90%
5	less than 80%

For the 2009-2010 ISAG Horse Comparison Test, Genotyping Accuracy and the corresponding Rating will be determined by genotyping results for the current 9 ISAG recommended Horse STR DNA Markers: AHT4, AHT5, ASB2, HMS3, HMS6, HMS7, HTG10, HTG4, VHL20.

Workshop members discussed the “Absolute Genotype Error” Rating versus the “Relative Genotype Error” Rating. Concerns were raised that the two different methods of determining a laboratory’s rating would create confusion for equine breed societies and stud books. The workshop expressed a desire to implement a single rating system for reporting the results of the horse comparison test, and that a single rating be shown on any Certificate issued by ISAG. The workshop hoped that a single rating system would avoid potential confusion created by having two different rating systems and would ensure that breed societies will be comparing “like-with-like” if they request sight of ISAG Comparison Test Certificates from a number of different laboratories.

Workshop members discussed which of the two ratings should be reported on the ISAG Horse Comparison Test Certificates. The “Absolute Genotype Error” Rating was considered preferable because it is the higher genotyping quality standard, and because of the increased potential for false-positive qualification of foals if incomplete DNA profiles were used in a parentage analysis.

Workshop members discussed the results of the 2009-2010 ISAG Horse Comparison Test in the context of the Absolute Genotype Error Rating System and the Relative Genotype Error Rating System. The following points were noted with regard Absolute, vs. Relative Genotyping Rating Systems:

Of the 82 laboratories that participated in the 2009-2010 ISAG HCT, there are 12 cases in which the “Absolute Percentage Correct Genotypes”, is different compared to “Relative

Percentage Correct Genotypes”. That is, 12 participating laboratories did not report one or more alleles of the nine ISAG recommended Equine DNA Markers.

Across these 12 cases, the differences between Absolute versus Relative “Percentage Correct Genotypes” ranged from 0.6% to 38.9%. In most of these cases (7 out of 12), the difference between the Absolute and Relative Percentage Correct Genotypes made no difference to the Rating that the laboratory would receive under the proposed criteria shown above.

However, in 5 cases, the difference between the Absolute Percentage Correct Genotypes, and the Relative Percentage Correct Genotypes would result in a different rating. In 3 of the 5 cases, the rating band would increase by three divisions.

These 12 cases, along with the corresponding Absolute and Relative Percentage Correct Genotypes and the Absolute and Relative Ratings, are shown in the following Table.

Case	Number of Unreported Alleles	Absolute Genotyping Accuracy (%)	Relative Genotyping Accuracy (%)	Difference	Absolute Genotyping Rating	Relative Genotyping Rating	Difference in Rating Band
A	1	96.1	96.7	0.6	2	2	0
B	1	99.4	100.0	0.6	1	1	0
C	1	99.4	100.0	0.6	1	1	0
D	4	90.6	92.8	2.2	3	3	0
E	4	95.6	97.8	2.2	2	2	0
F	4	96.7	98.9	2.2	2	1	1
G	8	81.7	86.1	4.4	4	4	0
H	8	90.0	94.4	4.4	3	3	0
I	19	86.1	96.7	10.6	4	2	2
J	20	87.8	98.9	11.1	4	1	3
K	20	88.9	100.0	11.1	4	1	3
L	70	56.1	95.0	38.9	5	2	3

To allow laboratories to establish internationally compatible equine DNA profiling procedures, laboratories and organisations participating in an ISAG Horse Comparison Test for the first time may choose NOT to be rated.

Following discussion of the “Absolute” versus “Relative” methods of assessing genotyping accuracy and assignment of the corresponding rating, the Chair put the following Motion to the workshop.

**MOTION:** The ISAG Equine Genetics and Parentage Testing Workshop proposes the use of “Absolute Genotyping Accuracy” as the single rating system for horse genotyping and reporting on ISAG issued certificates of participation in ISAG Horse Comparison Tests.

The Chair declared voting rights as one vote per ISAG Institutional Member. One representative from each ISAG Institutional Member organisation present at the workshop voted on the motion by a “show of hands”.

The result of the vote count was:

	TALLY
IN FAVOUR of the Motion	32
OPPOSED to the Motion	3
ABSTAIN	1

**The Motion was CARRIED by clear majority and without dissent.**

## 5 ISAG Horse Comparison Test 2011-2012

### 5.1 Appointment of Duty Laboratory for 2011-2012 HCT

Dr Hitoshi Gawahara from the Laboratory of Racing Chemistry (LRC), Japan volunteered to undertake the important role of “Duty Laboratory” for preparation and distribution of purified Horse DNA samples (1 reference sample plus 20 unknown samples) for the 2011-2012 ISAG Horse Comparison Test.

The 2009-2010 Duty Laboratory (AEGRC, University of Queensland, Australia) agreed to provide advice in undertaking this role.

Other Institutional Members of ISAG were given the opportunity to nominate from the floor for the role of Duty Laboratory for the 2011-2012 ISAG HCT. No other nominations were made.

**The Laboratory of Racing Chemistry (Japan), represented by Dr Hitoshi Gawahara, was appointed as the Duty Laboratory for the 2011-2012 ISAG Horse Comparison Test.**

The participants of the workshop expressed their sincere thanks to Dr Hitoshi Gawahara, on behalf of the LRC (Japan), for undertaking this increasingly onerous and very important role.

### 5.2 Appointment of Results Analysis Laboratory for 2011-2012 ISAG HCT

Dr Lee Millon from the Veterinary Genetics Laboratory, University of California at Davis (VGL-UC Davis), USA, volunteered to undertake the role of “Results Analysis Laboratory” for the collation and analysis of results reported by participating laboratories for the 2011-2012 ISAG Horse Comparison Test.

Other Institutional Members of ISAG were given the opportunity to nominate from the floor for the role of Results Analysis Laboratory for the 2011-2012 ISAG HCT. No other nominations were made.

**Dr Lee Millon, on behalf of VGL-UC Davis (USA), was appointed as the Results Analysis Laboratory for the 2011-2012 ISAG Horse Comparison Test.**

The participants of the workshop expressed their sincere thanks to Dr Lee Millon, on behalf of VGL-UC Davis (USA), for undertaking this increasingly complex and very important role.

## **6 Inclusion of Three Additional Equine STR DNA Markers to the ISAG Recommended International Panel of Equine STR DNA Markers**

The current (at July 2010) ISAG International Panel of Equine STR DNA Markers includes 9 Equine STR DNA Markers (AHT4, AHT5, ASB2, HMS3, HMS6, HMS7, HTG10, HTG4, VHL20) that are recommended to be included in all Thoroughbred horse DNA profiles determined by all ISAG Institutional Member laboratories world-wide.

The inclusion of a common panel of Equine STR DNA Markers in all Equine DNA profiles facilitates the international import/export of Thoroughbred horses, and other horse breeds. Equine DNA Profiles shared between affiliated Stud Books and Breed Registries can then be used for parentage verification and identity confirmation by recipient Stud Books and their Equine DNA Profiling laboratories.

The current ISAG recommended panel of 9 Equine STR DNA Markers provides a very high level of confidence for use in “Comparison Tests” to confirm the identity of individual horses by DNA Profile Analysis.

However, equine parentage verification requires the inclusion of additional, common, Equine STR DNA Markers to achieve a similarly high level of confidence in the parentage analysis.

The 2008 ISAG Equine Genetics and Parentage Analysis Workshop (held at the 2008 ISAG Conference – Amsterdam) requested that ISAG Institutional Member Laboratories undertake DNA profiling of six additional Equine STR DNA Markers (ASB17, ASB23, CA425, HMS2, HTG6 and HTG7) and report DNA profiling results for these markers in the 2009-2010 ISAG Horse Comparison Test. This would allow population genetic data and “Power of Exclusion” for each marker to be analysed, and assessment of the performance of each DNA marker in the 2009-2010 International Horse Comparison Test. The three most informative, and best performing DNA Markers could then be selected for inclusion in the ISAG recommended panel of Equine STR DNA Markers at the 2010 ISAG Equine Genetics and Parentage Analysis Workshop.

The 2010 workshop discussed the “Power of Exclusion” and accuracy of DNA Profiling during the 2009-2010 ISAG Horse Comparison Test, of the six Equine STR DNA Markers under consideration. Following this discussion and consultation, the 2010 workshop recommended that ASB17, ASB23 and HMS2 Equine STR DNA Markers be included in the ISAG



International Panel of Equine STR DNA Markers for all new Equine DNA Profiles produced after 1<sup>st</sup> January 2011. For clarity, the workshop confirmed that there is no expectation that existing Equine DNA Profiles, produced prior to the 1<sup>st</sup> January 2011, be re-tested to include the three new DNA STR Markers. Some of the larger ISAG Institutional Member laboratories have 100,000's to 1,000,000's of stored, historical Equine samples. The workshop agreed that re-DNA Profiling historical Equine samples would place unacceptable operational and financial burdens on ISAG Institutional Member laboratories and the international equine industry. Following consideration of these matters, the Chair put the following Motion to the workshop.

**MOTION:** That, for all new horse DNA Profiles produced from 1<sup>st</sup> January, 2011, the number of core markers in the ISAG recommended Horse STR DNA Marker Panel is increased from 9 STR DNA Markers to 12 STR DNA Markers by inclusion of ASB17, ASB23, and HMS2. Therefore, from 1<sup>st</sup> January, 2011, the ISAG recommended Horse STR DNA Marker Panel will consist of: AHT4, AHT5, ASB17, ASB2, ASB23, HMS2, HMS3, HMS6, HMS7, HTG10, HTG4, VHL20.

One representative from each ISAG Institutional Member organisation present at the workshop voted on the motion by a "show of hands".

The result of the vote count was:

	TALLY
IN FAVOUR of the Motion	39
OPPOSED to the Motion	1
ABSTAIN	1

**The Motion was CARRIED by clear majority and without dissent.**

## 7 New Information Regarding the ISAG Recommended Secondary Panel of Equine STR DNA Markers: TKY STR DNA Markers

The TKY Panel of Equine STR Markers was recommended for use as a routine secondary panel of STRs by the Equine Genetics and Parentage Analysis Workshop held at the 2006 ISAG Conference (Reference: Tozaki T, Kakoi H, Mashima S, Hirota K, Hasegawa T, Ishida N, Miura N, Choi-Miura NH, Tomita M. (2001) Population study and validation of paternity testing for Thoroughbred horses by 15 microsatellite loci. *J Vet Med Sci.* **63**(11):1191-7).

The following new information was reported to the 2010 workshop regarding some technical issues for 2 of the STRs in the TKY Panel of Equine STR Markers:

- TKY337: a null allele has been identified for this STR in some horses
- TKY297: some laboratories have reported poor amplification resulting in low signal strength (peak height) for this STR



## 8 Guidelines on Exclusions for International Stud Book Committee (ISBC) – Thoroughbreds

One of the roles of the ISAG Standing Committee for Equine Genetics and Thoroughbred Parentage Testing Standardization is to make recommendations to Stud Books and Breed Registries on the scientific standards that should be applied to equine genetics testing, parentage and identification analysis. ISAG makes these recommendations on the basis of knowledge of the genetic structure of equine breeds.

Workshop members discussed a range on matters relating to scientific quality standards applied to equine genetics testing and analysis. The following consensus opinion emerged and the Workshop Chair proposed that ISAG Institutional Member Organisations adopt the following thirteen standards for Thoroughbred genetics testing and analysis:

1. Organisations must be Institutional Members of the International Society of Animal Genetics.
2. Organisations must participate in each, biennial ISAG Horse Comparison Test.
3. Organisations must achieve Rating 1 (98-100% accuracy) in the ISAG Horse Comparison Test.
4. Organisations issuing International DNA Certificates must include their laboratory's current ISAG Institutional Membership Code (5-digit number: eg. 84414) on the Certificate.
5. The minimum number of DNA Markers recommended by ISAG for equine parentage analysis is increased from 9 to 12. The new DNA Markers are ASB17, ASB23 and HMS2.
6. The new DNA Markers are to be included in NEW equine DNA profiles determined after 1<sup>st</sup> January 2011.
7. From 1<sup>st</sup> January 2011, the twelve ISAG recommended Equine STR DNA Markers are: AHT4, AHT5, ASB17, ASB2, ASB23, HMS2, HMS3, HMS6, HMS7, HTG10, HTG4, VHL20.
8. Equine identification can be accurately determined by use of nine of the twelve ISAG recommended equine STR DNA Markers.
9. The minimum recommendation for equine parentage analysis is the use of the twelve ISAG recommended equine STR DNA Markers.
10. For Equine parentage analysis: in the case of a single-system exclusion occurring in the twelve ISAG recommended equine STR DNA Markers (Primary Equine DNA Panel), at least twelve additional STR DNA Markers must be tested in the sire, dam and foal.
11. The twelve additional STR DNA Markers must be twelve, of the available fifteen, TKY STR DNA Markers (Secondary Equine DNA Panel – see Item 7).
12. If, after testing both the Primary and Secondary Equine STR DNA Panels, only a single-system exclusion remains, then the foal cannot be excluded (qualifies) as the offspring of the nominated sire and dam.
13. Blood Typing is no longer recommended by ISAG for either equine parentage or identification analysis.

No dissent was made; therefore, adoption of these thirteen standards for Thoroughbred genetics testing and analysis was the formal decision by the workshop committee.

These scientific quality standards for equine genetics analysis will be made available to the International Stud Book Committee (ISBC), and to other equine breed societies, registries and regulatory bodies to assist these bodies in making informed decisions regarding their choice of organisations to conduct equine genetics analysis on their behalf.

## 9 Principles for Sharing of Equine DNA Profiles (Genotypes) Between ISAG Member Laboratories

Sofia Mikko brought to the attention of the workshop the WorldFengur (WF) organisation and their requests to ISAG member laboratories to disclose the DNA profiles of Icelandic horses tested by the laboratories.

ISAG member laboratories have previously agreed a set of principles in respect to sharing Horse DNA Profiles between laboratories. These principles are:

- The client, i.e. breed association or horse owner, owns the DNA Profile/genotype information and the results of any analysis (e.g. parentage).
- DNA Profiles, genotypes and analysis results should never be given to any 3<sup>rd</sup> party, without prior written approval or instructions from the client – the owner or breed society that submitted the original sample for DNA analysis.
- ISAG member laboratories will send the DNA profile/genotype of a horse to another ISAG member laboratory at the specific request of the client, the horse owner or breed society, usually for a specific parentage analysis or identification case.
- If an anomaly (possible exclusion) arises in a case involving a DNA profile provided by separate laboratory, then all DNA profiles are confirmed with the laboratory/ies that originally determined each DNA profile.

WorldFengur (WF) currently hosts an online database of DNA profiles and pedigree information of Icelandic horses. Clients of WF (owners and breed societies) can log onto the WF database and test the parentage of a horse based on the stored DNA profiles.

Members of the workshop expressed considerable concern regarding the results of any parentage analysis undertaken by the WF database for the following reasons:

- The complexities of parentage analysis using STR DNA profiles are not considered by this system
- Single system exclusions are not considered
- There is no opportunity to test additional DNA STR Markers, such as the TKY Panel of Equine STR DNA Markers, to resolve single system exclusion cases
- The number of common STR DNA markers between samples being analysed is not considered
- Laboratories that determined the original DNA profiles do not have the opportunity to apply appropriate quality control checks, such as checking independent information regarding the sample submitted for DNA Profile analysis (such as hair colour of the submitted sample), before parentage analysis is undertaken
- It is highly likely that parentage analyses undertaken under these circumstances will return both false-positive (qualifications) and false-negative (exclusions) parentage results.

The Chair proposed that:

1. the existing principles governing the sharing of Horse DNA Profiles between ISAG member laboratories be endorsed, and
2. that DNA Profiles, genotypes and analysis results should never be given to any 3<sup>rd</sup> party, without prior written approval or instructions from the client – the owner or breed society that submitted the original sample for DNA analysis.

No dissent was made; therefore, this was the formal decision by the workshop committee.

## 10 Status of SNP Testing for Parentage Analysis of Horses

Workshop members discussed the possibility of using single nucleotide polymorphisms (SNPs) for equine parentage analysis as an alternative to the currently used STR DNA Markers. The following matters were discussed in relation to the use of SNPs for equine parentage analysis:

### **Power of Exclusion:**

Genotyping of 300 SNPs in all samples would be required to give a similar Power of Exclusion in parentage analysis to that obtained from the 12 multi-allele STR Equine DNA markers recommended by ISAG (see item 6). 300 SNPs would be the minimum number of SNPs needed to undertake equine parentage analysis.

In up to 10% of current equine parentage cases, additional STR markers are needed to resolve the parentage of the foal. For example, in single system exclusion cases, and some double-mating cases. In such cases it is common to use the TKY Panel of up to 15 additional STR Equine DNA markers. To resolve these parentage cases, all samples involved would need to be genotyped for an additional 300 SNPs.

### **Cost of SNP Genotyping:**

While the cost per genotype can be much lower for SNPs, compared to STR DNA Markers, the need to genotype orders of magnitude more SNPs for equivalent power parentage analysis means that the overall cost of parentage analysis would increase. Equine parentage analysis is already a very price sensitive product and the horse industry would not be willing to pay a higher price for parentage analysis.

### **Failure Rate in SNP Genotyping:**

With any multi-locus genotyping system, for any given sample some SNPs will fail to produce any data. The percentage of SNPs that fail per sample will also be impacted by the purity of the DNA sample that is being tested. Many laboratories undertaking high-throughput parentage analysis are able to use whole cell lysates as the template DNA in STR based parentage testing. This is desirable for economic reasons.

The use of whole cell lysates as the template DNA in a SNP genotyping system is likely to increase the percentage of SNPs that fail to produce data for each sample.

To obtain a similar power of exclusion in a parentage analysis, as a 12 STR DNA Marker Panel, you need to obtain data from 300 SNPs in common in all samples (foal plus sire and/or dam). If you assume a 10% SNP failure rate per sample, you would need to start with a primary panel of at least 400 SNPs to be confident of obtaining data for 300 SNPs in common across all samples. Also, a secondary panel of at least another 400 SNPs would be needed to resolve parentage in the cases that currently require the use of additional STR DNA Markers (TKY Panel).

### **Genotyping of Historical Samples:**

Mares and Stallions that are producing the current foal crops have been entered into Stud Books following parentage analysis based on either Blood Typing or STR DNA Marker analysis. To change over to using SNP genotyping for the new foals, then all the existing mares and stallions would have to be re-genotyped for the new SNP panels. For many parentage analysis laboratories this would mean re-genotyping 100,000's to 1,000,000's of stored samples. The horse industry will not pay for the re-genotyping of existing samples and the parentage analysis laboratories do not have the capacity to absorb the costs of SNP genotyping all the historical samples.

**Other Issues Associated with Shifting to SNP Genotyping for Parentage Analysis:***Capital Equipment:*

Implementation of large scale SNP genotyping would require a change in technology. The majority of equine parentage analysis laboratories use capillary electrophoresis to determine Equine STR DNA Profiles. While SNP genotyping can be achieved with capillary electrophoresis, it is considerably more expensive than other technologies on the market, such as Sequenom Mass Array SNP genotyping or Illumina GoldenGate SNP genotyping. The Capital Equipment costs of implementing either the Sequenom or Illumina systems are substantial (approx \$500,000) and neither system is capable of STR DNA Profile determination.

*Result Reporting and Data Analysis Databases:*

Many ISAG member laboratories have developed customised databases for STR DNA Marker Parentage and Identification Analysis and Result Reporting to clients (owners and breed registries). These databases would be completely redundant and new databases designed to securely hold and analyse 1,000's of genotypes per sample, rather than the current 12-30 genotypes per sample, would have to be developed.

*International Standardisation of Genotype Reporting:*

International transfers of Horse DNA profiles are essential to the international movement of horses and the world-wide horse industry. ISAG member laboratories have well established protocols for ensuring international compatibility of horse STR DNA profiles produced by different laboratories across the world.

Establishing similar world-wide standards for Equine SNP genotyping data would be necessary before any move to the use of SNP genotyping data for parentage and identification could be contemplated. This would require a large international effort and would add further costs to the implementation of SNP genotyping for parentage analysis.

Workshop members acknowledged that the genome-wide equine SNP Chips are powerful tools for equine genomics research.

**Workshop Decision:**

A consensus opinion emerged that a move to SNP genotyping for equine parentage analysis cannot currently be justified.

The Chair proposed that STR DNA Markers continue to be used for Equine parentage and identification analysis according to the standards described in Item 8.

No dissent was made; therefore, this was the formal decision by the workshop committee.

**11 DNA Testing for Disease and Colour Markers - Standardization**

Many ISAG member laboratories that undertake Equine DNA Profiling also provide genotyping for an increasing number of inherited diseases and other physical characteristics.

With an increasing number of genetic diagnostic tests being available and offered, there is a need for international standardisation in result reporting nomenclature.

The ISAG Equine Standing Committee will discuss this matter and provide a recommendation on standardised reporting nomenclature for genetic diagnostic test results.

ISAG member laboratories are encouraged to apply any genetic diagnostic tests they offer to the ISAG Horse Comparison Test Samples and report results as part of the ISAG Horse Comparison Test process.

With an increasing range of genetic diagnostic tests being offered, it is not feasible for the Horse Comparison Test Duty Laboratory to ensure that the HCT samples include a range of genotypes for each diagnostic test. Therefore, there is no expectation or obligation on the HCT Duty Laboratory to provide samples that include different genotypes across the various genetic diagnostic tests that are now offered.

## 12 Blood Typing of Horses and Neonatal Isoerythrolysis

Very few ISAG member laboratories continue to offer horse blood typing and, of those that do, most offer testing for only a limited selection of blood type markers.

There's also an increasingly limited availability of anti-sera for various blood typing tests.

Given the limited availability of horse blood typing reagents, and the limited number of laboratories offering horse blood typing across a restricted range of blood typing markers, ISAG no longer recommends blood typing for either parentage or identification analysis in horses.

The following laboratories provide the listed Equine Blood Typing Services:

Laboratory	Blood Typing Services
Ireland	Protein polymorphisms (P.A.G.E)
Kentucky	All blood groups i.e. Red cell and protein polymorphisms
Japan	All blood groups i.e. Red cell and protein polymorphisms
Argentina	Reduced markers
Poland (Gregorz Cholewinski)	All blood groups i.e. Red cell ( except P system)and protein polymorphisms
New Zealand	Some blood groups
Germany (Uwe Hertner)	Reduced panel and only type once a year.
India	Protein polymorphisms only
Sweden	Only typing once more.
Italy	Protein polymorphisms (P.A.G.E)

The following laboratories are producing the listed Equine Blood Typing Reagents:

Laboratory	Blood Typing Reagents
Poland ( Gregorz Cholewinski)	Red cell Anti-sera
Poland ( Gregorz Cholewinski)	Complement (twice a year)
Argentina	Complement

The following laboratories continue to provide testing for NI:

- Ireland
- Kentucky U of K
- VGL- UC Davis
- Italy

### 13 Election of Committee

#### 2006-2010 ISAG Equine Standing Committee

Alan Guthrie - Chair (OPVGL, South Africa)

Romy Morrin (Weatherbys, Ireland)

Sofia Mikko (SLU, Sweden)

Ann Trezise (AEGRC-UQ, Australia)

Hitoshi Gawahara (LRC, Japan)

Lee Millon (VGL-UCD, USA)

The term of all voted committee members is lapsed. Romy, Sofia, Ann, Hitoshi are prepared to serve another term.

Membership of the new 2010-2014 ISAG Equine Standing Committee was voted and endorsed by the workshop.

#### 2010-2014 ISAG Equine Standing Committee

Ann Trezise - Chair (AEGRC-UQ, Australia): ann.trezise@uq.edu.au

Romy Morrin-O'Donnell (Weatherbys, Ireland): rmorrin@weatherbys.ie

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Hitoshi Gawahara (LRC, Japan): h-gawahara@lrc.or.jp

Elena Genzini (LGS Cremona, Italy): elenagenzini@lgscr.it

Lee Millon (VGL-UCD, USA): lvmillon@ucdavis.edu

## 14 Meeting Closed

Minutes compiled by Ann Trezise (AEGRC-UQ, Australia): [ann.trezise@uq.edu.au](mailto:ann.trezise@uq.edu.au)

Minutes reviewed by:

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