UK NEQAS

Histocompatibility & Immunogenetics

Annual Report
2015

Contents:

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1. INTRODUCTION

This is my first time of writing as the new Director of UK NEQAS for H&I. April 2015 saw the retirement of Dr Chris Darke who has been in this position for over 20 years. He has worked tirelessly in support of the underpinning ethos of EQA which is to educate and improve standards in clinical laboratories. During his time as Director he has overseen the expansion and modification of the schemes to support modern day clinical practice. A testament to this is the international recognition of UK NEQAS for H&I which has over 200 international participants. He will be a hard act to follow, but I have excellent support from the Steering Committee, chaired by Judith Worthington, the Schemes Manager Deborah Pritchard and her small team of dedicated staff.

Recognising the need to continually evolve we have introduced a number of changes to make our processes more efficient and enable us to focus on improving our service to participants. Some of these changes are detailed below. Of particular note is our new educational scheme aimed at mimicking the clinical interpretation of a number of test results to provide clinical advice. Thus as part of the educational scheme in 2016, participants will be able to register to receive blood and serum samples for combined crossmatching, HLA typing and HLA antibody detection/specification. Participants will be expected to report the results of all the individual test components, but to also provide an interpretation of the results if they were obtained in a clinical kidney transplant setting. Full instructions and details will be provided at the time of sample distribution. The results will not be formally assessed.

We have also launched three new pilot schemes for HPA, KIR and MICA typing and would welcome feedback from participants on how to operate this to best suit clinical practice. On this note I would like to take this opportunity to thank our participants for their suggestions for scheme improvements to enable us to develop and modify our schemes accordingly.

Steering Committee
There is one change to the UK NEQAS for H&I Steering Committee for 2016. Fotini Partheniou has completed two terms on the Committee and I would like to thank her for 6 years service and commitment to the Steering Committee. I also welcome our new Steering Committee Member, Anthony Poles, who joins the committee in 2016.

Scheme Result Forms
Scheme result forms will no longer be printed and included in the box with distributed samples. Instead, participants can download the relevant scheme forms from our website on receipt of samples http://www.wtail.org.uk/neqas/resultsforms.asp. The forms are in 'Microsoft Word' format which allow results to be directly typed into them. They can also be printed and handwritten. Please note that the version in use may change slightly throughout the year, so please check that you are using the most up to date report form for each distribution of samples. We would encourage result

submission by e-mail where possible to enable confirmation of receipt. Scheme result deadlines can be found in the Participant Manual and on the UK NEQAS for H&I website (http://www.wtail.org.uk/neqas/deadline.asp).

Reports/Performance Correspondence
Scheme reports/performance correspondence will no longer be posted to participants, but e-mailed in PDF format. This will enable faster distribution of reports to participants and reduce postage costs. The registration forms have been updated to collect e-mail addresses for recipients of reports. Where possible we would advise that a group e-mail address or several contacts are provided to ensure timely receipt in the event of staff absences.

Scheme method/technique data collection
Detailed method information will be collected on separate forms to the scheme results from 2016. Ordinarily this information will only need to be completed once each year (after receipt of the first set of samples), unless changes to the technique/methods being used are made. This will reduce the duplication of information collected with each distribution of samples for labs with consistent testing methodology.

Dr Tracey Rees, UK NEQAS for H&I Director

2. OBSERVATIONS ON THE SCHEMES

SCHEME 1A: HLA PHENOTYPING

The purpose of this scheme is to assess the ability to use serological and supplementary methods to correctly identify HLA specificities. Participants can register for HLA-A, B, C, DRB1, DQB1 typing or any combination. Two random donor samples are sent 5 times in a year giving a total of 10 samples for HLA typing. Participation in the scheme in 2015 is summarised in table 1 below:

Table 1: Scheme 1A Participation

HLA	Number of Participants	
	Total	UK
Any	42-45	8-9
A	42-45	8-9
B	42-45	8-9
Cw	6-7	1
DR	29-31	8-9
DQ	29-27	8-9
A, B	10	0
A, B, C	3	0
A, B, DR	2	0
A, B, DR, DQ	24-26	7-8
A, B, C, DR, DQ	3-4	1

Ranges reflect changes in participant number over the distribution cycles

Assessment

Scoring of HLA type is based on 75% consensus. Each complete HLA type in agreement with the consensus phenotype is deemed acceptable. Each complete HLA type not in agreement with the consensus phenotype is deemed unacceptable. Satisfactory performance is obtaining nine or more complete HLA types in agreement with consensus in a calendar year.

Methods: Typing trays used

Participants used a range of typing trays from a variety of manufacturers: One lambda (30 labs); Biotest (2 labs); BioRad (3 labs) Innotrain (1 lab), and 8 labs using a combination of manufacturers.

Cell preparation

The majority of laboratories undertook testing using separated T cell and B cell preparations (19 labs), whilst 6 laboratories tested samples using unseparated cells. Eight laboratories used T cells only, 5 used unseparated cells plus B cells, 1 lab used unseparated cells plus T cells and 2 labs used unseparated cells plus T cells and B cells.

Table 2: Incorrect assignments in 2015

Sample	Report	Consensus	Lab Number
1A01	B44, blank	B44, B51	232
	DR7, DR3	DR7, DR17	194
	DQ2, DQ1	DQ2, blank	120
1A02	DR7, DR3	DR7, DR17	194
1A03	DR15, DR3	DR15, DR17	301
1A04	DR1, DR4	DR103, DR4	163, 301
	DQ5, DQ3	DQ5, DQ7	301
1A06	DR8, DR3	DR8, DR17	238
1A07	DQ2, DQ3	DQ2, DQ9	163, 315
1A08	B40, blank	B60, blank	315
	DR4, DR10	DR4, blank	181
	DQ3, blank	DQ8, blank	163, 315
1A09	DR11, DR3	DR11, DR17	262

Performance in 2015

Incorrect assignments (table 2) fell into 4 categories:

i Failure to split a broad specificity
ii Missed specificities
iii Incorrect specificities
iv Incorrect nomenclature

There were no incorrect assignments made by laboratories from UK or Ireland in 2015. There were 5 incorrect assignments due to missed or incorrect specificities made by 5 Rest of the World (RoW) laboratories. There was no correlation with reagents or testing strategy used and the misassignments reported. Incorrect assignments due to failure to split a broad specificity occurred on 14 occasions in 2015, involving 6 laboratories (all RoW).

There were 4 unsatisfactory performers in 2015 (table 3).

Table 3: Scheme 1A Unsatisfactory Performance

Scheme 1A Unsatisfactory Performance	2013	2014	2015
Number of Participants	30	42	45
Number with Unsatisfactory Performance (< 90%)	0	8	4
% Unsatisfactory Performance	0.0%	19.0%	8.9%

Dr Leigh Keen, Histocompatibility & Immunogenetics Department, NHSBT, Filton

SCHEME 1B: HLA-B27 TESTING

The purpose of this scheme is to assess ability to correctly determine HLA-B27 status. Participants in this scheme are asked to report results as HLA-B27 positive or HLA-B27 negative. Two random donor samples are sent 5 times a year (5 cycles) giving a total of 10 samples for analysis. HLA-B27 status is determined by at least 75% agreement on the presence or absence of HLA-B27.

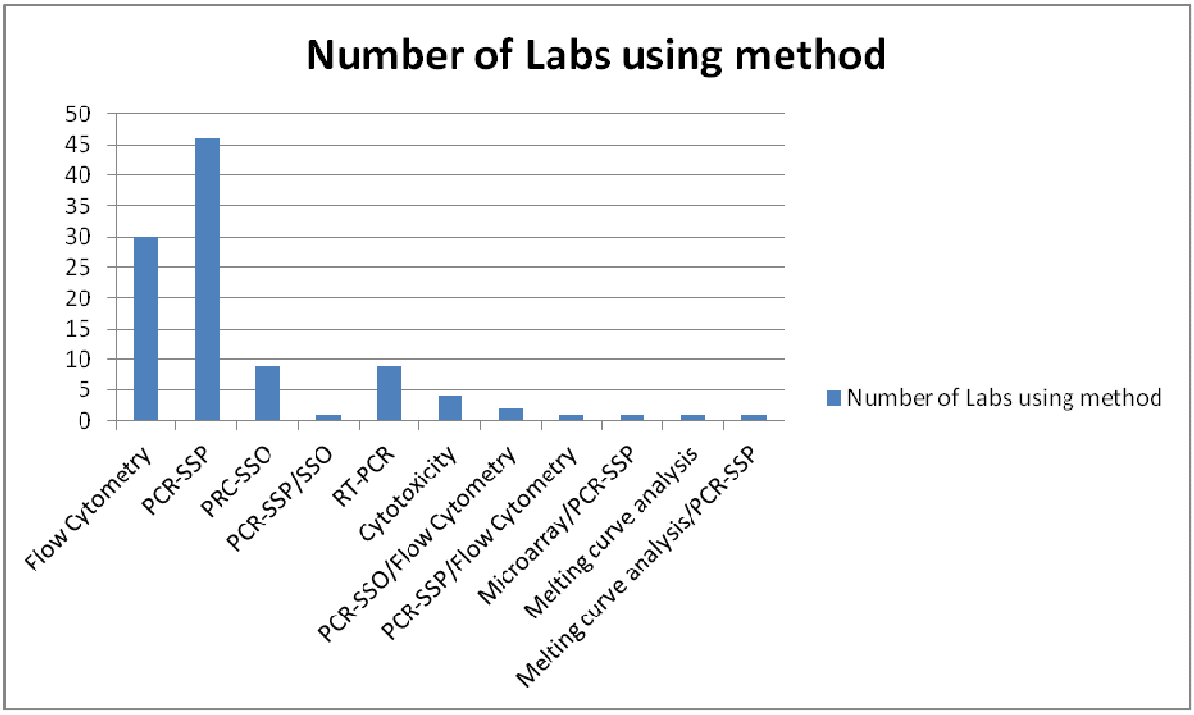
In 2015 there were 115 participants in the scheme (54 UK&I laboratories).

Assessment

A result in agreement with the consensus HLA-B27 status is deemed acceptable and a result not in agreement with the consensus HLA-B27 status is deemed unacceptable. Satisfactory performance is making 10 sample reports in agreement with consensus in a calendar year.

Methods: Technique

Participants used a variety of techniques for HLA-B27 typing, with the most common techniques being PCR-SSP or flow cytometry. Some laboratories use techniques in combination (see below).



Methods: Monoclonal antibodies (B27 detection)

A variety of monoclonal antibodies were used for detection of HLA-B27, with 3 main suppliers (Becton Dickinson, One Lambda and Beckman Coulter)

Performance

In 2015, six samples distributed were HLA-B27 positive. Ten assignments were made outside of consensus (see table 1). Three misassignments were made by laboratories using flow cytometry, one by PCR-SSO and one by flow/SSO combination. There were therefore 8 unsatisfactory performers in 2015, 6.9% of the participants (Table 2).

Table 1: Scheme 1B Incorrect Assignments

Sample	Result	Lab Number	Technique	HLA-B Type
1B01	False Pos	129	PCR-SSO	B50, B62
1B02	False Pos	129	PCR-SSO	B44, B60
1B04	False Neg	21, 40, 256	Flow	B8, B27
1B05	False Pos	257	PCR-SSO	B7, B51
1B06	False Neg	236, 257	Flow/PCR-SSO	B27, B73
1B08	False Neg	71	Flow	B8, B27
1B09	False Neg	27	Flow	B27, B62

Table 2: Scheme 1B Unsatisfactory Performance

	2013	2014	2015
Number of Participants	96	107	115
Number with Unsatisfactory Performance (< 100%)	4	4	8
% Unsatisfactory Performance	4.2%	3.7%	6.9%

Ruhena Sergeant, Clinical Immunology Laboratory, Hammersmith Hospital, London

SCHEME 2A: CYTOTOXIC CROSSMATCHING

Introduction: The purpose of Scheme 2A is to assess the participants' ability to correctly determine cell/serum cytotoxic crossmatch status. Participants may register to test peripheral blood lymphocytes (PBL)/T-cells and/or B-cells, with and/or without dithiothreitol (DTT) treatment of sera. A total of ten blood samples and forty serum samples were sent as five distributions.

Changes in 2015: There were a number of changes to Scheme 2A in 2015.

1) Participants were able to register for result assessment with dithiothreitol (DTT) treatment of sera. Results obtained after DTT treatment were considered independently from results without DTT treatment.
2) PBL/T-cell & B-cell assessments were linked for laboratories registered for T and B cells - both had to be in line with the consensus results for satisfactory performance.
3) 3 different blood units were distributed for each sample;
    1. 1 unit for UK&I laboratories
    2. 1 unit for RoW laboratories who receive whole blood (WB)
    3. 1 unit for RoW laboratories who receive isolated lymphocytes (IL).

Participation: Table 1 Scheme 2A Participants in 2015

	Number of Participants = 77			
	UK & I	**RoW WB**	**RoW IL**	**Total**
PBL/T & B	20	19*	24*	63
PBL/T	1	4	9	14
PBL/T & B + DTT	17	16	22	55
PBL/T + DTT	1	2	6	9
* 1 RoW laboratory initially received WB and changed to IL during the assessment year.				

PBL/T cell methodology: 48/77 (62%) of laboratories used beaded cells compared to 50% last year. There was the usual variety of pre- and post-complement incubation times ranging from 20 to 60 minutes pre-complement with the majority using 60 minutes. Post-complement the incubation times varied from 30 to 120 minutes with the majority using 60 minutes. There were 16 different incubation time combinations compared to 14 combinations last year.
EB/AO remains the most popular method for visualisation.

B cell methodology: 62/63 (98%) of laboratories used beaded cells.
Incubation times varied between laboratories, ranging from 30-75 minutes pre-complement with the majority using 60 minutes. Post complement the incubation times varied from 30 to 120 minutes with the majority using 60 minutes. There were 17 different post complement incubation time combinations.

Assessment and Performance: The status or result for each cell/serum combination was determined by 75% consensus between laboratories. A result in agreement with consensus was "acceptable" one not in agreement with consensus was "unacceptable". Satisfactory performance within this scheme was 85% of all reports in agreement with the consensus results within the calendar year.

The performance results without DTT are shown in Table 2. The performance results with DTT are shown in Table 3.

Table 2: Scheme 2A 2015 Performance without DTT

		UK&I	RoW WB	RoW IL
Number of Participants		21	23*	34*
Number XM Reports Assessed (Combined PBL/T & B Cell XM = 1 report)		40 /40	38/40	40/40
PBL/T Cell	No XM Assessed	34/40	37/40	37/40
	Positive XM	9	4	5
	Negative XM	25	33	32
	% of Results Not Tested	5.7%	11.8%	18.4%
B Cell	No XM Assessed	34/40	30/40	35/40
	Positive XM	23	10	10
	Negative XM	11	20	25
	% of Results Not Tested	6.6%	11.6%	20.5%
Incorrect assignments		62 (9.1%)	77 (9.7%)	111 (10.2%)
	False Positive	40	48	78
	False Negative	22	29	33
Unsatisfactory Performance		2 (84%, 82%)	6 (50-82.6%)	8 (0-84.4%)

Table 3: Scheme 2A 2015 Performance With DTT

		UK&I	RoW WB	RoW IL
Number of Participants		18	18	28
Number of XM Reports Assessed (Combined PBL/T & B Cell XM = 1 report)		40 /40	37/40	40/40
PBL/T Cell	No of XM Assessed	38	37	37
	Positive XM	8	2	5
	Negative XM	30	35	32
	% of Results Not Tested	7.2%	11.8%	23.3%
B Cell	No of XM Assessed	33	31	39
	Positive XM	15	8	11
	Negative XM	18	23	28
	% of Results Not Tested	8.5%	13%	21.6%
Incorrect assignments		48 (7.2%)	63 (10.4%)	94 (10.3%)
	False Positive	28	37	56
	False Negative	20	26	38
Unsatisfactory Performance		0	4 (52.2%-81.1%)	5 (0%-81.3%)

Satisfactory Performance in 2015

61/77 (79%) of laboratories achieved a satisfactory performance without DTT and 55/64 (86%) of laboratories achieved a satisfactory performance with DTT in 2015. It isn't possible to directly compare the performance in 2015 to the performance in previous years because of the changes that were made to the scheme in 2015.

Table 4: Scheme 2A Performance 2013-2014

	PBL/T Cells		B Cells	
	2013	2014	2013	2014
Number of Participants	65	78	50	61
Number with Unsatisfactory Performance (< 85%)	5	6	5	7
% Unsatisfactory Performance	7.7%	7.7%	10%	11.5%

Table 5: Scheme 2A Performance 2015

2015 (PBL/T Cells & B Cells)	Without DTT	With DTT
Number of Participants	77	64
Number with Unsatisfactory Performance (< 85%)	16	9
% Unsatisfactory Performance	20.8%	14.0%

Patrick Flynn, The Transplantation Laboratory, Manchester Royal Infirmary

Scheme 2A – Standard Method Exercise for Cytotoxic Crossmatching (UK&I Only)

At the 2014 UK NEQAS for H&I's Participant Meeting, data was presented on Scheme 2A which highlighted there were a number of different cytotoxic crossmatch methodologies in use by UK and Irish (UK&I) laboratories, with up to 11 different combinations of pre- and post-complement incubation times for PBL/T cells and 12 for B-cells.

It was also highlighted that a significant proportion of crossmatch results did not reach consensus (that is ≥ 75% of laboratories reporting the same positive/negative result), and are therefore not assessed. In 2014, 20% of the 40 cell-serum crossmatch results were not assessed for UK &I participants for both PBL/T cells and B-cells.

It was suggested by participants that the variations in the methods used could be contributing to the number of non-assessed results. An 'educational exercise' was proposed to see if using a 'standard method' would increase test concordance between labs. This suggestion was discussed in detail at the recent UK NEQAS for H&I Steering Committee meeting and the committee identified a 'standard protocol' based on the most common methodology in use by UK &I participants.

UK and Ireland participants were invited to test Scheme 2A samples using both their usual method and the standard method so that the results could be directly compared. The results were not formally assessed. A total of 16 labs participated.

The standard protocol was as follows:

- Isolate T/B cells using immunobeads
- Incubate 1µl of T/B cell suspension (2 × 106 cells/mL) with 1µl of serum for 60 minutes at room temperature.
- Add 5µl of complement and incubate for a further 60 minutes at room temperature.

The complement source/supplier was not standardised. However, all but one of the 16 laboratories used complement from Cedarlane. The remaining 1 lab used complement from TSC Biosciences.

Out of a total of 96 individual T/B cell-serum tests, 15 (15.6%) failed to reach consensus when laboratories used their own method compared to 13 (13.5%) results which failed to reach consensus when the standard method was used.

The percentage of laboratories reporting the same individual cell-serum test result (i.e. the consensus rate) was no different between the standard method and laboratories' own methods for 51% of results. For 22.9% of results there was an increase in the consensus rate. However for 26.0% of results the consensus rate was lower using the standard method.

Therefore the committee made the decision not to continue the standard method for 2016 as it was thought not to make an improvement on the number of laboratories reaching consensus.

Felicity May, UK NEQAS for H&I Operations Manager

SCHEME 2B - CROSSMATCHING BY FLOW CYTOMETRY

The purpose of this scheme was to assess participant's ability to correctly determine cell/serum flow cytometry crossmatch status.

The 2015 scheme consisted of 5 distributions of 2 blood samples plus 4 test sera per sample giving a total of 10 blood samples and 40 sera. Participants were able to register for assessment of the T cell crossmatch only or both the T cell and B cell crossmatch.

Participants were asked to assess the reactivity of a serum against a particular cell in relation to the local AB negative control serum and report the crossmatch as either positive or negative. The consensus crossmatch status of each sample was determined by at least 75% of laboratories agreeing on the positivity or negativity of each test; crossmatching tests failing to reach the 75% consensus level were not assessed. For 2015 T-cell & B-cell assessment was linked such that both results were required to be in line with the consensus results for acceptable performance.

To achieve a satisfactory performance, participants had to obtain 85% of reports on all sera in agreement with the consensus findings in the calendar year.

Performance

The majority of participants achieved a satisfactory performance, however there were 13 laboratories with unsatisfactory performance (Tables 1-3, figure 1). Please note that UK&I and RoW receive different blood samples to ensure enough cells for testing.

Table 1: Scheme 2B T Cell Result Summary

Scheme 2B T Cell Results	UK&I	RoW
Number of participants	23	50
Number of XM assessed (>75% consensus)	34/40	31/40
Number of Positive XM	10	7
Number of Negative XM	24	24
Number of incorrect assignments	39 (5.1%)	96 (6.8%)
Number of False Pos	32	66
Number of False Neg	7	30
Number of Unsatisfactory Performers (< 85% correct) (T&B combined where applicable)	3	10

Table 2: Scheme 2B B Cell Result Summary

Scheme 2B B Cell Results	UK&I	RoW
Number of participants	20	47
Number of XM assessed (>75% consensus)	29/40	31/40
Number of Positive XM	14	12
Number of Negative XM	15	19
Number of incorrect assignments	32 (5.7%)	114 (9%)
Number of False Pos	26	58
Number of False Neg	6	56

Figure 1: 2015 Scheme 2B Performance

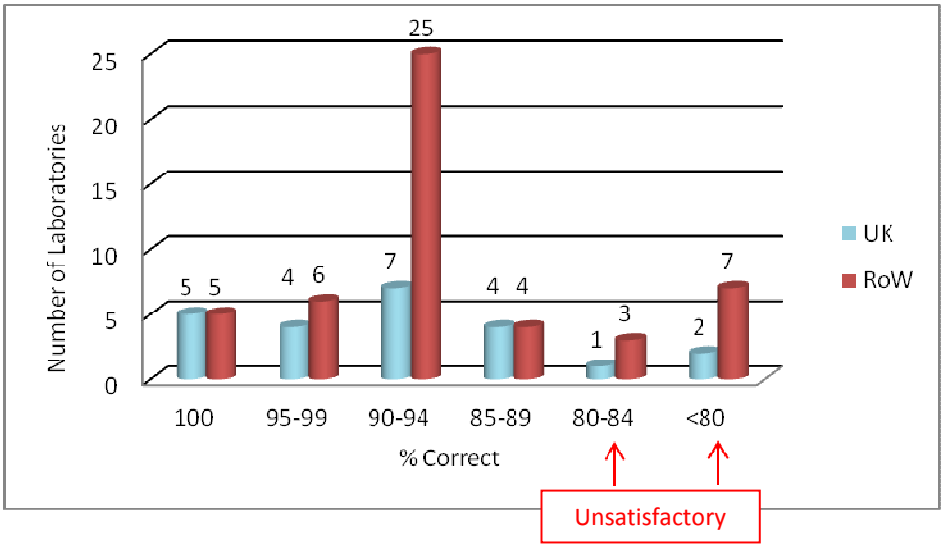


Table 3: Scheme 2B Performance

	PBL/T Cells				B Cells			
	2012	**2013**	**2014**	**2015**	**2012**	**2013**	**2014**	**2015**
Number of Participants	60	69	71	73	53	63	65	67
Number with Unsatisfactory Performance	10	6	6	13	8	10	12	N/A
% Unsatisfactory Performance	16.7%	8.7%	8.5%	17.8%	15.1%	15.9%	18.5%	N/A

Please note for 2015 T-cell & B-cell assessment was linked such that both results were required to be in line with the consensus results for acceptable performance. It is therefore not possible to directly compare the performance in 2015 to the performance in previous years because of this change.

Jeanette Ayers, Transplant Immunology Laboratory, Churchill Hospital, Oxford

SCHEME 3: HLA ANTIBODY SPECIFICITY ANALYSIS

Purpose of scheme

Scheme 3 focuses on HLA antibody specificity analysis. Five sera are sent out on two separate occasions, and these should be tested and reported using a laboratory's routine testing method(s). Participants can register for class I and/or class II and must report results within 10 weeks of sample receipt. Scoring is via a consensus system, with 75% consensus required to score specificity positive and 95% consensus required to score specificity negative. Individual laboratory performance is assessed via agreement with consensus, being either acceptable or unacceptable. Overall, laboratories must detect 75% of the positive specificities and not detect 75% of the negative specificities for acceptable performance.

Participants

This year 81 laboratories registered for Scheme 3, 24 from the UK&I. For class I antibody analyses, 79 laboratories participated. Seventy nine laboratories also registered for class II antibody specificity analysis.

Methods

The majority of participants tested the samples using Luminex technology (78/81 participants), 64 participants tested the samples using Luminex only, 14 used Luminex in combination with CDC, 1 lab used ELISA & Luminex, 1 used ELISA, Flow cytometry and Luminex and one laboratory provided no data.

There were more participants that used Luminex kits from One Lambda for testing the samples (57, 70.3%), than used Lifecodes kits (11, 13.6%). 10 participants used a mixture of kits from both suppliers (12.3%) and 3 (3.7%) provided no information about the kits being used.

There was considerable variation noticed in the bead and serum volume used by participants in the Luminex assay, as well as the MFI cut off value used to assign positive specificities. 23 labs reported the use of EDTA to treat the serum, 2 labs reported the use of heat inactivation, 1 reported the use of dilution and 1 the use of DTT.

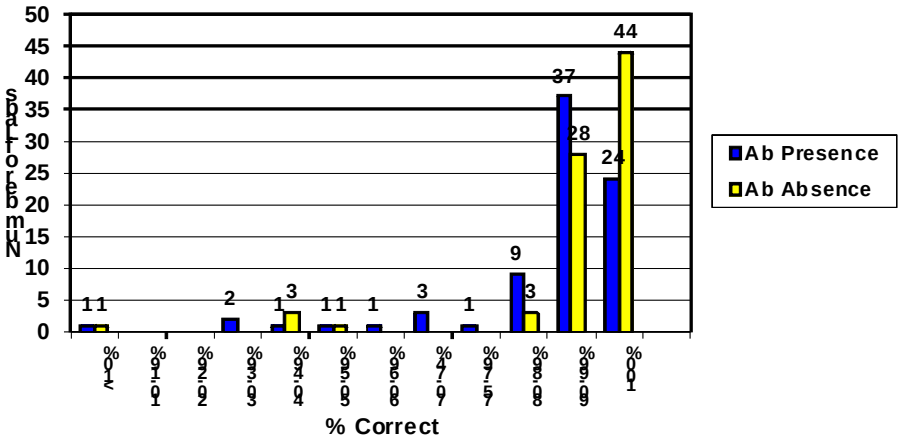
Performance

11 participants had unsatisfactory performance for Class I specificity analysis; 9 labs for antibody presence analysis, and 2 labs for antibody absence analysis (figure 1).

7 participants had unsatisfactory performance for Class II specificity analysis; 4 labs for antibody presence analysis, and 3 lab for antibody absence analysis (figure 2).

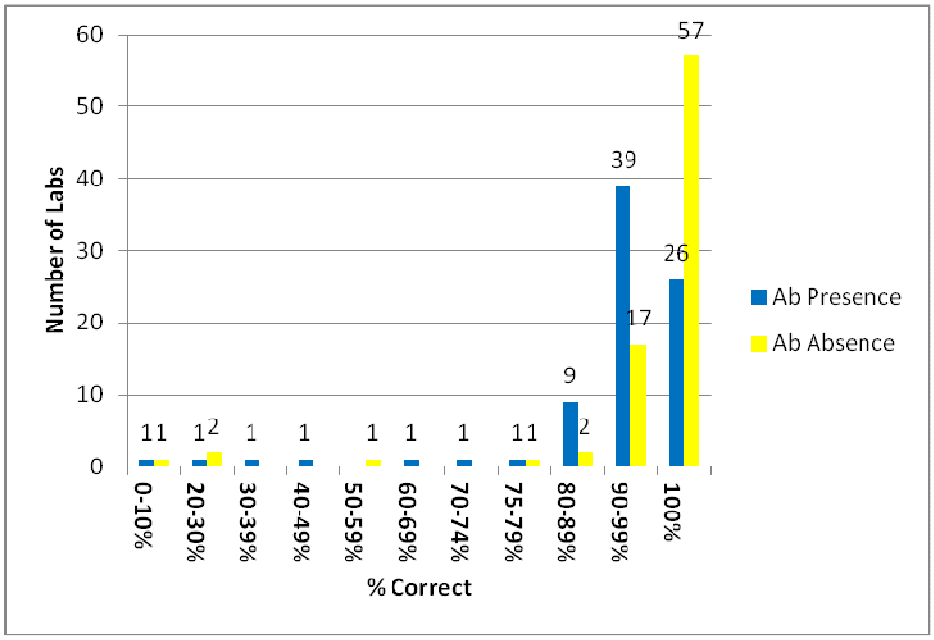
There was no clear correlation of unsatisfactory performance with Luminex kits.

Figure 1: Class I Performance



Scheme 3 Class I Performance	2013	2014	2015
Number of Participants	66	78	81
Number with Unsatisfactory Performance (< 75%) Presence / Absence	11/2	15/1	9/2
% Unsatisfactory Performance Presence / Absence	16.7% 3.0%	19.2% 1.3%	11.1% 2.5%

Figure 2: Class II Performance



Scheme 3 Class II Performance	2013	2014	2015
Number of Participants	63	76	81
Number with Unsatisfactory Performance (< 75%) Presence / Absence	5 / 0	5 / 2	4/3
% Unsatisfactory Performance Presence/ Absence	7.9% 0.0%	6.6% 2.6%	4.9% 3.7%

Table 1: Scheme 3 Unsatisfactory Performers 2015

Lab No	Class I/II Presence/ Absence	Technique/ Kit(s) Used		%
9	**CI P**	LS1A04	One Lambda	74.6
197	**CI P** **CII P** **CII A**	Information not provided		71.1 44.4 45.5
210	**CI P** **CII P** **CII P** **CII A**	No results received *(No reason submitted)*		0
218	**CI P**	LSAI	Immucor	72.9
235	**CI P**	LS1A04	One Lambda	66.1

Lab No	Class I/II Presence/ Absence	Technique/ Kit(s) Used		%
267	**CI P**	LSMUTR LSAI LMI	One Lambda Immucor	63.6
268	**CI P**	LMX LM1	Immucor	66.1
293	**CI P** **CII P** **CII A**	Information not provided		65.0 72.3 58.1
301	**CI P** **CI A** **CII P**	LSAI LSAII	Immucor	55.9 57.9 60.8

James Kelleher, NHISSOT, Beaumont Hospital

SCHEME 4A1 - DNA HLA TYPING AT 1ST FIELD LEVEL

Format and specification

The aim is to assess participants' ability to correctly determine HLA alleles at the 1st field level of resolution.

10 samples are distributed each year comprising 2 send outs of 5 blood samples from local donors.

Participants may register for 1st field assessment of HLA-A, B, C, DRB1, DQB1, DQA1, DPA1 and for 1st field or presence of DRB3, DRB4 and DRB5. Participating laboratories are only assessed on the loci for which they have registered.

Alleles that fail to reach 75% consensus level are not assessed. Only those alleles listed in the latest full HLA nomenclature report are assessed.

Performance

Satisfactory performance involves obtaining 9 or more full HLA genotypes in agreement with consensus in a calendar year. Whilst the majority of laboratories submitting results scored 100%, there were 7 laboratories classified as unsatisfactory performers in 2015 (Table 1).

There were 33 incorrect assignments reported by 15 labs in 2015 (Table 2).

- 17 incorrect assignments (e.g. A80 instead of A23)
- 5 missed assignments (e.g. reported homozygous/blank)
- 6 incorrect nomenclature (e.g. DRB1*17 instead of DRB1*03)
- 5 reported DRB3/4/5 present (lab registered for DRB3/4/5 1st Field)

The most errors were made typing for HLA-B (Figure 1). Of the 15 laboratories that submitted incorrect results (Table 2), 8 used Luminex 4 used SSP and 3 used a combination of SSP and Luminex.

Figure 1: Scheme 4A1 errors by HLA locus

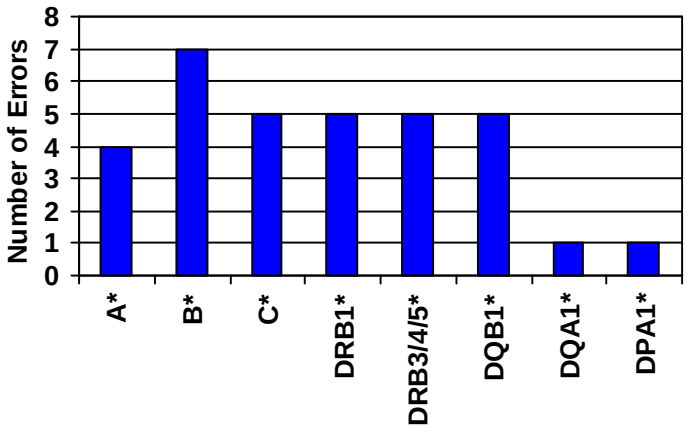


Table 1: Scheme 4A1 Performance

Scheme 4A1 Performance	2013	2014	2015
Number of Participants	96	96	100
Number with Unsatisfactory Performance (< 90%)	5	9	7
% Unsatisfactory Performance	5.2%	9.4%	7.0%

Table 2: Scheme 4A1 Incorrect Assignments

Sample	Report	Consensus	Method	Lab Number
4A1 01	A*80, 24	A*23, 24	SSP (Olerup)	172
	C*04, 04	C*03, 04	Luminex (One Lambda)	248
	DQB1*03, 03	DQB1*02, 03	SSP (CTS)	112
	DRB4*present	Registered for DRB3/4/5 1st Field	Luminex (Immucor)	231
4A1 02	C*03, 04	C*03, 05	Luminex (One Lambda)	127
	C*03, 08		Luminex (One Lambda)	197
	DRB3*present	Registered for DRB3/4/5 1st Field	Luminex (Immucor)	231
4A1 03	B*08, 60	B*08, 40	SSP (ROSE GenTec)	78
	DRB1*03, 13	DRB1*03, 08	Luminex (One Lambda)	215, 216
	DRB3*present	Registered for DRB3/4/5 1st Field	Luminex (Immucor)	231
4A1 04	C*02, 02	C*02, 16	Luminex (One Lambda)	248
	DRB4*present	Registered for DRB3/4/5 1st Field	Luminex (Immucor)	231
4A1 05	DRB1*03, blank	DRB1*04, blank	SSP (ROSE GenTec)	78
	DRB4*present	Registered for DRB3/4/5 1st Field	Luminex (Immucor)	231
4A1 06	B*35, 18	B*35, blank	SSP (One Lambda)	190
	DRB1*01, 16	DRB1*01, blank	Luminex (Immucor)	189
4A1 07	B*07/42, 08	B*07, 08	Luminex	103
	B*07, 42		Luminex (One Lambda)	215

4A1 08	DRB1*17, 12 DQB1*02, 07	DRB1*03, 12 DQB1*02, 03	SSP (One Lambda)	190
	DPA1*01, blank	DPA1*01, 02	SSP/Lumimex (Readygene/One Lambda)	14
4A1 09	A*03, 31 B*35, 44	A*02, 68 B*07, 44	Luminex (One Lambda)	155
	C*08, 07	C*05, 07	SSP/Luminex (Olerup, GenProbe)	197
	DQB1*07, blank	DQB1*03, blank	SSP (One Lambda)	190
4A1 10	A*02, 68 B*07, 44	A*02, 31 B*27, 40	Luminex (One Lambda)	155
	DQB1* 07, 08	DQB1*03, 03	SSP (One Lambda)	190
	DQA1*05, blank	DQA1*05, 03	SSP/SSOP (Immucor)	19

Scheme 4A1 - Interpreted DNA Results

Participants were invited to interpret the DNA based typing results for Scheme 4A1 samples and additionally report results at the split specificity level (e.g. DQB1*03:01 allele group reported as DQ7). These 'converted' results were not formally assessed.

There were 185 incorrect 'interpreted' assignments reported by 32 labs. The majority (135) of these errors were reports of broad rather than split specificity (e.g. Cw3 not Cw9). The remaining errors could be categorised as follows:

- 23 reports of the wrong split (e.g. DR1 instead of DR103)
- 14 incorrect/didn't report Bw4/6
- 10 incorrect DR51/52/53
- 3 antigen mis-assignments (e.g. A2 instead of A1)

Dr Leigh Keen, Histocompatibility & Immunogenetics Department, NHSBT, Filton

SCHEME 4A2: DNA HLA TYPING TO 2ND FIELD RESOLUTION

Format and specification

The aim is to assess participants' ability to correctly determine HLA alleles to the 2nd field level.

10 samples are distributed each year comprising 2 send outs of 5 blood samples from local donors.

Participants may register for 2nd field assessment of HLA-A, B, C, DRB1, DQB1, DQA1, DPA1, DPB1 and for 2nd field. Participating laboratories are only assessed on the loci for which they have registered.

Alleles that fail to reach 75% consensus level are not assessed. Allele groups may be reported, provided that participants include the consensus allele and resolve all ambiguities resulting from polymorphisms located within exons 2 and 3 for HLA class I and exon 2 for HLA class II. Only those alleles listed in the latest full HLA nomenclature report are assessed.

Performance

Satisfactory performance involves obtaining 9 or more full HLA genotypes in agreement with consensus in a calendar year.

The number of participating laboratories (59) is the same as the previous year. However, the number of unsatisfactory performers (7) has increased by two from 2014 (Table 1).

The highest number of errors were made typing for HLA Class I, in particular HLA-C (Figure 1).

Figure 1: Scheme 4A2 errors by HLA locus

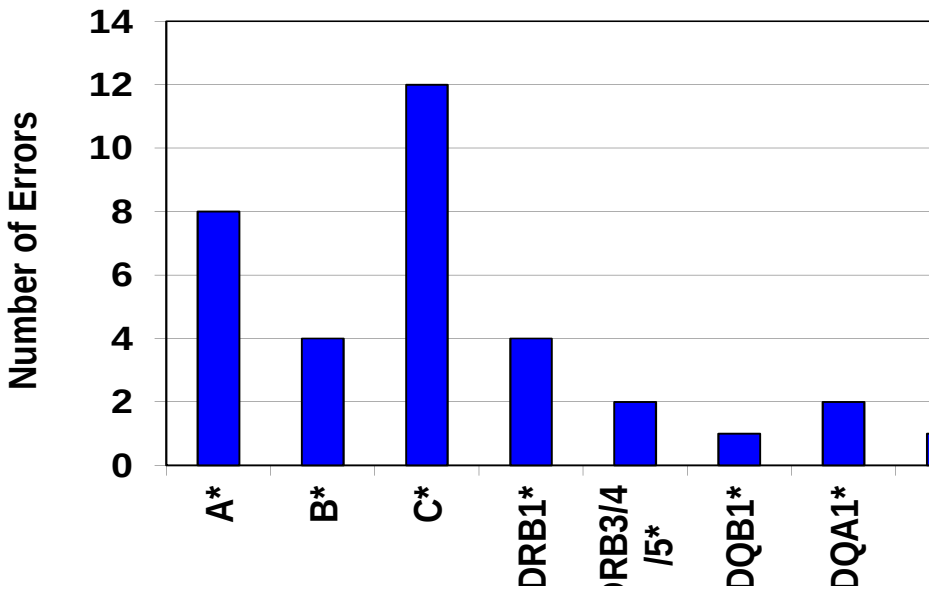


Table 1: Scheme 4A2 Performance

Scheme 4A2 Performance	2013	2014	2015
Number of Participants	58	59	59
Number with Unsatisfactory Performance (< 90%)	5	5	7
% Unsatisfactory Performance	8.6%	8.5%	11.9%

Table 2: Scheme 4A2 Incorrect Assignments

Sample	Report	Consensus	Lab Number
4A2 01	B*07:02, blank	B*07:02, 57:01	15
	C*06:02, 06:02	C*06:02, 07:02	248
4A2 02	A*03:01, 29:01	A*03:01, 29:02	248
	DQA1*01:05, 01:02	DQA1*01:01, 01:02	34
	DPB1*02:01, 04:02	DPB1*02:01, 04:01	42
4A2 03	DRB1*01:02, 07:01	DRB1*01:01, 07:01	112
4A2 04	C*04:01, 07:02	C*04:09N, 07:02	15, 20,123, 133, 312
	DQA1*01:03, 02:01	DQA1*01:02, 02:01	126
4A2 05	B*07:01, 38:01	B*07:02, 38:01	24
	B*07:02, 37:01		48
	DRB1*04:01, 06:01	DRB1*04:01, 16:01	165
4A2 06	C*01:02/11/25, 05:01/03	C*01:02, 05:01	15
	C*12:09, 05:01		126
	DRB1*01:01, 13:02	DRB1*01:01, 01:03	267
	DQB1*03:01/13, 05:01	DQB1*03:01, 05:01	331

4A2 07	C*07:01/02, blank	C*07:02	165
	DRB1*07:01, 14:01	DRB1*07:01,14:54	142
	DRB4*01:03	DRB4*01:03N	149
4A2 08	C*07:01/06/08, 08:02	C*07:01, 08:02	267
	DRB3*01:01/04	DRB3*01:01	165
4A2 09	A*02:01, 03:01	A*02:66, 03:01	113, 126, 156, 165, 248, 259, 260
	B*27:01, 55:01/03,	B*27:01, 55:01	165
	C*01:02/11/25, 03:03/62	C*01:02, 03:03	15
4A2 10	C*01:02/11/25, 05:01/03	C*01:02, 05:01	15

Changes for 2016

HLA nomenclature – IMGT/HLA database updates

Previously UK NEQAS for H&I have only considered alleles reported in most recently published FULL WHO Nomenclature Report as the 'reference' baseline nomenclature. The last full report was published in 2010 and given the increasing number of HLA alleles being detected it is unlikely that further full publications will be made.

Therefore from 2016, the IMGT/HLA database update (http://www.ebi.ac.uk/ipd/imgt/hla/docs/release.html) from the January two years prior to start of the Scheme will be taken as the 'reference' allele baseline for the entire year and participants will be expected to report their findings in accord with this report as a minimum. (e.g in 2016 the IMGT/HLA release version 3.15.0 01-2014 will be used throughout 2016).

For typing to the 2nd field, HLA alleles should continue to be assigned on the basis of differences in exons 2 and 3 for class I and exon 2 for class II, as a minimum requirement.

Allele resolution typing

Participants performing HLA typing at the allelic resolution (e.g. using next generation sequencing) are able to report these results using scheme 4A2 samples. Results reported above the 2nd field will not be formally assessed in 2016 but summarised to allow comparison with other laboratories performing allelic level typing.

Dr Leigh Keen, Histocompatibility & Immunogenetics Department, NHSBT, Filton

SCHEME 4B: ABO GROUPING BY DNA METHODS

This scheme is designed to assess participants' ability to correctly determine ABO blood groups using DNA-based methodology. The scheme utilises scheme 4A1 samples

In 2015 there were 7 participants. All participants used PCR-SSP technology with 5 using commercial kits and the remainder using 'in house' developed primer sets.

There were no unsatisfactory performers in 2015.

Scheme 4B Performance	2012	2013	2014
Number of Participants	7	7	10
Number with Unsatisfactory Performance (< 100%)	1	1	0
% Unsatisfactory Performance	14.3%	14.3%	0%

Dr Leigh Keen, Histocompatibility & Immunogenetics Department, NHSBT, Filton

SCHEME 5A: HFE TYPING

This scheme is designed to assess participants' ability to correctly determine HFE mutations, to do so the participants were required to report on codon 63 and 282 and could also report codon 65.

Satisfactory performance is correctly assigning all 10 samples.

Table 1: Scheme 5A samples distributed in 2014

5A Samples Distributed			
Codon 63	**Codon 282**	**Codon 65**	**Number Of Samples**
HD	CC	SC	2
HD	CC	SS	2
HH	CC	SS	3
HH	YY	SS	3
HH	CY	SS	1

Performance

In 2015 there were 60 participants; 26 reported codon 65 results, 60 reported codon 282 and 59 reported on codon 63. A variety of techniques were used including RT-PCR, PCR-SSP and PCR melt curve analysis.

There were no laboratories with unsatisfactory performance

Scheme 5A Performance	2013	2014	2014
Number of Participants	58	59	60
Number with Unsatisfactory Performance (< 100%)	2	2	0
% Unsatisfactory Performance	3.9%	3.4%	0%

Ruhena Sergeant, Clinical Immunology Laboratory, Hammersmith Hospital, London

SCHEME 5B: INTERPRETATIVE: HFE GENOTYPE AND HEREDITARY HAEMOCHROMATOSIS

Introduction

The purpose of this scheme is to assess participants' ability to make an accurate, clear, concise and timely clinical report, appropriate for the range of clinical staff involved in a patient's care and treatment, given HFE genotype and other relevant clinical information.

Format

Two fictitious patient scenarios with HFE genotype (for C282Y and H63D mutations) and clinical information were provided in each of two distributions during the year, coinciding with the scheme 5A sample distributions. The scenarios were devised based on real cases and typical experience. Participants were expected to return a report within 4 weeks, in a format identical to that used for routine clinical reporting in their laboratories, providing appropriate interpretation and suggested actions.

Assessment

While designing the scenarios, the three expert assessors agreed on aspects of the report that were considered essential and what specific errors should attract penalty points, depending on their importance.

Criteria were classed under five general headings (describe the result, advise actions to be taken, state disease risk for patient, advise on risk to family members and on testing, and an open heading of common sense/other error). Allowing for one penalty award under each heading makes a maximum of five possible penalties.

Performance by a laboratory was classified "unacceptable" for any scenario where more than 50% of the possible penalty points were allocated, *i.e.* three penalties. Satisfactory performance for 2014 was achieved by obtaining four 'acceptable' classifications in the year.

Participation and results

Returns were received from 18 participants for the both distributions of scenarios 1-4. The maximum possible penalty was 5 points per scenario, 20 points in total.

2	labs got	0 penalty points
4	labs got	1 penalty point
4	lab got	2 penalty points
5	labs got	3 penalty points
2	labs got	4 penalty points
0	lab got	5 penalty points
1	labs got	6 penalty points

Average Annual total points was 2.28.

Satisfactory performance was achieved by all 18 participants in 2015 with none receiving >3 penalty points for any of the four scenarios.

Table 1. Performance Summary

	Scenario 1	Scenario 2	Scenario 3	Scenario 4
No. of labs with 0 penalty points	**11**	**7**	**9**	**10**
No. of labs with 1 penalty point	**6**	**9**	**6**	**8**
Labs with 0 or 1 penalty points	**94 %**	**89%**	**83 %**	**100 %**
Average penalty	**0.44**	**0.72**	**0.67**	**0.44**
No. of labs with classification "unacceptable" (3+ pts)	**0**	**0**	**0**	**0**

General deficiencies identified in reports included the following:

- Not advising further investigation of raised ferritin (e.g. infection, inflammatory disorders or malignancy).
- Not suggesting that secondary causes of iron overload should be considered
- Advising repeat testing of ferritin on fasting sample (fasting is not relevant to serum ferritin concentration, but to serum iron and transferrin saturation).
- Failing to advise testing of first degree relatives.
- Advising family testing but not advising against genetic testing of minors for this adult-onset condition.
- Not stating that other rarer mutations or types of haemochromatosis were not ruled out.
- Not mentioning that offspring's genotype unknown and therefore the patient's risk depends on whether offspring's genotype has HFE or other HH mutations.
- Advising indices of iron overload should be assessed, having said patient is unlikely to be affected with iron overload.
- Inclusion of minimal statements about the genotyping method used, no statement of specificity and sensitivity of the method.
- Less than half of the reports included full HGVS nomenclature for description of mutations.

Participants in the 5b scheme should be aware of new EMQN best practice guidelines published in 2015following the Best Practice Meeting held in Porto, May 2014:

> EMQN Porto G, Brissot P, Swinkels DW, *et al*., EMQN best practice guidelines for the molecular genetic diagnosis of hereditary hemochromatosis (HH). Eur J Hum Genet. 2015 Jul 8. PubMed PMID: 26153218

The 5b assessors will be taking in to consideration the recommendations within these guidelines in the assessment of scenarios in 2016.

Carol Hardy, West Midlands Regional Genetic Laboratory, Birmingham, UK.

SCHEME 6: HLA ANTIBODY DETECTION

Overview

The purpose of Scheme 6 is to assess participant's ability to correctly determine the likely presence of HLA specific antibodies. A total of 20 serum samples are sent each year as two distributions of ten serum samples. At registration participants may opt for class I only or class I and class II antibody assessment, results are to be reported within 8 weeks. In 2015 there were 97 participants. Consensus Class I/Class II positivity or negativity of each sample is determined by at least 75% of laboratories agreeing, samples failing to reach 75% consensus will not be assessed. Each report in agreement with the consensus is considered Acceptable and each non agreement Unacceptable. Satisfactory performance is making 80% of reports on all sera in agreement with the consensus in a calendar year.

Methodology

Details of methodology used are requested as part of the reporting process. The methodology used to test the samples is shown in Table 1.

Table 1: Methodology

Technique	1st cycle	2nd cycle
CDC only	2	1
ELISA only	0	0
FLOW only	0	2
LUMINEX only	64	71
Luminex + CDC	24	20
Luminex + ELISA	1	1
Luminex + Flow	2	1
Luminex + CDC + Flow	1	0

Performance: Satisfactory performance is making 80% of reports on all sera in agreement with consensus in a calendar year. In 2015 6 laboratories failed to reach 80% these are summarised in Figure 1 and Table 3. Overall there were more false positive results (UK&I 88%, ROW 71%) than false negative results. In 2014 there were more false negative (57%) than false positive results.

Figure 1: Scheme 6 Performance

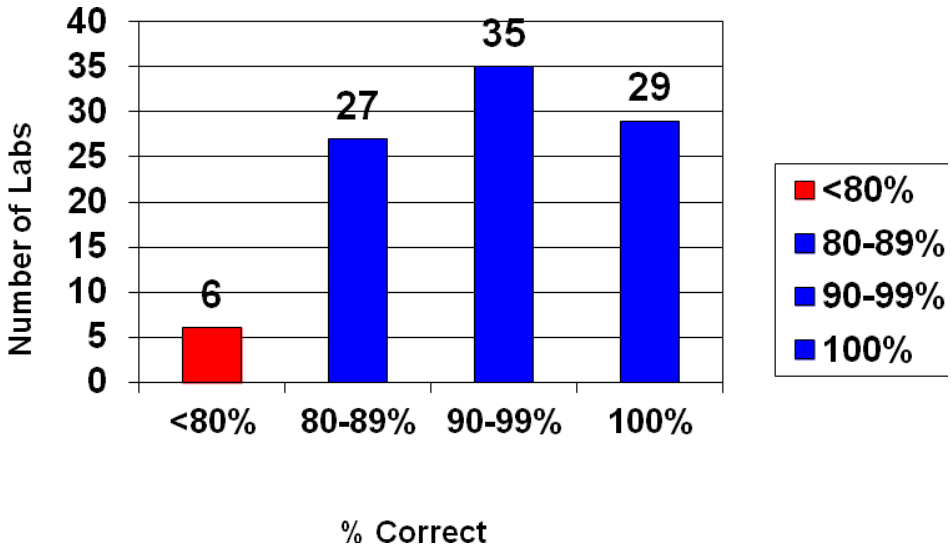


Table 3: Scheme 6 incorrect assignments

Lab No	Techniques Used	% Correct
20	CDC & LSM12 (One Lambda)	75.0%
28	CDC & LSM12 (One Lambda)	60.0%
34	SAB, LSM12 (One Lambda), ID Immucor	70.0%
149	LSM12 (One Lambda)	60.0%
258	LMX (Immucor)	60.0%
292	LSM12 (One Lambda)	65.0%

Table 4: Scheme 6 Performance

Scheme 6 Performance	2013	2014	2015
Number of Participants	68	83	97
Number with Unsatisfactory Performance (< 80%)	3	5	6
% Unsatisfactory Performance	4.4%	6.0%	6.2%

James Kelleher, NHISSOT, Beaumont Hospital

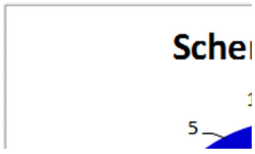
SCHEME 7- HLA-B*57:01 TYPING FOR DRUG HYPERSENSITIVITY

The requirement for B*57:01 typing is founded on the finding that hypersensitivity to abacavir - a nucleoside analogue reverse transcriptase inhibitor used to treat HIV and AIDS patients - is strongly associated with possession of B*57:01. HIV/AIDS treatment guidelines firmly recommend B*57:01 testing prior to abacavir treatment and withholding the drug from B*57:01 'positive' patients.

The purpose of this scheme, therefore, is to assess participants' ability to correctly determine HLA-B*57:01 status. Accordingly, participants were required to report on the samples' B*57:01 'positive' or 'negative' status and, for information only, to specify any B*57 positive non-B*57:01 alleles identified.

Scheme assessment was based on the usual 75% consensus level and satisfactory performance was achieving all 10 reports in accord with the consensus findings.
In 2015 two distributions were made of 5 blood samples each and there were 62 participants. The methods used to test the samples are shown in figure 1.

Figure 1: Scheme 7 testing methods



Of the 10 samples supplied 4 were from B*57:01 positive donors and 6 were from B*57:01 negative donors.

There was no laboratory with unsatisfactory performance in 2015.

Table 1: Scheme 7 number participants

Scheme 7 Performance	2013	2014	2015
Number of Participants	47	56	26
Number with Unsatisfactory Performance (< 100%)	0	01	10
% Unsatisfactory Performance	0%	1.8%	0%

Ruhena Sergeant, Clinical Immunology Laboratory, Hammersmith Hospital, London

SCHEME 8 – HLA AND DISEASE TYPING FOR HLA-DR/DQ/DP ONLY

This scheme is aimed at enabling participants to external quality assess their HLA typing for conditions associated with HLA Class II alleles. The diseases commonly typed include: coeliac disease, narcolepsy, rheumatoid arthritis and type I diabetes.

The purpose of the scheme, therefore, is to assess participants' ability to correctly determine HLA-DR/DQ/DP allele families/alleles.

In 2015 there were 2 sample distributions – each of 5 DNA preparations. Importantly, all of these samples had previously been tested in Scheme 4A2 – DNA HLA Typing to the 2nd Field - so possessed well documented HLA types.

Laboratories were required to report their Class II findings at a resolution as required or as a HLA type or presence/absence.
Assessment was made for the loci reported and for the presence or absence.

Satisfactory performance was achieved by obtaining at least 10 genotypes in accord with the consensus type.

There were 30 participants in 2015. 13 laboratories reported both presence/absence and class 2 type, 11 reported presence/absence only and 6 reported class 2 type only. 8 laboratories had unsatisfactory performance (Table 1). There were 11 misassignments made in 2015. 6 of the 10 samples had reporting errors, all errors were related to reporting of presence/absence (Table 2).

Table 1: Scheme 8 Unsatisfactory Performance

Scheme 8 Unacceptable Performance	2013	2014	2015
Number of Participants	19	21	30
Number with Unsatisfactory Performance (< 90%)	2	3	8
% Unsatisfactory Performance	10.5%	14.3%	26.7%

Table 2: Scheme 8 incorrect assignments

Sample	Lab No	Reported	Method
801	285	DQB1*02:02 Present	SSP (BAG)
803	113	DQB1*02 Absent	SSP/Lum (Olerup/One Lambda)
804	223	DQA1*01:02 Absent	SSP (Olerup)
808	274, 276, 278	DQB1*03:02 Present	SSOP/SSP
	278	DQA1*03:01 Present	SSP
809	278	DQB1*03:02 Present	SSP
	278	DQA1*03:01 Present	SSP
810	276	DQB1*03:02 Absent	SSP (Olerup)
810	278	DQA1*03:01 Present	SSP

Ruhena Sergeant, Clinical Immunology Laboratory, Hammersmith Hospital, London

EDUCATIONAL SCHEME SAMPLES

The purpose of this Scheme is to provide a variety of interesting HLA alleles/specificities that offer an educational element. The material is normally acquired from the Welsh Bone Marrow Donor Panel of some 87,000 HLA typed donors.

There were 48 participants in 2015, of which 22 were from the UK & Ireland.

In 2015 all 4 Educational Scheme samples were sent as DNA extracts. The suggested procedure is to perform "low resolution" typing by DNA- based method of HLA-A, B, C, DR, DQ and focus on the area of interest for further typing, if required.

The alleles of interest were: ED01/15 – A*25:04, ED02/15 – B*44:22, ED03/15 – B15:34, ED04/15 – A*03:162N. 48 laboratories reported on the samples – the findings were:

- **ED01/15 – HLA-A*25:04**

48 DNA-based HLA-A findings:

38 reports of A*25:04 – thus 79.1% of labs identified this allele
10 reports of A*25

A*25:04 differs from A*25:01:01 by two nucleotides at positions 538 T>C and 539 G>A (codon 156 TGG>CAG) resulting in an amino acid change, 156W (tryptophan) is changed to 156Q (glutamine) in the alpha helix of the alpha 2 domain (*Tissue Antigens 2003*, **62**, 256-258 and *International Journal of Immunogenetics 2008*, **35,** 481-510).

- **ED02/15 – HLA-B*44:22**

48 DNA-based HLA-B findings:

35 reports of B*44:22 - thus 72.9% of labs identified this allele
11 reports of B*44
2 reports of B*44:02

B*44:22 differs from B*44:02:01:01 by one nucleotide at position 106 A>G (codon 12 ATG>GTG) resulting in an amino acid change, 12M (methionine) is changed to 12V (valine) in the β strand region of the alpha 1 domain (*Tissue Antigens 2002*, **59**, 338-340 and *International Journal of Immunogenetics 2008*, **35,** 481-510).

- **ED03/15 – HLA-B*15:34**

45 DNA-based HLA-B findings:

32 reports of B*15:34 and 1 of B*15:01/26N-28/34 – thus 73.3% of labs identified, or came close to identifying, this allele
10 reports of B*15
1 report of B*15:26N
1 report of B*15:01/01N/26N-343

B*15:34 differs from B*15:01:01:01 by one nucleotide at position 379 G>C (codon 103 GTG>CTG) resulting in an amino acid change, 103V (valine) is changed to 103L (leucine) in the β strand region of the alpha 2 domain (*Human Immunology 1997*, **56**, 84-93 and *European Journal of Immunogenetics 2002*, **29,** 351-370).

- **ED04/15 – HLA-A*03:162N**

45 DNA-based HLA-A findings:

19 reports of A*03:162N – thus 42.2% of labs identified this allele
14 reports of A*03
2 reports of A*03:01
1 report of A*03:01/01N-209
1 report of A*03:01/08
1 report of A*03:01:01
1 report of A*03:01:01G
1 report of A*03:01/20/21N/26/112/129N/132/134/162N
1 report of A*03:01/20/26/37/45/78/112/118/132/134/162N
1 report of A*03:1/81N/112/129N
1 report of A*03:132
1 report of A*03:AEGDD
1 report of A*03:Nul?

A*03:162N differs from A*03:01:01:01 by a CATG insertion in exon 4 beginning at position 665. This causes a frameshift and changes codon 198 from GAG (glutamic acid E) to GCA (alanine A) and codon 199 from GCC (alanine A) to TGA (a termination codon) (*Tissue Antigens 2014*, **83**, 53-54).

Felicity May, UK NEQAS for H&I Operations Manager

INTERPRETATIVE EDUCATIONAL SCHEME CLINICAL SCENARIOS

The introduction of clinical interpretative scenarios (iED) has been a very popular addition to UK NEQAS for H&I repertoire.

These scenarios are based around a case study, with set questions regarding the testing and clinical advice participants would provide given the information presented in the scenario. Three scenarios were distributed in 2015 and this year the participants were given the option to register for the different scenarios independent of whether they participated in the corresponding EQA scheme. This change was made in recognition of the educational value to our participants irrespective of whether they perform the task routinely.

Participants were given 6 weeks to return the results. These scenarios are not formally assessed and result summaries are returned to each laboratory that submits a response.

Clinical Scenario 1: Solid Organ Transplantation

The first scenario was based on a cardiothoracic case.

The HLA typing information of the recipient and 2 potential deceased donors were presented along with HLA antibody testing results. Participants were asked to complete questions based on the results provided. This included what specificities would represent a high risk for transplant and for the 2 donor offers participants were asked to assign a risk level.

Results were received from 50 participants and the difference in responses between laboratories probably reflected those that were working within the Cardiothoracic Transplant Advisory Group (CTAG) recommendations and laboratories either overseas or not routinely supporting a cardiothoracic programme.

Clinical Scenario 2: Haematopoietic Stem Cell Transplantation

The second scenario was based on a based on a patient with Hurlers Syndrome who required a haematopoietic stem cell transplant (HSCT).

Information was provided on the HLA type, CMV status, weight and blood group of the patient. Te results of a cord blood unit (CBU) search and post-transplant chimerism monitoring results.

Participants were asked to complete questions based on the results provided. This included the selection of suitable donors from the CBU search and the clinical advice that would be given based on the chimerism results.

Results were received from 43 participants. The first choice CBU was almost unanimous with all but one laboratory selecting the same unit. The 2nd and 3rd choices were more varied reflecting individual unit policies as a result of clinician's preference.

Clinical Scenario 3: Platelet Transfusion Case

The final scenario for 2015 was a patient with AML requiring platelet support.

Information was provided on the patient's ABO, CMV status, HLA type and Luminex Single Antigen bead data. In addition a platelet unit search was included and post infusion increment data.

Results were received from 27 participants. The initial question was based on the Single Antigen bead results which antigens would be avoided in a platelet donor. Generally all laboratories agreed that median fluorescent levels greater than 10,000 would be avoided if possible. The only exception to this was HLA-Cw where only 57.7% would avoid. This split probably reflects again the difference between laboratories that provide a routine service and those using the iED as a "teaching" exercise. There was a clear first choice platelet unit selected by around 80% of laboratories. The consensus for the increment data was that the patient had failed to increment and alternate strategies were proposed.

For 2016

Feedback at the AGM suggested that participants were keen to continue with the iED and therefore three clinical scenarios are to be distributed again in 2016.

The iED Scheme Clinical Scenarios will be distributed to participants by e-mail in 2016. Please ensure a relevant e-mail address for receipt of the scenarios is completed on the registration forms.

Judith Worthington, The Transplantation Laboratory, Manchester Royal Infirmary

PILOT GENOTYPING SCHEMES

Three Pilot Schemes were launched in 2015 for Genotyping of the following; HPA (Human Platelet Antigen), KIR (Killer-cell immunoglobulin-like receptor) and MICA (MHC class I polypeptide-related sequence A)

Participants were provided with 5 blood samples to use for all three schemes. The results were not formally assessed. All three schemes will be continued in 2016.

Pilot HPA Genotyping

Participants able to report any of the following: HPA-1, HPA-2, HPA-3, HPA-4, HPA-5, HPA-6, HPA-15 as well as any other HPA polymorphisms detected, for information. There were 14 participants in 2015. All 14 labs reported HPA-1, 2 , 3, 5 and 15. 13 labs also reported HPA-4, 9 labs also reported HPA-6 and 1 lab also reported HPA-9

There were 5 reports out of consensus, these are summarised in Table 1.

Table 1: HPA Genotyping Reports Out of Consensus

Sample	Report	Consensus	Method	Lab Number
4A1 08/2015	6a6b	6a6a	SSP	127
	15a15a	15a15b	SSP (Protrans)	164
4A1 09/2015	6a6b	6a6a	SSP	127
	15a15a	15a15b	SSP (Protrans)	164
4A1 10/2015	6a6b	6a6a	SSP	127

Pilot KIR Genotyping

Participants able to report any of the following: KIR2DL1, KIR2DL2, KIR2DL3, KIR2DL4, KIR2DL5, KIR3DL1, KIR3DL2, KIR3DL3, KIR3DS1, KIR2DS1, KIR2DS2, KIR2DS3, KIR2DS4, KIR2DS5, KIR2DP1, KIR3DP1. Participants were also able to report any other KIR polymorphisms they detected for information.

There were 7 participants in 2015 and there were no reports out of consensus.

Pilot MICA Genotyping

Participant asked to report the MICA alleles as fully as possible using the appropriate nomenclature. There were 4 participants in 2015, each reporting in varying levels, therefore there was difficulty reaching consensus. However the scheme will be continued in 2016 to see if this improves with more participants.

Felicity May, UK NEQAS for H&I Operations Manager

NUMBER OF PARTICIPANTS DURING 2015

The number of Schemes' participants varies slightly during the course of any one year. However, the following table shows the approximate figures for each Scheme for 2015.

Scheme	UK and ROI	RoW
Scheme 1A	9	36
Scheme 1B	54	61
Scheme 2A	21	56
Scheme 2B	23	50
Scheme 3	24	57
Scheme 4A1	29	71
Scheme 4A2	20	39
Scheme 4B	4	3
Scheme 5A	49	11
Scheme 5B	18	1
Scheme 6	24	73
Scheme 7	26	36
Scheme 8	8	22
Educational Scheme Samples	22	27
iED Scenario 1	16	34
iED Scenario 2	15	27
iED Scenario 3	15	12
Pilot HPA Genotyping	3	11
Pilot KIR Genotyping	1	6
Pilot MICA Genotyping	2	2

ROI – Republic of Ireland
RoW – Rest of the World
iED – Interpretive Educational

3. 2015 ANNUAL PARTICIPANT MEETING – BIRMINGHAM

The UK NEQAS for H&I Annual Participant Meeting was held on the 7th December at a new venue – the Aston Conference Centre in Birmingham. 65 delegates representing 29 laboratories attended. The new venue was well received and will be used for the 2016 Annual Participant Meeting.

Slides from all of the annual meeting presentations may be downloaded from: http://www.wtail.org.uk/neqas/presentations.asp or requested from Felicity May, UK NEQAS for H&I Operations Manager.

The 2016 UK NEQAS for H&I participant meeting is valid for 3 Royal College of Pathologists' CPD points and 0.3 Credits for the Institute of Biomedical Science's CPD Scheme. It constitutes an appropriate meeting to attract BSHI CPD scheme points and should be documented by attendees who are BSHI Diploma Trainees.

4. FOR 2016 PLEASE NOTE

Laboratories will retain their code numbers for 2015. Laboratory code information is known only to the Scheme Manager and UK NEQAS for H&I staff.

An up-to-date list of contact names is provided in the Participant Manual

Important UK NEQAS for H&I dates for distributions, result deadlines, reporting and meetings are provided in the Participant Manual. Please see the 2016 Participant Manual for full details of the assessment system which is available to download from the website:

http://www.wtail.org.uk/neqas/participantmanual.asp