



Welcome and Introduction Judith Worthington Chair of UK NEQAS for H&I Steering Committee

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International Quality Expertise

Histocompatibility & Immunogenetics **Annual Participant's Meeting 2018**

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2018 Steering Committee

- · Judith Worthington (Chair)
- Arthi Anand
- Patrick Flynn
- James Kelleher
- Anthony Poles
- Ruhena Sergeant
- John Smith retired November 2018
- Helena Lee (BSHI Representative to UK NQAAP)
- Rommel Ravanan (Clinical Representative)
- Kathryn Robson (Lead Expert Advisor Scheme 5B)
- Alan Balfe (Expert Advisor Scheme 5B)
- Gavin Willis (Expert Advisor Scheme 5B)

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Notes

- Presentation focus on performance, interesting trends, discussion points, changes for 2019
- Labs 1-100 are from the UK and Ireland (UK&I)
- Labs 101 + are from the rest of the world (RoW)
- Please ask questions!

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- Scheme Assessment
 Most Schemes assessed on a consensus basis using a 75% consensus level i.e. 75% of reports must agree on a result for it to be assessed
- Reference typing results are used for typing/disease schemes if consensus not reached and any educational/pilot schemes
 - Scheme 5B: Interpretative HFE
 - Scheme 8: HLA Genotyping for HLA Associated Diseases
 - Scheme 4A1: HLA Typing at 1st Field Resolution DPB1 assessment using a reference result
 - Scheme 4A2: HLA Typing to 2nd/3rd Field Resolution, Scheme 7: HLA-B*57:01 Typing for Drug Sensitivity, Scheme 9: KIR Genotyping, Scheme 10: HPA Genotyping a reference result used for assessment if consensus is not reached
- All Not tested (NT) results excluded from assessment
- Equivocal result only accepted for Scheme 2B
- Labs that fail to return results, or provide valid reason for NT are assessed as unacceptable

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Unsatisfactory Performance (UP)

- Each scheme has minimum annual performance criteria
 - HLA Typing schemes 90%
 - Crossmatching 85%
 - Disease Association Schemes 100%
 - Antibody Specificity 75%
 - Antibody Detection 80%
- Participants that do not meet the minimum criteria are classed as unsatisfactory performers
- Must complete a root cause analysis and CAPA form

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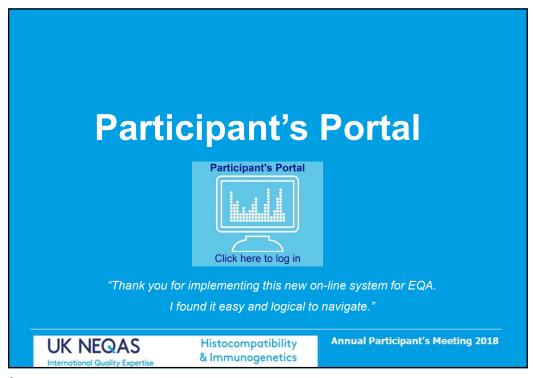
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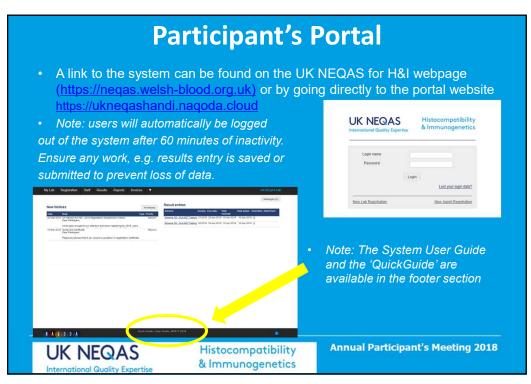
Changes for 2019

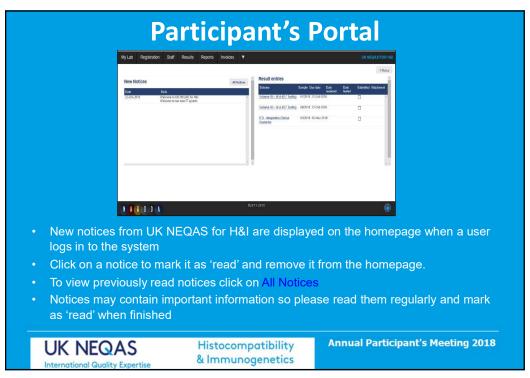
- Steering Committee
 - Tim Clench and Marian Hill (Expert Advisor Scheme 5B)
 - John Smith Retired
 - Helena Lee replaced by Elizabeth Wroe
- NEQAS Operations Manager covering maternity leave
- · Financial year operation has been implemented
- The 'Participant's Portal' bespoke EQA IT system has been introduced

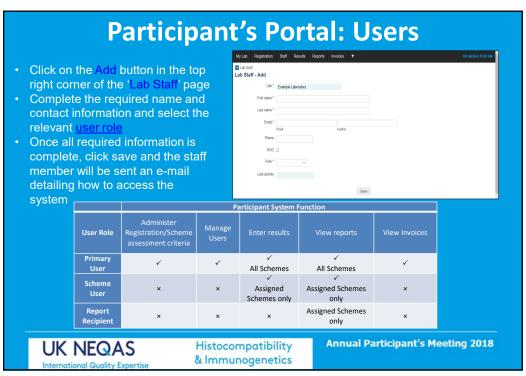
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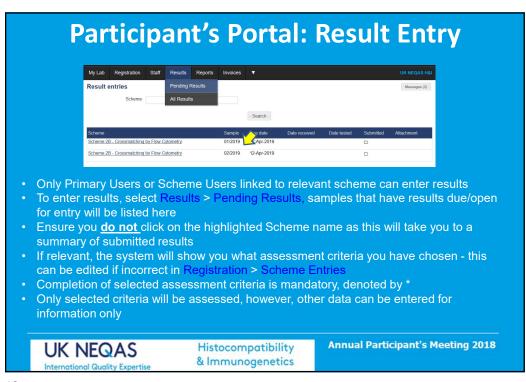
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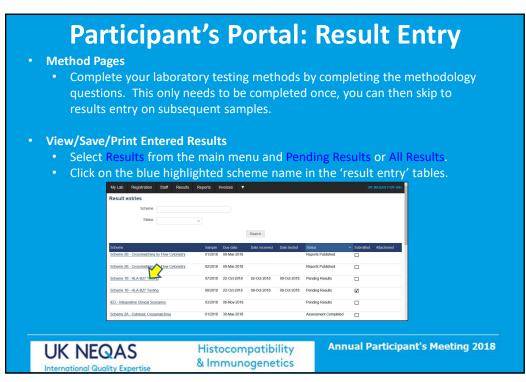


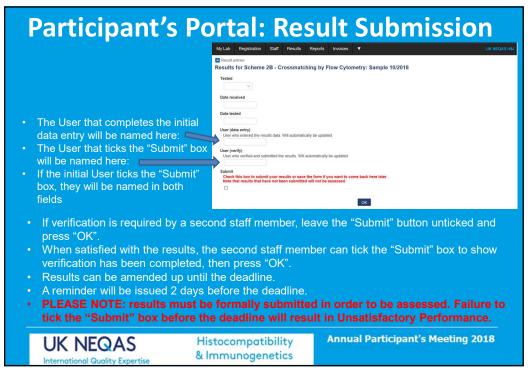


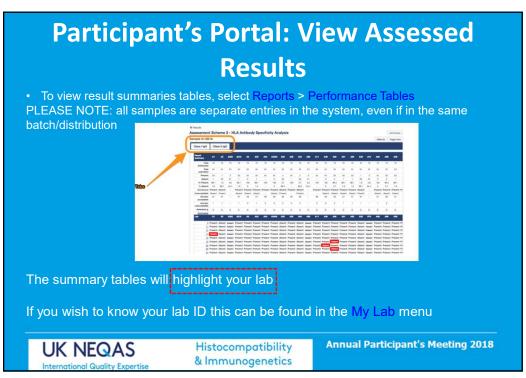












Participant's Portal: View Assessment Reports

Once assessment of samples is complete notification will be sent that your report is available to view in the Participant System.

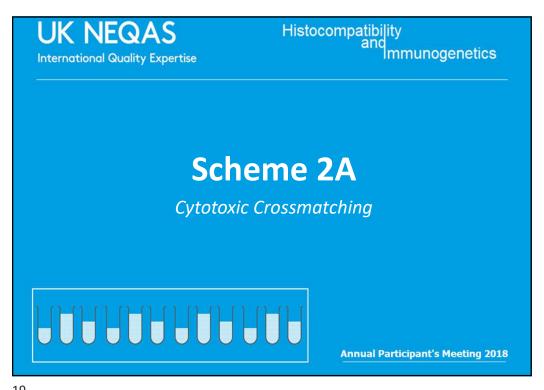
• Click on Reports and Performance Reports to access all laboratory reports.

The table will display a list of available distribution reports. Unsatisfactory performance notifications, close-out letters and annual performance reports will also appear in this list.



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Scheme 2A

- *Purpose:* To assess participants' ability to correctly determine cell/serum cytotoxicity crossmatch status
- 10 blood samples and 40 serum samples sent in five distributions
- *Consensus*: determined by at least 75% agreement on a positive or negative result
- Satisfactory Performance: Making 85% of reports in agreement with the consensus result in a distribution year for each cell/DTT type.

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Scheme 2A Performance

• 16 Unsatisfactory Performers (7 UK & Ireland)

All cells with and without DTT	2015 +DTT	2016 +DTT	2017	2018
Number of Participants (UK&I)	64 (18)	64 (18)	75 (19)	71 (18)
Number with Unsatisfactory Performance (< 85%) (UK&I)	9 (0)	13 (6)	16 (6)	16 (7)
% Unsatisfactory Performance (UK&I)	14.0% (0%)	20.3% (33.3%)	21.3% (31.6%)	22.5% (38.8%)

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UK&I 2018 Performance

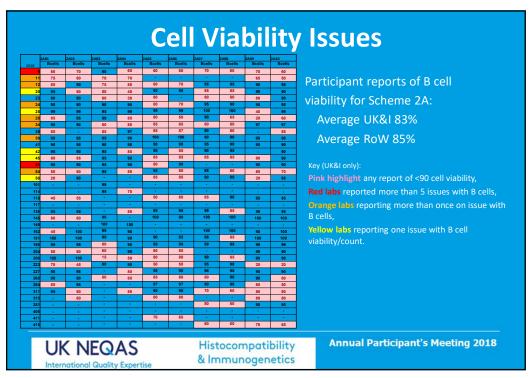
	PBL	PBL +DTT	T Cell	T Cell +DTT	B Cell	B Cell +DTT
Crossmatches assessed (n=40)	37	38	34	39	23	33
% NT	7.9%	8.3%	6.8%	12.0%	14.7%	19.3%
NT	19	20	41	72	100	131
% incorrect assignments	5.0%	1.3%	6.9%	2.9%	13.0%	5.9%
False Positive	10	2	35	17	41	33
False Negative	1	1	0	0	10	0

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	Un	acce	ptabl	e Perfo	rmer	s 2018	3
	PBL -DTT	T -DTT	B -DTT	PBL + DTT	T + DTT	B + DTT	Lab Identified Error
25			82.6%				Cell viability
34			56.5%				Cell viability
38			78.3%				Unclear
39			75.0%				Cell viability
41		79.4%			84.6%	75.8%	Waiting for a response
51			78.3%			84%	Cell viability
54			81.3%			84%	Technical issues and cell viability
112	40%						No response
193			77.8%			81.8%	No response
197		69.6%	64.3%		66.7%	78.9%	No response
252			81.8%				No response
292			83.3%				Cell viability
293		0%	0%		0%	0%	Cell viability (transport)
351		0%	0%		0%	0%	No response
406	0%	0%	0%				No response
411		63.2%	50.0%		66.7%	55.6%	No response
	EQAS Quality Expert	t.		npatibility nogenetics	Annua	l Participan	t's Meeting 2

Labs r	ep <u>c</u>	orting <u>iss</u>	sues wi	th B cel <u>l v</u>	iability or	count
	. 2A Sample	UK&I Labs	% With an Issue (n=17)	RoW WB % With an Issue (n=18)	RoW PC % With an Issue (n=36)	
0)1	9, 45, 54, 58	23.5%	16.7%	27.8%	
0	12	9	5.9%	16.7%	25.0%	
0	13	9, 34	11.8%	27.8%	13.9%	
0	14	9, 20, 34	23.5%	27.8%	5.6%	
0)5	9 , 11, 12, 39, 51	29.4%	22.2%	16.7%	
0	16	9, 11, 12, 24, 28, 39, 51	41.2%	11.1%	27.8%	
0	17	51	5.9%	5.6%	41.7%	
0	8	9, 11 , 24, 28 , 51, 54	35.3%	27.8%	36.1%	
0	9	9, 25, 28, 38, 42, 51, 54, 58	47.1%	22.2%	38.9%	
1	.0	9, 24, 28, 42, 51, 54	35.3%	16.7%	33.3%	



Participant reports of cell viability	for Sch	eme 2	A in co	mnari	son to	comm	ents re	gardin	g noor		
viability and results submitted:											
	Labs	1	2	3	6 Viable B	5	6	7	8	9	10
	9	80	70	90	60	60	60	70	60	70	60
	11	75	60	70	70					65	50
	12	85	90	75	85	60	70	95	95	95	98
	15	99	99	80	100	80	90	99		90	90
	20	95	80	80	40	90	90	85	85	90	90
	23	90	90	80	30	80		80	80	80	90
	24	90	90	90	95	80	70	95	90	95	95
	25	99	99	95	99	99	99	100	100	40	99
	28	85	95	99	85	80	50	90	65	20	60
	34	90	90	80	85	85	85	80	80	97	97
	38	85		85	97	85	87	90	80		85
	39	98	98	95	90	100	100	90	90	98	98
	41	90	95	90	90	98	90	95	90	90	90
	42	95	90	95	85	95	85	90	95		90
y: Highlight denotes a comment on poor	45	80	85	95	90	85	85	85	85	80	90
	51	90	90	95	90	80	90			90	90
ability was made for that sample	54	50	80	95	85	95	80	95	<80		70
d Highlight = B cell results not submitted	58	20	90			85	85	90	90	20	95
low Highlight = some B cell results submitted,	Range	20-99	60-99	70-99	30-100	60-100	60-100	70-100	60-100	20-98	50-99
	Average	83	88	88	81	85	82	89	84	74	85
	Neqas Check	98	98	100	99	100	100	100	100	90	95
	Consensus	8/8	8/8	6/8	4/8	6/8	4/8	7/8	7/8	0/8	6/8

		2B 01-10/2018 % Viable B Cells Reported by UK&I Labs													
	Date	Bled:	19-Mar	Date	Bled:	04-Jun	04-Jun Date Bled:		10-Sep	Date Bled:		19-Nov Date		e Bled: 22-Jan	
Lab	01	02	Age When Tested (Days)	03	04	Age When Tested (Days)	05	06	Age When Tested (Days)	07	08	Age When Tested (Days)	09	10	Age When Tested (Days)
9	80	70	3	90	60	3	60	60	3	70	60	3	70	60	2
11	75	60	3	70	70	3	N/A	N/A	2	N/A	N/A	4	65	50	2
12	85	90	2	75	85	2	60	70	2	95	95	2	95	98	1
15	99	99	2	80	100	2	80	90	2	99	N/A	3	90	90	1
20	95	80	4	80	40	3	90	90	3	85	85	2	90	90	2
23	90	90	2	80	30	2	80	N/A	2	80	80	2	80	90	1
24	90	90	3	90	95	3	80	70	3	95	90	3	95	95	2
25	99	99	2	95	99	2	99	99	2	100	100	2	40	99	1
28 34	85 90	95	2	99	85 85	2	80 85	50 85	2	90 80	65 80	2	20 97	60 97	1
38	85	N/A	2	85	97	2	85	87	2	90	80	2	N/A	85	1
39	98	98	2	95	90	2	100	100	2	90	90	2	98	98	1
41	90	95	2	90	90	2	98	90	2	95	90	2	90	90	1
42	95	90	3	95	85	3	95	85	2	90	95	2	N/A	90	1
45	80	85	2	95	90	3	85	85	2	85	85	3	80	90	3
	90	90	3	95	90	3	80	90	3	N/A	N/A	4	90	90	2
54	50	80	3	95	85	3	95	80	3	95	<80	3	60	70	2
58	20	90	2	N/A	N/A	2	85	85	2	90	90	2	20	95	1
High	diaht -	R coll	recults not	cuhmi	ttod	Yellow Highl	iaht -	come	B call result	e cuhn	nittad	Groom High	allahe	- all :	l S coll recults

Cell Viability Issues

- NEQAS performed an investigation into cell viability and serum stability at different temperature ranges to establish whether whole blood and lymphocytes were stable when stored for up to 72 hours (3 days)

 Serum stability was also assessed and no evidence of antibody degradation was found after 72 hours incubation at temperatures up to 45°C

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Participant Feedback on Viability

- The high percentage of serum / B cell samples Not Assessed due to labs reporting samples as Not Tested – laboratories frequently report poor cell viability as the stated reason for not reporting.
- Can NEQAS comment on the high percentage of B cell samples that are Not Assessed / Not Reported and whether this has changed over time?

2A Performance	No of Reports Assessed +DTT	B+DTT % NT	B+DTT % Incorrect	No of Reports Assessed -DTT	B-DTT % NT	B-DTT % Incorrect	%UP UK&I
2016	27/40	11.1%	4.2%	34/40	13.4%	5.1%	19.25%
2017*a	29/36	25.8%	5.4%	27/36	19.9%	5.1%	31.6%
2018	33/40	19.3%	5.9%	23/40	14.7%	13%	38.8%

Excludes sample 2A 02/2017 which was not assessed due to poor sample quality

^a Higher number of B cell results not tested due to dynabead product recall

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Not Assessed Samples

15% of cell/serum combinations for 2018 were not assessed

2018 (n=36/240)	-DTT	+DTT
PBL	3	2
T cell	6	1
B cell	17	7
Total	26	10

- The percentage agreement for each cell type and whether the result was positive or negative usually falls at approximately 60% in NA samples:
- Is NA an indicator of cell viability??

T-DTT T+DTT 55.2 58 62.1 58 62.1 58 62.1 58 62.1 58 62.1 58 62.1 58 62.1 58 62.3 58 62.3 58 62.3 58

53.8 74.1 66.7 63.3 76 57.7 60 72 68.8 51.7 52.2 61.6

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Participant Feedback: Splitting Assessment for UK&I from RoW

• 17 UK&I are assessed with 20 labs from the RoW that also receive whole blood.

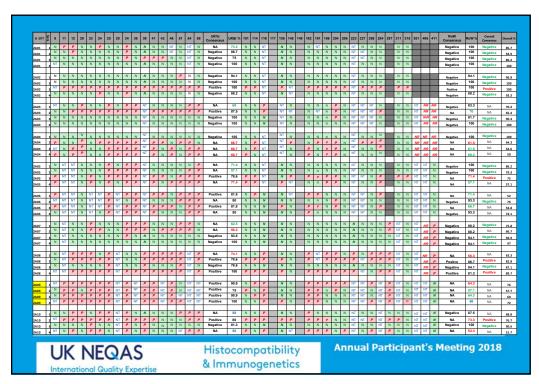
	UK -DTT	RoW -DTT	UK +DTT	RoW +DTT
PBL	6	2	6	1
T Cell	15	20	15	17
B Cell	17	20	17	17

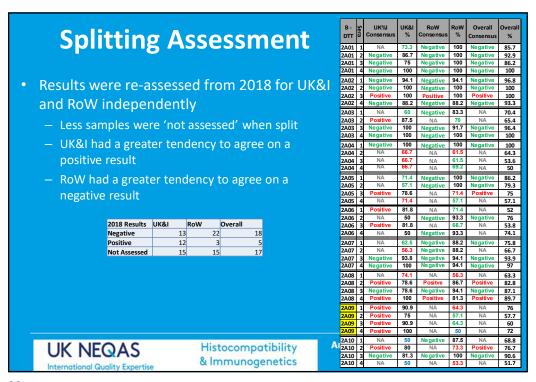
 Suggestion that UK&I labs should only be compared to other UK&I labs.

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				01		B cell With	I I	1112	0010.4				
	2A01&02	2A03&04	2018 Asse 2A05&06		2A09&10	T-4-1	0404000	UK only 2A03&04	y 2018 Ass	2A07&08	6 Correct)	Total	Lab Performance
UK&I						Total	100.0%		2AU5&U6		2A09&10	84.0%	Lab remorniance
11	100.0% 87.5%	100.0%	100.0% NT	80.0% NT	100.0%	96.0% 95.0%	100.0%	75.0% 75.0%	100.0% NT	80.0% NT	66.7% 100.0%		
12	75.0%	100.0%	NT	100.0%	100.0%	93.0%	83.3%	100.0%	NT	100.0%	66.7%	91.0% 87.0%	 Original assessment:
15	13.070	100.070	141	100.070	100.070	33.0 /6	00.070	100.070	141	100.070	00.770	67.078	
20	100.0%	100.0%	75.0%	100.0%	100.0%	95.0%	100.0%	100.0%	0.0%	100.0%	66.7%	73.0%	6 UK&I labs <75%
23	100.0%	100.0%	100.0%	83.3%	50.0%	86.0%	100.0%	100.0%	100.0%	83.3%	66.7%	90.0%	O UKQI Idbs 3/0</td
24	75.0%	100.0%	66.7%	100.0%	100.0%	88.0%	83.3%	100.0%	0.0%	83.3%	66.7%	66.0%	
25	100.0%	100.0%	25.0%	83.3%	100.0%	81.0%	100.0%	100.0%	100.0%	83.3%	66.7%	90.0%	4 RoW labs <75%
28	100.0%	100.0%	66.7%	100.0%	NT	91.0%	100.0%	100.0%	100.0%	100.0%	NT	100.0%	
34	50.0%	100.0%	50.0%	50.0%	50.0%	60.0%	66.7%	100.0%	100.0%	50.0%	33.3%	70.0%	
38	100.0%	100.0%	25.0%	66.7%	100.0%	78.0%	100.0%	100.0%	100.0%	66.7%	100.0%	93.0%	
39	87.5%	NT	NT	66.7%	50.0%	68.0%	100.0%	100.0%	NT	66.7%	66.7%	83.0%	
41	87.5%	100.0%	100.0%	100.0%	100.0%	97.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	 Split assessment
42	87.5%	100.0%	100.0%	100.0%	50.0%	87.0%	100.0%	100.0%	100.0%	83.3%	66.7%	90.0%	
45	100.0%	100.0%	75.0%	100.0%	50.0%	85.0%	100.0%	100.0%	33.3%	83.3%	66.7%	76.0%	7 UK&I labs <75%
51	87.5%	100.0%	75.0%	66.7%	50.0%	76.0%	83.3%	100.0%	66.7%	66.7%	33.3%	58.0%	/ UNQI IdDS 5%</td
54	100.0%	100.0%	50.0%	66.7%	100.0%	83.0%	100.0%	100.0%	100.0%	66.7%	66.7%	86.0%	
58	100.0%	100.0%	25.0%	100.0%	100.0%	85.0%	100.0%	100.0%	100.0%	100.0%	66.7%	93.0%	4 new labs now <75%
RoW	400.00/		iginal 201	100.0%		400.00/	400.00/	400.000	oW only 20		nent	400.00/	Thew labs now 47570
101	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	3 now >75%
116	NT	100.0%	100.0%	100.0%	100.0%	100%	NT	100.0%	100.0%	100.0%	66.7%	92.0%	3 HOW 2/3%
117	INI	100.0%	100.0%	100.0%	100.0%	100.0%	INI	100.0%	100.0%	100.0%	00.7%	92.0%	0 111 750/1 11
136	100.0%	NT	75.0%	100.0%	100.0%	94%	100.0%	NT	100.0%	100.0%	100.0%	100.0%	2 still <75% but improved
145	100.0%	100.0%	100.0%	66.7%	100.0%	94%	100.0%	100.0%	100.0%	71.4%	100.0%	94.0%	
149	100.070	100.070	100.070	00.170	100.070	0470	100.070	100.070	100.070	71.470	100.070	04.070	1 still <75% but got worse
162	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	66.7%	93.0%	
181	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	4 RoW labs <75%
186	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	4 NOW Idus 3/0</td
204	100.0%	66.7%	75.0%	100.0%	50.0%	78%	100.0%	66.7%	50.0%	100.0%	66.7%	76.0%	
206	100.0%	100.0%	75.0%	100.0%	50.0%	85.0%	100.0%	100.0%	100.0%	100.0%	66.7%	93.0%	same labs still <75%
223	NT	NT	NT	100.0%	NT	100.0%	NT	NT	NT	100.0%	NT	100.0%	
227	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	1 still <75% but improved
268	100.0%	100.0%	75.0%	83.3%	100.0%	91.0%	100.0%	100.0%	100.0%	85.7%	100.0%	97.0%	1 3till <7370 but illiproved
284	100.0%	100.0%	100.0%	100.0%	NT	100%	100.0%	100.0%	100.0%	100.0%	NT	100.0%	1 still <7E0/ but set were
297	NT	NT	NT 400.00/	83.3%	100.0%	91.0%	NT	NT	NT	71.4%	100.0%	85.0%	1 still <75% but got worse
311	100.0%	100.0%	100.0%	NT oo 70/	100.0%	100.0%	100.0%	100.0%	100.0%	NT	100.0%	100.0%	
315 351	100.0% NT	100.0%	100.0%	66.7% NT	50.0%	87.0% 0.0%	100.0% NT	100.0%	100.0%	57.1% NT	66.7% 0.0%	85.0% 0.0%	
406	NT NT	0.0% NT	0.0%	0.0%	0.0%	0.0%	NT NT	0.0% NT	0.0%	0.0%	0.0%	0.0%	
411	NT	NT	75.0%	33.3%	50.0%	42.0%	NT	NT	100.0%	28.6%	66.7%	48.0%	
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Interesting Results: 2A01

- Query from UK lab regarding Sample 2A01 serum 3
 - Multiple UK&I labs called this B cell positive but the consensus was negative (all RoW labs reported negative): 86.2% negative -DTT, 76.9% negative +DTT
 - SAB testing performed by 5 labs:
- HLA PHENOTYPE OF BLOOD DONOR: HLA-A2, A3; B7, B60; Cw3, Cw7; DR4, DR15; DQ6, DQ8

SAB Defin	ed 'DSA'
A2	19,430
DR51	20,824
DQ6	21,559
Cumulative	61, 813

SAB Defin	ed 'DSA'	SAB 'DSA' +EDTA		
A2	15,281	A2	2,300	
DR4	5,103	A3	9,600	
DR51	15,825	B7	2,900	
DQ6	16,433	Cw7	1,100	
DQ8	1,221	Cumulative	15,900	
Cumulative	53,863			

SAB 'DSA' +EDTA				
A2	>10,000			
DR51	14,000			
DQ6	>8,000			
Cumulative	32,000			

SAB 'DSA'	+EDTA
A2	17,300
B56	1,300
B57	16,000
Cw1	1,700
DR1	21,000
DQ5	18,500
DR51	14,000
DRB1*04:01	5,300
Cumulative	~95.000

- Shouldn't a cumulative MFI of 61,813 cause a positive CDCXM?????
 - Other labs reported that the PBL and T cell crossmatch was Negative although some reported PBL and T cell positives
 - Non-complement fixing antibodies?
 - Prozone effect? Not when PBLs tested in dilution:
 - Neat Positive (4), 1:2 Positive (4), 1:4 Positive (2), 1:8 Negative

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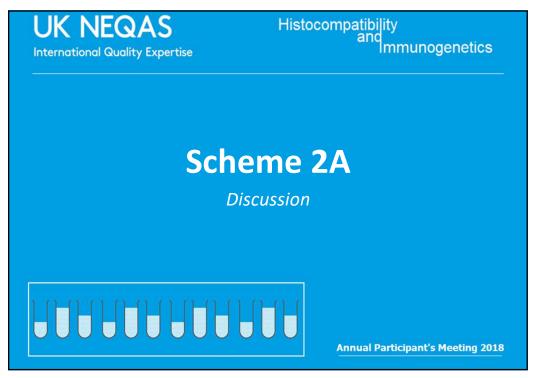
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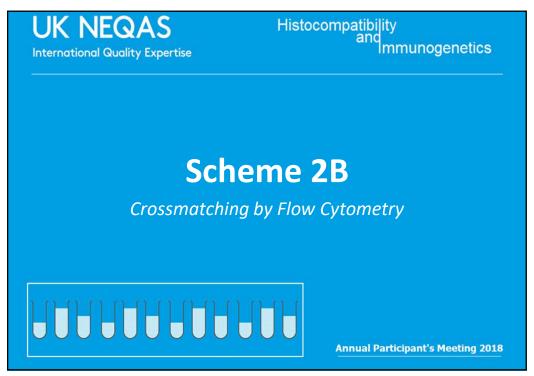
Discussion

- Not all Scheme 2A results will reach consensus (that's ok!)
- B-cells are difficult (transport, non-specific binding)
- Only partially emulates clinical practice
- 2A is a technical assessment of cytotoxic crossmatching and should not be 'interpreted'
- Lab's need to ensure that all test parameters and acceptance criteria are met prior to reporting NEQAS samples.
- CDC assays are not quantitative so reliant on subjective assessment.

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Scheme 2B

- *Purpose:* To assess participants' ability to correctly determine cell/serum flow crossmatch status
- 10 blood samples and 40 serum samples sent in five distributions
- Consensus: determined by at least 75% agreement on a positive, negative or equivocal result
- **Satisfactory Performance**: Making 85% of reports in agreement with the consensus result in a distribution year for each cell type.

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Reporting of Equivocal Results

- In 2018 Equivocal results were assessed
 - i.e if 75% or more of participants report positive/negative, any laboratories reporting 'equivocal' were assessed as 'unacceptable'
 - If a 75% consensus result is not reached when including the equivocal reports, the sample was not assessed.
- Technical issues and invalid results (e.g control failures, replicate issues, sample quality issues) should be reported as 'Not Tested' with the reason stated.

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Scheme 2B Performance

• 15 Unsatisfactory Performers (2 UK & Ireland)

Scheme 2B	2015	2016	2017	2018
Number of Participants (UK&I)	73	76	85	83
	(23)	(23)	(22)	(22)
Number with Unsatisfactory Performance (< 85%) (UK&I)	13	13	8	15
	(3)	(1)	(1)	(2)
% Unsatisfactory Performance	17.8%	17.1%	8.7%	18.1%
	(13.0%)	(4.3%)	(4.5%)	(9.1%)

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Scheme 2B Summary

	T Cells				B Cells	
	UK&I	RoW PC	RoW WB	UK&I	RoW PC	RoW WB
Number of participants	22	48	19	22	48	19
Number of XM assessed (>75% consensus)	34/40	32/40	34/40	36/40	36/40	30/40
Number of Positive XM	15	9	7	24	17	12
Number of Negative XM	19	23	27	12	19	18
Number of incorrect assignments	36 (4.8%)	64 (4.7%)	34 (4.7%)	32 (4.0%)	82 (6.9%)	36 (5.5%)
Number of False Pos	23	34	21	22	40	19
Number of False Neg	13	30	13	10	42	17
Number of equivocal assignments Number of NT assignments	22 (2.5%) 48 (5.5%)	35 (2.0%) 230 (13.1%)	10 (1.2%) 146 (17.4%)	5 (0.6%) 83 (9.4%)	24 (1.4%) 215 (12.2%)	11 (1.3%) 147 (17.5%)

UK&I and RoW receive different blood samples

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Unacceptable Performers 2018

• 15 labs with UP (<85%)

Lab	T Cell	No. of results submitted	B Cell	No. of results submitted	Root Cause
28	69.2%	30/40	100%	25/40	Cell viability and reporting Equivocal
51	79.4%	40/40	88%	28/40	Cell viability and reporting Equivocal
139	84.2%	24/40	90.5%	24/40	No response
142	82.4%	40/40	93.3%	40/40	Technical issue
169	75%	32/40	61.1%	32/40	No response
189	75%	40/40	69.4%	40/40	Cell viability issue
218	81.0%	28/40	68.0%	28/40	No response
230	85.3%	40/40	76.7%	40/40	Technical issue
240	90.6%	40/40	66.7%	40/40	No response
271	94.4%	20/40	83.3%	21/40	Technical issue
315	47.1%	23/40	50.0%	23/40	Technical issue
351	83.3%	24/40	78.3%	24/40	No response
374	85.3%	40/40	73.3%	40/40	Technical issues
380	42.9%	8/40	38.5%	8/40	No response
392	0%	0/40	0%	0/40	No response

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Reporting of Equivocal Results

- 2018 Summary
 - 67 T cell equivocal results (from 3022 = 2.2%)
 - 42 B cell equivocal results (from 2809 = 1.5%)
 - 22 T cell equivocal results assessed as unacceptable (0.7%)
 - 20 B cell equivocal results assessed as unacceptable (0.7%)

2018	T cell Total		B cell Equivocal	Total	Equivocal Assessed as Unacceptable Result		
2016	Results	Results Results Results	Results	T cell	B cell		
1+2	23	608	11	550	3	7	
3+4	9	648	13	587	5	1	
5+6	14	632	6	578	4	4	
7+8	9	553	7	569	3	5	
9+10	12	581	5	525	7	3	
Totals	67	3022	42	2809	22	20	

2018	No of Labs Reporting Equivocal	No. of Labs Reporting >1 Equivocal Result
UK (n=22)	10 (45%)	6 (27%)
OS (n= 61)	34 (56%)	22 (36%)
Total (n=83)	44 (53%)	28 (34%)

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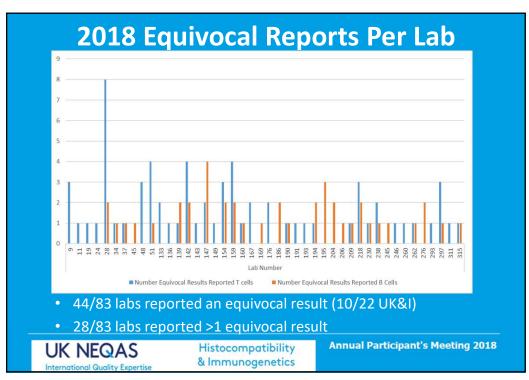
Reporting of Equivocal Results · Compared to 2017 assessment criteria 4 sera changed consensus (3 T cell, 1 B cell - RoW only) T Cell 2B01 2018 160 (11.9%) 293 297 2B05 2018 OS PC 154 Assessed (21.4%) (9.5%) 159 (69%) 218 2B09 2018 Serum 1 142 (11.8%) (70.6%) 2B09 2018 OS WB 315 Assessed (6.7%) (73.3%) (20.0%)

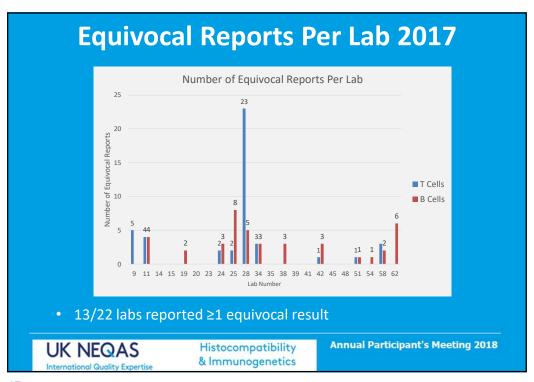
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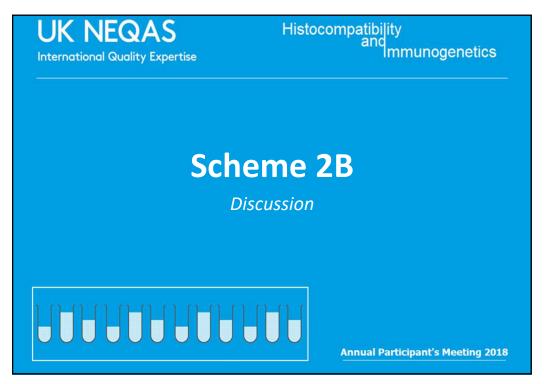
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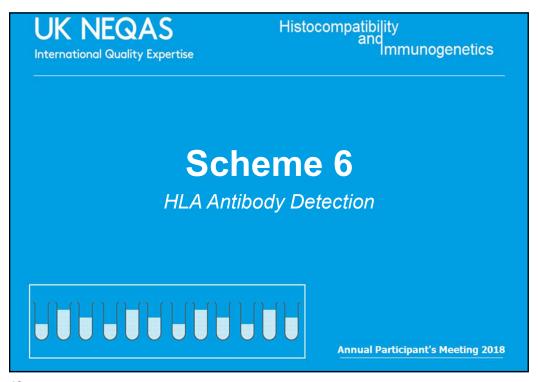
45

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Scheme 6

- *Purpose:* To assess participants' ability to correctly determine the presence of HLA antibodies
- 12 serum samples sent in two distributions
- *Consensus*: determined by at least 75% agreement on a presence or absence of an antibody
- **Satisfactory Performance**: Making 80% of reports in agreement with the consensus result in a distribution year.

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Scheme 6 Performance

• 5 Unsatisfactory Performers (0 UK & Ireland)

	2015	2016	2017	2018
Number of Participants (UK&I)	97	98	101	88
Number of Participants (OR&I)	(24)	(24)	(24)	(25)
Number with Unsatisfactory Performance (< 80%) (UK&I)	6 (3)	18 (4)	21 (0)	5 (0)
% Unsatisfactory Performance	6.2% (12.5%)	18.4% (16.7%)	20.8%	5.7% (0%)

The 5 labs with unacceptable performance:

- 1 used Immucor kits only (1 mixed)
- 4 gave no information as to kit usage

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Not Assessed Samples							
2018 Sample	Class I All Labs (n=90)	Class I UK&I (n=25)		Class II All Labs (n=88)	Class II UK&I (n=24)		
601	92.9%	96%		97.5%	100%		
602	90.5%	100%		98.8%	100%		
603	90.4%	96%		91.3%	96%		
604*	56.6%	52%		100%	100%		
605	100%	100%		100%	100%		
606	95.2%	100%		61.3%	60%		
607	98.8%	100%		100%	100%		
608	75.3%	100%		100%	100%		
609	100%	100%		100%	100%		
610	100%	100%		100%	100%		
611*	70.2%	52%		100%	100%	Green denote agreement or	
612*	74.1%	56%		51.2%	62.5%	negative resu	
* Denotes samples were sourced from non-transfused male donors							
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Scheme 6 Errors

58/1573 (3.7%) results out of consensus (7 UK&I)

More false negative results in RoW but UK&I tendency for more false positive results

Non-specific binding an issue (sample 604, 611 612)

Error	UK&I	RoW
Class I only	5	43
Class II only	2	2
Class I & II	0	6

	Cla	ss I	Class II		
	False False Neg		False Pos	False Neg	
UK&I	3	2	2	0	
RoW	13	30	5	3	

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Interesting Results: 608/2018

- Class I Consensus Positive (overall 75.3%, UK&I 100%)
 - 63 labs reported positive, 21 reported negative
- 18 Labs that use Immucor kits, 11 of them reported a Negative result
- 29 Labs use One Lambda kits all reported a Positive result

	Sample 60	8/2018 Kit Breakdown	Pos	Neg	NT	Total
Not:	stated		29	9	3	41
cor	LM1	Class I ID Kit	3	0	0	3
Immunco	LMX	Lifecodes Lifescreen Deluxe Kit	2	11	0	13
<u>Ē</u>	LSAI	Lifecodes Lifescreen SA Class I	1	1	0	2
oda	LSM12	LS Mixed Class I&II	18	0	0	18
One Lambda	LS1PRA	LABScreen PRA Class I	4	0	0	4
Je L	LS12PRA	LABScreen PRA Class I&II	1	0	0	1
ō	LS1A04	LS SA Class I	6	0	0	6
		Totals	64	21	3	88

- Labs used numerous different kits to detect the presence/absence of antibodies
- Should we standardise?
 - Scheme 6 operates purely as a detection scheme. We do not state what detection methods have to be used to achieve this but it is important that the techniques used reflect clinical practice.

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Kit Differences Affecting Consensus

- Five 2018 non-consensus results were re-analysed by kit manufacturer.
- For labs reporting using One Lambda kits only (n=28)
 - 1/5 results reached consensus (sample 612 CII).
- For Immucor only users (n=15)
 - 3/5 results reached consensus (sample 611 CI, 612 CI and CII).
- In 3/5 results the consensus/majority result differed between the manufacturers
 - 604, 606, 612

2018 Samples	All Labs (n=Cl 90, Cll 88)	One Lambda (n=28)	Lifecodes (n=15)
604 Class I	56.6%	51.9%	60.0%
606 Class II	61.3%	64.3%	64.3%
611 Class I	70.2%	53.6%	78.6%
612 Class I	74.1%	64.3%	78.6%
612 Class II	51.2%	75.0%	84.6%

Green denotes agreement on negative result, red denotes agreement on positive result

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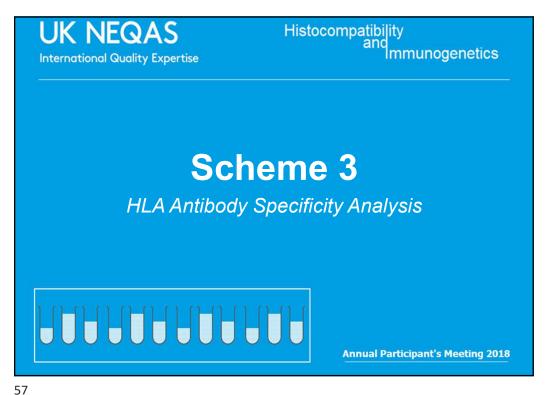
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Mixed v Single Antigen

- · Mixed kits have an 'undetermined' region
- · Scheme requires 'positive' or 'negative' result
 - Test using additional kits
- Known sensitivity difference between mixed and SA beads
 - Could account for not-assessed results
 - Many labs reported testing using single antigen beads
- Result interpretation
- · Samples containing marginal antibodies

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Scheme 3

- *Purpose:* To assess participants' ability to correctly determine the specificity of HLA antibodies
- 10 serum samples sent in two distributions
- *Consensus*: Presence of a specificity is determined by at least 75% of labs agreeing, absence is determined by at least 95% of labs agreeing
- Satisfactory Performance: Making at least 75% of specificities in agreement with the consensus result in a distribution year.

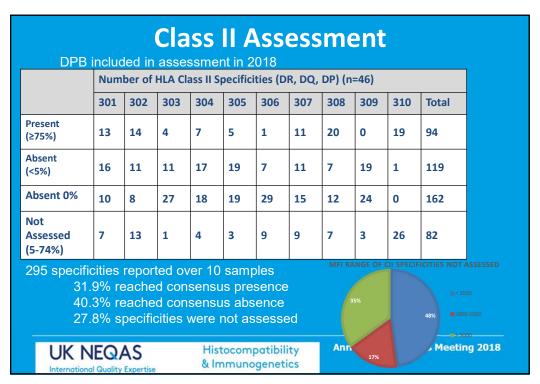
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Class I		2015	2016	2017	2018
Number of Participants (UK&I)		81 (24)	85 (24)	72 (24)	73 (25)
Number with Unsatisfactory	Presence	9 (1)	8 (0)	10 (0)	15 (1)
Performance (UK&I)	Absence	2 (0)	3 (0)	3 (0)	5 (0)
0/ 11	Presence	11.1%	9.4%	13.8%	20.5%
% Unsatisfactory Performance	Absence	2.5%	3.5%	4.2%	6.8%
Class II		2015	2016	2017	2018
Number of Participants (UK&I)		81 (24)	85 (24)	72 (24)	75 (25)
Number with Unsatisfactory	Presence	4 (0)	5 (0)	5 (0)	12 (0)
	Absence	3 (0)	4 (0)	2 (0)	3 (0)
Performance (UK&I)		4.00/	5.9%	6.9%	16.0%
Performance (UK&I) % Unsatisfactory Performance	Presence	4.9%	1 -1	1	

17 John		Cla	ss I	Clas	Class II		
• 17 labs	Lab	Presence	Absence	Presence	Absence	Kit	
(1 UK&I) with	100	64.9%	98.8%	84.0%	95%	Lifecodes	
ID (< 7E0/)	133	73.3%	100%	96.0%	100%	Lifecodes	
JP (<75%)	197	59.1%	94.6%	54.3%	84.9%	No Info	
	212	53.3%	72.5%	47.9%	89.1%	Lifecodes	
	214	47.1%	95.7%	76.6%	95.8%	Lifecodes	
	216	27.1%	98.4%	60.6%	99.2%	Lifecodes	
	218	69.3%	99.6%	76.6%	100%	Lifecodes	
	222	80.9%	59.7%	83.0%	73.9%	No Info	
	229	0%	0%	0%	0%	No Info	
	230	46.2%	83.7%	64.9%	100%	Lifecodes	
	242	56.4%	100%	51.1%	99.2%	One Lambda	
	252	22.2%	94.6%	40.4%	99.2%	Lifecodes	
	268	90.2%	100%	73.4%	100%	One Lambda	
	293	71.6%	95.7%	79.8%	94.1%	One Lambda	
	302	70.2%	76.0%	64.9%	75.6%	Lifecodes	
	392	0%	0%	0%	0%	No Info	
	401	0%	0%	0%	0%	No Info	

	Number of HLA Class I Specificities (n=89)										
	301	302	303	304	305	306	307	308	309	310	Total
Present (≥75%)	33	13	7	23	12	5	23	37	27	45	225
Absent (<5%)	30	44	20	29	41	24	25	16	28	1	258
Absent 0%	11	27	52	17	19	44	18	8	13	4	213
Not Assessed (5-74%)	15	5	10	20	17	16	23	28	21	39	194
7 specificities reported over 10 samples 33.2% reached consensus presence 38.1% reached consensus absence 28.7% specificities were not assessed											



DPB only

	Numb	Number of HLA DPB Specificities (n=19)										
	301	302	303	304	305	306	307	308	309	310	Total	
Present (≥75%)	0	10	0	0	0	0	0	4	0	0	14	
Absent (<5%)	10	1	1	4	7	1	5	4	6	1	40	
Absent 0%	9	6	17	11	12	17	12	10	11	0	105	
Not Assessed (5-74%)	0	2	1	4	0	1	2	1	2	18	31	

2 samples had DPB1 specificities that reached consensus

85 specificities reported over 10 samples

16.5% reached consensus presence

47.1% reached consensus absence

36.4% specificities were not assessed

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DPA and **DQA**

- Labs reported DQA (=53) and DPA (n=44)
- Continue to report DQA and DPA, but these will not be assessed in 2019

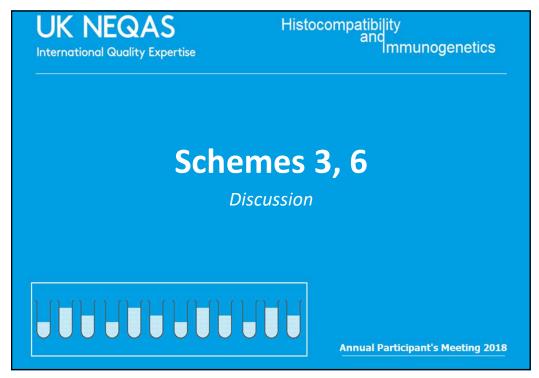
	Numbe	Number of HLA DQA Specificities										
	301	302	303	304	305	306	307	308	309	310	Total	
Present (≥75%)	0	0	0	0	0	0	0	0	0	0	0	
Absent (<5%)	2	6	4	5	3	2	2	0	1	0	25	
Not Assessed (5-74%)	5	3	4	2	2	1	6	10	0	12	45	

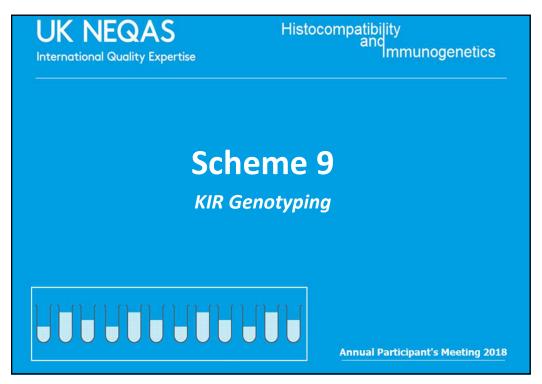
	Number of HLA DPA Specificities										
	301	302	303	304	305	306	307	308	309	310	Total
Present (≥75%)	0	0	0	0	0	0	0	0	0	0	0
Absent (<5%)	0	1	0	3	0	0	0	1	3	0	8
Not Assessed (5-74%)	1	4	0	0	0	0	0	6	0	7	18

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Scheme 9

- Purpose: To assess participants' ability to correctly determine the presence or absence of specific KIR genes
- 10 blood samples sent in two distributions
- Consensus: Genotype is determined by at least 75% of laboratories agreeing the presence/absence of each gene. Where consensus can't be reached a reference type will be used
- **Satisfactory Performance**: Obtaining 9 or more full KIR genotypes in agreement with the consensus result in a distribution year.

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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.
- Also able to report any other KIR polymorphisms they detected for information
- Participants can also report an 'A' or 'B' haplotype for each sample based on the gene content of the sample

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Performance 2018

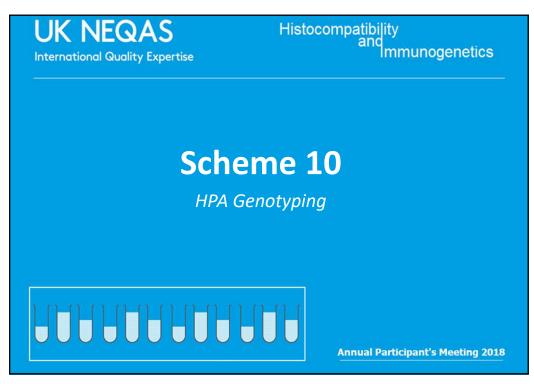
- 3 Errors
- 1 Unsatisfactory Performer
 - 10 samples distributed, must make 9 or more full KIR genotypes in agreement with consensus

	2015 Pilot	2016 Pilot	2017	2018
Number of Participants (UK&I)	7 (1)	11 (2)	8 (3)	9 (1)
Number with Unsatisfactory Performance (UK&I)	N/A	N/A	0 (0)	1 (0)
% Unsatisfactory Performance (UK&I)	N/A	N/A	0%	11.1%

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Scheme 10

- Purpose: To assess participants' ability to correctly determine HPA polymorphisms
- 10 blood samples sent in two distributions
- Consensus: determined by at least 75% of labs agreeing the presence/absence of each allele, a reference result is used for results failing to reach consensus
- **Satisfactory Performance**: Obtaining 9 or more full HPA types in agreement with the consensus/reference result in a distribution year.

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HPA Genotyping

- Participants able to report any of the following: HPA-1, HPA-2, HPA-3, HPA-4, HPA-5, HPA-6, HPA-15
 - 25/37 reported HPA-1, 2, 3, 4, 5 and 15
 - 30/37 labs reported HPA-4
 - 24/37 labs reported HPA-6
- Also able to report any other HPA polymorphisms detected, for information

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Performance 2018

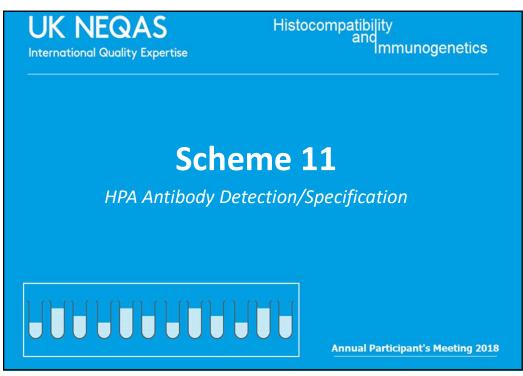
- 3 Errors (RoW only)
- 1 Unsatisfactory Performer

	2015 Pilot	2016 Pilot	2017	2018
Number of Participants (UK&I)	14 (3)	12 (4)	15 (5)	37 (6)
Number with Unsatisfactory Performance (< 100%) (UK&I)	N/A	N/A	1 (0)	1 (0)
% Unsatisfactory Performance (UK&I)	N/A	N/A	6.7%	2.7%

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Scheme 11

- Purpose: To assess participants' ability to correctly determine the presence and specificity of HPA antibodies
- 8 serum/plasma samples sent in two distributions
- Consensus: Presence of a specificity is determined by at least 75% of labs agreeing, absence is determined by at least 95% of labs agreeing
- Satisfactory Performance: Making at least 75% of specificities in agreement with the consensus result in a distribution year.

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Performance 2018

• 1 Unsatisfactory Performer (0 UK & Ireland)

	2017 Pilot	2018
Number of Participants (UK&I)	13 (3)	35 (4)
Number with Unsatisfactory Performance (< 75%) (UK&I)	N/A	1 (0)
% Unsatisfactory Performance (UK&I)	N/A	2.9%

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• NIBSC participants offered to transfer to UK NEQAS for H&I

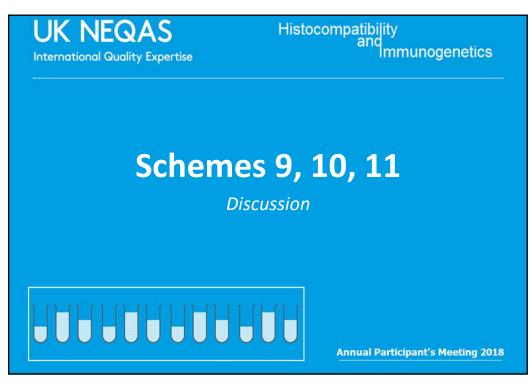
												HPA Ant	tibody ID
			2018 Sample	HPA Detection	HLA Detection	Presence	Absence						
			1	100% Neg	100% Neg	100%	6 Neg						
			2	100% Pos	100% Pos	HPA-5b 96.9%	3.1% HPA-3b, 5a, 15a						
			3	Not Assessed (64.5% Pos)	100% Neg	Not Assessed	3.2% GPIIa/IIIb						
			4	90% Neg	100% Pos	96.79	% Neg						
Result for Methor Sample 3 Detect		mber Labs	5	76.5% Neg	92.9% Neg	Not Assessed	77.1% HPA Neg						
Negative MAIPA		Lans	6	100% Neg	100% Pos	100%	6 Neg						
Positive Lumine			7	100% Pos	100% Pos	HPA-5b 97.1%	HPA-15b 2.9%						
MAIPA			8	94.1% Neg	89.3% Neg	Not Assessed	91.4% HPA Neg						
Lumine	ex/MAIPA 8												

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Quantitative Measurement of HLA Specific Antibodies

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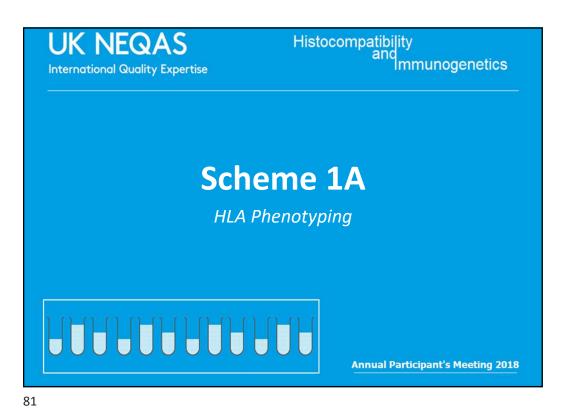
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Dr Martin Rutter

Islet Cell Transplantation: A Clinical Perspective

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Scheme 1A

- Purpose: To assess participants' ability to correctly use serological and supplementary methods to correctly identify HLA specificities
- 10 blood samples sent in two distributions
- Consensus: Presence of a specificity is determined by at least 75% of labs in agreement
- **Satisfactory Performance**: Making 9 or more complete HLA phenotypes in agreement with the consensus result in a distribution year.

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1A Performance 2018

• 6 labs with Unsatisfactory Performance (1 UK&I)

	2012	2013	2014	2015	2016	2017	2018
Number of Participants (UK&I)	22 (10)	30 (10)	42 (9)	45 (9)	41 (7)	38 (6)	38 (6)
Number with Unsatisfactory Performance (< 90%) (UK&I)	1 (0)	0 (0)	8 (0)	4 (0)	3 (0)	1 (0)	6 (1)
% Unsatisfactory Performance	4.5%	0.0%	19.0%	8.9%	7.3%	2.6%	15.8%

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2018 Incorrect Assignments

Sample	Lab Number	Consensus	Report
1A 02	62	DQ2, DQ8	DQ2, DQ7
	181		DRB1*04:01, 13:01; DQB1*06:03, 03:01
1A 03	286	A2, A25; B51, B55; Cw9, Cw14; DR4, DR13; DQ6, DQ7	A*02:01:01:01, A*25:01:01:01; B*51:01:01:01, B*55:01:01; C*03:03:01:01, C*14:02:01:01; DRB1*04:01:01:02, DRB1*13:01:01:01; DQB1*06:03:01:01, DQB1*03:01:01:01
	62, 163		DR1, -
	181		DRB1*01:01, DRB1*01:03; DQB1*05:01, -
	194		A2, A69
	225	AO AGO, D40 DEZ, OE	B18, B58
1A 04	286	A2, A68; B18, B57; Cw5, Cw6; DR1, DR103; DQ5, -	A*02:01:01:01, A*68:02:01:01; B*18:01:01:02, B*57:01:01:01; C*05:01:01:02, C*06:02:01:01; DRB1*01:01:01, DRB1*01:03:01; DQB1*05:01:01:02, -
315, 401			DR1, -
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2018 Incorrect Assignments

Sample	Lab Number	Consensus	Report
1A 05	159, 401	B7, B61	B7, B40
	223		A*02 , A25
1A 09	315	A2,A25; DR4, DR7; DQ2, DQ8	A*02, A25; DRB1*04, DRB1*07; DQB1*02, DQB1*03:02
	223	AQ AQ DZ DQQ	A*02, A*03; B*07 , B38
1A 10	315	A2, A3; B7, B38; DQ6, -	A*02, A*03; B*07 , B38; DQB1*06, -

17/380 (4.5%) incorrect HLA types in 2018 reported by 10 labs;

5 reports of incorrect broad/split specificity

8 reports of molecular based nomenclature

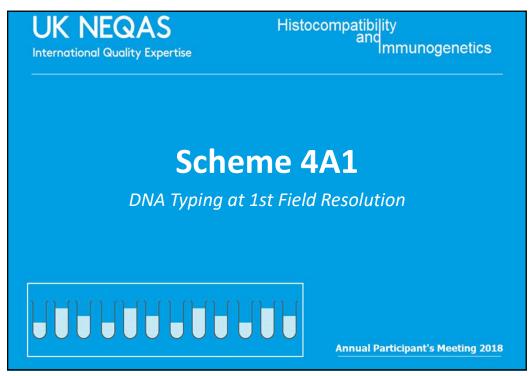
4 reports of missed specificity (i.e. reported blank)

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Scheme 4A1

- Purpose: To assess participants' ability to correctly determine HLA types at the 1st field
- 10 blood samples sent in two distributions
- Consensus: Presence of an allele is determined by at least 75% of labs agreeing, a reference result is used for those failing to reach consensus and for DPB1 assessment
- Satisfactory Performance: Making at least 9 full HLA types in agreement with the consensus/reference result in a distribution year.

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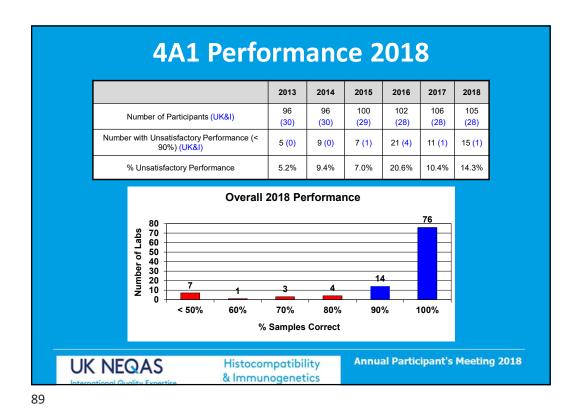
87

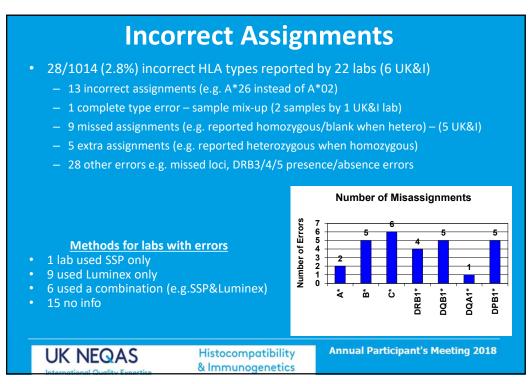
Changes Introduced in 2018

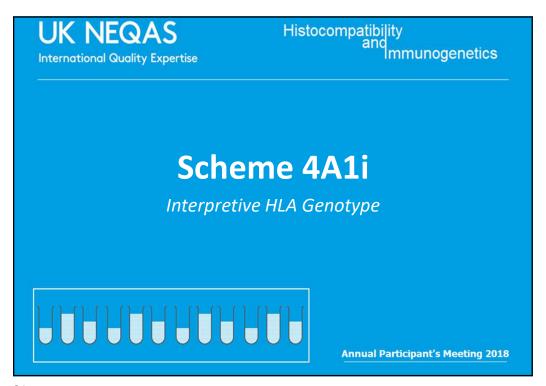
- Participants can register for DPB1 assessment at low/medium resolution (i.e. SSP/SSO results)
- Assessed against a reference type
- Report DPB1 alleles at the resolution applicable to clinical need
- Strings of alleles not penalised if reference allele is present

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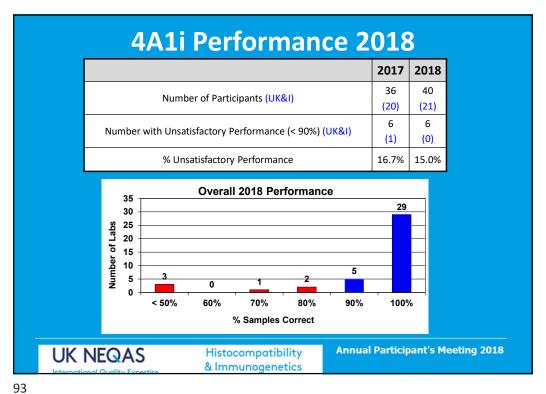


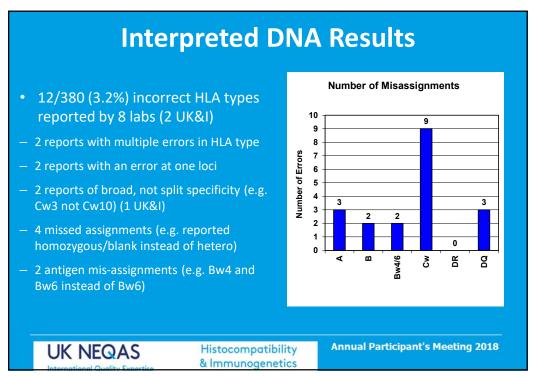
Scheme 4A1i

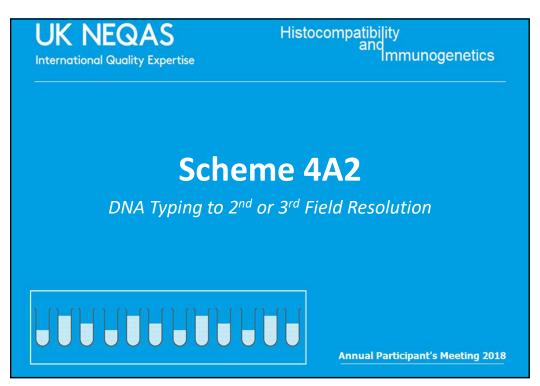
- Purpose: To assess participants' ability to correctly interpret their 4A1 result to the 'split' specificity level
- 10 blood samples sent in two distributions
- Consensus: HLA type is determined by 75% of labs agreeing each specificity, a reference result is used for results failing to reach consensus
- Satisfactory Performance: Making at least 9 full HLA types in agreement with the consensus/reference result in a distribution year.

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Scheme 4A2

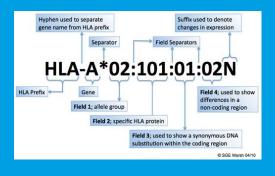
- *Purpose:* To assess participants' ability to correctly determine HLA type to the 2nd or 3rd field
- 10 blood samples sent in two distributions
- Consensus: Genotype is determined by 75% of labs agreeing each allele. If consensus is not reached a reference result will be used
- Satisfactory Performance: Making 9 or more full HLA types in agreement with consensus/reference genotype in a distribution year

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Introduced in 2018

 Participants can register for assessment of 3rd field results in Scheme 4A2



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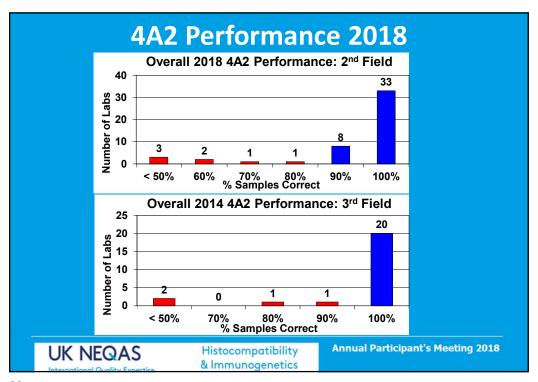
4A2 Performance 2018

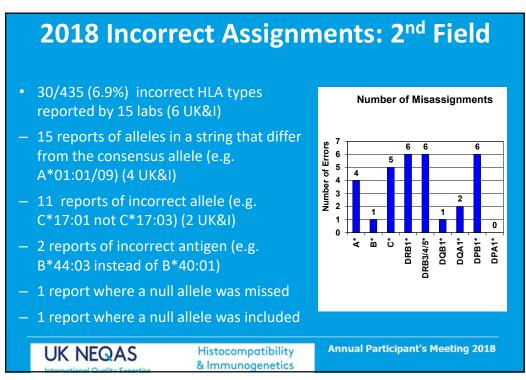
• 9 Unsatisfactory Performers (2 UK & Ireland)

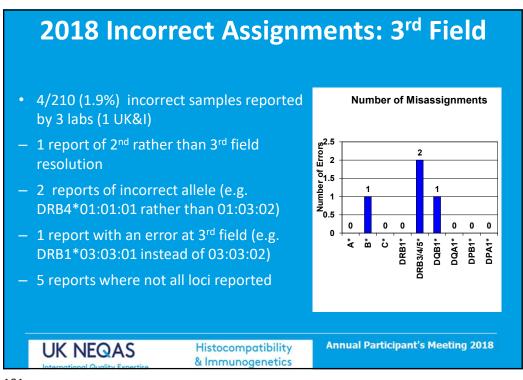
	2014	2015	2016	2017	2018
Number of Participants (UK&I)	59 (21)	59 (<mark>20</mark>)	63 (<mark>21</mark>)	66 (<mark>21</mark>)	63 (<mark>20</mark>)
Number with Unsatisfactory Performance (< 90%) (UK&I)	5 (1)	7(1)	8 (2)	4 (0)	9 (2)
% Unsatisfactory Performance	8.5%	11.9%	12.7%	6.1%	14.3%

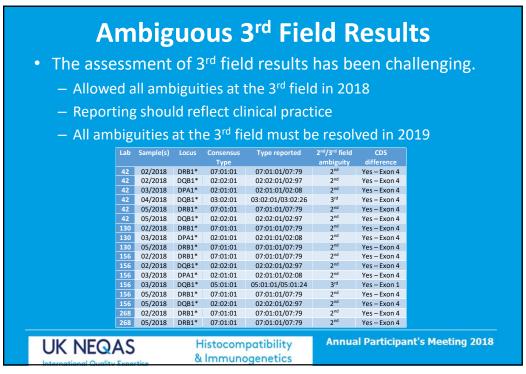
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Clinical Reporting

- Resolution being reported should reflect clinical practice
- NEQAS asked participants what level of resolution labs report at clinically 17 (27%) responses (5 from UK&I, 12 from RoW):
 - What clinical services do you provide and what's the highest resolution do you report at clinically?

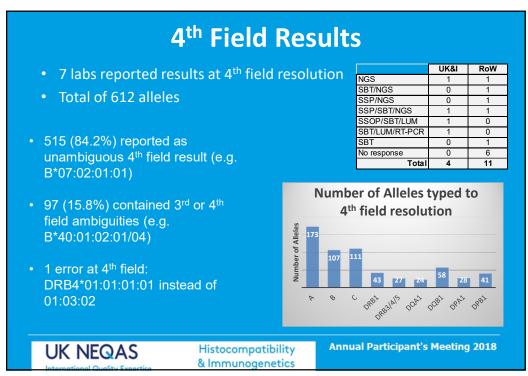
	Solid Organ Transplant	HSCT	Disease Association	Specify
First Field	6	0	1	3 (HLA Selected Platelets)
Second Field	5	12	12	4 (Refractoriness to Platelet Transfusions and Special Requests)
Third Field	0	3	0	1 (Research Projects only)
No Response	6	2	4	9

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New for 2019

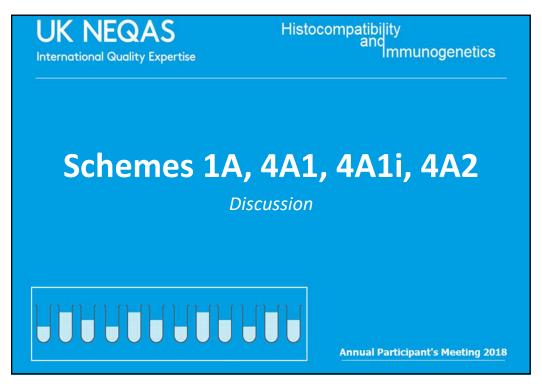
- More stringent assessment of 3rd field resolution
 - Participants must sequence all exons to resolve all ambiguities
 - E.g. DRB1*07:01:01/07:79 or DQB1*03:02:01/03:02:26 would be unacceptable as ambiguities in exon 4 have not been resolved
- Results at the 4th field can be reported, but will not be assessed

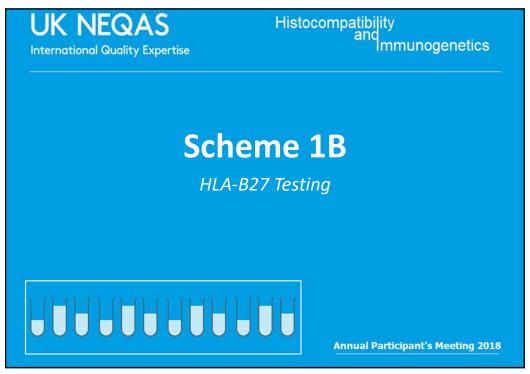
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HLA-B27 Testing

- Purpose: To assess ability to correctly determine HLA-B27/2808/B*27 status
- 10 random donor samples sent in five distributions
- *Consensus*: B27 status determined by at least 75% agreement on presence or absence of HLA-B27
- **Satisfactory performance**: Making 10 reports in agreement with consensus in a distribution year

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2018 Incorrect Assignments									
Sample	Result	Lab Number	Technique	HLA Type	Lab Identified Cause				
1B01	False Neg	106*, 256, 279	Serological	B27, B47	No reply Low lymphocyte reactivity				
1B02	False Neg	67, 83, 106*, 256, 279	Serological	B27, B60	Kit Ambiguity No response Transcription Error Low lymphocyte reactivity				
1B05	False Neg	10*, 372	Serological	B27, B65	Delay in testing causing poor viability No response				
1B06	False Pos	106*	*Unknown	B38, B50	No response				
1B09	False Pos	10*, 372	Serological	B27, B65	Delay in testing causing poor viability No response				
1B10	False Pos	106*	*Unknown	B38 B50	No response				
6/10 samples distributed were HLA-B27 positive 14 errors: 10 False Neg, 4 False Pos									
UK NEQAS International Quality Expertise Histocompatibility & Immunogenetics			Annual Particip	oant's Meeting 2018					

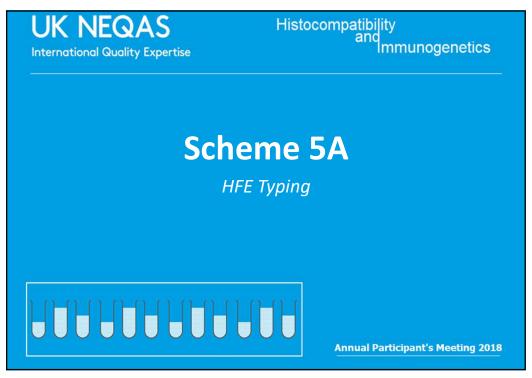
Performance 2018

• 10 Unsatisfactory Performers (3 UK & Ireland)

	2013	2014	2015	2016	2017	2018
Number of Participants (LIKS)	96	107	115	123	127	133
Number of Participants (UK&I)	(47)	(51)	(54)	(54)	(52)	(54)
Number with Unsatisfactory Performance (< 100%) (UK&I)	4 (1)	4 (2)	8 (4)	15 (6)	7 (2)	10 (3)
	4.2%	3.7%	6.9%	12.2%	5.5%	7.5%
% Unsatisfactory Performance (UK&I)	(2.1%)	(3.9%)	(7.4%)	(11.1%)	(3.8%)	(5.6%)

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Scheme 5A

- Purpose: To assess participants ability to correctly determine HFE mutations
 - 3 mutations assessed:
 - Codon 63: Histidine63Aspartic acid (H63D)
 - Codon 282: cysteine282tyrosine (C282Y)
 - Codon 65: Serine63Cysteine (S65C)
- 10 random donor samples sent in two distributions
- *Consensus*: determined by at least 75% agreement with the consensus/reference result
- **Satisfactory Performance**: 10 reports in agreement with consensus in a distribution year

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Scheme 5A Performance

• No Unsatisfactory Performers

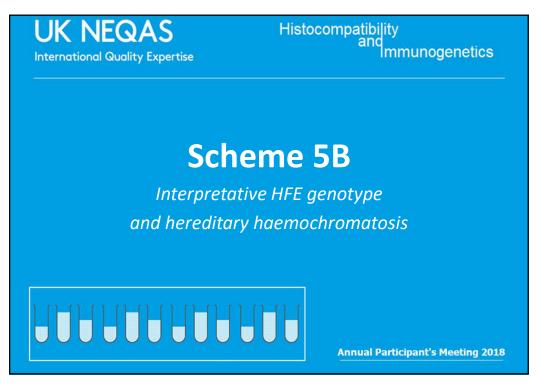
	2013	2014	2015	2016	2017	2018
Number of Participants (UK&I)	58 (10)	59 (50)	60 (49)	58 (49)	56 (42)	58 (44)
Number with Unsatisfactory Performance (< 100%) (UK&I)	2 (2)	2 (2)	0 (0)	3 (2)	3 (2)	0 (0)
% Unsatisfactory Performance	3.9%	3.4%	0%	5.2%	5.3%	0%

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Scheme 5B

- Purpose: to assess participants' ability to make an accurate, clear and concise clinical report
- Twice a year, 2 clinical scenarios:
 - HFE genotype provided, together with various pieces of clinical information
- Reports must be identical in format to that used for routine clinical reporting in participants' laboratories
- Interpretative criteria expected to be covered by the reports are identified and agreed by the expert assessors.
 - Penalty points awarded, if >50% of the available penalty points are awarded then performance is unacceptable

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Performance

2018 – all 4 scenarios

5 penalty points per scenario, 20 in total

3 labs got 1 penalty point

4 labs got 2 penalty points

7 labs got 3 penalty points

2 labs got 5 penalty points

2 labs got 6 penalty points

1 lab got 7 penalty points

1 lab got 8 penalty points

1 lab got Multiple penalty points (sent wrong report)

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Scheme 5B Performance

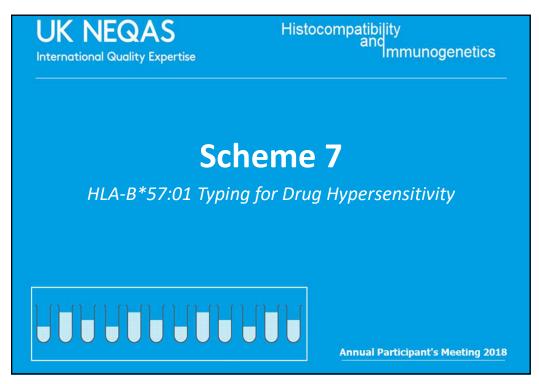
• 1 Unsatisfactory Performer (1 UK&I)

	2012	2013	2014	2015	2016	2017	2018
Number of Participants	21	19	20	18	19	20	21 (18)
Number with Unsatisfactory Performance	3	3	5	0	0	0	1 (1)
% Unsatisfactory Performance	14.3%	15.8%	25.0%	0%	0%	0%	4.8%

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Scheme 7

- *Purpose:* To assess participants' ability to correctly determine HLA-B*57:01 status.
- 10 random donor samples sent in two distributions
- *Consensus*: determined by at least 75% agreement with the consensus/reference result
- Satisfactory Performance: Making ten sample reports in agreement with the consensus HLA-B*57:01 status in a distribution year.

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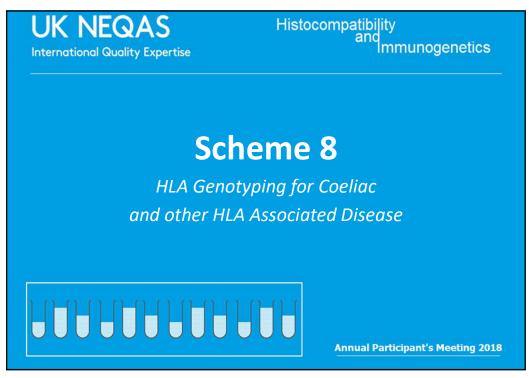
Scheme 7 Performance

- 7/10 samples distributed were HLA-B*57:01 positive
- 2 labs with unacceptable performance
 - Both did not return results

	2013	2014	2015	2016	2017	2018
Number of Participants (UK&I)	47	56	62	62	64	67
Number of Participants (ORM)	(23)	(24)	(26)	(25)	(26)	(27)
Number with Unacceptable Performance (< 100%) (UK&I)	O (O)	1 (0)	0 (0)	1 (1)	4 (1)	2 (0)
% Unsatisfactory Performance	0.0%	1.8%	0.0%	1.6%	6.3%	3.0%

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Scheme 8

- Purpose: To assess participants' ability to correctly determine HLA type associated with various diseases e.g. coeliac disease and narcolepsy
- 10 blood samples sent in two distributions
- Consensus: determined by assessment against the reference result
- **Satisfactory Performance**: Making ten sample reports in agreement with the reference genotype in a distribution year.

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Scheme 8 Performance

• 14 Unsatisfactory Performers (4 UK & Ireland)

	2013	2014	2015	2016	2017	2018
Number of Participants (LIKS)	19	21	30	39	45	52
Number of Participants (UK&I)	(8)	(9)	(8)	(8)	(9)	(10)
Number with Unsatisfactory Performance (< 100%) (UK&I)	2 (1)	3 (2)	8 (0)	8 (3)	15 (2)	14 (4)
% Unsatisfactory Performance	10.5% (12.5%)	14.3% (22.2%)	26.7% (0%)	20.5% (37.5%)	33.3% (22.2%)	26.9% (40%)

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2018 Unacceptable Performance by Disease

Disease	HLA Association	Number of Participants	No. of Participants with Unacceptable Performance
Coeliac	DQ2, DQ8, DQA	50	11
Narcolepsy	DQB1*06:02	21	3
Actinic Prurigo	DRB1*04:07	4	1
Birdshot	A*29	9	1
Retinopathy			
Behçet's	B*51	6	0
Rheumatoid	DRB1*04	2	0
Arthritis			
Diabetes	DR3. DR4	4	1

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Sample	Lab	Result	HLA Type	Error
	85	Negative for DQ2 and DQ8		Interpretation issue
	185	DRB1*04, DRB1*07, DQA1*02:01, DQA1*03:02, DQB1*02:02, DQB1*03:01		Transcription error
	255	HLA-DQ2: NEG HLA-DQ8: NEG	DRB1*04:01,	Interpretation issue
801	801 278 Beta-subunit HLA DQ8, HLA DQ8 epnotype DQA1*02:01, DQA1*02	DQB1*02:02, DQB1*03:01;	No response	
	279	DRB1 *04; *07, DQB1 *02:02; *03:01 DQA1 *02:01; *03:01		Technical issue
	319	DQ2: NEG DQ8: NEG]	Interpretation issue
	78 DQ2 and DQ8 ABSENT			Technical issue
802	185	DRB1*03, DRB1*04, <i>DQA1*03:02</i> , DQA1*05:01, DQB1*02:01, DQB1*03:01	DRB1*03:01/124/132/137, DRB1*04:08; DQB1*02:01, DQB1*03:01; DQA1*03:03, DQA1*05:01	Transcription error
	279	DRB1 *03; *04 DQB1 *02:01; *03:01 DQA1 *03:01; *05:01	- DQA1*05:01	Technical issue
803	159	DQA1*01:01-05, *05:05 DQB1*03:01, *05:01	DRB1*11:01/97, DRB1*15:01/141; DQB1*03:01, DQB1*06:02; DQA1*01:02/11, DQA1*05:05	Kit issue
804	159	DQA1*01:01-05, *05:05 DQB1*03:01, *05:01	DRB1*01:03, DRB1*13:01/117/190/215; DQB1*03:01, DQB1*06:03; DQA1*01:03, DQA1*05:05	Kit issue

Sample	Lab Number	Result	HLA Type	Error		
806	86	Coeliac disease-associated HLA alleles present: DOB1*03:01 DR81*13:01, DR81*13:01, DR81*13:03; DOA1*05:05 DOA1*05:14. A DO8: PRESENT - HLA DOB1*03*05*103, DOA1*01:03, DOA1*05:05 DOA1*05. HLA DO8: ABSENT		Kit issue		
	123	DQB1*07, DQB1*03:03		No response		
808	319	DQ2: NEG DQ8: NEG (A1*05: NEG, B1*02: POS, B1*0302: NEG)	DRB1*07:01, DRB1*09:01; DQB1*02:02, DQB1*03:03; DQA1*02:01, DQA1*03:02	No response		
	129	DRB1*0401, -	DRB1*04:01. DRB1*07:01:	Interpretation issue		
809	319	DQ2:NEG, DQ8:POS (A1*05: NEG, B1*02: POS, B1*0302: POS)	DQB1*02:02, DQB1*03:02; DQA1*02:01, DQA1*03:01	No response		
810	17	HLA-DQA1*05:01; DQB1*02:01 Positive HLA-DQA1*03; DQB1*03:02 Negative	DRB1*04:01, DRB1*15:01; DQB1*03:01, DQB1*06:02;	Technical issue		
	279	DRB1*04; DQB1*03:01,*05:01; DQA1*03:01	DQA1*01:02, DQA1*03:03	Kit issue		
18 incorrect assignments in 2018 (4 UK&I), 17/18 in Coeliac Disease – Also 2 labs did not report any results for samples 801-805/2018						

Participant Issues

- CAPA responses show some common problems:
 - sample handling or technical error 2 labs (18%)
 - misinterpretation of a correct HLA type 3 labs (27%)
 - ambiguous kit results or resolution issue 4 labs (37%)
 - 2 labs (18%) did not respond
- Labs struggled with the interpretation of a correct HLA type
 - a lab reported that DQ2 was present or "Half DQ2 positive" when they had detected HLA-DQB1*03:01, DQA1*05:05 as they wanted to report they had detected the DQA1*05 subunit.

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Participant Issues

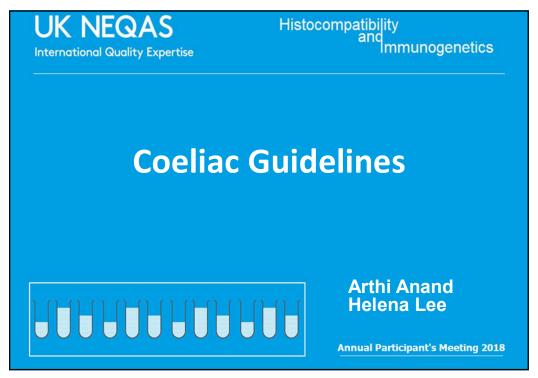
 Commercial kits also been to be the cause of some issues due to deficiencies in resolution and the interpretation of results:

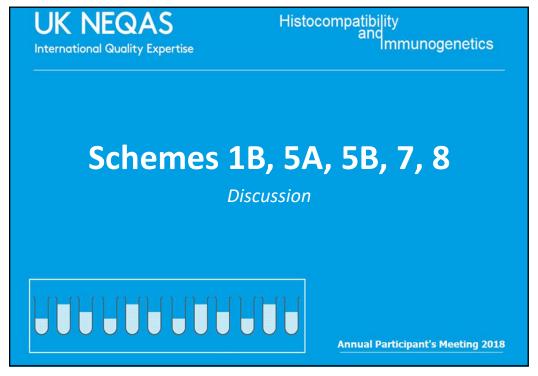
	Mix DQA1*05	Mix DQB1*02	Mix DQB1*03:02	HLA-Genotype
	-	2	+	DQ8
	100	(+	DQ8
E	+		+	DQ8
Signa	+	+	+	DQ2 and DQ8
	+	+	-	DQ2
	+	-	-	A genetic predisposition for
	100	+	-	Coeliac Disease is unlikely
	-	-	-	

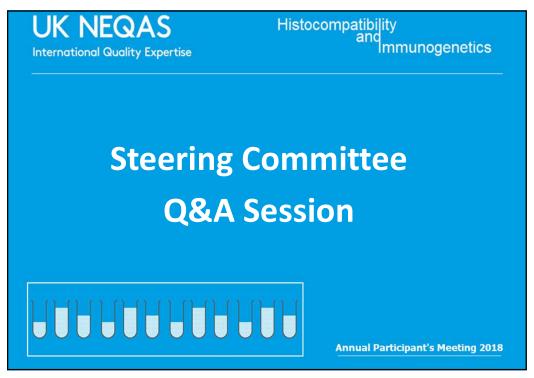
- This table taken from a commercial kit insert shows how misleading it can be especially for labs with limited H&I experience
- · Currently interpretative comments are collected but not assessed
- · Examples from UK labs for the same sample:
 - This patient is DQ2.2 positive, heterozygous. This patient is DQ2 positive which is associated with Coeliac Disease.
 - This individual does not carry the HLA-DQ variants associated with Coeliac Disease.
 - This patient is Heterozygous POSITIVE for HLA-DQ2 (but is DQA1*05 NEGATIVE) and NEGATIVE for HLA-DQ8 (DQA1*03, DQB1*03:02). Patients with this genotype have a LOW RISK of predisposition to Coeliac disease.

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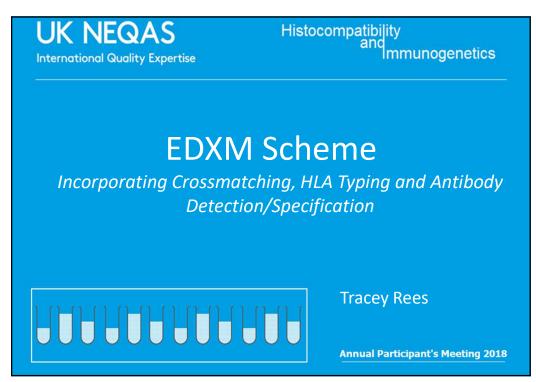
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	2013	2014	2015	2016	2017	2018
	2013	0	0	2016	2017	2018
Scheme 1A					-	
Scheme 1B	1	2	4	6	3	3
Scheme 2A Without DTT	2	6	2	3	6	7
Scheme 2A With DTT	N/A	N/A	0	6	8	′
Scheme 2B	0	2	3	1	1	2
Scheme 3 Class I	1	0	1	0	0	1
Scheme 3 Class II	0	0	0	0	0	0
Scheme 4A1	0	0	1	4	1	1
Scheme 4A1i	N/A	N/A	N/A	N/A	1	0
Scheme 4A2	2	1	1	2	1	2
Scheme 5A	2	2	0	2	2	0
Scheme 6	0	1	3	4	0	0
Scheme 7	0	0	0	1	1	0
Scheme 8	1	2	0	3	2	4
Scheme 9	N/A	N/A	N/A	N/A	0	0
Scheme 10	N/A	N/A	N/A	N/A	0	0
Scheme 11	N/A	N/A	N/A	N/A	N/A	0
To	tal 9	16	15	32	15	21



'Whole Process' EQA

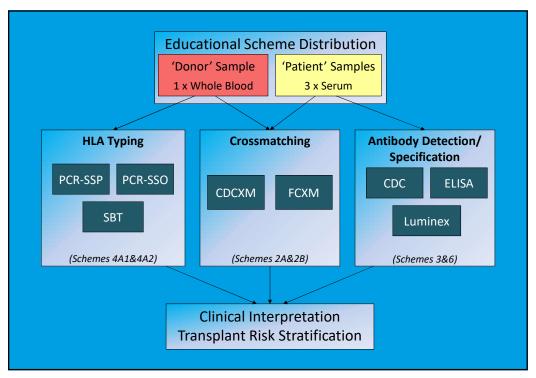
- UK NEQAS for H&I
 - Scheme 1A, 4A1, 4A2 HLA Typing
 - Scheme 6 HLA Antibody Detection
 - Scheme 3 HLA Antibody Specification
 - Schemes 2A and 2B Crossmatching
 - Solid Organ Interpretive Scenarios (Paper based)

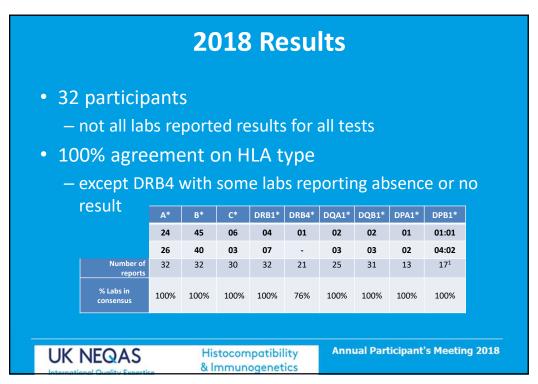
"Schemes should relate more closely to clinical scenarios rather than testing individual test assays."

- Clinical decision making based on results from multiple assays
- Each assay only gives part of the picture
- Results from one assay can influence the interpretation of another
- Variation between centres
 - Sensitivity/cut offs
 - Assay repertoires

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Serum 1 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Positive	84%	5 labs reported negative (143, 190, 238, 260, 262)
HLA Class II Antibodies	Positive	100%	
DSA	Yes	97% (28/29)	Huge range in MFI reported e.g. DR4 3,287-17,567 DSA included A24, Cw6, DR4, DR7, DQ8, DR53 and DQA
CDC XM	Negative	100% (15/15)	
FCXM T Cell	Not Assessed	65.4% (17/26)	65.4% positive, 34.6% negative
FCXM B Cell	Positive	86.4% (19/23)	Lab 14, 112 reported negative, Lab 28, 54 reported equivocal
Transplant Risk	Contraindication /High	62% (18/29)	11 labs reported medium risk (9, 11, 24, 38, 48, 54, 62, 112, 149, 238, 262)

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Serum 2 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Positive	100%	
HLA Class II Antibodies	Positive	100%	
DSA	Yes	96.6% (28/29)	Huge range in MFI reported e.g. DQ2 9,025-34,845 DSA included B45, DR7, DQ2, DQ8, DR53, DPB1*01:01, DPB1*04:02, DQA and DPA
CDC XM	B cell Positive T cell Negative	100% (15/15) 92.3% (12/13)	PBL –DTT 80% Positive, +DTT Not Assessed (57% Positive)
FCXM T Cell	Negative	84.6% (22/26)	4 Labs reported Positive (Lab 11, 19, 20 and 38), 1 reported Equivocal (Lab 122)
FCXM B Cell	Positive	100% (25/25)	
Transplant Risk	Contraindication /High	97% (28/29)	One Lab (195) reported medium risk

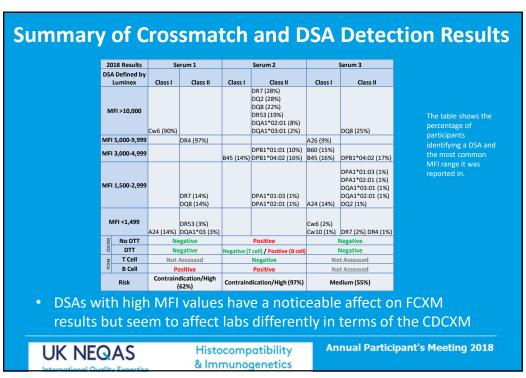
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Serum 3 Results Result % Consensus Comments 94% **HLA Class I Antibodies** Positive **HLA Class II Antibodies** Positive 100% DSA included A24, A26, B60, B45, Cw6, Cw10, DR4, DSA 86.2% (25/29) Yes DR7, DQ2, DQ8, DPB1*04:02, DQA and DPA CDC XM Negative 100% FCXM T Cell Not Assessed 66.7% (18/27) 66.7% reported Negative, 33.3% Positive FCXM B Cell Not Assessed 58.3% (14/24) 58.3% reported Negative, 41.7% Positive 5 labs reported a low risk (15, 23, 34, 39, 149, 194, Transplant Risk Medium Risk 55% (16/29) 260), 3 a high risk (28, 48, 58) and 5 a contraindication (122, 162, 195, 220, 284) **UK NEQAS Annual Participant's Meeting 2018** Histocompatibility

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Benefits

- Participants able to:
 - Monitor performance of multiple techniques within a single scheme
 - Make clinical interpretations based on their own results
 - Compare local policies for clinical assessment
- Educational
 - Monitor concordances
 - Review variations
 - Trainees
- Competency
 - Laboratory staff
 - Consultants

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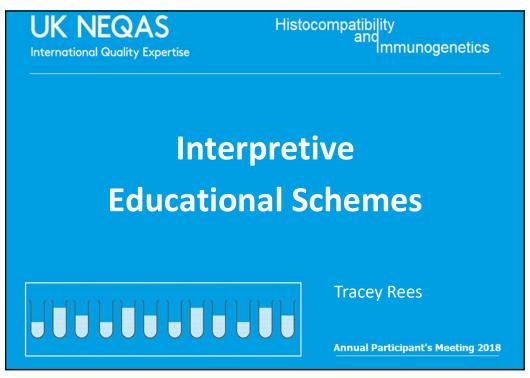
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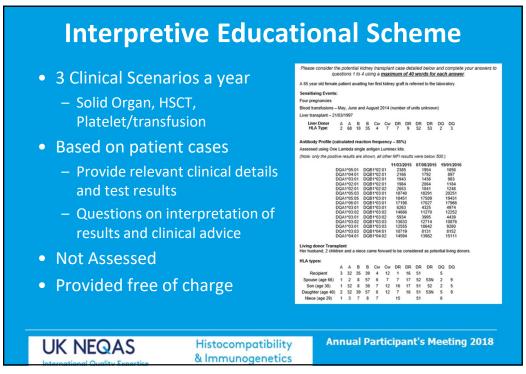
Future Considerations

- Could the scheme form the basis of future formal EQA scheme design?
- Workload
 - Participants
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- Assessment complexity
 - Consensus?
 - Incorrect result, correct interpretation?

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Clinical Scenarios

	Solid Organ	нѕст	Platelet/ transfusion
2013	Live kidney transplant	Matched unrelated donor selection	N/A
2014	Deceased kidney transplant	Mismatched unrelated donor selection	N/A
2015	Cardiothoracic transplant	Paediatric cord blood donor selection	Platelet refractory
2016	Deceased donor virtual XM	Donor search for patient with unusual HLA type	Platelet refractory
2017	Cardiothoracic transplant	Haploidentical donor selection	TRALI
2018	Live kidney transplant	Unrelated donor selection permissive/non-permissive	NAIT

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Scenario 1- Kidney Transplant Case

Offer of kidney transplant to your centre and selection of recipients

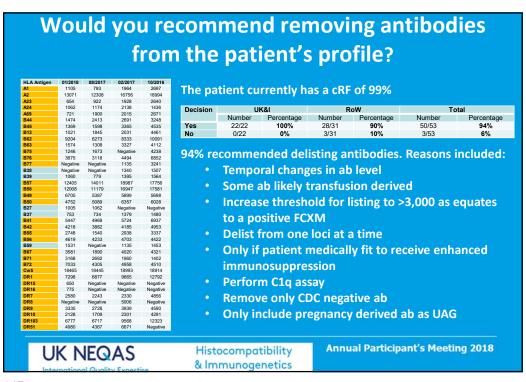
Provided

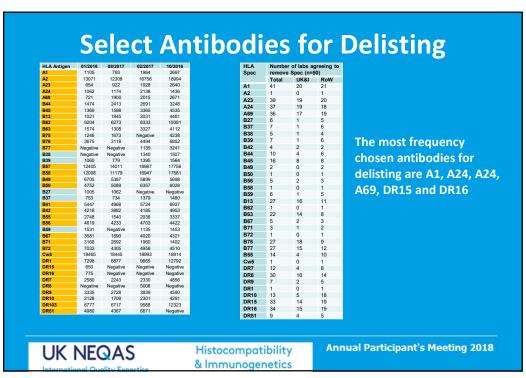
- Patient HLA type and ABO (O)
- HLA antibody profile
- Information on potential recent sensitising events
- Crossmatching results
- 53 returns (22 UK&I)

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Would you perform additional testing or give recommendations to increase the chance of deceased donor transplantation?

Decision	U	UK&I		oW	Total		
	Number	Percentage	Number	Percentage	Number	Percentage	
Yes	20/22	91%	28/31	90%	48/53	91%	
No	2/22	9%	3/31	10%	5/53	9%	

91% of respondents answered that they would perform additional testing. Examples of which included:

- EDTA treat serum samples
- Test using alternative method e.g. Lifecodes or C1q
- Perform 3rd party crossmatches
- Eplet study or HLA Matchmaker
- Consider live donor options
- · Check ABO ab titres for ABOi transplant consideration
- Review local DCD/Fast Track local policy for priority allocation
- Plasma exchange/plasmapheresis
- · Allow repeat mm to partner
- · Perform an autologous crossmatch

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Based on the results given what would you recommend?

Potential	ABO	HLA type	Current CDC XM Result	Current FCXM Result
Donor				
Niece	Α	A2, A68; B44, B51;	PBL Positive (scored "6"	T Cell (LCS 232)
		Cw5, Cw14; DR4,	with and without DTT)	B cell (LCS 264)
		DR13; DQ6, DQ7	B cell Positive (scored "4"	Strong Positives
			with and without DTT)	

Recommendations:

- Discontinue transplant work up, high risk ABOi and HLAi
- Transplant veto as CDCXM and FCXM positive
- · Perform autologous crossmatches, discuss at MDT meeting
- · Repeat pregnancy haplotype mismatch with antibody, poor prognosis
- · Patient unlikely to respond to desensitisation
- Enter pair into the Kidney Sharing Scheme

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What antibody profile would you use to register the pair in the kidney sharing scheme?

		UK&I (n=22)		RoW (n=31)		Total	%
		Number	Percentage	Number	Percentage	(n=53)	70
Option 1	Same profile as original deceased donor profile	0	0%	4	13%	4	8%
Option 2	Modified deceased donor profile	16	73%	20	65%	36	68%
Option 3	Other	6	27%	7	22%	13	24%

Registration with the a reduced UAG profile was the most popular option (68%). The reasons cited included:

- To increase the chances of getting a match
- Use a conservative approach and delist in subsequent matching runs
- Local policy is to list of ab with MFI >3,000
- Patient has limited vascular access, may need to take additional risks and delist further
- Option to use pre and post transplant desensitisation

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Predict the CDCXM and FCXM result for the new donor

Some antigens were removed from the patient's unacceptable antigen profile and a match was identified in the kidney sharing scheme (mm in red, patient DP type unknown)

ABO O A1, A24; B8, B51; Cw1, Cw7; DR11, DR17; DR52; DQ2, DQ7; DPB1*02:01, -

		Predicted Crossmatch Result									
	P	ositive			Negative			Other			
	UK&I	RoW	Total	UK&I	RoW	Total	UK&I	RoW	Total		
CDC	0	0	0	22	30	32	0	0	0		
Flow Cytometry	1	5	6	11	17	28	10	8	18		

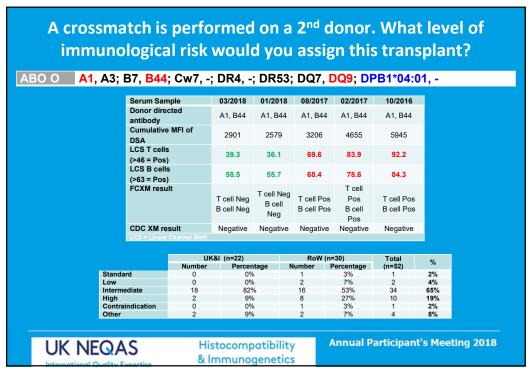
Most respondents predict the CDCXM and FCXM will be negative. The reasons cited included:

- Cumulative DSA MFI not expected to cause a positive result
- Possible historic positive, current negative crossmatch
- Patient has A1 and A24 DSA these antigens don't share any antibodyverified eplet with the sensitising event ab
- Wet crossmatch recommended

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Serum Samp Donor direct antibody Cumulative DSA LCS T cells (>46 = Pos) LCS B cells	ted	03/2018 A1, 24 2867	01/201 A1, 24 2167	A	3/ 2017 41, 24 1967	02/201 A1, 24	A1,	24	
DSA LCS T cells (>46 = Pos)	MFI of		2167		1967	4102	/11	33	
(>46 = Pos)						7102	410	,,	
LCS B cells		40.1	38.1	:	35.6	68.1	88	.2	
(>63 = Pos)		58.5	59.7		55.5	71.1	82		
FCXM result		T cell Neg B cell Neg	T cell No	eg Bo	ell Neg ell Neg	T cell P B cell P	os B cell	Pos	
CDC XM res	ult hannel Shift	Negative	Negativ	e Ne	egative	Negativ	e Nega	itive	
respondents state		UK&I (n=22)	centage		W (n=30)	entage	Total (n=52)	%	
Standard	1		4%	0		1%	1	2%	
Low	3		14%	4		3%	7	13%	
Intermediate	18		82%	20		7%	38	73%	
100.00			0%	5 1		7% 8%	5 1	10% 2%	
High Control diseases						70	- 1	270	
Contraindication Other	0		0% 0%	0	(1%	0	0%	
Contraindication	ded: SSHI Gu		0%		ch, lov	v leve	l DSA		
Contraindication Other asons cited including Following BTS/E	ded: SSHI Gu	ric posit	0%	ssmato	ch, lov	v leve			1 eeting



What level of immunological risk would you assign this transplant?

Most respondents stated this would be a Intermediate risk transplant.

The reasons cited included:

- BSHI/BTS Guidelines categorise historic positive current negative T/B cell FCXM (CDCXM negative) due to current IgG class I DSA as intermediate risk.
- The risk of hyperacute rejection is low. However risk of accelerated antibody mediated rejection due to memory response is higher due to historically positive Flow crossmatch.
- DSA is due to a known sensitisation event, pregnancy.
- Transplant possible with augmented immunosuppression and posttransplant monitoring.
- Recent cumulative DSA is ~3,000MFI, historically ~6,000

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What clinical advise would you give?

Most common answers included:

- BSHI/BTS Guidelines state transplant is recommended given the anticipated loss of vascular access
- Clinical caution with proactive use of immunosuppression and posttransplant monitoring
- Discuss with MDT if sufficient time to enter another cycle of the sharing scheme

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Scenario 2 – HSCT Scenario

- 42 year old female with high-risk ALL
- Blood group: O Rh Positive
- CMV status: Negative
- HLA Type:

A*02:01, A*24:02; B*07:02, B*51:01; C*02:02, C*07:02; DRB1*15:01, -; DQB1*06:02, -; DPB1*03:01, DPB1*04:01

- Patient only has half-siblings
- Unrelated donor search performed

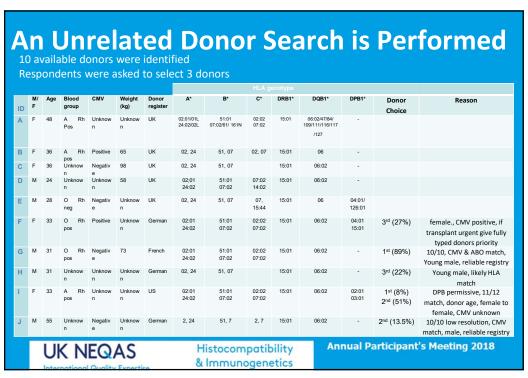
37 responses received

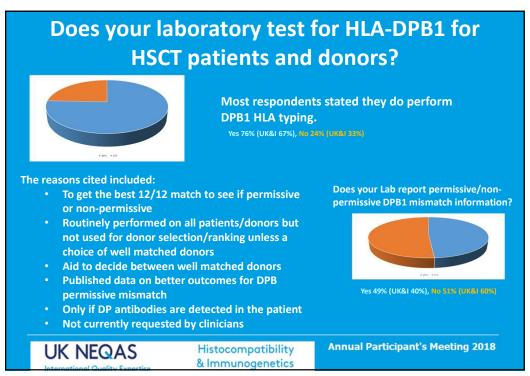
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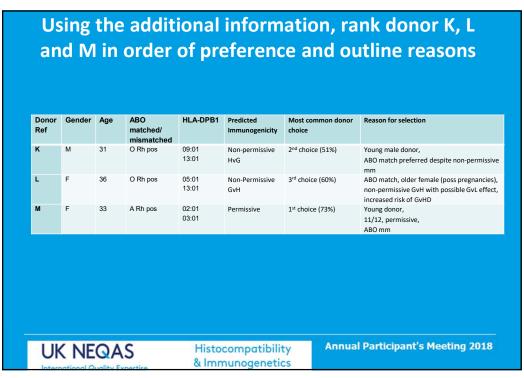
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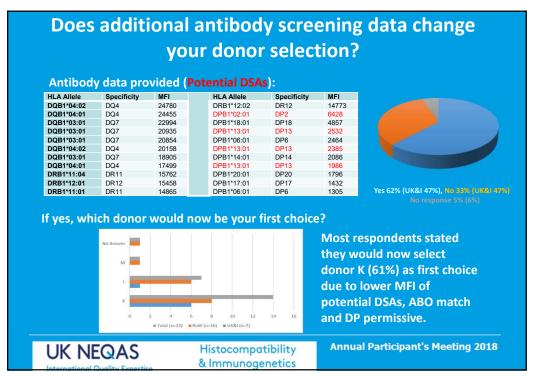
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Comment on the likelihood of finding a donor Summary of responses from UK and Ireland (UK&I) Likely to find a 10/10 matched donor There is a high likelihood of finding a matched unrelated donor - although maybe not an optimal donor for non-HLA reasons as the number found would be quite small. Would be a challenging search due to rare/intermediate B/C association and homozygous DRB1/DQB1. HLA-B*51:01 is associated with several different HLA-C alleles (e.g. C*01:02, C*14:02, C*15:02 and C*16:02) and is less frequently associated with C*02:02, making it less likely a 10/10 match will be found, particularly if registry HLA-C data is not provided. HLA-C typing can be missing from some donors, this makes it difficult to predict if these donors are potentially fully matched or mismatched at HLA-C. Summary of responses from Rest of World (RoW) The haplotype A*02:01 C*02:02 B*07:02 DRB1*15:01 DQB1*06:02 is not very frequent and it could represent a challenge in donor search. The patient has a frequent HLA haplotype found in Caucasian populations with high probability to find an identical HLA 10/10 donor. The difficulty will be to find among the 30 donors 10/10 identified in the BMDW a rapidly available and CMV Identification of HLA matched unrelated donor could be challenging due to DRB1, -DQB1 homozygosity; HLA-B*51:01 that could be associated with different HLA-C alleles and therefore HLA-C allele MM could be expected. The patient carries the variant HLA-B*51 that can be associated with several HLA-C alleles, but in this phenotypic context, the haplotype A24, B7, Cw7, DR15 and DQ6 is common. Unusual HLA-B/C linkage disequilibrium (B*51:01/C*02:02): 8% (NMDP data for CAU ethnic code). **UK NEQAS Annual Participant's Meeting 2018** Histocompatibility & Immunogenetics









Scenario 3 – Neonatal Alloimmune Thrombocytopenia (NAIT)

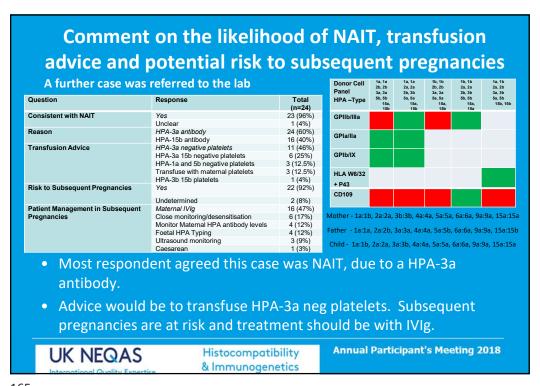
- A suspected case of NAIT is referred for investigation.
- Maternal platelet count
- HPA type of mother, father and child
- Indirect MAIPA results
- 24 responses received (11 UK&I)

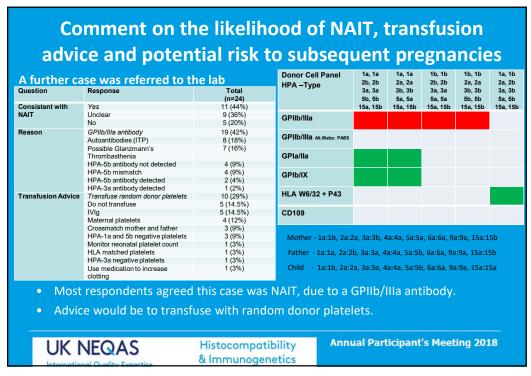
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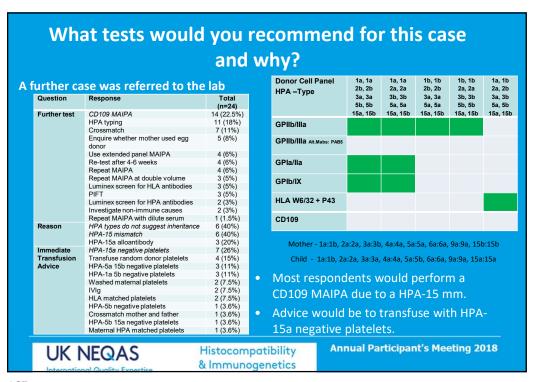
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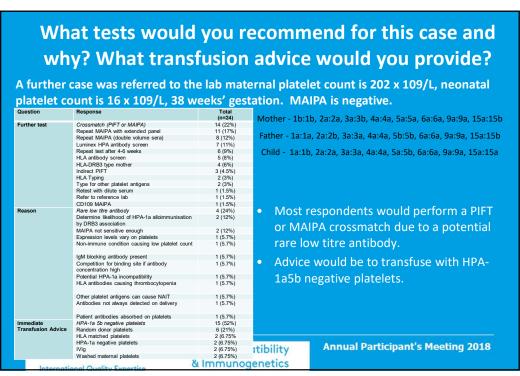
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Comment on the likelihood of NAIT, transfusion advice and potential risk to subsequent pregnancies Question Response Total (n=24) Panel HPA -Type Highly Likely Likely HPA-1a antibody HPA-3a antibody 14 (56%) 11 (44%) 18 (90%) Likelihood of NAIT Defined antibody GPIIb/IIIa PAB 1 HPA-3a antibody HPA-1b antibody HPA-1a negative platelets HPA-1a and 5a negative platelets 1 (5%) 1 (5%) 18 (75%) 6 (25%) Transfusion Advice GPIb/IX HLA W6/32 + Risk to Subsequent Pregnancies 22 (100%) Maternal IVIg Foetal HPA Typing Ultrasound monitoring Monitor Maternal HPA antibody levels P43 17 (34%) Patient Management in Subsequent 5 (10%) 4 (8%) 3 (6%) Mother - 1b:1b, 2a:2a, 3a:3b, 4a:4a, 5a:5a, 6a:6a, 9a:9a, 15a:15b Father - 1a:1b, 2a:2b, 3a:3a, 4a:4a, 5b:5b, 6a:6a, 9a:9a, 15a:15b Transfuse HPA-1a negative platelets Counselling Transfuse HPA-1a 5b negative platelets Childs - 1a:1b, 2a:2a, 3a:3a, 4a:4a, 5a:5b, 6a:6a, 9a:9a, 15a:15a Most respondents agreed that NAIT was highly likely, due to a HPA-1a antibody. Advice would be to transfuse HPA-1a neg platelets. Subsequent pregnancies are at risk and treatment should be with IVIg. **UK NEQAS Annual Participant's Meeting 2018** Histocompatibility & Immunogenetics









What tests would you recommend for this case and why?

A further case from a South East Asian family was referred to the lab. The MAIPA result is negative but the PIFT is positive with the mother's serum.

Question	Response	Total (n=24)
Further test	Crossmatch	10 (21%)
	GPIV/CD36 Typing/MAIPA	8 (17%)
	HLA antibody screening	6 (12%)
	Luminex HPA Antibody Screen	5 (10%)
	HLA Type	4 (8%)
	PIFT	3 (6%)
	HPA Type	3 (6%)
	NGS Sequencing	3 (6%)
	Investigate maternal auto-antibodies	3 (6%)
	Test for platelet disorder e.g. Glanzmann's	1 (2%)
	MAIPA with reduced serum volume	1 (2%)
	Platelet counts	1 (2%)
	Non-immune investigations	1 (2%)
Reason	CD36 clinically relevant in Asian populations	8 (35%)
	HLA Class I antibodies causing positive PIFT	4 (18%)
	Low frequency antibodies/antigens	4 (18%)
	Maternal auto-antibody	3 (13%)
	Anti-CD36 implicated in NAIT	1 (4%)
	Alloimmunisation to atypical HPA	1 (4%)
	Alloimmunisation to blood group antigens	1 (4%)
	Possible platelet disorder	1 (4%)
1.00		

Mother - 1a:1a, 2a:2a, 3a:3a, 4a:4a, 5a:5a, 6a:6a, 9a:9a, 15a:15b Father - 1a:1a, 2a:2a, 3a:3a, 4a:4a, 5a:5a, 6a:6a, 9a:9a, 15a:15b Child - 1a:1a, 2a:2a, 3a:3a, 4a:4a, 5a:5a, 6a:6a, 9a:9a, 15a:15b

Most respondents would perform a crossmatch as CD36 is clinically relevant in Asian populations.

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iED Discussion

- Questions / comments ?
 - Ideas for cases
 - Result feedback
 - Format of cases
 - Complexity level
 - Educational benefit
 - Number of questions

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Educational Scheme: Interesting Result

Sample ED03/18 probable HLA type

 $\mathsf{HLA} - \mathsf{A}^*02:01, \, \mathsf{A}^*29:02; \, \mathsf{B}^*44:03, \, \textcolor{red}{\mathbf{B}^*44:221}; \, \mathsf{C}^*05:01, \, \mathsf{C}^*16:01; \, \mathsf{DRB1}^*11:04, \, \mathsf{DRB1}^*15:01; \, \mathsf{DRB1}^*11:04, \, \mathsf{DRB1}^*1$

DRB3*02; DRB5*01; DQB1*03:01, DQB1*06:02; DPB1*02:01, DPB1*04:01

	Allele 1	Allele 2				
Report	Number of Participants	Report	Number of Participants			
	(n= 39)		(n= 39)			
B*44 homozygous	8 (21%)	B*44 homozygous	8 (21%)			
B*44:02	6 (15%)	B*44:221	10 (26%)			
B*44:03	10 (26%)	B*44:258	6 (15%)			
B*44:02/03/	11 (28%)	B*44:221/258	11 (28%)			
B*44:02/221	2 (5%)	B*44:03/258	2 (5%)			
B*44:104	1 (2.5%)	B*44:224	1 (2.5%)			
B*35:01	1 (2.5%)	B*38:01	1 (2.5%)			

- 10/39 (4/19 UK&I) labs correctly reported B*44:03, B*44:221
- 11/39 (6/19 UK&I) labs reported the correct type as part of a string e.g. B*44:02/03, B*44:221/258
- 6/39 (4/19 UK&I) labs reported B*44:02, B*44:258
- 2/39 (2/19 UK&I) labs reported B*44:02/221, B*44:03/258

Discrepancies in type caused by a cis/trans ambiguity

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