UK NEQAS Histocompatibility & Immunogenetics

UK NEQAS H&I

Annual Participant's Meeting 2022-23

WIFI: _Conference WIFI Password: Jerseyroyal

@UKneqasHI
@UK_NEQAS

Key Data from the Schemes

Amy De'Ath
UK NEQAS for H&I Operations Manager

GIG CYMRU NHS WALES
Ymddiriedolaeth GIG Prifysgol Felindre
Velindre University NHS Trust

Welsh Blood Service

Meet The Team!

Director: Dr Tracey Rees

Deputy Director: Deborah Pritchard

Operations Manager: Amy De'Ath

Deputy Manager: Melanie Bartley

Healthcare Scientist Practitioner: Geraint Clarke

QA Technical Officer: Jack Jefferies

MLA: Nicola Davies

UK NEQAS for H&I Steering Committee 2022-23

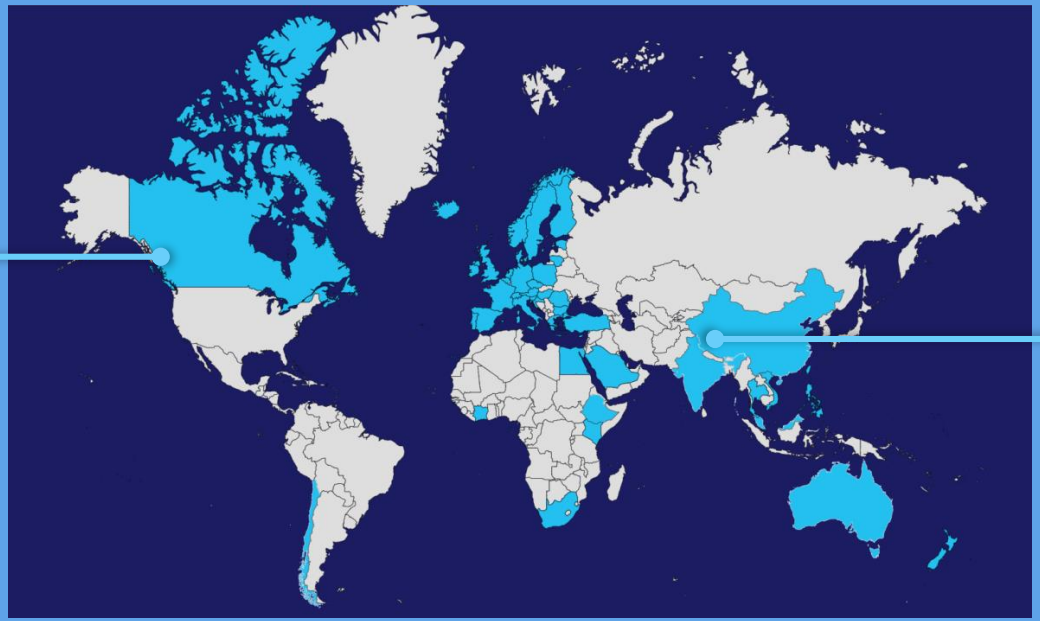
Helena Lee (Chair)
Arthi Anand
Katy Derbyshire
Sylvia McConnell
Katherine Mounsey
Anthony Poles
Sunil Daga (Clinical Representative)
Elizabeth Wroe (BSHI Representative to UK NQAAP)

Anthony Calvert
Rhys Goodhead (Expert Advisor Scheme 5B)

Kathryn Robson (Expert Advisor Scheme 5B)
Barbara McNamara (Expert Advisor Scheme 5B)
Tim Clench (Expert Advisor Scheme 5B)

UK NEQAS for H&I: An Overview

>320 participants



>50 countries

Things To Note...

Presentation Focus...

Performance, key trends, discussion points and 2023 changes

Further Details...

The presentation will be available to view on our website.

Lab Locations...

Generally:
1-100 = UK & Ireland.
101+ = Rest of the world

Scheme Assessments

- 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 plus educational schemes where required:

  - *e.g. Scheme 8: HLA Genotyping for Coeliac and Other HLA Associated Diseases*
    Scheme 4A1: HLA Typing at 1st Field Resolution - DPB1 assessment using a reference result

- Equivocal result only accepted for Scheme 2B.
- All Not Tested (NT) results excluded from assessment.
- Labs that fail to return results or do not a provide valid reason for NT are assessed as unacceptable.

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.

Changes for 2023-24

Steering Committee

New Members

Participant's Portal

Continuing improvements
Report format

Webinars

iED feedback continuing

Scheme Changes

Scheme 2A – Group changes
Scheme 8 – Pharmacogenetic reactions: Phenytoin and Carbamazepine
Scheme 9 – KIR haplotype assessment

Scheme 2A

Cytotoxic Crossmatching

Scheme 2A – Cytotoxic Crossmatch

Purpose

Assess participants ability to determine cell/serum cytotoxicity crossmatch status

Consensus

At least 75% agreement on pos/neg result

Satisfactory Performance

85% of reports agree with consensus in distribution year for each cell/DTT type

10 blood samples, 40 serum samples over 5 distributions

Scheme 2A: Performance

All cells with and without DTT	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	75 (19)	71 (18)	71 (22)	66 (16)	63 (15)	59 (15)
Number with Unsatisfactory Performance (< 85%) (UK&I)	16 (6)	16 (7)	5 (1)	7 (0)	4 (0)	6 (3)
% Unsatisfactory Performance (UK&I)	21.3% (31.6%)	22.5% (38.8%)	7.0% (4.5%)	10.6% (0)	6.3% (0)	10.2% (20%)

2022: 6 Unsatisfactory Performers (3 UK & Ireland)

Scheme 2A: UK&I Performance

	PBL	PBL +DTT	T Cell	T Cell +DTT	B Cell	B Cell +DTT
Crossmatches assessed (n=40)	33	33	36	35	31	31
% NT – Assessed samples only	25.8%	28.7%	22.7%	19.6%	29.8%	25.3%
% incorrect assignments	4%	3.8%	2.5%	2.5%	3.6%	4.1%
False Positive	85%	75%	66%	50%	33%	46%
False Negative	15%	25%	34%	50%	67%	54%

Scheme 2A: Unacceptable Performers 2022

Lab ID	PBL -DTT	T -DTT	B -DTT	PBL + DTT	T + DTT	B + DTT	Lab Identified Error
11			33%			33%	Test no longer performed
28			79%				*Under investigation*
45						84%	*Under Investigation*
143		57%			57%		Poor cell viability – low testing numbers
218			71%				No response
239	81%						Poor cell viability – delivery delay

Scheme 2A: 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

Scheme 2B

Crossmatching by Flow Cytometry

Scheme 2B: Crossmatching by Flow Cytometry

Purpose

Assess participants ability to determine cell/serum flow crossmatch status

Satisfactory Performance

85% reports agree with consensus in distribution year for each cell type

Consensus

At least 75% agreement on pos/neg or equivocal result

10 blood samples, 40 serum samples over 5 distributions

Scheme 2B: Performance

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	85 (22)	83 (22)	84 (23)	80 (21)	80 (22)	84 (19)
Number with Unsatisfactory Performance (< 85%) (UK&I)	8 (1)	15 (2)	12 (1)	11 (0)	5 (0)	6 (2)
% Unsatisfactory Performance (UK&I)	8.7% (4.5%)	18.1% (9.1%)	14.2% (4.3%)	13.8% (0)	6.3% (0)	7.1% (10.5%)

2022: 6 Unsatisfactory Performers (2 UK & Ireland)

Scheme 2B: Summary

	T Cells			B Cells		
	UK&I	RoW PC	RoW WB	UK&I	RoW PC	RoW WB
Number of participants	21	30	32	20	29	31
Number of XM assessed (>75% consensus)	37/40	31/40	34/40	38/40	30/40	37/40
Number of Positive XM	29	22	27	33	29	33
Number of Negative XM	8	9	7	5	1	4
Number of incorrect assignments	25 (3.2%)	36 (3.8%)	40 (3.6%)	15 (2%)	27 (3.1%)	42 (3.7%)
Number of False Pos	9 (1.2%)	20 (2.2%)	14 (1.3%)	4 (0.5%)	5 (0.6%)	10 (0.9%)
Number of False Neg	16 (2.1%)	16 (1.7%)	26 (2.4%)	11 (1.4%)	22 (2.5%)	32 (2.8%)
Number of equivocal assignments Number of samples NT	1 (0.1%) 16 (2.1%)	1 (0.1%) 80 (8.6%)	2 (0.2%) 136 (12.5%)	2 (0.3%) 15 (2%)	1 (0.1%) 56 (6.4%)	4 (0.3%) 157 (13.7%)

UK&I and RoW receive different blood samples

Scheme 2B: Unacceptable Performers 2022

Lab	T Cell	No. of results submitted	B Cell	No. of results submitted	Issue
42	100%	40/40	84%	40/40	Validation issue of reagent
48	84%	40/40	97%	40/40	False negs –known sensitivity issue
139	97%	40/40	77%	40/40	No response
191	93%	32/40	79%	32/40	No response
260	87%	40/40	83%	40/40	No response
1360	85%	40/40	83%	38/40	False neg/pos – sensitivity issues

6 labs with UP (<85%)

Scheme 6

HLA Antibody Detection

Scheme 6: HLA Antibody Detection

Purpose

Assess participants ability to determine **presence or absence** of HLA antibodies

Consensus

At least 75% agreement on presence/absence of HLA antibodies

Satisfactory Performance

80% reports agree with consensus in distribution year

12 serum samples over 3 distributions

Scheme 6: Performance

4 Unsatisfactory Performers (0 UK&I)

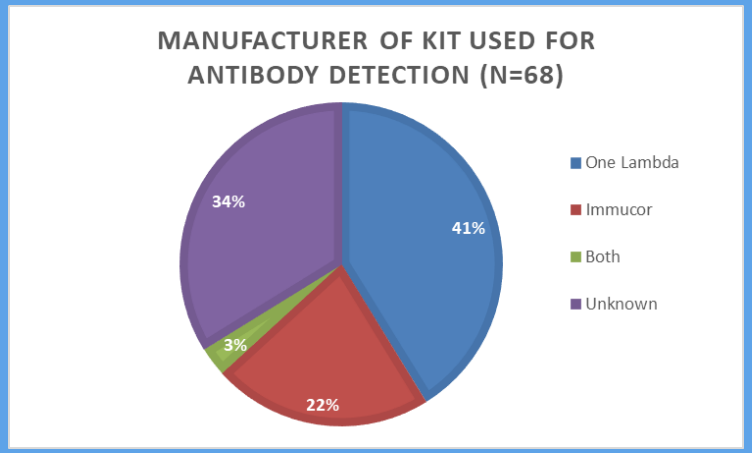
	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	101 (24)	88 (25)	82 (25)	74 (25)	71 (23)	68 (23)
Number with Unsatisfactory Performance (< 80%) (UK&I)	21 (0)	5 (0)	8 (0)	2 (0)	0 (0)	4 (0)
% Unsatisfactory Performance	20.8% (0%)	5.7% (0%)	9.7% (0%)	2.7% (0%)	0% (0%)	5.0% (0%)

42% negative

54% positive

4% samples not assessed (1 Class II, 54% neg)

Scheme 6: Kit Use and Performance



2022	Class I				Class II			
	One Lambda (n=28)	%	Immucor (n=15)	%	One Lambda (n=28)	%	Immucor (n=15)	%
601	Pos	100	Pos	100	Neg	100	Neg	100
602	Pos	100	Pos	100	Neg	96	Neg	80
603	Neg	100	Neg	100	Neg	100	Neg	100
604	Pos	100	Pos	100	Pos	100	Pos	100
605	Pos	100	Pos	93	Pos	100	Pos	87
606	Neg	100	Neg	93	Neg	100	Neg	93
607	Pos	100	Pos	100	Pos	100	Pos	100
608	*Neg*	*96*	*No Consensus*	*60*	Neg	96	Neg	80
609	Pos	100	Pos	100	Pos	100	Pos	100
610	Pos	100	Pos	93	*No consensus*	*56*	*No consensus*	*60*
611	Pos	100	Pos	100	Pos	100	Pos	100
612	Neg	96	Neg	93	Neg	96	Neg	100

Scheme 3

HLA Antibody Specificity Analysis

Scheme 3: HLA Antibody Specificity Analysis

Purpose

Assess participants ability to determine **specificity** of HLA antibodies

Satisfactory Performance

75% reports agree with consensus in distribution year

Consensus

At least 75% agreement on presence of HLA antibodies, 95% agreement on absense.

10 serum samples over 3 distributions

Scheme 3: Performance

Class I		2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)		72 (24)	73 (25)	70 (25)	64 (24)	65 (24)	65 (24)
Number with Unsatisfactory Performance (UK&I)	Presence	10 (0)	15 (1)	3 (0)	1 (0)	1 (0)	1 (0)
	Absence	3 (0)	5 (0)	2 (0)	1 (0)	1 (0)	1 (0)
% Unsatisfactory Performance	Presence	13.8%	20.5%	4.2%	1.6%	1.5%	1.5%
	Absence	4.2%	6.8%	2.6%	1.6%	1.5%	1.5%

Overall 2 labs with UP (0 UK&I)

Class II		2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)		72 (24)	75 (25)	69 (25)	63 (24)	64 (24)	64 (24)
Number with Unsatisfactory Performance (UK&I)	Presence	5 (0)	12 (0)	5 (0)	2 (0)	3 (0)	1 (0)
	Absence	2 (0)	3 (0)	2 (0)	1 (0)	1 (0)	1 (0)
% Unsatisfactory Performance	Presence	6.9%	16.0%	7.2%	3.2%	4.7%	1.6%
	Absence	2.8%	4.0 %	2.8%	1.6%	1.6%	1.6%

Scheme 3: Unacceptable Performers 2022

2 labs (0 UK&I) with UP (<75%)

Lab	Class I		Class II		CAPA	Kit
	Presence	Absence	Presence	Absence		
302	79%	38%	57%	56%	No reply	No info
1349	73%	100%	89%	100%	False neg	Immucor

Scheme 3: Class I Assessment

	Number of HLA Class I Specificities (n=65)										
	301	302	303	304	305	306	307	308	309	310	Total
Present (≥75%)	34	43	11	11	11	18	17	13	15	1	174
Absent (<5%)	28	24	8	35	32	20	41	35	35	5	263
Negative 0%	16	11	67	35	30	33	20	32	26	76	351
Not Assessed (5-74%)	10	10	3	8	16	18	11	3	11	7	79

516 (absent 0% not included in analysis) specificities reported over 10 samples

- 33.7% reached consensus presence
- 51.0% reached consensus absence
- 15.3% specificities were not assessed

Scheme 3: Class II Assessment

(DPB included in assessment from 2021)

	Number of HLA Class II Specificities (DR, DQ, DP) (n=64)										
	301	302	303	304	305	306	307	308	309	310	Total
Present (≥75%)	0	0	4	0	20	0	0	19	10	10	63
Absent (<5%)	1	24	11	17	10	19	13	10	12	6	123
Negative 0%	42	17	29	27	10	20	26	12	20	21	208
Not Assessed (5-74%)	3	5	2	2	3	7	7	5	3	9	46

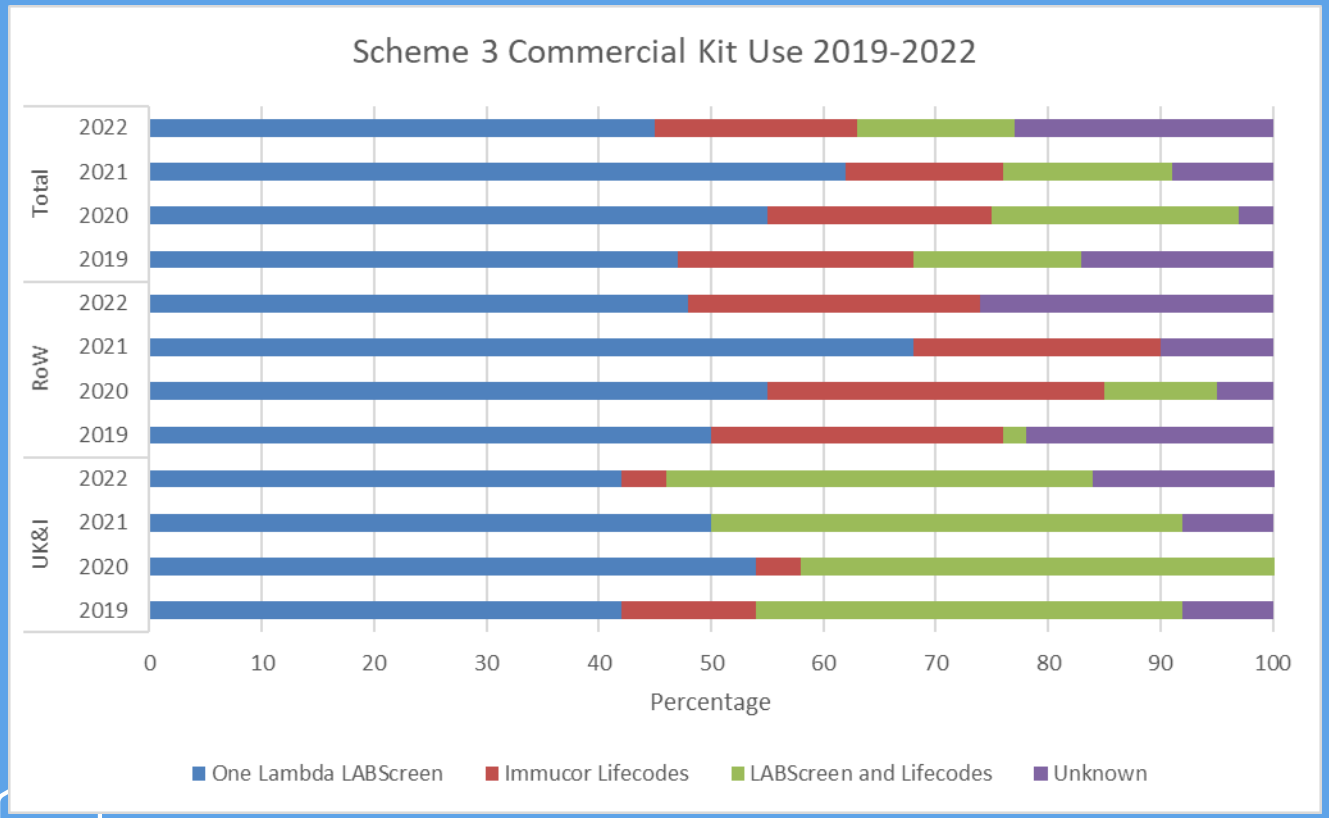
232 specificities (absent 0% not included in analysis) reported over 10 samples

27.1% reached consensus presence

53.0% reached consensus absence

19.8% specificities were not assessed

Scheme 3: Kit Use 2019-2022

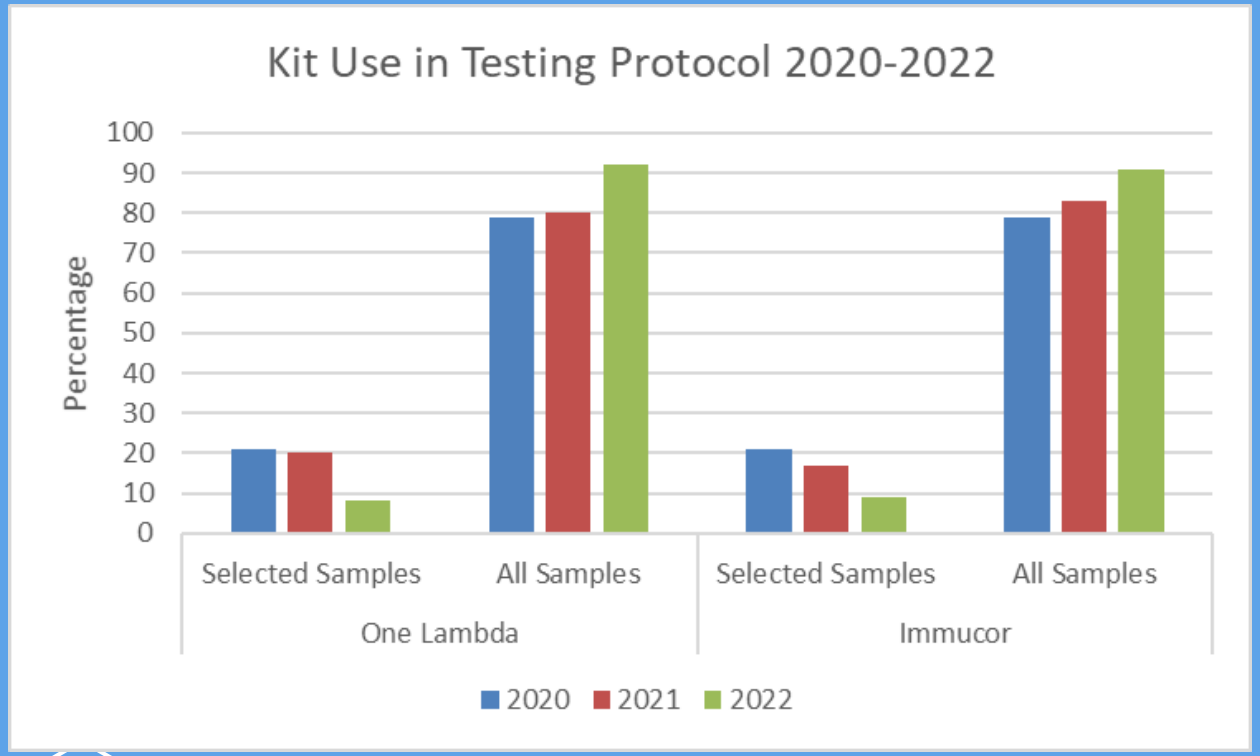


Overall OL kits are the most widely used

UK&I labs are more likely to use a combination of kits

Immucor only kit use more prevalent in RoW labs

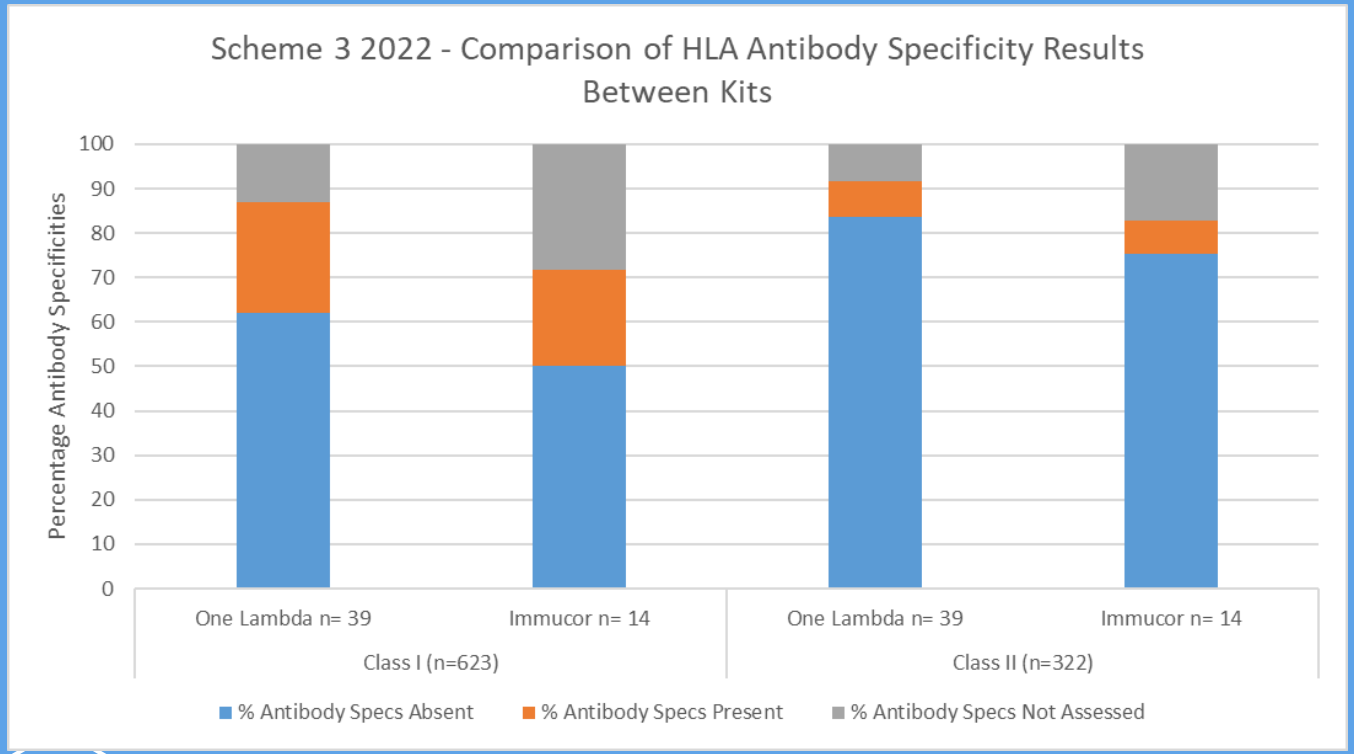
Scheme 3: Kit Use in Testing Protocol



Majority of labs use their kit of choice to test all samples

This strategy has been gaining popularity since 2020

Scheme 3: Results by Kit Use



Similar percentage of antibodies reach consensus present in both kits

Less concordance in 'absent' antibodies

Greater percentage of Class I antibodies classed as not assessed

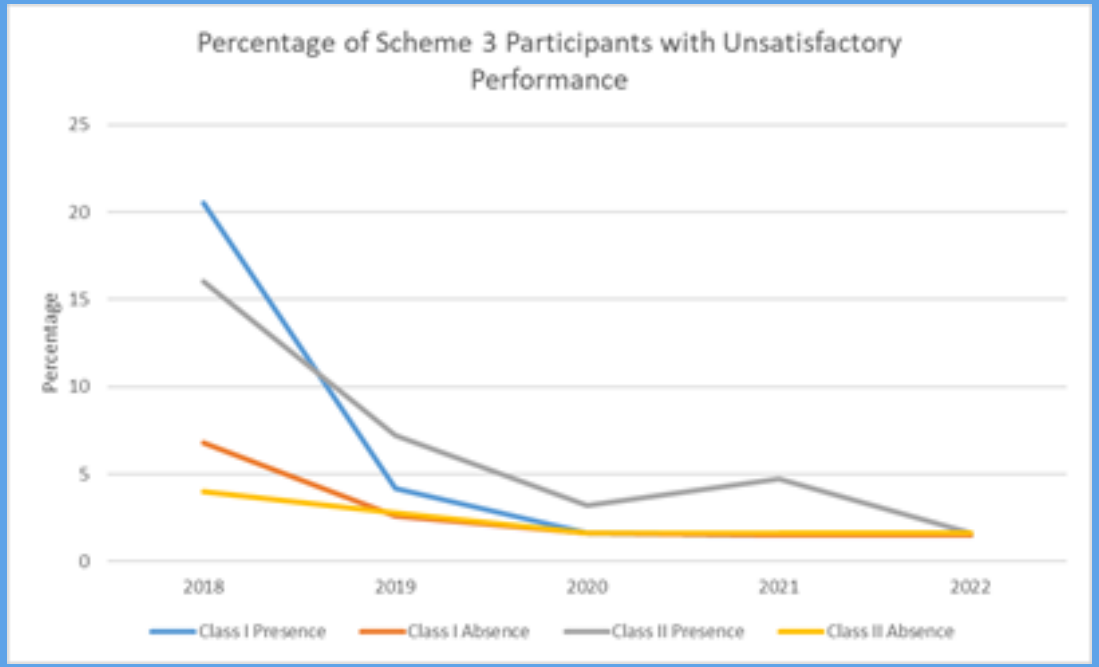
Scheme 3: Kit Use and Performance

Average Performance	Class I		Class II	
	OL	Imm	OL	Imm
Presence	97.4%	86.9%	96.1%	89.0%
Absence	98.5%	95.4%	98.4%	95.6%

Average overall performance for detecting the 'presence' of antibodies it was marginally higher for users of OL kits.

For the confirmation of 'absence' of antibodies the difference in overall performance was also comparable between kit users.

Scheme 3: Unsatisfactory Performance

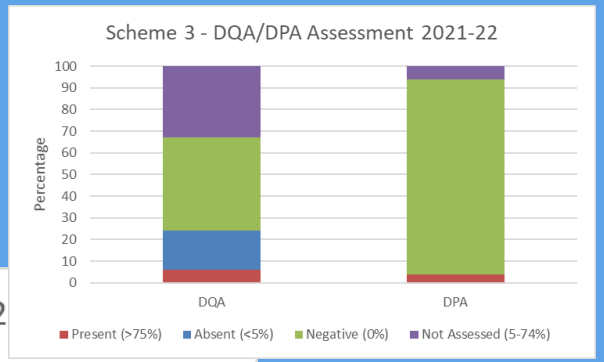


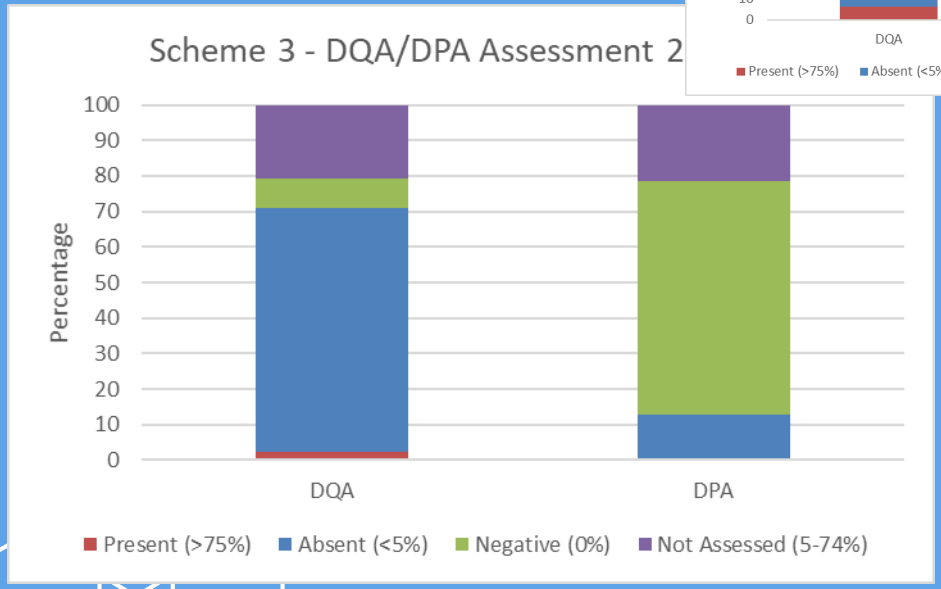
Overall percentage of UP has generally decreased over the last 5 years

UP rate over last 3 years typically <2% (exception in 2021 CII presence <5%)

Scheme 3: DQA/DPA Antibody Reporting

Reporting of antibodies to HLA-DQA and –DPA is optional and not assessed.
51.5% report DQA, 45.5% report DPA.





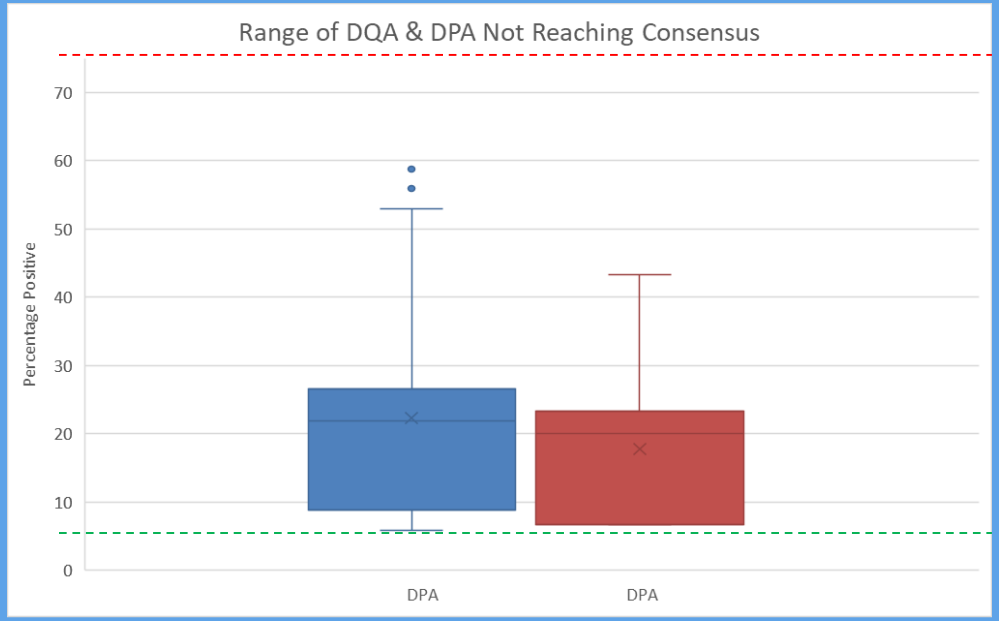
An analysis of the data submitted for DQA and DPA antibodies in 2022-23 and 2021-22 was performed.

Large proportion of samples are negative or consensus absent.

Very few positives.

Approx 20% not assessed.

Scheme 3: DQA and DPA Antibody Reporting



Scheme 11

HPA Antibody Detection/Specification

Scheme 11: HPA Antibody Detection/Specification

Purpose

Assess participants ability to correctly determine pesence and specificty of HPA antibodies.

Satisfactory Performance

At least 75% of specificities in agreement with the consensus result in a distribution year.

Consensus

Presence of specificity determined by at least 75% agreement and absence determined by at least 95% agreement.

8 serum/plasma samples over 2 distributions

Scheme 11: Performance

- 2 Unsatisfactory Performers (0 UK&I)

	2017 Pilot	2018	2019	2020	2021	2022
Number of Participants (UK&I)	13 (3)	35 (4)	39 (5)	42 (4)	43 (4)	43 (4)
Number with Unsatisfactory Performance (< 75%) (UK&I)	N/A	1 (0)	1 (0)	3 (0)	6 (0)	2 (0)
% Unsatisfactory Performance	N/A	2.9%	2.6%	7.1%	13.9%	4.5%

Scheme 11: HPA Antibody Detection/Specification

2022 Sample	HPA Detection	HLA Detection	HPA Antibody ID	
			Presence	Absence
1	97.6% Neg	100% Neg	N/A	HPA-1a 97.6%
2	92.9% Neg	94.1% Neg	N/A	HPA-3a 92.9%
3	87.8% Pos	97.0% Neg	HPA-1a 87.8%	HPA-1b, 3a 97.6% GP11b/111a 85.4%
4	97.6% Neg	94.1% Pos	N/A	HPA-GP1b 97.6%
5	95.3% Pos	50.0% Pos	HPA-3a 95.3%	HPA4a, 4b, 15a, GP11b/111a 97.7%
6	100% Pos	100% Pos	HPA-5b 100%	HPA-1b, GP11b/111a 97.7%
7	100% Neg	97.0% Pos	N/A	N/A
8	97.6% Pos	100% Pos	HPA-1a 97.6%	HPA-4a, 5b 97.6% 4b, GP11b/111a, GP 1b 95.2%

Scheme 11: HPA Antibody Detection/Specification

Sample	Expected Results	Consensus Present	Not Assessed
1	HPA neg, HLA neg	**None**	None
2	3a	**NEG**	3a (93% absent)
3	1a	**1a**	3b (93% absent) 4b (93% absent) GPIIb/IIIa (85% absent)
4	HPA neg, HLA neg	**None**	None
5	3a (NIBSC)	**3a**	1a (90% absent)
6	5b	**5b**	None
7	HLA pos only	**None**	None
8	1a	**1a**	3a (90% absent)

Scheme 11: NIBSC 3a Detection

NIBSC Standards used in 2021:

ID	Sample	Dilution	Result Positive	Unacceptable Positives
1101/2021	NIBSC Standard HPA-1a (05/106)	1:4	HPA-1a (90.7%)	HPA-3a (n=1 (267)), HPA-3b (n=1 (387)), HPA-4b (n=1(1346))
1102/2021	NIBSC Standard HPA-3a (03/190)	1:8	HPA-3a (76.7%)	HPA-1a (n=1 (180)), HPA-4b (n=1 (1346))
1103/2021	NIBSC Standard HPA-5b (99/666)	1:2	HPA-5b (100%)	GP Ia/IIa (n=2 (130, 394))
1104/2021	NIBSC Standard HPA-15b (18/220)	1:16	HPA-15b (14%)	

HPA-3a Standard	Dilution	Result	Unacceptable Positives
2021	1:8	76.7%	HPA-1a, HPA-4b
2022	1:4	95.3%	HPA-1a, HPA-4a, HPA-4b, HPA-15a

Scheme 11: Unacceptable Performers 2022

Lab	HPA Presence	HPA Absence	Samples reported	Method	Error
388	33%	82%	8/8	PAK Plus	Procedural issues
389	50%	100%	8/8	MAIPA in house	Interpretation issues

2 labs with UP (<75%)

Scheme 11: Analysis of Errors

- Summary of false negative and false positive errors 2020-2022.
- Error rate extremely low 0.54% but errors often at clinically relevant polymorphisms.
- Most errors found at HPA-1a (n=19, error rate 1.47%), 1b (n=19, error rate 1.47%), 3a (n=18, error rate 1.39%).

Errors 2020-2022	HPA-1 a	HPA-1 b	HPA-2 a	HPA-2 b	HPA-3 a	HPA-3 b	HPA-4 a	HPA-4 b	HPA-5 a	HPA-5 b	HPA-6 a	HPA-6 b	HPA-15 a	HPA-15 b	Total
False Pos	4	3	2	1	6	5	3	10	6	4	0	0	1	4	49
False Neg	15	16	0	0	12	0	0	0	0	6	0	0	0	0	49
Total Errors	19	19	2	1	18	5	3	10	6	10	0	0	1	4	98
% Error Rate	1.47	1.47	0.15	0.08	1.39	0.39	0.23	0.77	0.46	0.77	0.00	0.00	0.08	0.31	0.54
Total Tested	1295	1295	1295	1295	1295	1295	1295	1295	1295	1295	1295	1295	1295	1295	18130

- Even split of false positive (n=49) and false negative (n=49) errors.
- In the last 3 years: most labs had only 1 error

Number of Labs	Number of Errors
14	1
8	2
3	3
3	4
4	5
4	>5

Scheme 11: Factors Affecting Performance

- Limitations of commercial kits
- Scheme Design
    - lack of genotype
- Sample quality
    - volume of sample – increasing to 1.5ml in 2022-23
    - complexity of sera
- Individual testing strategy
    - ability to detect certain antibodies e.g. HPA-15

Do you have any questions?

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Key Data from the Schemes

Deborah Pritchard
UK NEQAS for H&I Deputy Director

Scheme 1A

HLA Phenotyping

Scheme 1A: HLA Phenotyping

Purpose

Assess participants ability to use serological and supplementary methods to correctly identify HLA phenotype

Satisfactory Performance

9 or more complete HLA phenotypes in agreement with consensus per distribution year.

Consensus

At least 75% agreement on each specificity.

10 blood samples over 5 distributions

Scheme 1A: Performance

- 2 labs with unsatisfactory performance (0 UK&I).

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	38 (6)	38 (6)	38 (5)	34 (4)	33 (2)	28 (1)
Number with Unsatisfactory Performance (< 90%) (UK&I)	1 (0)	6 (1)	8 (1)	3 (1)	2 (0)	2 (0)
% Unsatisfactory Performance	2.6%	15.8%	21.1%	8.8%	6.1%	7.1%

Scheme 1A: 2022 Incorrect Assignments

10/280 (3.5%) incorrect HLA types in 2022 reported by 8 labs:

10 reports that contained broad not split specificity (e.g. B40 v B60)
0 reports that contained an incorrect split specificity (e.g. DR4 v DR13)
0 reports with molecular based nomenclature (e.g. A01 v A1)

0/2 labs with unsatisfactory performance completed CAPA

Scheme 4A1

DNA Typing at 1st Field Resolution

Scheme 4A1: DNA Typing at 1st Field Resolution

Purpose

Assess participants ability to correctly determine HLA genotypes at the 1st field resolution.

Satisfactory Performance

9 or more full HLA types in agreement with consensus/reference result in a distribution year.

Consensus

At least 75% agreement on each allele. When consensus is not met, a reference result is used. Reference result is always used for DPB1 assessment

10 blood samples over 3 distributions

Scheme 4A1: Performance

- 6 labs with unsatisfactory performance (0 UK&I)

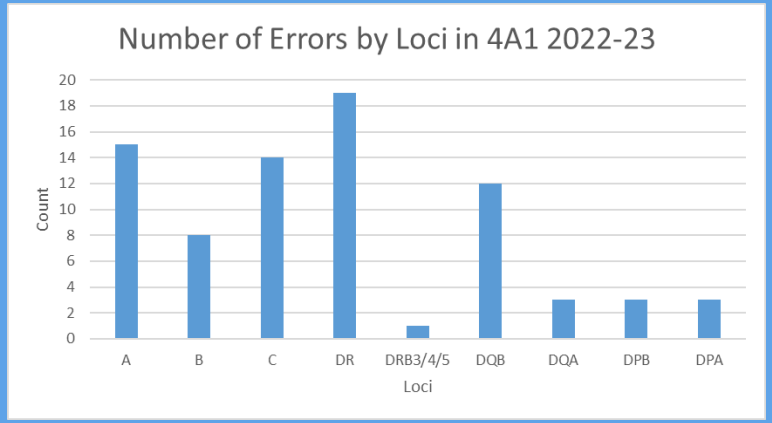
	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	106 (28)	105 (28)	100 (28)	88 (26)	82 (25)	81 (25)
Number with Unsatisfactory Performance (< 90%) (UK&I)	11 (1)	15 (1)	4 (1)	8 (0)	6 (1)	7 (0)
% Unsatisfactory Performance	10.4%	14.3%	4%	9.1%	7.3%	8.4%

Scheme 4A1: 2022-23 Incorrect Assignments

78/10880 (0.7%) errors reported by 17 different labs (4 UK&I)

- 8 samples with incorrect uses of nomenclature (e.g. C*5 instead of C*05) (1 UK&I)
- 6 samples with incorrect assignments (e.g. A*02 instead of A*68)
- 5 samples where HLA types not reported
- 3 missed assignment (reported homozygous when heterozygous) (1 UK&I)
- 2 samples with additional assignment (reported heterozygous when homozygous) (1 UK&I)
- 2 samples with data entry errors (1 UK&I)
- 0 HLA types completely incorrect

9 HLA types with multiple errors
12 HLA types with one error



Scheme 4A1: Unacceptable Performers 2022

Lab	Sample	Error	CAPA Response
1386	01-03	No results returned	Reagent issue/service suspended
172	04 + 06 + 07	Multiple reporting errors	No reply
379	05 + 06 + 07	DRB3* incorrect assignments	Revise registration issue
1352	01 + 07	Incorrect DPB1* types	No reply
1395	04 - 07	Incorrect nomenclature & not reporting registered loci	No reply
103	08 - 10	No results returned	No reply
1403	08 - 10	Incorrect nomenclature	Reporting/clerical error

Scheme 4A1i

Interpretive HLA Genotype

Scheme 4A1: Interpretive HLA Genotype

Purpose

Assess participants ability to correctly interpret their 4A1 genotype result to the 'split' specificity level.

Satisfactory Performance

9 or more full HLA types in agreement with consensus/reference result in a distribution year.

Consensus

At least 75% agreement on each specificity. When consensus is not met, a reference result is used.

10 HLA genotypes from Scheme 4A1

Scheme 4A1i: Performance

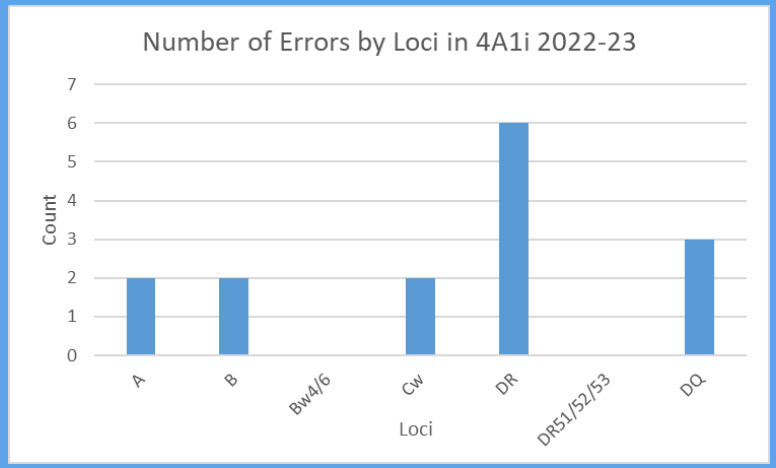
- 2 labs with unsatisfactory performance (0 UK&I)

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	36 (20)	40 (21)	44 (22)	44 (22)	42 (21)	40 (21)
Number with Unsatisfactory Performance (< 90%) (UK&I)	6 (1)	6 (0)	8 (1)	6 (2)	5 (1)	2 (0)
% Unsatisfactory Performance	16.7%	15.0%	18.1%	13.6%	11.9%	5.0%

Scheme 4A1i: 2022-23 Incorrect Assignments

- 15/5448 (0.28%) incorrect results reported by 5 different labs (2 UK&I)
  - 3 samples where HLA types not reported
  - 2 reporting at broad not split specificity level
  - 2 incorrect assignments (e.g. DQ8 instead of DQ9) (1 UK&I)
  - 2 reporting 'null' instead of Cw12
  - 1 data entry error (1 UK&I)

1 HLA type with multiple errors
6 HLA types with single errors



Scheme 4A1i: Unacceptable Performers 2022

Lab	Sample	Error	CAPA Response
1352	01 + 03 + 08	Reported homozygous/incorrect split	No reply
1379	01 + 07	Reported broad not split	Reporting error

Scheme 4A2

DNA Typing to 2nd or 3rd Field Resolution

Scheme 4A2: DNA Typing to 2nd or 3rd Field Resolution

Purpose

Assess participants ability to correctly determine HLA type to 2nd or 3rd field.

Consensus

At least 75% agreement on each allele. If consensus is not met, a reference result is used.

Satisfactory Performance

9 or more full HLA types in agreement with consensus/reference genotype in a distribution year.

10 blood samples over 3 distributions

Scheme 4A2: Performance

- 46/61 participants registered for 2nd field
- 15/61 participants registered for 3rd field

- 4 labs with unsatisfactory performance (0 UK&I)

4/4 labs with unsatisfactory performance completed CAPA

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	66 (21)	63 (20)	62 (20)	64 (20)	63 (22)	61 (23)
Number with Unsatisfactory Performance (< 90%) (UK&I)	4 (0)	9 (2)	9 (1)	7 (0)	6 (0)	4 (0)
% Unsatisfactory Performance	6.1%	14.3%	14.5%	11.0%	11.1%	6.5%

Scheme 4A2: Incorrect Assignments: 2nd Field

13/8420 (0.15%) incorrect HLA alleles reported by 8 labs (3 UK&I)

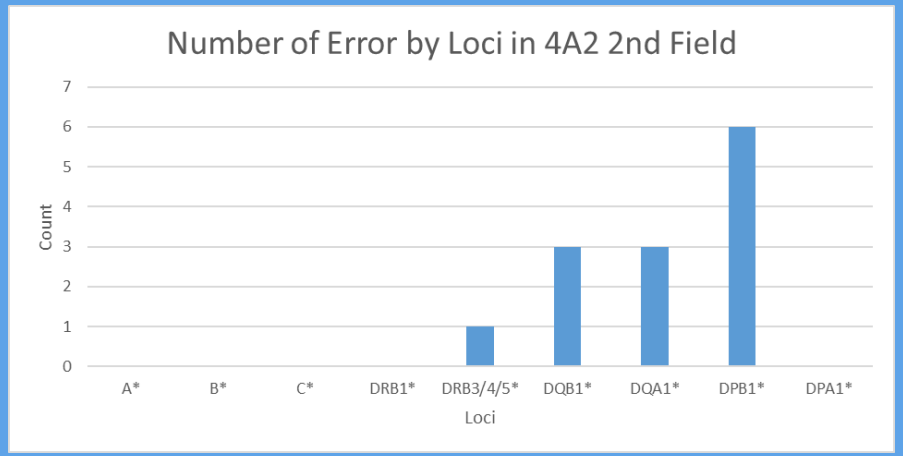
- 4 samples with alleles in a string that should have been resolved

(e.g. DQB1*06:03/14/41/44)

- 4 reports of errors at the 2nd field (e.g. DQB1*02:01 rather than 02:02)
- 1 reports of homozygous type when heterozygous (e.g. DRB4*01:03/134, - rather than DRB4*01:01, 01:03)
- 1 report of heterozygous type when homozygous

(e.g. DQB1*03:03, 06:02 rather than DQB1*06:02, -)

3 HLA types with multiple errors
7 HLA types with single errors

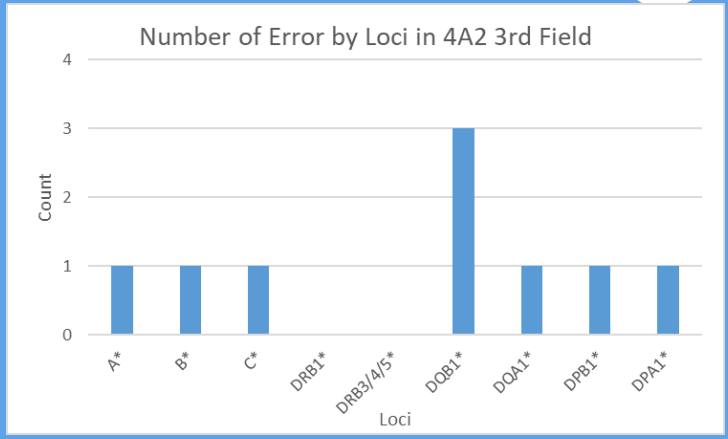


Scheme 4A2: Incorrect Assignments: 3rd Field

9/2280 (0.39%) incorrect HLA alleles reported by 4 labs (1 UK&I)

- 2 samples with reports of unresolved ambiguities (e.g. DQB1*06:02:01/06:02:49)
- 2 samples with errors at 2nd field (e.g. DQB1*06:01:01 rather than 06:02:01)
- 2 samples with errors at 3rd field (e.g. B*08:01:01 rather than 08:01:20)
- 1 sample report incorrect allele (e.g. A*11:353 instead of 11:01:01)
- 1 sample with a data entry error (e.g. C*6:02:01)

1 HLA type with multiple errors
7 HLA types with single errors

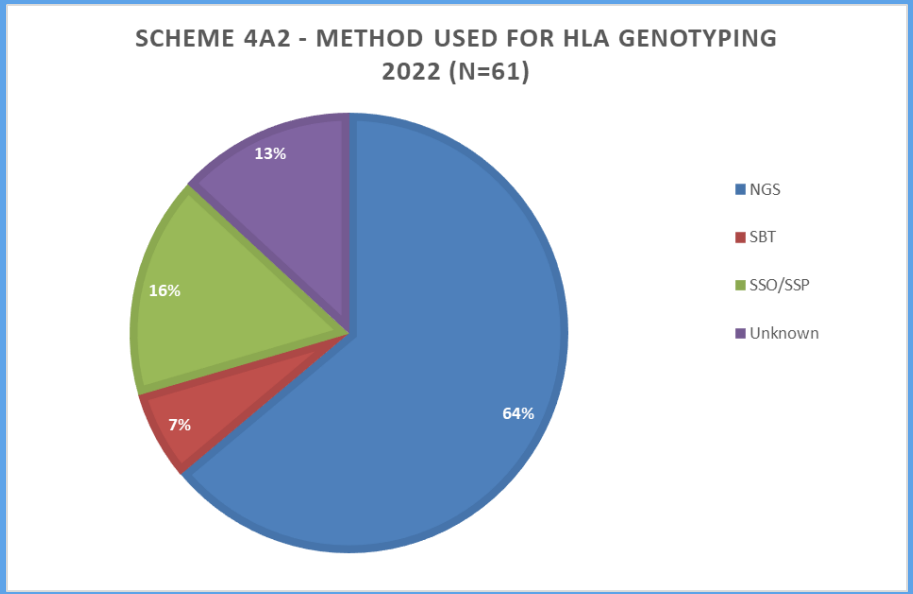


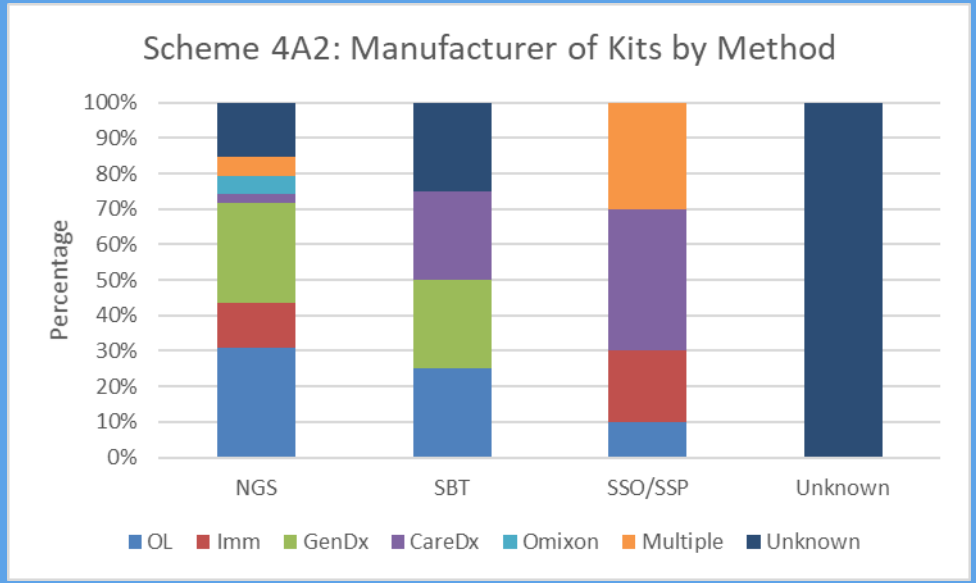
Labs with 4A2 Errors		Method	Manufacturer
2nd Field Error	25	NGS	One Lambda
	41	NGS	Omixon
	54	NGS	GenDx
	112	SSO	Immucor
	127	NGS	One Lambda
	286	NGS	Unknown
	367	SSP	CareDx
	374	Unknown	Unknown
3rd Field Error	35	NGS	One Lambda
	132	NGS	Unknown
	267	NGS	Unknown
	309	NGS	Immucor

Scheme 4A2: Unacceptable Performers 2022

Lab	Sample	Error	Field	CAPA Response
309	01+03+ 05+09	4A2 01/2022: Ambiguity reported for DPB1* 4A2 03/2022: Incorrect types reported for DQA1* and DPA1* 4A2 05/2022 3rd field: Reported DQB1*06:01:01, consensus DQB1*06:03:01 4A2 09/2022: Reported DQA1*05:01:01, consensus 05:03:01	3rd	Kit issues & poor sample quality & reporting/transcription error
374	01+02	4A2 01/2022: Report Unacceptable ambiguity (DQB1*06:14) 4A2 02/2022: Reported DQB1* 03:03, 06:02 when samples was DQB1*06:02 homozygous	2nd	Software issues/staff interpretation
267	03+07	4A2 03/2022 3rd field: Reported B*08:01:01, consensus B*08:01:20 4A2 07/2022 3rd field: Reported A*11:353, consensus A*11:01:01	3rd	Clerical/technical errors
127	08+10	4A2 08/2022: Reported DQA1*05:01, consensus 05:05 4A2 10/2022: Reported DQB1*02:01, consensus 02:02	3rd	Result entry errors

Scheme 4A2: Testing Methods





Scheme 9

KIR Genotyping

Scheme 9: KIR Genotyping

Purpose

Assess participants ability to correctly determine the presence or absence of specific KIR genes.

Satisfactory Performance

9 or more full KIR genotypes in agreement with consensus/reference genotype in a distribution year.

Consensus

At least 75% agreement on the presence/abesence of each gene. Reference type used where consensus is not met

10 blood samples over 2 distributions

Scheme 9: 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

Scheme 9: Performance

- 0 lab with unsatisfactory performance (multiple errors)

	2016 (Pilot)	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	11 (2)	8 (3)	9 (1)	12 (1)	12 (1)	15 (1)	15 (1)
Number with Unsatisfactory Performance (UK&I)	*N/A*	0 (0)	1 (0)	3 (0)	0 (0)	1 (0)	0 (0)
% Unsatisfactory Performance	*N/A*	0%	11.1%	25%	0%	6.7%	0%

Scheme 10

HPA Genotyping

Scheme 10: HPA Genotyping

Purpose

Assess participants ability to correctly determine HPA polymorphisms.

Consensus

At least 75% agreement on the presence/abesence of each allele. Reference type used where consensus is not met

Satisfactory Performance

9 or more full HPA types in agreement with consensus/reference genotype in a distribution year.

10 blood samples over 2 distributions

Scheme 10: HPA Genotyping

- Participants able to report any of the following: *HPA-1, HPA-2, HPA-3, HPA-4, HPA-5, HPA-6, HPA-15*
  - 34/39 reported HPA-1, 2 , 3, 4, 5 and 15
  - 34/39 labs reported HPA-4
  - 30/39 labs reported HPA-6
- Also able to report any other HPA polymorphisms detected, *for information*

Scheme 10: HPA Genotyping

- 2 errors
- 1 lab with unsatisfactory performance

	2016 Pilot	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	12 (4)	15 (5)	37 (6)	38 (6)	40 (0)	38 (6)	39 (6)
Number with Unsatisfactory Performance (< 100%) (UK&I)	N/A	1 (0)	1 (0)	3 (0)	0 (0)	0 (0)	1 (0)
% Unsatisfactory Performance	N/A	6.7%	2.7%	7.9%	0%	0%	2.6%

Scheme 10: Errors in HPA Genotypes

- Summary of false negative and false positive errors 2017-2022.
- Error rate extremely low 0.1% but errors often at clinically relevant polymorphisms.
- Most errors found at HPA-15b (n=7, error rate 0.35%), 3b (n=6, error rate 0.2%), 1b (n=5, error rate 0.25%), 15a (n=5, error rate 0.26%), 5b (n=4, error rate 0.2%) and 3a (n=3, error rate 0.15%).

Errors 2017-22	HPA-1 a	HPA-1 b	HPA-2 a	HPA-2 b	HPA-3 a	HPA-3 b	HPA-4 a	HPA-4 b	HPA-5 a	HPA-5 b	HPA-6 a	HPA-6 b	HPA-15 a	HPA-15 b	Total
False Neg	2	4	1	0	2	4	0	0	0	0	1	0	2	3	19
False Pos	0	1	0	1	1	2	0	1	0	4	0	1	3	4	18
Total Errors	2	5	1	1	3	6	0	1	0	4	1	1	5	7	30
% Error	0.10	0.25	0.05	0.05	0.15	0.30	0.00	0.06	0.00	0.20	0.07	0.07	0.26	0.35	0.1
Total Tested	2028	2028	1988	1988	1988	1988	1698	1698	2018	2018	1460	1460	1888	1988	26236

- Even split of false positive (n=18) and false negative (n=19) errors.
- In the last 3 years: 4 labs with 1 error and 1 lab with 3 errors (SSP technical issue - gel labelling)
- There was no correlation in errors made and the method of detection noted.

Scheme 1B

HLA-B27 Testing

Scheme 1B: HLA-B27 Testing

Purpose

Assess participants ability to correctly determine HLA-B27/2708/B*27 status.

Satisfactory Performance

Making 10/10 reports that are in agreement with consensus in a distribution year.

Consensus

At least 75% agreement on B27 status. Reference type used where consensus is not met

10 blood samples sent over 5 distributions

Scheme 1B: Performance

- 8 labs with unsatisfactory performance (0 UK&I)

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	127 (52)	133 (54)	133 (53)	141 (52)	141 (50)	139 (49)
Number with Unsatisfactory Performance (< 100%) (UK&I)	7 (2)	10 (3)	4 (1)	12 (2)	3 (0)	8 (0)
% Unsatisfactory Performance (UK&I)	5.5%	7.5%	3.0%	8.5%	2.1%	5.7%

Scheme 1B: 2022 Incorrect Assignments

Sample	Result	Lab Number	Technique	HLA Type	Lab Identified Cause
1B 03	False neg	129 409 1375	Molecular Serological Serological	B27 B44	Storage/temp issues Reagent issues No reply
1B 04	False pos	153 256 1371	Serological Not known Serological	B7 B7	Interpretation/training issues Borderline result No reply
1B 09	False neg	327 1376	Molecular Unknown	B8 B27	No reply No reply
1B 09 & 10	False neg & false pos	324	Serological	B8 B27 B13 B44	Sample mix up

- 2/10 samples distributed were HLA-B27 positive
- 8 errors: 5 false neg, 3 false pos
- 5/8 errors involved serological technique
- 1 sample mix up

4/8 labs with unsatisfactory performance completed CAPA

Scheme

5A

HFE Typing

Scheme 5A: HFE Testing

Purpose

Assess participants ability to correctly determine HFE mutations.

3 mutations assessed:

- Codon 63: Histidine63Aspartic acid (H63D)
- Codon 282: cysteine282tyrosine (C282Y)
- Codon 65: Serine63Cysteine (S65C)

Satisfactory Performance

10 reports in agreement with consensus/reference result in a distribution year.

Consensus

At least 75% agreement on each HFE mutation. Reference type used where consensus is not met

10 donor samples sent over 3 distributions

Scheme 5A: Performance

- 4 labs with unsatisfactory performance (3 UK&I)

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	56 (42)	58 (44)	51 (38)	49 (36)	45 (32)	37 (27)
Number with Unsatisfactory Performance (< 100%) (UK&I)	3 (2)	0 (0)	2 (1)	1 (1)	1 (1)	4 (3)
% Unsatisfactory Performance	5.3%	0%	3.9%	2.0%	2.2%	10.8%

CAPA responses

- Sample/labelling mix up
- Some did not report as now outsourcing the service/no longer testing

Scheme 5B

Interpretive HFE genotype and Hereditary Haemochromatosis

Scheme 5B: Interpretive HFE genotype and Hereditary Haemochromatosis

Purpose

Assess participants ability to produce an accurate, clear and concise clinical report. HFE genotype and various clinical information provided

Satisfactory Performance

Must have <50% of available penalty points available to be considered acceptable.

Assessment

Reports must be identical in format to those typically produced by lab. Penalty points awarded for failure to cover interpretive criteria identified and agreed by the expert assessors.

Twice a year, 2 clinical scenarios

Scheme 5B: Performance

- 2 labs with unsatisfactory performance (1 UK&I)

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	20	21 (18)	21 (17)	19 (15)	16 (12)	15 (11)
Number with Unsatisfactory Performance (UK&I)	0	1 (1)	3 (1)	1 (0)	0 (0)	2 (1)
% Unsatisfactory Performance	0%	4.8%	14%	5.3%	0%	13%

Scheme 5B: Performance

- 2022 – All 4 scenarios:

  maximum 6 penalty points per scenario, 24 in total.

2	labs got	0-1 penalty points
2	got	1.5-2 penalty points
4	got	2.5-3 penalty point
3	got	3.5-4 penalty points
2	got	4.5-5 penalty points
2	labs got	>12 penalty points

Both the labs with >12 points, did not submit reports for 2 scenarios

Scheme 7

HLA-B*57:01 Typing for Drug Hypersensitivity

Scheme 7: HLA-B*57:01 Typing for Drug Hypersensitivity.

Purpose

Assess participants ability to correctly determine HLA-B*57:01 status

Satisfactory Performance

Making 10 sample reports in agreement with the consensus/reference result in a distribution year.

Consensus

At least 75% agreement on the status of HLA-B*57:01. Reference result used when consensus not met.

10 blood samples over 3 distributions

Scheme 7: Performance

- 6/10 samples distributed were HLA-B*57:01 positive
- 3 labs with unacceptable performance

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	64 (26)	67 (27)	67 (27)	67 (27)	64 (25)	52 (18)
Number with Unacceptable Performance (< 100%) (UK&I)	4 (1)	2 (0)	0 (0)	2 (0)	1 (1)	3 (0)
% Unsatisfactory Performance	6.3%	3.0%	0.0%	3.1%	1.6%	5.8%

Scheme 7: Unacceptable Performers 2022

Lab	Sample	Error	CAPA Response
223	03	False negative	Sample mix up
360	01-03	No results returned	Staffing issue
1470	08	False positive	Technical issue (unspecific weak pos)

Scheme 8

HLA Genotyping for Coeliac and other HLA Associated Disease

Scheme 8: HLA Genotyping for Coeliac and other HLA Associated Disease.

Purpose

Assess participants ability to correctly determine HLA type associated with various diseases e.g. coeliac disease, narcolepsy.

Satisfactory Performance

Making 10 sample reports in agreement with the reference genotype in a distribution year.

Assessment

Lab results reported in format identical to clinical report. Reference HLA result used for assesment.

10 blood samples over 3 distributions

Scheme 8: Performance

- 25 Unsatisfactory Performers (5 UK&I)

	2017	2018	2019	2020	2021	2022
Number of Participants (UK&I)	45 (9)	52 (10)	50 (11)	55 (12)	55 (10)	54 (11)
Number with Unsatisfactory Performance (< 100%) (UK&I)	15 (2)	14 (4)	13 (2)	17 (5)	12 (2)	25 (5)
% Unsatisfactory Performance	33% (22%)	27% (40%)	26% (18%)	31% (42%)	22% (20%)	46.3% (45.5%)

CAPA responses

- Sample mix up
- Transcription errors
- Kit interpretation error
- Reporting error

19/25 labs with unsatisfactory performance completed CAPA

Scheme 8: Unacceptable Performance by Disease

Disease	HLA Association	Number of Participants	No. of Participants with Unacceptable Performance
Coeliac	DQ2.5, DQ8, DQ2.2	54	25 (46%)
Narcolepsy	DQB1*06:02	21	5 (24%)
Actinic Prurigo	DRB1*04:07	3	0
Birdshot Retinopathy	A*29	9	0
Behçet's	B*51	15	1 (7%)
Rheumatoid Arthritis	DRB1*04	6	0
Diabetes	DR3, DR4	8	2 (25%)
Psoriasis	C*06	3	0
Allopurinol Hypersensitivity	B*58	3	0

Scheme 8: Coeliac Disease – Interesting Sample

Reference Genotype: DRB1*04:03, 11:01; DQB1*03:01 (DQ7), **03:05 (DQ8)**; DQA1*03:01, 05:05

- Performance:

  18/52 unacceptable performers
- Unusual HLA type

  DQB1*03:05 = DQ8

  Prevalence <1% population
- Issues

  Difference in detection capabilities

  Some commercial kits cannot detect DQB1*03:05

  Labs did not interpret DQB1*03:05 as DQ8

Submitted Result	Detection Limitation (where specified)	Assessment	Reason for Decision
HLA-DQB1*03:02 detected/positive		Unacceptable	HLA-DQB1*03:02 is not present
DQ8 negative		Unacceptable	DQ8 is present
DQ2.2 DQ2.5 DQ8 and beta subunit all negative	B-subunit HLA DQ2.2/2.5	Acceptable	DQ8 not listed in detection criteria
HLA-DQ8: Neg	HLA-DQB1	Unacceptable	Lab should be able to detect all DQB alleles
Absence of alleles DQB1*02 and DQB1*03:02	DQB1*02, DQA1*05 and DQB1*03:02	Acceptable	Lab can only define DQB1*03:02

Scheme 8: Summary of Unacceptable Performers 2022

Lab Details		Disease				CAPA Response Categories					
Location	Count	Behcets	Narcolepsy	Diabetes	Coeliac Disease	Sample Mix Up	Transcription Error	Interpretation of Results	Kit Issue	Technical Failure	No response
UK&I	5	1	0	0	5	1	0	2	3	0	1
RoW	20	0	4	2	19	2	4	5	3	2	6

CD Sample 10		Transcription Error	Interpretation of Results	Kit Issue	Technical Failure	No response
UK&I	4	0	2	2	0	1
RoW	11	2	3	3	1	5

UK NEQAS and BSHI Guideline: Laboratory Testing and Clinical Interpretation of HLA Genotyping Results supporting the Diagnosis of Coeliac Disease

Pritchard D, Anand A, De'Ath A, Lee H, Rees MT

Abstract/Summary

Coeliac disease is a common immune-mediated inflammatory disorder caused by dietary gluten in genetically susceptible individuals. While diagnosis of coeliac disease is based on serological and histological criteria, HLA-DQ genotyping can be useful, especially in excluding the diagnosis in patients who do not carry the relevant DQ heterodimers; *DQA1*05 DQB1*02, DQB1*03:02* or *DQA1*02 DQB1*02* (commonly referred to as DQ2.5, DQ8 and DQ2.2 respectively). External quality assessment results for HLA genotyping in coeliac disease have revealed concerning errors in HLA genotyping, reporting, and clinical interpretation. In response, these guidelines have been developed as an evidence-based approach to guide laboratories undertaking HLA genotyping for coeliac disease and provides recommendations for reports to standardise and improve communication of results.

UK NEQAS for H&I will be publishing a set of guidelines ratified by BSHI on Laboratory Testing and Clinical Interpretation of HLA Genotyping Results in the Diagnosis of Coeliac Disease.

Scheme 8: CD Interpretative Comments

- Option to record interpretative comments
- 56% currently report
- These comments are not currently assessed

Introduce formal assessment of these interpretative comments

Variety in format and level of detail:

Reference type - DQB1*02:01 (DQ2), 03:02 (DQ8); DQA1*03:01, 05:01

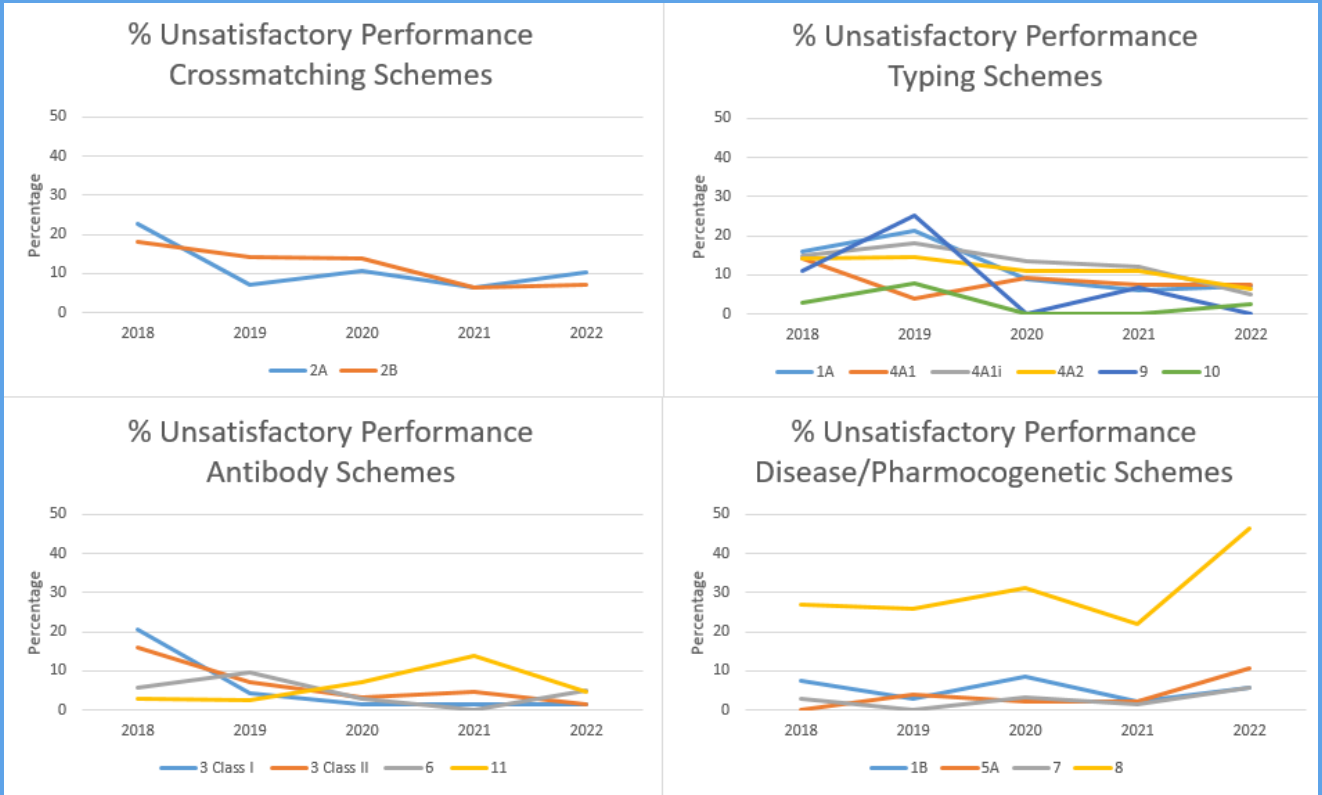
- The presence of HLA-DQ2 and DQ8(3) is associated with, but not diagnostic for, coeliac disease. HLA-DQ2 and DQ8(3) are present in about 21%and 10% respectively of caucasians in the normal population.
- This genotype is associated with genetic susceptibility for coeliac disease.
- This individual carries both the DQA1*05:01, DQB1*02:01 (HLA-DQ2) variant and the DQB1*03:02 (HLA-DQ8) variant associated with coeliac disease (Very high risk).
- Présence des allèles HLA-DQB1*02 (DQ2), DQA1*05 et DQB1*03:02 (DQ8). Risque très élevé de prédisposition à la maladie cœliaque.
- Coeliac Disease association positive, high risk.

Join a panel incorporating members of the UK NEQAS for H&I Steering Committee, Clinicians and volunteers dedicated to developing *proposed assessment* criteria for interpretative comments relating to Coeliac Disease.

Scheme Summary

Performance Summary for all Schemes

5 Year Trends in Unsatisfactory Performance



Do you have any questions?

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UK NEQAS for H&I
Educational Crossmatch Scenario (EDXM)

Dr Tracey Rees
UK NEQAS for H&I Director

UK NEQAS
Histocompatibility
& Immunogenetics

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

Whole Process ‘EQA’

Assessed Schemes

- 1A, 4A1, 4A2 – HLA Typing
- 6 – HLA Antibody Detection
- 3 – HLA Antibody Specification
- 2A, 2B – Crossmatching

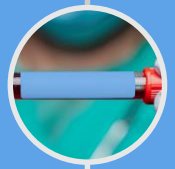
Educational Schemes

- Interpretative Educational Scenarios
- Educational Crossmatch Scheme
  - 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 (repertoires, cut-offs)

Educational Scheme Distribution

Educational Scheme Distribution

‘Donor’ Sample

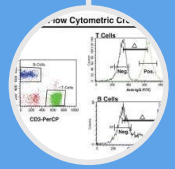


‘Patient’ Samples

3 x Serum Samples

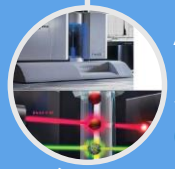
HLA Typing

(Schemes 4A1 & 4A2)



Crossmatching

(Schemes 2A & 2B)



Antibody Detection / Specification

(Schemes 3 & 6)

Clinical Interpretation
Transplant Risk Stratification

2022 Submissions

- 33 participants submitted results
- Not all labs reported results for all tests

- HLA genotype:

Consensus HLA Type	A*	B*	C*	DRB1*	DRB3*	DQA1*	DQB1*	DPA1*	DPB1*
	01	37	06	03 (17)	01	01	02	01	04:01
	02	57	06	13	02	05	06	01	04:02
Number of reports	33	33	33	33	26	31	33	24	29
% Labs in consensus	100%	100%	100%	100%	88%	100%	100%	100%	97%

DRB3 - 88% reported DRB3*01, DRB3*02; 8% reported DRB3*01, DRB3*-; 4% reported DRB3*02:02, DRB3*03:03.

DPB1 - 97% reported DPB1*04:01, DPB1*04:02; 3% reported DPB1*04:01, DPB1*04:01/10.

01

Serum 1

Results

Serum 1 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Positive	100% (32/32)	Multiple Cw antibodies >10,000 MFI
HLA Class II Antibodies	No Consensus	41% (13/32 Pos)	
DSA	Yes	100% (33/33)	Cw6 detected by 100% at range of 11088-27000 B57 detected by 70% at a range of 657-3036
CDC XM	PBL Negative T cell Negative B cell Negative	100% (4/4) 100% (14/14) 77% (10/13)	CDC Negative FCXM Positive
FCXM T Cell	Positive	96% (27/28)	
FCXM B Cell	Positive	85% (22/26)	
Transplant Risk	Contraindication/ High	81% (26/32)	19% stated medium risk
Immunological Advice	Not suitable for transplantation. High risk of AMR. Donor is homozygous Cw6 (antibody detected at >10,000).		
Recommendations	Seek alternative donor. Consider de-sensitisation. Monitor antibodies over time to consider de-listing.		

Serum 1 Results

EDXM Serum 1 also tested in Scheme 3 06/2022

	EDXM	No of labs	% consensus	Scheme 3	No of labs	% consensus
Number of Specificities Absent (reported by < 5% labs)	57			43		
Number of Specificities Present (reported by ≥ 75% labs)	16			18		
MFI >10000	Cw2, Cw4, Cw5, Cw6, Cw12, Cw15, Cw18	33	100%	Cw2, Cw4, Cw5, Cw6, Cw12, Cw15, Cw18	66	98.5-100%
MFI 5000 - 9999	B63, Cw1, Cw9, Cw10, Cw14, Cw16, Cw17		91-100%	Cw1, Cw9, Cw10, Cw14, Cw16, Cw17		92.5-100%
MFI 2000 - 4999	B49, Cw7, Cw8		64-100%	B63, Cw8		97-100%
MFI 1000-1999			N/A	A32 B49 B51		77.3-78.8%

02 Serum 2

Results

Serum 2 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Negative	94% (30/32)	
HLA Class II Antibodies	Positive	100% (32/32)	Multiple DR antibodies >10,000 MFI
DSA	Positive	97% (32/33)	DR13 and 17 detected by 97% at range of 11274-30740 DQ6 detected by 88% at a range of 817-18504
CDC XM	PBL No Consensus T cell Negative B cell Positive	50% (4/8) 93% (13/14) 100% (14/14)	T cell negative B cell positive
FCXM T Cell	Negative	86% (24/28)	
FCXM B Cell	Positive	100% (26/26)	
Transplant Risk	Contraindication/ High	97% (31/32)	1 lab defined this as a medium risk transplant
Immunological Advice	Not suitable for transplantation. High risk of hyperacute rejection.		
Recommendations	Seek alternative donor. Consider de-sensitisation. Monitor antibodies over time to consider de-listing.		

03 Serum 3

Results

Serum 3 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Negative	87% (27/31)	
HLA Class II Antibodies	Negative	97% (30/31)	
DSA	Negative	97% (32/33)	One lab reported DSA against DQA1*05:01 (9481 MFI)
CDC XM	PBL Negative T cell Negative B cell Negative	100% (4/4) 100% (14/14) 100% (14/14)	Negative
FCXM T Cell	Negative	100% (28/28)	
FCXM B Cell	Negative	100% (26/26)	
Transplant Risk	Standard/Low Risk	100% (32/32)	
Immunological Advice	Suitable for transplantation.		
Recommendations	Confirm ABO compatibility. Standard immunosuppression and post-transplant monitoring protocols.		

Summary of Crossmatch and DSA Detection Results

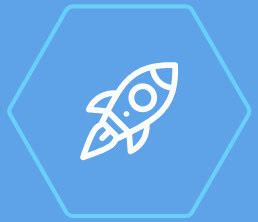
2022 Results		Serum 1		Serum 2		Serum 3	
DSA Defined by Luminex		Class I	Class II	Class I	Class II	Class I	Class II
MFI >10,000		Cw6 (100%)	N/A	N/A	DR17 (97%) DR13 (97%) DR52 (82%)	N/A	N/A
MFI 5,001-9,999		N/A	N/A	N/A	DQ6 (88%)	N/A	DQA1*05 (3%)
MFI 2,501-5,000		N/A	N/A	N/A	N/A	N/A	N/A
MFI <2,500		B57 (70%) B37 (3%)	DQ6 (18%)	N/A	DQA1*05 (3%)	N/A	N/A
CDCXM B CELL	No DTT	No consensus		Positive		Negative	
	DTT	Negative		Positive		Negative	
FCXM	T Cell	Positive		Negative		Negative	
	B Cell	Positive		Positive		Negative	
Risk		Contraindication/High (81%) Medium (19%)		Contraindication/High (97%) Medium (3%)		Standard (100%)	

The table shows the percentage of participants identifying a DSA and the most common MFI range it was reported in.

Benefits

Benchmarking

Monitor performance of multiple techniques
Make clinical interpretations on own results
Compare local policies for clinical assessment



Education

Monitor concordances
Review variations
Staff training

Competency

Laboratory staff
Clinical staff

Future Considerations

Formal Assessment

Basis of future scheme design

Complexity

How to assess the correct clinical interpretation

Workload

Participants
NEQAS team

Competency

Individual competency assessment

Any ideas?

Do you have any questions?

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