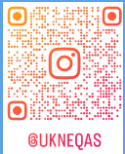


UK NEQAS H&I

Annual Participant's Meeting 2025-26



@UKNEQAS



Key Data from the Schemes
Amy De'Ath
UK NEQAS for H&I Manager





Meet The Team!

Director: Deborah Pritchard

Manager: Amy De'Ath

Deputy Manager: Melanie Bartley

Healthcare Scientist Practitioner: Geraint Clarke

QA Technical Officer: Jack Jefferies

MLA: Sue Davies



UK NEQAS for H&I Steering Committee 2025-26



Helena Lee (Chair)

Arthi Anand

Katy Derbyshire

Sylvia McConnell

Katherine Mounsey

Anthony Calvert

Sunil Daga (Clinical Representative)

Fotini Partheniou (BSHI Representative)



Rhys Goodhead (Expert Advisor Scheme 5B)

Barbara McNamara (Expert Advisor Scheme 5B)

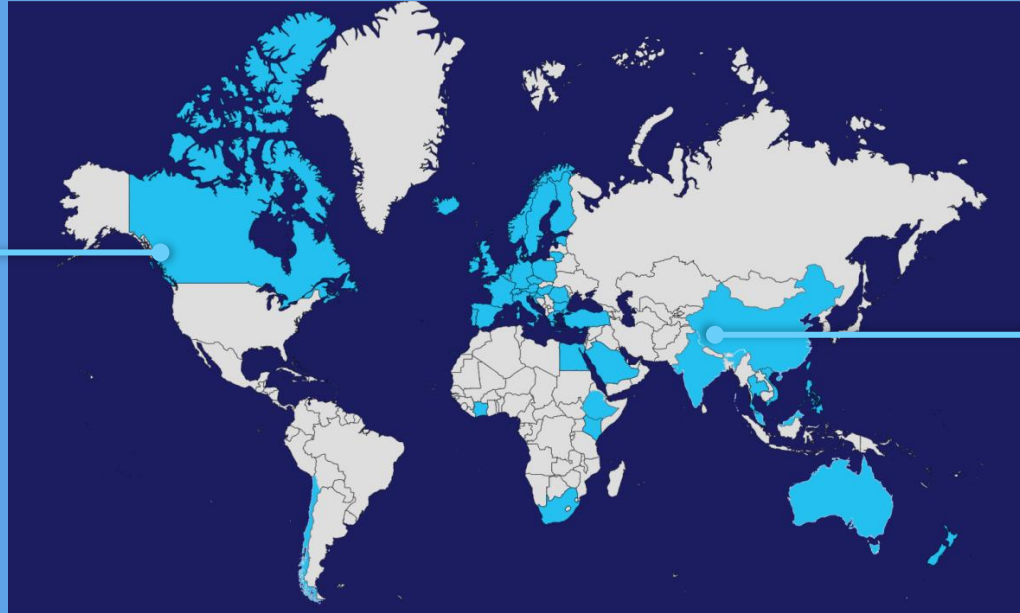
Tim Clench (Expert Advisor Scheme 5B)



UK NEQAS for H&I: An Overview



>320 participants



>50 countries



Things To Note...



Presentation Focus...

Performance, key trends, discussion points and 2026 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 disease association and drug hypersensitivity schemes or in some schemes if consensus not reached
 - ▶ *e.g. Scheme 8: HLA Genotyping for Coeliac and Other HLA Associated Diseases*
- Equivocal result only accepted for Scheme 2B.
- All Not Tested (NT) results excluded from assessment.
- Labs that fail to return results or do not provide a 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 2026-27

Schemes



- Scheme 5A – result deadline extended
- Scheme 10 – HPA-9 added
- Scheme 12 – HNA Genotyping
- Scheme 13 – HNA Antibody Detection

Portal

New Participant Portal



Pilot Scheme

Interpretative comments for Coeliac Disease



Sustainability

Paperless: no distribution slips
Packaging: reduce plastic



New Participant Portal



Old System



End of life



Commercial system – expensive to buy and run



Expensive to develop functionality



New System



Increased security



Easier to use, Microsoft based



Increased functionality and management





Scheme



2A

Cytotoxic Crossmatching



Scheme 2A – Cytotoxic Crossmatch



Purpose

Assess participants ability to determine cell/serum cytotoxicity crossmatch status



Satisfactory Performance

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



Consensus

At least 75% agreement on pos/neg result

10 blood samples, 40 serum samples over 5 distributions

Scheme 2A: Performance



All cells with and without DTT	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	71 (22)	66 (16)	63 (15)	59 (15)	47 (10)	47 (8)	45 (8)
Number with Unsatisfactory Performance (< 85%) (UK&I)	5 (1)	7 (0)	4 (0)	6 (3)	2 (2)	5 (0)	5 (0)
% Unsatisfactory Performance (UK&I)	7.0% (4.5%)	10.6% (0)	6.3% (0)	10.2% (20%)	4.2% (20%)	10.8% (0%)	11.1% (0%)

2025: 5 Unsatisfactory Performers (0 UK & Ireland)



Scheme 2A: Performance by category



	PBL	PBL +DTT	T Cell	T Cell +DTT	B Cell	B Cell +DTT
Crossmatches assessed (n=40) (UK&I)	35 (35)	36 (36)	38 (39)	38 (39)	32 (28)	35 (34)
NT – Assessed samples only	10.4%	13.4%	8.9%	8.1%	14.6%	12.3%
% incorrect assignments	3.6%	3.6%	2.8%	2.1%	4.8%	3.8%
False Positive	2.3%	2.8%	1.7%	1.5%	2.4%	2.0%
False Negative	1.3%	0.8%	1.1%	0.6%	2.4%	1.8%



Scheme 2A: Unacceptable Performers 2025



Lab ID	PBL -DTT	T -DTT	B -DTT	PBL + DTT	T + DTT	B + DTT	Lab Identified Error
147						79%	<i>No response</i>
189	81%						Technical issue– new controls implemented
232			76%			72%	Sample delivery delay - poor cell prep
1399			82%				Human error - report mix up & technical interpretation
1412		56%	36%				<i>No response</i>





Scheme 2A: Discussion

- Not all Scheme 2A results expected to reach consensus
- 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



Consensus

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



Satisfactory Performance

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



10 blood samples, 40 serum samples over 5 distributions



Scheme 2B: Performance



	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	84 (23)	80 (21)	80 (22)	84 (19)	83 (21)	79 (20)	75 (20)
Number with Unsatisfactory Performance ($< 85\%$) (UK&I)	12 (1)	11 (0)	5 (0)	6 (2)	10 (0)	4 (0)	4 (1)
% Unsatisfactory Performance (UK&I)	14.2% (4.3%)	13.8% (0)	6.3% (0)	7.1% (10.5%)	12% (0)	5% (0)	5.3% (5%)

2025: 4 Unsatisfactory Performers (1 UK & Ireland)



Scheme 2B: Performance by Category



	T Cells			B Cells		
	UK&I	RoW PC	RoW WB	UK&I	RoW PC	RoW WB
Number of participants	20	25	30	20	25	28
Number of XM assessed (>75% consensus)	34/40 (85%)	32/40 (80%)	38/40 (95%)	35/40 (87.5%)	33/40 (82.5%)	35/40 (87.5%)
Number of Positive XM	15 (47%)	12 (31%)	17 (45%)	24 (69%)	21 (64%)	23 (66%)
Number of Negative XM	18 (53%)	20 (63%)	21 (55%)	11 (31%)	12 (36%)	12 (34%)
Number of incorrect assignments	12	18	39	31	36	55
Number of False Pos	6	6	9	16	9	10
Number of False Neg	6	9	25	15	23	41
Number of equivocal assignments	0	3	5	0	4	4
Number of samples NT	27	86	39	65	95	40

UK&I and RoW receive different blood samples



Scheme 2B: Unacceptable Performers 2025

Lab	T Cell	No. of results submitted	B Cell	No. of results submitted	Issue
23	94%	40/40	81%	40/40	Sensitivity issues/cut off values
139	94%	40/40	72%	39/40	<i>No response</i>
142	88%	40/40	83%	40/40	To review cut off values
1463	89%	32/40	76%	32/40	Sensitivity issue (delivery delays/poor cell prep)

4 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

Satisfactory Performance

80% reports agree with consensus in distribution year



Consensus

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

12 serum samples over 3 distributions





Scheme 6: Performance

8 Unsatisfactory Performers (6 UK&I)

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	82 (25)	74 (25)	71 (23)	68 (23)	68 (23)	67 (24)	62 (22)
Number with Unsatisfactory Performance (< 80%) (UK&I)	8 (0)	2 (0)	0 (0)	4 (0)	3 (0)	3 (1)	8 (6)
% Unsatisfactory Performance	9.7% (0%)	2.7% (0%)	0% (0%)	5% (0%)	4.4% (0)	4.4% (4.1%)	13% (27%)

63% negative
29% positive
8% samples not assessed





Scheme 6: Unacceptable Performers 2025

Lab	Performance (<80%)	Issue	CAPA
14	75%	False Pos CI and CII	Kit / bead reactivity
20	50%	False Pos CI and CII	Interpretation (pos cut off)
25	67%	False Pos CI and CII	Interpretation (pos cut off)
35	58%	False Pos/Neg CI and CII	Reagent / testing issues
45	75%	False Pos CI	Sensitivity issues
48	75%	False Pos CI and CII	Sensitivity issues
189	75%	False Pos/Neg CII	Interpretation / cut off values
1418	25%	False Pos CI and CII	Interpretation / kit issue

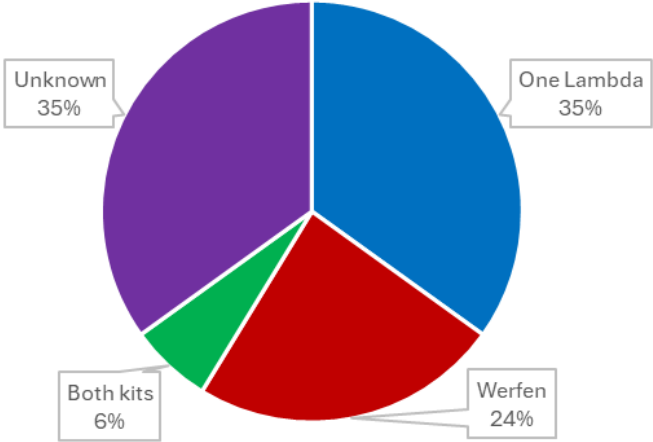
8 labs with UP (<85%)



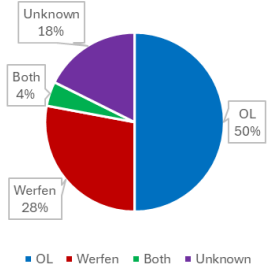
Scheme 6: Kit Use



Manufacturer of Kit Used for Antibody Detection 2025-26
(n=63)



Manufacturer of Kit Used for Antibody Detection
(n=68)



Scheme 6: Kit Use and Performance



2025-26	Consensus		Class I						Class II					
	Class I	Class II	One Lambda (n=22)	%	Both (n=4)	%	Werfen (n=15)	%	One Lambda (n=22)	%	Both (n=4)	%	Werfen (n=15)	%
601	Negative	Negative	Negative	86%	Negative	75%	Negative	93%	Negative	91%	Negative	100%	Negative	100%
602	Positive	Positive	Positive	100%	Positive	100%	No Consensus	60%	Positive	100%	Positive	100%	Positive	100%
603	Positive	Positive	Positive	100%	Positive	100%	Positive	100%	Positive	100%	Positive	100%	Positive	100%
604	Negative	Negative	Negative	95%	Negative	100%	Negative	100%	Negative	86%	No Consensus	50%	Negative	87%
605	Negative	No Consensus	Negative	95%	Negative	100%	Negative	100%	No Consensus	59%	Negative	75%	Positive	92%
606	Positive	Positive	Positive	100%	Positive	100%	Positive	93%	Positive	100%	Positive	100%	Positive	100%
607	Negative	Negative	Negative	77%	Negative	75%	Negative	100%	Negative	91%	Negative	100%	Negative	100%
608	Negative	Negative	Negative	91%	No Consensus	50%	Negative	93%	Negative	82%	Negative	100%	Negative	93%
609	Negative	Negative	No Consensus	68%	No Consensus	50%	Negative	100%	Negative	86%	Negative	100%	Negative	100%
610	Negative	Positive	Negative	95%	Negative	100%	Negative	100%	Positive	100%	Positive	100%	Positive	100%
611	Negative	Negative	Negative	95%	No Consensus	50%	Negative	100%	Negative	91%	No Consensus	50%	Negative	100%
612	Negative	No Consensus	Negative	95%	Negative	100%	Negative	100%	No Consensus	73%	Positive	100%	Negative	92%



Scheme

3

HLA Antibody Specificity Analysis



Scheme 3: HLA Antibody Specificity Analysis



Purpose

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



Consensus

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

Satisfactory Performance

75% reports agree with consensus in distribution year



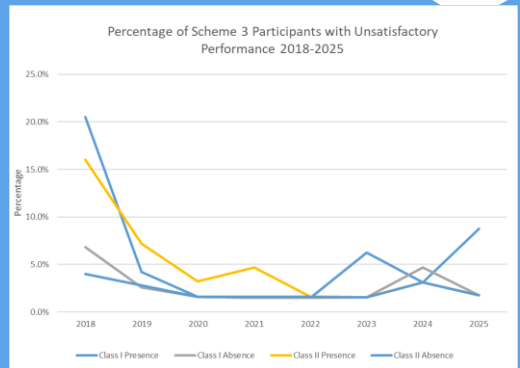
10 serum samples over 3 distributions



Scheme 3: Performance



Class I		2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)		70 (25)	64 (24)	65 (24)	65 (24)	64 (24)	63 (23)	58 (23)
Number with Unsatisfactory Performance (UK&I)	Presence	3 (0)	1 (0)	1 (0)	1 (0)	4 (0)	2 (0)	5 (1)
	Absence	2 (0)	1 (0)	1 (0)	1 (0)	1 (0)	3 (0)	1 (0)
% Unsatisfactory Performance	Presence	4.2%	1.6%	1.5%	1.5%	6.3%	3.2%	8.6%
	Absence	2.6%	1.6%	1.5%	1.5%	1.5%	4.8%	1.7%



Overall: 6 labs with UP (2 UK&I)

Class II		2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)		69 (25)	63 (24)	64 (24)	64 (24)	64 (24)	63 (23)	58 (23)
Number with Unsatisfactory Performance (UK&I)	Presence	5 (0)	2 (0)	3 (0)	1 (0)	1 (0)	2 (0)	1 (0)
	Absence	2 (0)	1 (0)	1 (0)	1 (0)	1 (0)	2 (0)	2 (0)
% Unsatisfactory Performance	Presence	7.2%	3.2%	4.7%	1.6%	1.6%	3.2%	1.7%
	Absence	2.8%	1.6%	1.6%	1.6%	1.6%	3.2%	3.4%





Scheme 3: Unacceptable Performers 2025

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

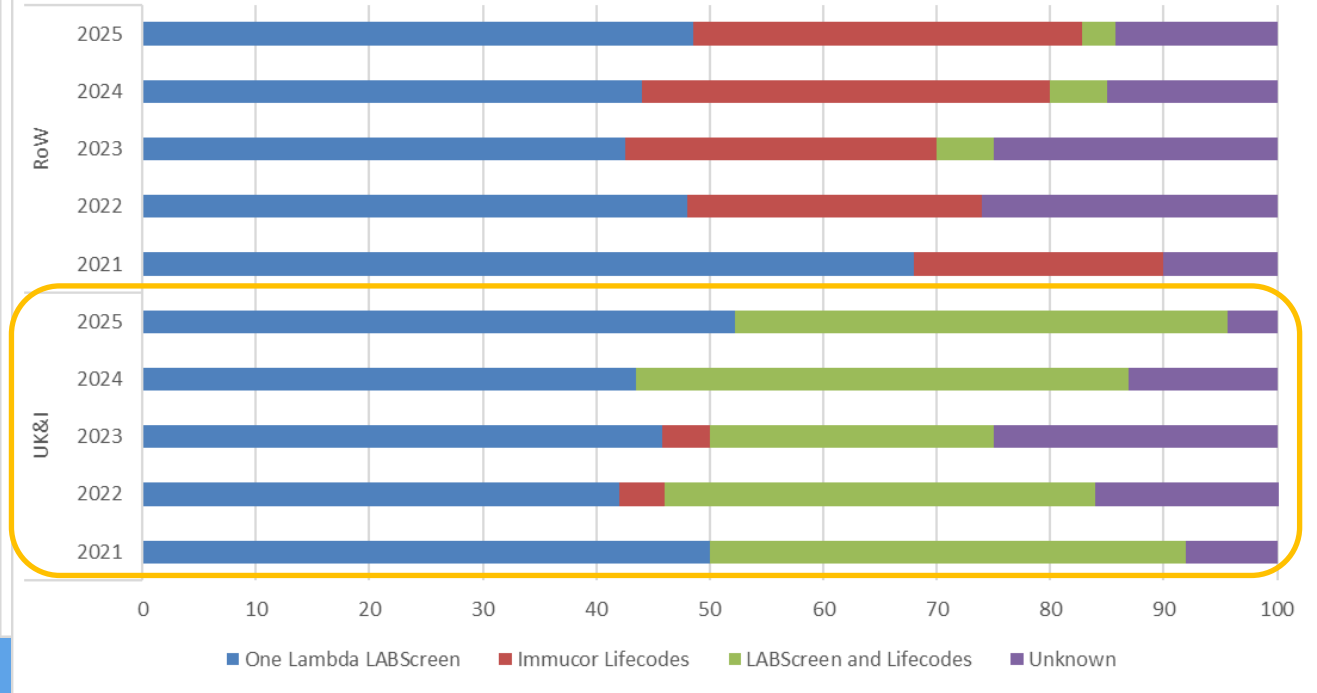
Lab	Class I		Class II		CAPA	Kit
	Presence	Absence	Presence	Absence		
15	67%				Clerical reporting error	One Lambda
35	74%				Analyser issues & testing strategy	One Lambda
112	73%				Only use one kit for testing	Werfen
302		69%	51%	56%	<i>No response</i>	One Lambda
361	68%				Only use one kit for testing	Werfen
1412	40%				<i>No response</i>	Werfen



Scheme 3: Kit Use 2021-2025



Scheme 3 Commercial Kit Use 2021-2025



Overall OL kits are the most widely used

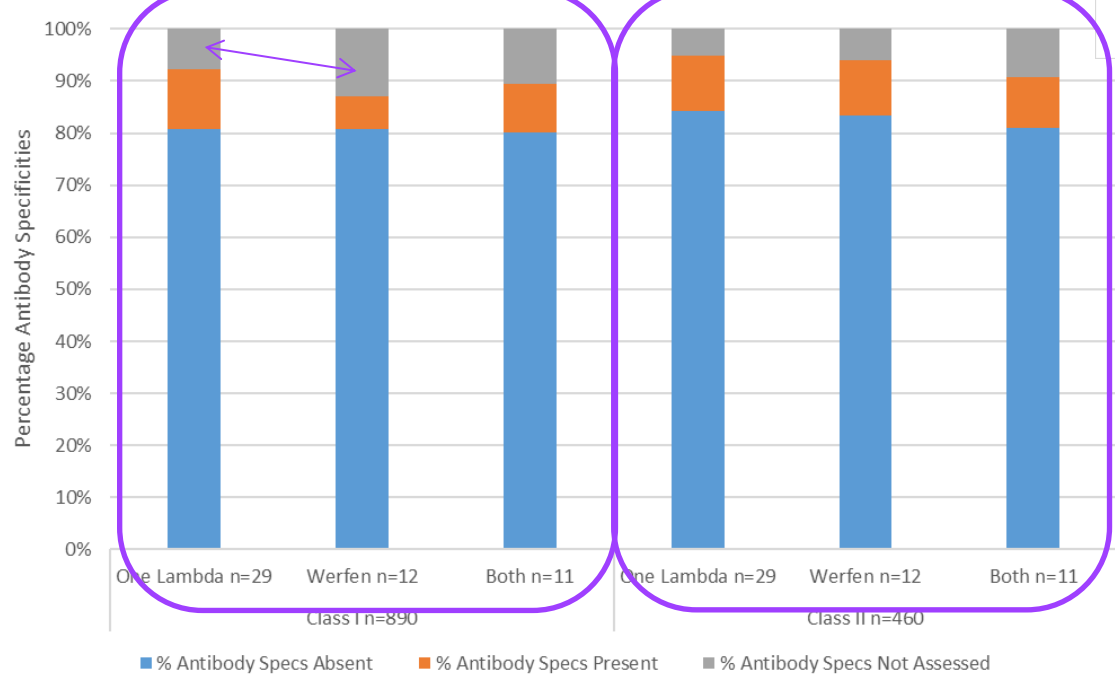
UK&I labs are more likely to use a combination of kits

Werfen only kit use more prevalent in RoW labs

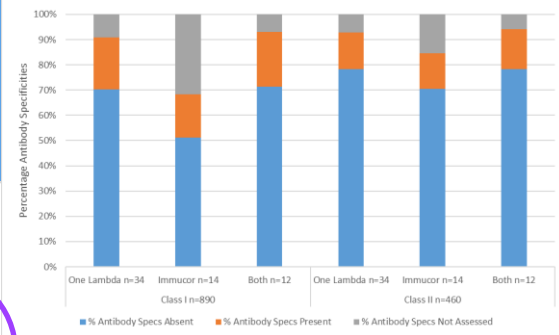
Scheme 3: Results by Kit Use



Scheme 3 2025 - Comparison of HLA Antibody Specificity Results Between Kits



Scheme 3 2024 - Comparison of HLA Antibody Specificity Results Between Kits



Similar percentage of antibodies reach consensus present (orange) in both kits

Slightly less concordance in 'present' CI antibodies

Marginally more antibodies classed as not assessed in Werfen group

Scheme 3: Kit Use and Performance



Average overall satisfactory performance for detecting the 'presence' and 'absence' of antibodies:

Average Performance	Class I			Class II		
	One Lambda (n=29)	Werfen (n=12)	Both kits (n=11)	One Lambda (n=29)	Werfen (n=12)	Both kits (n=11)
2025-26						
Presence	95.1%	76.7%	89.4%	98.3%	92.9%	92.2%
Absence	98.4%	96.7%	99.3%	98.4%	98.0%	98.5%

Average Performance	Class I			Class II		
	One Lambda (n=34)	Werfen (n=14)	Both (n=12)	One Lambda (n=34)	Werfen (n=14)	Both (n=12)
2024-25						
Presence	94.1%	86.5%	97.2%	94.5%	89.7%	97.8%
Absence	97.5%	94.2%	99.5%	97.4%	95.3%	99.5%

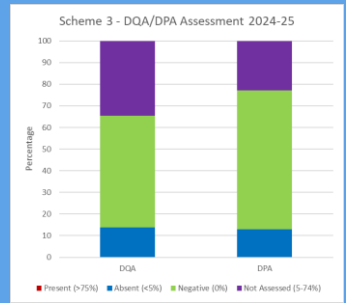
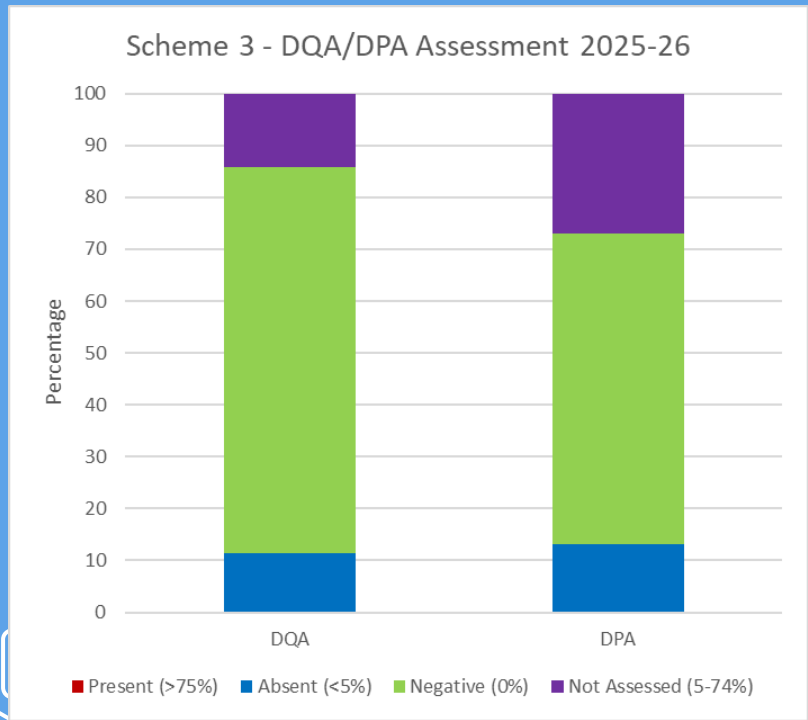
Scheme 3: DQA/DPA Antibody Reporting



Reporting of antibodies to HLA-DQA and -DPA is optional and not assessed.

Overall 44/60 (73%) report DQA, 38/60 (63%) report DPA

Previously 67% and 60%



An analysis of the data submitted for DQA and DPA antibodies in 2025-26 and 2024-25 was performed.

Large proportion of samples are negative or consensus absent.

No antibodies deemed positives.

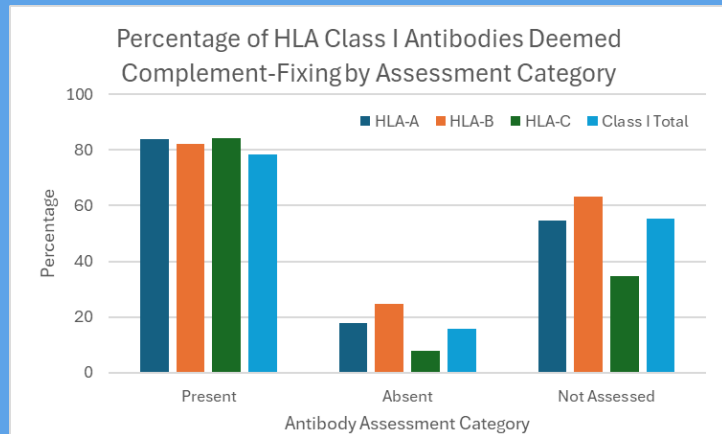
Approx 15-30% not assessed, higher in DPA.

Scheme 3: Reporting Complement Fixing Antibodies



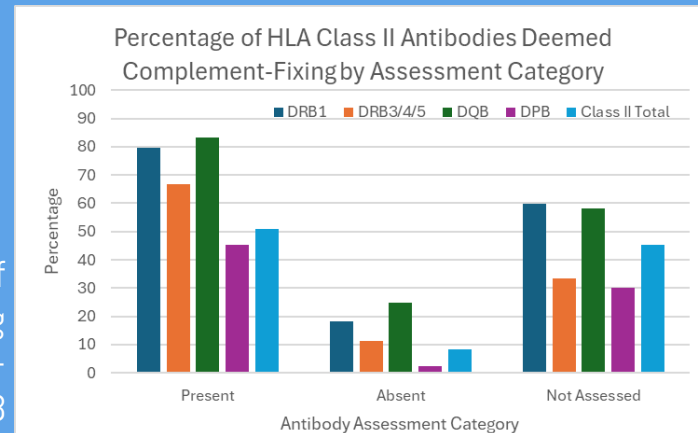
Option to report complement-fixing antibodies, but not formally assessed.

Max 22.9% (14/61) participants (6 UK&I) reported complement-fixing antibodies in at least one of the 10 samples in the 2024-25 distribution year.



The most frequent reporting of class I complement-fixing antibodies occurred at HLA-B>A>C

The most frequent reporting of class II complement-fixing antibodies occurred at HLA-DQB1>DRB3/4/5>DRB1>DPB





Scheme



11

HPA Antibody Detection/Specification



Scheme 11: HPA Antibody Detection/Specification

Purpose

Assess participants ability to correctly determine presence and specificity 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

- 5 Unsatisfactory Performers (0 UK&I)

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	39 (5)	42 (4)	43 (4)	43 (4)	43 (4)	44 (4)	43 (4)
Number with Unsatisfactory Performance (< 75%) (UK&I)	1 (0)	3 (0)	6 (0)	2 (0)	9 (0)	1 (0)	5 (0)
% Unsatisfactory Performance	2.6%	7.1%	13.9%	4.5%	20.9%	2.3%	11.6%



Scheme 11: HPA Antibody Detection/Specification

2025-26 Sample	HPA Detection	HLA Detection	Expected Result	HPA Antibody Consensus	
				Presence	Absence
1	87.5% Pos	62.5% Neg	HPA-3a	HPA 3a 87.5%	HPA 4a 97.3%
2	100% Neg	97.5% Neg	HPA neg, HLA neg	N/A	N/A
3	100% Pos	100% Pos	HPA-5b, HLA pos	HPA 5b 100%	HPA GP1a/11a 95%
4	100% Neg	97.5% Neg	HPA neg, HLA neg	N/A	N/A
5	97.6% Neg	90% Neg	HPA neg, HLA neg	N/A	HPA 5b 97.6%
6	95.1% Pos	100% Pos	HPA-1b 3b 5b	HPA 1b 95.1%, 3b 92.7%, 5b 97.6%	HPA 2b 97.4, 4b 97.2% GP1a/11a 97.5%
7	85.7% Pos	50% Pos	HPA-5b, HLA pos	HPA 5b 85.7%	HPA 11a/11b 97.5% 1a/11a 95%
8	100% Neg	100% Neg	HPA neg, HLA neg	N/A	N/A





Scheme 11: Unacceptable Performers 2025

Lab	HPA Presence	HPA Absence	Samples reported	Method	Error
180	67%	100%	8/8	Werfen PakPlus	Sensitivity / resolution issue
199	67%	88%	8/8	Werfen PakLx	Age of samples / sensitivity issues
281	100%	63%	8/8	Werfen PakLx	Interpretation issue
387	50%	100%	8/8	In house	<i>No response</i>
405	67%	100%	8/8	Werfen PakLx	Staff shortage, result entry error

5 lab with UP (<75%)

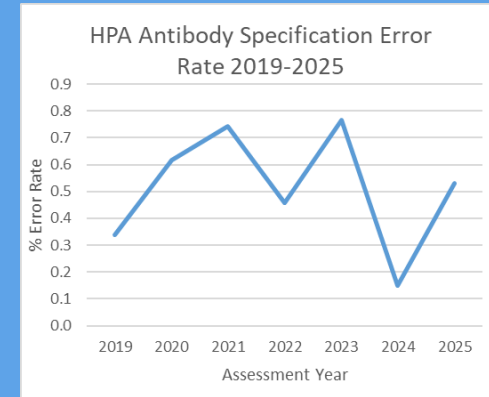




Scheme 11: Analysis of Errors 2025

- Error rate extremely low (overall 0.53%) but errors often at clinically relevant polymorphisms.
- Errors found at HPA-1b (n=2, error rate 0.6%), 2b (n=1, error rate 0.3%), 3a (n=5, error rate 1.5%), 3b (n=3, error rate 0.9%), 4a (n=1, error rate 0.3%), 5b (n=1, error rate 0.3%) and some glycoproteins.

Errors 2025	HPA-1a	HPA-1b	HPA-2a	HPA-2b	HPA-3a	HPA-3b	HPA-4a	HPA-4b	HPA-5a	HPA-5b	HPA-6a	HPA-6b	HPA-15a	HPA-15b	GP IIb/IIIa	GP Ia/IIa	GP Ib	GP IV	CD109	Total
False Pos	0	0	0	1	0	0	1	1	0	1	0	0	0	0	1	5	0	0	0	10
False Neg	0	2	0	0	5	3	0	0	0	7	0	0	0	0	0	0	0	0	0	17
Total Errors	0	2	0	1	5	3	1	1	0	8	0	0	0	0	1	5	0	0	0	27
% Error Rate	0.0	0.6	0.0	0.3	1.5	0.9	0.3	0.3	0.0	2.3	0.0	0.0	0.0	0.0	0.3	1.5	0.0	0.0	0.0	0.53
Total Tested	336	336	312	312	336	336	312	296	344	344	96	96	128	128	328	328	304	296	136	5104



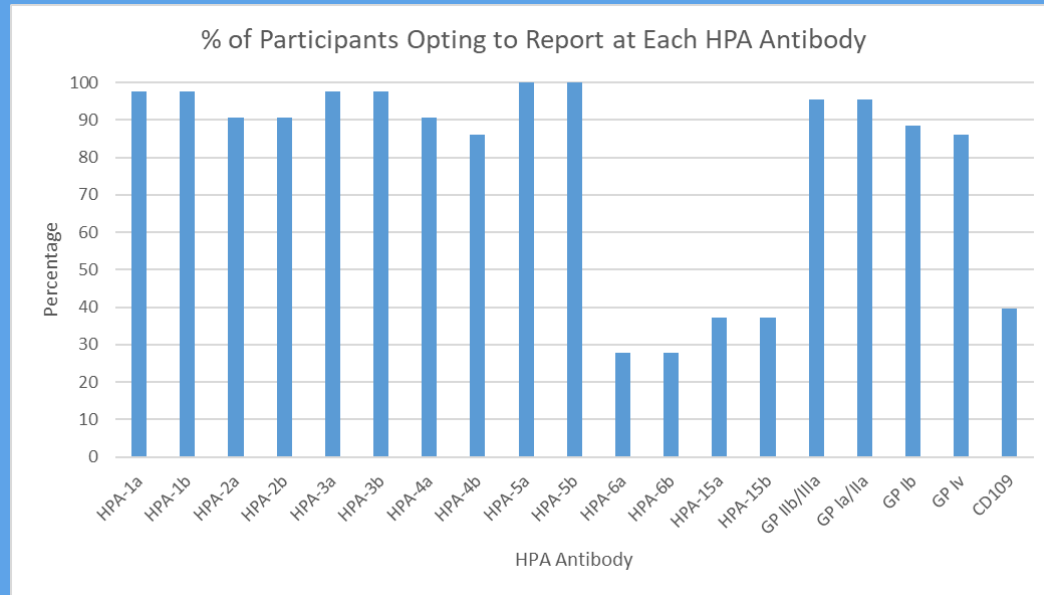
- False negative (n=17) more common than false positive (n=10) errors.
- Most labs had only 1 error

Number of Errors	Number of Labs
1	14
2	2
3	2



Scheme 11: Selection of HPA Antibodies for Assessment

- Originally introduced in 2024-25
- Labs can select any/all HPA antibodies for assessment based on their clinical strategy



Thanks!

Do you have any
questions?

UKNEQASHandl@Wales.NHS.UK

+44(0)1443 622185

www.ukneqashandi.org.uk



Key Data from the Schemes
Deborah Pritchard
UK NEQAS for H&I 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

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	38 (5)	34 (4)	33 (2)	28 (1)	23 (0)	19 (0)	14 (0)
Number with Unsatisfactory Performance (< 90%) (UK&I)	8 (1)	3 (1)	2 (0)	2 (0)	2 (0)	0 (0)	2 (0)
% Unsatisfactory Performance	21.1%	8.8%	6.1%	7.1%	8.7%	0%	14.3%






Scheme 1A: 2025 Incorrect Assignments

6/140 (4.3%) incorrect HLA types in 2025 reported by 3 labs:

- 4 reports that contained broad not split specificity (e.g. B40 v B60)
- 0 reports that contained an incorrect split specificity (e.g. B64 not B65)
- 0 reports with molecular based nomenclature (e.g. A01 v A1)
- 3 reports with incorrect specificity
- 0 reports of missed or homozygous assignments
- 0 clerical/typo error



2 labs with
unsatisfactory
performance



Scheme 1A: 2025 Incorrect Assignments (not resulting in UPs)



Lab ID	Sample	Report
120	03 10	1A 03/2025: Reported A1, 36 consensus A1,1 1A 10/2025: Reported DR1, 15 , consensus DR1,4
147	04 06 09 10	1A 04/2025: Reported B40 (broad), consensus B60 (split) 1A 06/2025: Reported B14 (broad), consensus B64 (split) 1A 09/2025: Reported B14 (broad), consensus B65 (split) 1A 10/2025: Reported B14 (broad), consensus B65 (split)



The background is a solid blue color. In the top left, there is a large white hexagon containing a smaller white hexagon with a dark blue 'Q' and a teal diagonal line. To its right is a white outline of a test tube. In the top right, there are several dark blue hexagons of varying sizes and a small light blue circle. In the bottom right, there is a white molecular structure consisting of interconnected hexagons and lines.

Scheme

4A1

DNA Typing at 1st Field Resolution

Scheme 4A1: HLA 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

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

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	100 (28)	88 (26)	82 (25)	81 (25)	81 (25)	84 (24)	85 (24)
Number with Unsatisfactory Performance (< 90%) (UK&I)	4 (1)	8 (0)	6 (1)	7 (0)	11 (1)	6 (2)	4 (0)
% Unsatisfactory Performance	4% (3.6%)	9.1% (0%)	7.3% (4%)	8.4% (0%)	13.6% (4%)	7.1% (8.3%)	4.7% (0%)



Scheme 4A1: 2025-26 Incorrect Assignments

40/11923 (0.34%) errors reported by 15 different labs (0 UK&I) – last year 0.12%

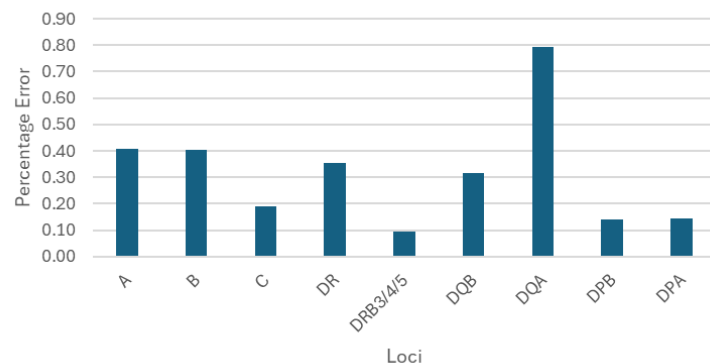
21 HLA types contained an error:

- 9 missed assignment (reported homozygous when heterozygous)
- 4 samples with the wrong genotype reported
- 3 samples with incorrect assignments *e.g. A*68 rather than A*24*
- 3 samples with no results submitted
- 1 reporting error (DQB results switched with DQA)
- 1 samples with DRB3/4/5 presence/absence reported incorrectly

12 (57%) HLA types with one error
9 (43%) HLA types with multiple errors

11 (73%) labs made 1 error
2 (13%) labs made 2 errors
2 (13%) lab made 3 errors

Scheme 4A1 - Percentage Error by Loci 25/26



Scheme 4A1: Unacceptable Performers 2025



Lab	Sample	Error	CAPA Response
133	09+10	? sample mix up	Transcription error
213	08-10	No results submitted	<i>No response</i>
1412	05+10	DQA1* and DQB1* missed assignments	Transcription error / reporting errors
1446	02+04	A* and DQA1* incorrect assignments	<i>No response</i>





Scheme



Interpretive HLA Genotype



Scheme 4A1: Interpretive HLA Genotype



Purpose

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



Consensus

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

Satisfactory Performance

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



10 HLA genotypes from Scheme 4A1





Scheme 4A1i: Performance

- 1 lab with unsatisfactory performance (0 UK&I)

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	44 (22)	44 (22)	42 (21)	40 (21)	40 (21)	41 (20)	42 (20)
Number with Unsatisfactory Performance (< 90%) (UK&I)	8 (1)	6 (2)	5 (1)	2 (0)	1 (0)	5 (0)	1 (0)
% Unsatisfactory Performance	18.1%	13.6%	11.9%	5.0%	2.5%	12.2%	2.4%

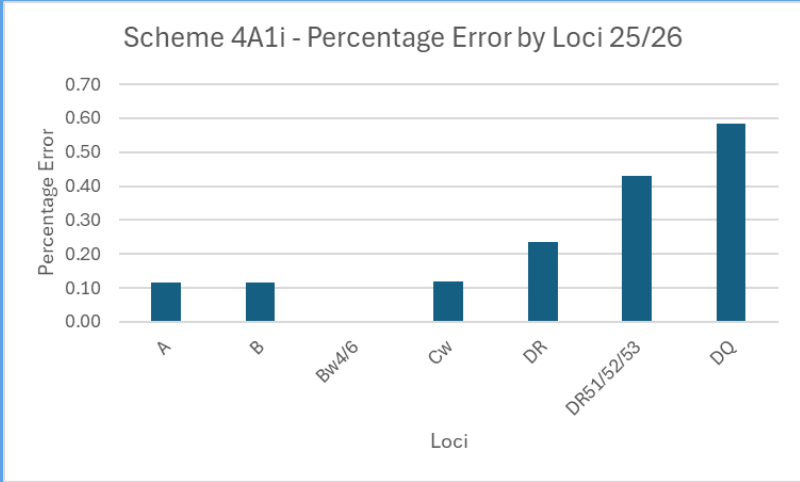
Scheme 4A1i: 2025-26 Incorrect Assignments



- 14/5874 (0.24%) incorrect results reported by 8 different labs (2 UK&I) – last year 0.22%
- 11 phenotypes contained an error:
 - 2 samples with missing assignment (reported homozygous when heterozygous)
 - 3 samples with errors at presence/absence of DR51/52/53 (2 UK)
 - 3 reporting at broad not split specificity level
 - 3 samples with incorrect assignments

7 (88%) labs made 1 error
1 (12%) lab made 4 errors

9 (81%) HLA types with single errors
2 (18%) HLA types with multiple errors



Scheme 4A1i: Unacceptable Performers 2025



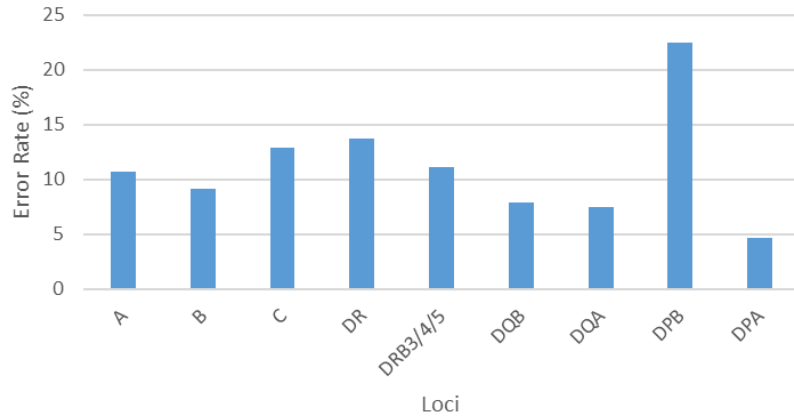
Lab	Sample	Error	CAPA Response
1418	03,04,05+10	Broads instead of splits/multiple reporting errors	<i>No response</i>



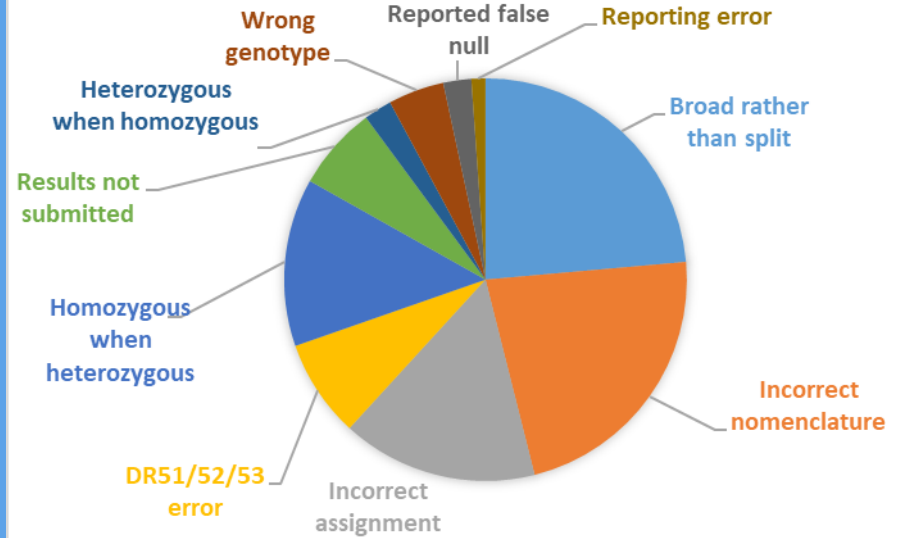


Scheme 4A1: Types of Errors 2020-2025

Scheme 4A1 - Error Rate by Loci (2020-2025)



SCHEME 4A1 - TYPES OF ERRORS (2020-2025)



Scheme 4A1i: Serological Equivalents



- 4A1i Interpretative HLA Genotyping, which allows participants to translate genotypes to phenotypes
- Participants are expected to report to the 'split' specificity level using serological nomenclature, e.g. HLA-DQB1*03:01 should be reported as DQ7 (DQ3)
- Knowledge and exposure of phenotyping and converting between genotypes and phenotypes may no longer be so commonplace

Reliance on LIMS/analysis software

No longer perform phenotyping

- Errors common due to reporting issues (broad rather split or using incorrect nomenclature)
- CAPA repeatedly cite issues due to staff training and knowledge
- Encourage utilisation of 4A1i for competency assessment

UK NEQAS have developed a template:

<https://ukneqashandi.org.uk/app/uploads/2025/03/Scheme-4A1i-Template.docx>

UK NEQAS
Education | Quality | Global

Histocompatibility & Immunogenetics

Scheme 4A1i – Competency Assessment Template

Task: Convert HLA genotypes reported in Scheme 4A1i to 'split specificity' level phenotypes (minimising computer aided assistance).

Learning Objective: Accurately demonstrate knowledge of serological equivalents.

Name _____ **Date** _____

Note resources used e.g. The HLA dictionary tool (if applicable): _____

Example:

Genotype	A*	A*	B*	B*		C*	C*	DR*	DR*	DRB3/4/5*	DRB3/4/5*	DQB1*	DQB1*	Score
Sample ID	01	11	55	57		03:03	06	03:01	07	DRB3*01	DRB4*01N	DQ	03:03	Acceptable
07/2024														
Phenotype	A	A	B	B	Bw4*	Bw6*	Cw	DR	DR	DRB1/52/53*	DRB1/52/53*	DQ	DQ	
Serological Equivalent	1	11	55	57	Present	Present	9	6	17	7	DR52	N/A	2	9
Assessment**	Correct	Correct	Correct	Correct	Correct	Correct	Correct	Correct	Correct	Correct	Correct	Correct	Correct	

**Indicate Presence or Absence
***Each full phenotype (compared to consensus result on UK NEQAS Portal) deemed acceptable

Genotype	A*	A*	B*	B*		C*	C*	DR*	DR*	DRB3/4/5*	DRB3/4/5*	DQB1*	DQB1*	Score
Sample ID														
XX/20XX														
Phenotype	A	A	B	B	Bw4*	Bw6*	Cw	DR	DR	DRB1/52/53*	DRB1/52/53*	DQ	DQ	
Serological Equivalent														
Assessment**														

**Indicate Presence or Absence
***Each full phenotype (compared to consensus result on UK NEQAS Portal) deemed acceptable





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

- 41/63 participants registered for 2nd field
- 21/63 participants registered for 3rd field

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

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	62 (20)	64 (20)	63 (22)	61 (23)	65 (23)	67 (23)	63 (23)
Number with Unsatisfactory Performance (< 90%) (UK&I)	9 (1)	7 (0)	6 (0)	4 (0)	9 (2)	8 (1)	5 (0)
% Unsatisfactory Performance	14.5%	11.0%	11.1%	6.5%	13.8% (8.7%)	11.9% (4.3%)	7.9%





Scheme 4A2: Incorrect Assignments: 2nd Field

71/8530 (0.83%) incorrect HLA alleles reported by 4 labs (0 UK&I) – last year (0.79%)

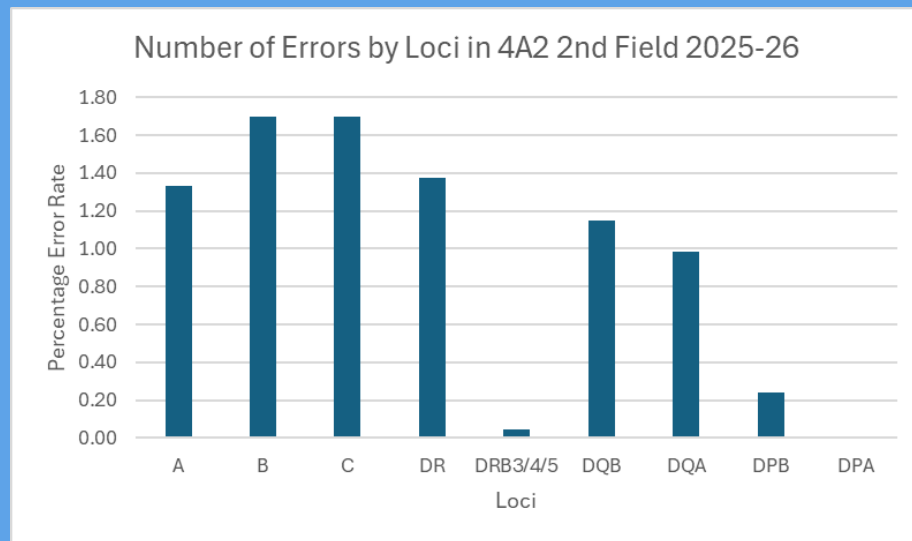
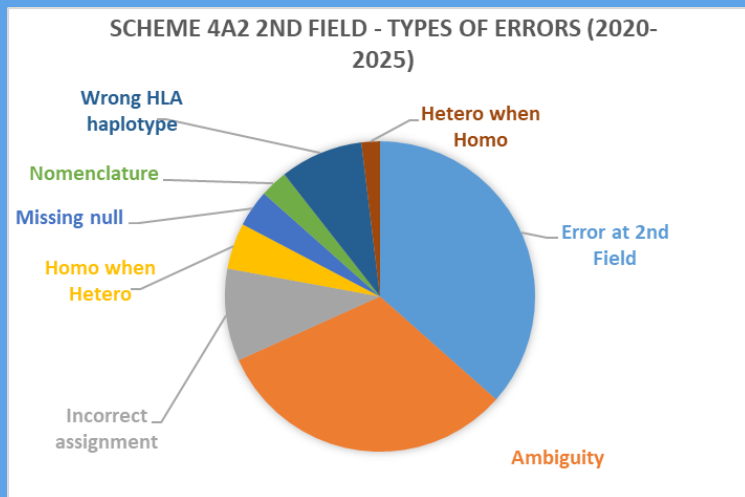
- 1 incorrect assignment
- 3 reports of errors at the 2nd field

*e.g. DQA1*03:02 rather than DQA1*03:03*

- 7 reports of the wrong HLA type

3 (27%) HLA types with a single error
8 (73%) HLA types with multiple errors

2 (50%) labs made 1 error
1 (25%) lab made 2 errors
1 (25%) lab made 7 errors



Scheme 4A2: Incorrect Assignments: 3rd Field

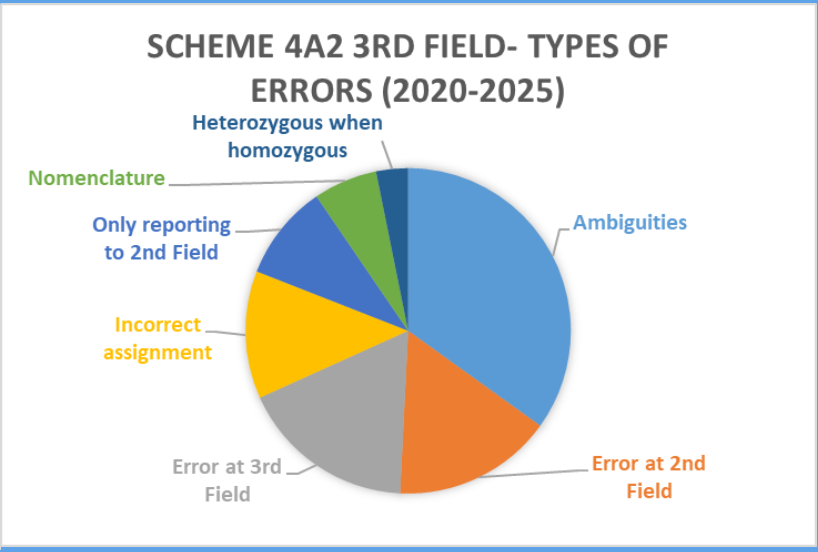
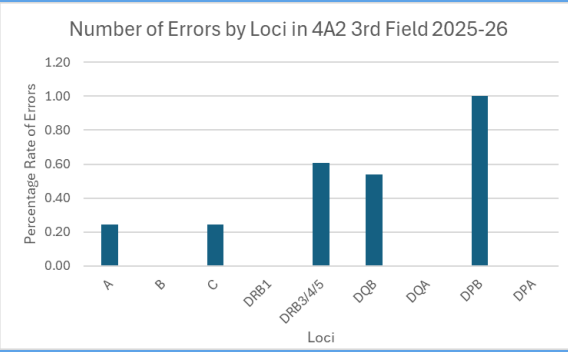


11/3420 (0.32%) incorrect HLA alleles reported by 5 labs (0 UK&I) – last year (0.32%)

- 3 errors at 3rd field e.g. DPB1*03:01:03 rather than DPB1*03:01:01
- 2 reported homozygosity but actually heterozygous
- 1 error at 2nd field e.g. C*03:03:01 rather than 03:321:XX
- 1 reported heterozygous but actually homozygous
- 1 3rd field not reported

1 (11%) HLA types with multiple errors
8 (89%) HLA types with a single error

3 (60%) labs made 1 error
1 (20%) lab made 2 errors
1 (20%) lab made 3 errors



Scheme 4A2: Unacceptable Performers 2025



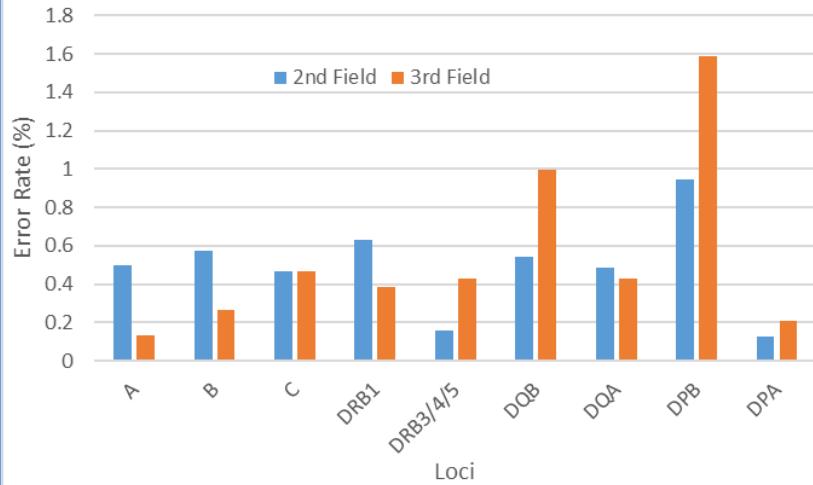
Lab	Sample	Error	Field	CAPA Response
112	04-10	Incorrect HLA types reported	2 nd	Incorrect results reported, mix-up of results, no second check
133	04+06	4A2 04/2025: Reported DPB1*04:01:01, 1321:01 , consensus DPB1*04:01:01, 04:01:01 4A2 06/2025: Reported DPB1*04:01:01, 1321:01 , consensus DPB1*04:01:01, 04:01:01	3 rd	Reporting error
361	03+07	4A2 03/2025: Reported A* 01:03 , 03:01, consensus A*01:01, 03:01 4A2 07/2025: Reported B* 27:03 , 44:02, consensus B*27:05, 44:02	2 nd	Kit resolution / interpretation issue
268	02+08	4A2 02/2025: Reported DRB4* 01:01 , consensus DRB4*01:01:01 4A2 08/2025: Reported DRB3* 01:01:01 , consensus DRB3*01:01:02	3 rd	Transcription / reporting errors
1411	01, 08+09	4A2 01/2025: Reported DPB1*04:01:01, 105:01:01 , consensus DPB1*04:01:01, 04:01:01 4A2 08/2025: Reported C*07:01:01, 07:01:01 , consensus C*07:01:01, 07:01:02 4A2 09/2025: Reported DQB1*02:01:01, 03:02:02 , consensus DQB1*02:01:01, 03:02:01	3 rd	Transcription / interpretation errors



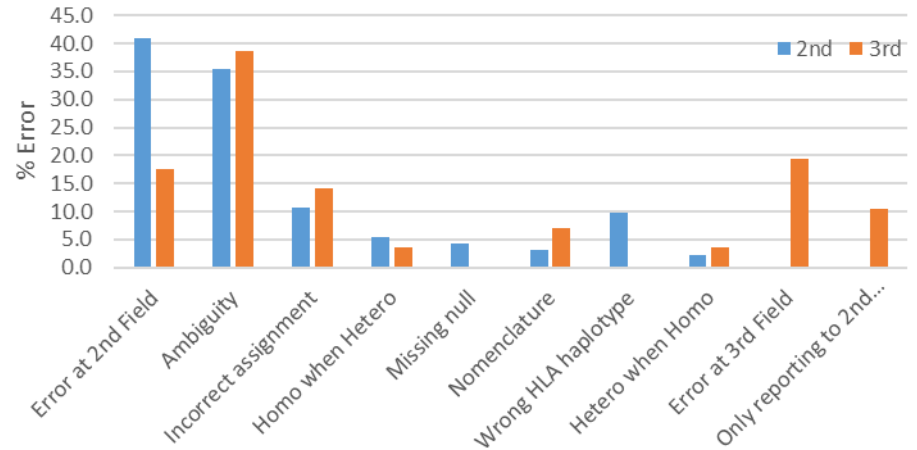
Scheme 4A2: Summary of Errors 2020-2025



Scheme 4A2 - Error Rate by Loci (2020-25)



4A2 - Types of Errors by Field (2020-25)





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/absence 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

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	12 (1)	12 (1)	15 (1)	15 (1)	15 (1)	13 (1)	13 (1)
Number with Unsatisfactory Performance (UK&I)	3 (0)	0 (0)	1 (0)	0 (0)	1 (0)	1 (0)	0 (0)
% Unsatisfactory Performance	25%	0%	6.7%	0%	6.7%	7.7%	0%





Scheme



10

HPA Genotyping



Scheme 10: HPA Genotyping

Purpose

Assess participants ability to correctly determine HPA polymorphisms.

Satisfactory Performance

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



Consensus

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

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*
 - 35/38 reported HPA-1, 2 , 3, 4, 5 and 15
 - 30/38 labs reported HPA-6
- Also able to report any other HPA polymorphisms detected, for information





Scheme 10: HPA Genotyping

- 1 lab with unsatisfactory performance

	2018	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	37 (6)	38 (6)	40 (0)	38 (6)	39 (6)	39 (6)	38 (6)	38 (6)
Number with Unsatisfactory Performance (< 100%) (UK&I)	1 (0)	3 (0)	0 (0)	0 (0)	1 (0)	1 (0)	0 (0)	1 (0)
% Unsatisfactory Performance	2.7%	7.9%	0%	0%	2.6%	2.6%	0%	2.6%

Scheme 10: Unacceptable Performers 2025



Lab	Error	CAPA Response
382	10 09/2025: False Pos HPA 3b 10 10/2025: False Neg HPA 3b	labelling error/sample mix up

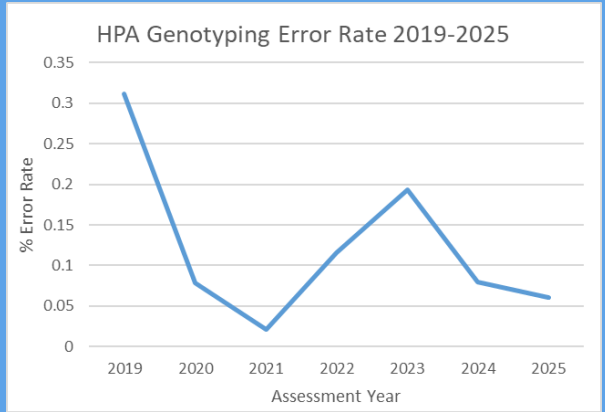


Scheme 10: Errors in HPA Genotypes 2025



- Error rate extremely low 0.06% but errors at some clinically relevant polymorphisms
- Errors found at HPA-3b (n=2), HPA-5a (n=1)

Errors 2025	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	0	0	0	0	0	1	0	0	1	0	0	0	0	0	2
False Pos	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Total Errors	0	0	0	0	0	2	0	0	1	0	0	0	0	0	3
% Error	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.06
Tested	380	380	380	380	380	380	340	340	380	380	290	290	380	380	5060



- Even split of false positive (n=1) and false negative (n=2) errors
- 2 labs made an error (1 lab made 1 error, 1 lab made 2 errors)





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

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

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	133 (53)	141 (52)	141 (50)	139 (49)	134 (50)	131 (49)	125 (48)
Number with Unsatisfactory Performance (< 100%) (UK&I)	4 (1)	12 (2)	3 (0)	8 (0)	11 (3)	16 (3)	10 (4)
% Unsatisfactory Performance (UK&I)	3.0% (1.9%)	8.5% (3.8%)	2.1% (0%)	5.7% (0%)	8.2% (6%)	12.2% (6%)	8% (8%)

- 4/10 samples distributed were HLA-B27 positive

Scheme 1B: 2025 Incorrect Assignments



Sample	Result	Lab Number	Technique	HLA Type	Lab Identified Cause
1B 05	False neg	1435	Unknown	B27 B44	No response
1B 05 & 06	False pos / false neg No results	130 324	Molecular Serological	B27 B44 B7 B8	Sample mix up No response
1B 06	False pos	55	Molecular	B7 B8	Reporting error
1B 07 & 08	False pos / false neg No results	31 334	Serological Unknown	B7 B39 B27 B51	Sample mix up No response
1B 08	False neg	8 40 256 372	Serological Unknown Serological Serological	B27 B51	Technical / reagent issue Incorrect storage, poor sample prep Delivery delay/storage issues/poor sample Delay to testing, poor sample prep
1B 09 & 10	No results	334	Unknown	B7 B8 B8 B35	No response

- 70% false negative, 30% false positive
 - 70% errors involved serological techniques
- Overall participants use: 78% use molecular methods, 22% use serological methods

7/10 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



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

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	51 (38)	49 (36)	45 (32)	37 (27)	38 (26)	37 (25)	33 (22)
Number with Unsatisfactory Performance (< 100%) (UK&I)	2 (1)	1 (1)	1 (1)	4 (3)	1 (1)	3 (1)	3 (2)
% Unsatisfactory Performance	3.9% (2.6%)	2.0% (2.8%)	2.2% (3.1%)	10.8% (11.1%)	2.6% (3.8%)	8.1% (4%)	9.1% (9.1%)

CAPA responses (n=1/3)

- Sample mix up – 33.3%
- No reply – 66.6%





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

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

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	21 (17)	19 (15)	16 (12)	15 (11)	12 (10)	9 (8)	7 (6)
Number with Unsatisfactory Performance (UK&I)	3 (1)	1 (0)	0 (0)	2 (1)	0 (0)	0 (0)	0 (0)
% Unsatisfactory Performance	14%	5.3%	0%	13%	0%	0%	0%





Scheme 5B: Performance

- 2025 – All 4 scenarios:
maximum 6 penalty points per scenario, 24 in total.

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





Scheme



7

HLA-related Pharmacogenetics



Scheme 7: HLA-related Pharmacogenetics



Purpose

Assess participants ability to correctly determine relevant HLA types for the drugs specified: Allopurinol, Carbamazepine, Oxcarbazepine, Lamotrigine, Flucloxacillin, Phenytoin & Tebentafusp

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 type. Reference result used when consensus not met.

10 blood samples over 3 distributions



Scheme 7: Performance

- 1 lab with unacceptable performance

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	67 (27)	67 (27)	64 (25)	52 (18)	50 (18)	46 (18)	48 (18)
Number with Unacceptable Performance (< 100%) (UK&I)	0 (0)	2 (0)	1 (1)	3 (0)	2 (0)	1 (0)	1 (0)
% Unsatisfactory Performance	0.0%	3.1%	1.6%	5.8%	4.0%	2.2%	2.1%

- 6/10 samples distributed were HLA-A*02:01 positive
- 3/10 samples distributed were HLA-A*31:01 positive
- 5/10 samples distributed were HLA-B*57:01 positive
- 2/10 samples distributed were HLA-B*58:01 positive
- 1/10 samples distributed were HLA-B*15:02 positive





Scheme 7: Unacceptable Performers 2025

Lab	Sample	Error	CAPA Response
413	08	Abacavir B*57:01 - False neg	Misinterpretation of results due to method used





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

- 17 Unsatisfactory Performers (2 UK&I)

	2019	2020	2021	2022	2023	2024	2025
Number of Participants (UK&I)	50 (11)	55 (12)	55 (10)	54 (11)	57 (11)	55 (11)	53 (11)
Number with Unsatisfactory Performance ($< 100\%$) (UK&I)	13 (2)	17 (5)	12 (2)	25 (5)	18 (2)	10 (1)	17 (2)
% Unsatisfactory Performance	26% (18%)	31% (42%)	22% (20%)	46.3% (45%)	31.6% (18%)	18.2% (9.1%)	32.1% (18.2%)

CAPA responses (n=13/17)

- Kit interpretation error – 38%
- Transcription errors – 31%
- Procedural error – 23%
- Reporting error – 8%



Scheme 8: Unacceptable Performance by Disease



Disease	HLA Association	Number of Participants	No. of Participants with Unacceptable Performance
Coeliac	DQ2.5, DQ8, DQ2.2	50	16 (32%)
Narcolepsy	DQB1*06:02	23	0
Actinic Prurigo	DRB1*04:07	5	1 (20%)
Birdshot Retinopathy	A*29	13	0
Behçet's	B*51	20	1 (5%)
Rheumatoid Arthritis	DRB1*04	5	2 (40%)
Diabetes	DR3, DR4	8	1 (12.5%)
Psoriasis	C*06	5	0





Scheme 8: Interpretative Comments

- Interpretation of the genotype in terms of predisposition to CD not currently assessed

iv. DQ2.5 heterozygous (cis or trans)	
HLA genotype result: HLA-DQA1*05, DQB1*02 HLA-DQA1*X, DQB1*X OR HLA-DQA1*05, DQB1*X HLA-DQA1*X, DQB1*02	HLA CD heterodimer result: HLA-DQB1*02, DQA1*05 (DQ2.5) positive HLA-DQB1*02, DQA1*02 (DQ2.2) negative HLA-DQB1*03:02 (DQ8) negative
Genotype comment: Positive for DQ2.5 (heterozygous)	
Interpretative comment < 1 > : This individual has a genotype which is associated with coeliac disease	
Interpretative comment < 2 > : This presence of DQA1*05, DQB1*02 (HLA-DQ2.5) has a strong association with coeliac disease in patients where laboratory tests or symptoms or endoscopic features suggest coeliac disease.	

- A pilot to establish a scoring system for assessment is underway



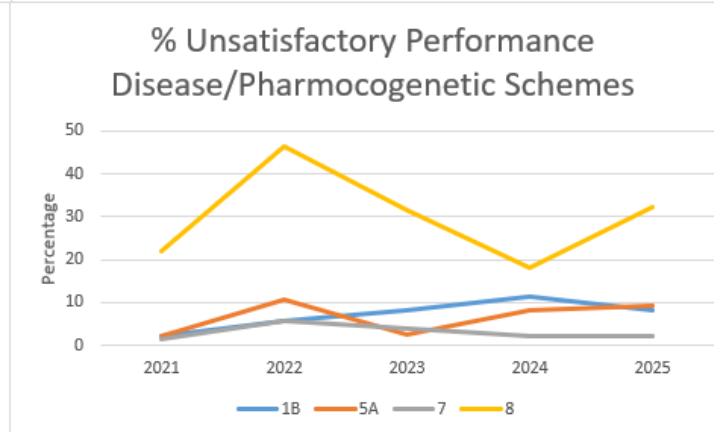
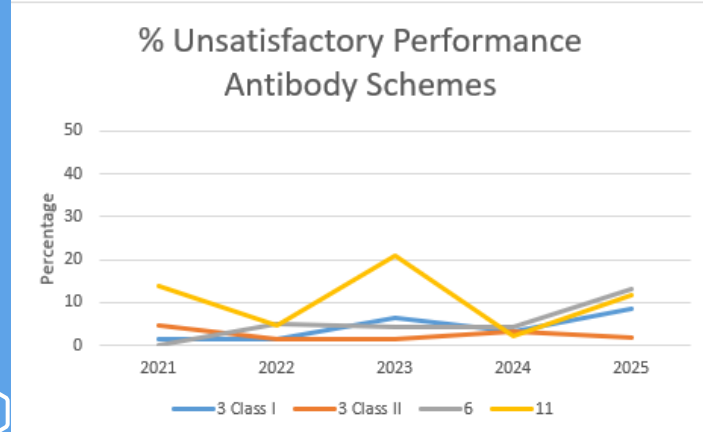
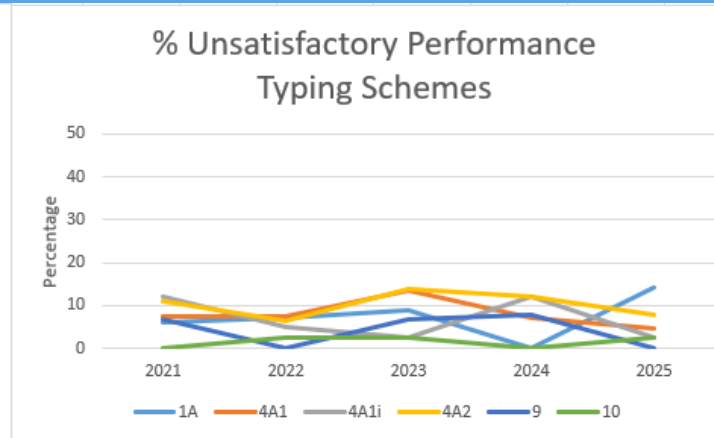
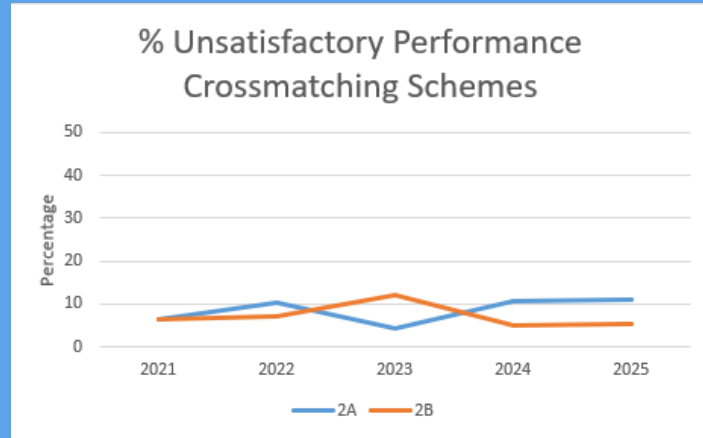


Scheme Summary

Performance Summary for all Schemes



5 Year Trends in Unsatisfactory Performance



Thanks!

Do you have any
questions?

UKNEQASHandl@Wales.NHS.UK

+44(0)1443 622185

www.ukneqashandi.org.uk



UK NEQAS for H&I
Educational Crossmatch Scenario (EDXM)
Amy De'Ath
UK NEQAS for H&I Manager





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



Whole Process 'EQA'



Educational Schemes

1. Educational HLA Typing (ED) – 4 samples
2. Interpretative Educational Scenarios (iED) – 3 scenarios
3. Educational Crossmatch Scheme (EDXM)
 - 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)



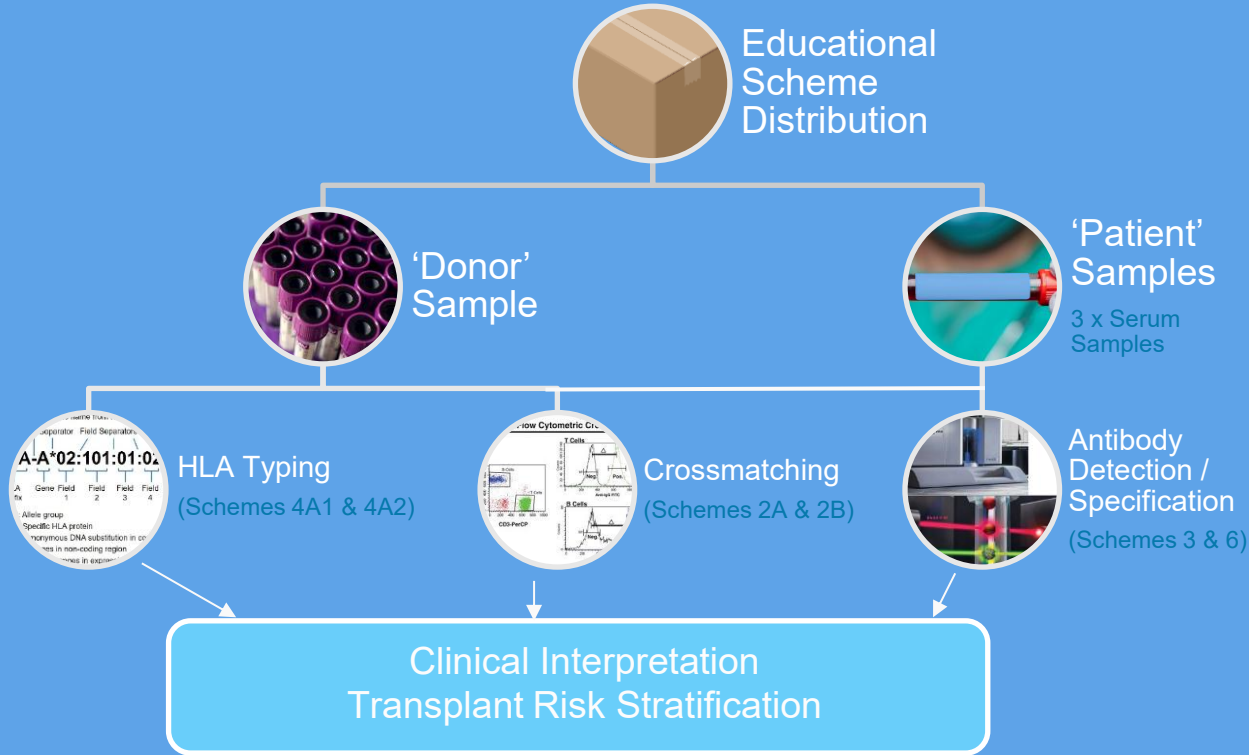
Assessed Schemes

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





Educational Scheme Distribution



2025 Submissions

- 32 participants submitted results
- Not all labs reported results for all tests
- HLA genotype:

Consensus HLA Type	A*	B*	C*	DRB1*	DRB3*	DRB5*	DQA1*	DQB1*	DPA1*	DPB1*
	03:01	07:02	07:02	13:01	01:01	01:01	01:02	06:02	01:03	02:01
	03:01	15:18	07:04	15:01			01:03	06:03	01:03	04:01
Number of reports	32	32	32	32	26	25	29	32	25	30
% Labs in consensus	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%

34% (n=11/32) of participants reported a phenotype or at the first field only

50% (n=16/32) reported to the 2nd field

16% (n=5/32) reported to the 3rd field



Serum 1

Results





Serum 1 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Positive	100% (32/32)	
HLA Class II Antibodies	Positive	100% (32/32)	
DSA	Present	100% (31/31)	MFI >20,000 for CI and CII
CDC XM	PBL Positive <i>T cell No Consensus</i> B cell Positive	100% (2/2) 70% (7/10 Pos) 100% (8/8)	
FCXM T Cell	Positive	100% (27/27)	
FCXM B Cell	Positive	100% (25/2)	
Transplant Risk	High/Contraindication	100% (31/31)	
Immunological Advice	Not suitable for direct transplantation. High risk of hyperacute rejection.		
Recommendations	Seek alternative donor. Consider de-sensitisation (assess with dilution testing). Discuss risk with patient.		



Serum 2

Results



Serum 2 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Positive	97% (31/32)	
HLA Class II Antibodies	Positive	97% (31/32)	
DSA	Present	100% (31/31)	CI MFI <10,000; CII MFI <15,000
CDC XM	PBL Negative T cell Negative B cell Negative	100% (2/2) 100% (10/10) 87.5% (7/8)	CDCXM Negative FCXM Positive
FCXM T Cell	Positive	78% (21/27)	
FCXM B Cell	Positive	88% (22/25)	
Transplant Risk	Intermediate High/Contraindication	19% (6/31) 81% (25/31)	
Immunological Advice	Not suitable for direct transplantation. High risk of AMR. If transplant proceeds use enhanced immunosuppression and post-transplant monitoring. Test for non-HLA and autologous antibodies.		
Recommendations	Seek alternative donor. Consider de-sensitisation. Monitor antibodies over time to consider de-listing. Discuss risk with patient.		



Serum 3

Results



Serum 3 Results

	Result	% Consensus	Comments
HLA Class I Antibodies	Not Assessed	62.5% Pos (20/32)	
HLA Class II Antibodies	Negative	78% (25/32)	
DSA	None	93.5% (29/31)	Two labs reported CI and CII DSA <5,000 MFI
CDC XM	PBL Negative T cell Negative B cell Negative	100% (2/2) 100% (10/10) 100% (8/8)	
FCXM T Cell	Negative	100% (27/27)	
FCXM B Cell	Negative	100% (25/25)	
Transplant Risk	Low/Standard Medium High/Contraindication	94% (29/31) 3% (1/31) 3% (1/31)	
Immunological Advice	Suitable for direct transplantation. HLA antibody present but not donor directed.		
Recommendations	Proceed to transplant. Standard immunosuppression and post-transplant monitoring. Post-transplant monitoring if clinical indication of rejection.		

UK NEQAS for H&I Comments



The same sample was used for both Serum 1 and Serum 2.

The sample was provided at neat for Serum 1 and at a dilution of 1:16 for Serum 2.

All antibodies reduced in MFI value upon dilution.

	Serum 1 (neat)	Serum 2 (1:16)
Consensus DSA	A3, B7, DR13, DR15 and DR52	A3, B7, DR13 and DR52
MFI range of DSA	965-31,318	628-12,133
Contraindication to Tx	100%	81%



Summary of Crossmatch and DSA Detection Results



2025 Results		Serum 1 NEAT		Serum 2 1:16		Serum 3	
DSA Defined by Luminex		Class I	Class II	Class I	Class II	Class I	Class II
MFI >20,000		A3 (100%) B7 (100%)	DR13 (100%) DR52 (97%)				
MFI 10,000 – 19,999					DR52 (97%)		
MFI 5,001-9,999				B7 (100%)	DR13 (100%)		
MFI 2,501-5,000			DR15 (74%)	A3 (94%)			DR52 (3%) DR13 (3%)
MFI <2,500			DQ6 (6%) DQA*01 (3%) DP2 (3%) DP4 (3%)			Cw7 (3%)	
CDCXM B CELL	No DTT	Positive		Negative		Negative	
	DTT	Positive		Negative		Negative	
FCXM	T Cell	Positive		Positive		Negative	
	B Cell	Positive		Positive		Negative	
Risk		Contraindication (100%)		Medium (19%) High/Contraindication (81%)		Contraindication (3%) Medium (3%) Low/Standard (94%)	

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

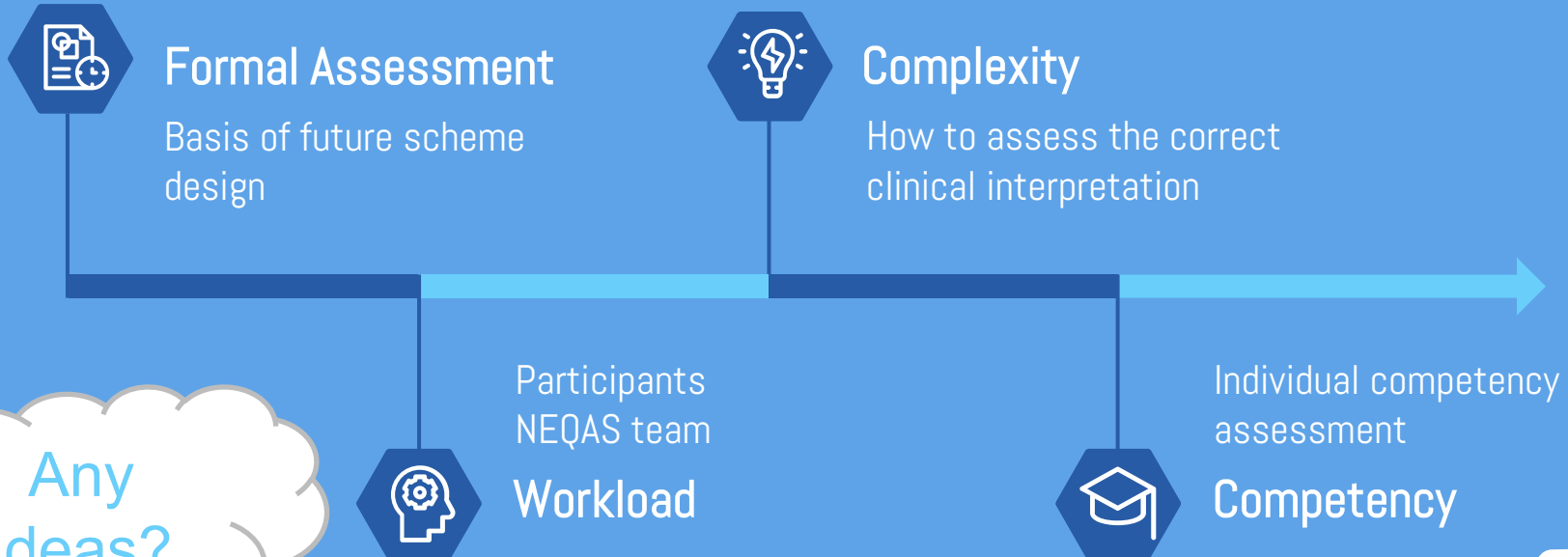
Monitor concordances
Review variations
Staff training



Competency

Laboratory staff
Clinical staff

Future Considerations



Any ideas?



Thanks!

Do you have any
questions?

UKNEQASHandl@Wales.NHS.UK

+44(0)1443 622185

www.ukneqashandi.org.uk

