UK NEQAS
International Quality Expertise

Histocompatibility & Immunogenetics

The Accuracy of HLA typing in the UK and Ireland for EQA Samples 2013- 2016

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Introduction

UK NEQAS for H&I's Scheme's 1A, 4A1 and 4A2 assesses participant's ability to correctly HLA type samples at the serological, 1st field or 2nd field resolution.

10 blood samples are distributed annually for each scheme. Participants can report results for any combination of HLA loci. Specificities/alleles reported by at least 75% of labs are taken as the consensus HLA type.

Here were report the results from labs in the UK and Ireland 2013-2016.

Scheme 1A – HLA Phenotyping

7-10 labs participated between 2013-2016, resulting in 340 HLA types. There were 4 incorrect HLA types reported (error rate 1.18%) made by 3 labs (Table 1). 3 errors were at DR and 1 at DQ. (Table 1).

Table 1: Scheme 1A Errors 2013-2016

Sample	Consensus Result	Error	Lab No.
1A03/2014	DR4, DR14	DR4, DR64	11
1A04/2014	DQ6, DQ7	DQ6, -	9
1A10/2014	DR103, DR4	DR1, DR4	20
1A10/2016	DR103, DR7	DR1, DR7	20

Scheme 4A1 – HLA Typing at 1st Field

28-30 labs participated during the time period. 19/1165 HLA types were incorrect (error rate 1.63%).

As shown in Table 2, errors were reported by 9 labs. 5 labs made errors on >1 sample. The highest error rate was for DRB3/4/5 (1.12%, n=11), DQA1/DPB1 (0.29%, n=4/1), A/DRB1 (0.17% n=4), B/DQB1 (0.13%, n=3), C (0.09%, n=2).

Table 2: Scheme 4A1 Errors 2013-2016

Sample	Consensus Result	Error	Lab No.
4A1 01/2013	DQA1*05, 06	DQA1* 05, 04	38
4A1 06/2013	A*02, 24	A*01, 24	11
4A1 10/2013	A*24, A*68	A*24, 69	78
4A1 05/2014	DRB3*03	DRB3*01	15
4A1 03/2015	B*08, 40	B*08, 60	78
4A1 05/2015	DRB1*04, -	DRB1*03, -	78
4A1 10/2015	DQA1*03, 05	DQA1*05, Blank	19
4A1 08/2015	DPA1*01, 02	DPA1*01, Blank	14
4A1 02/2016	DRB4*01	DRB4*01/02/03	62
4A1 04/2016	DRB4*01	DRB4*01/02/03	62
4A1 05/2016	DQA1*01, 04	DQA1*04, 06	14
4A1 06/2016	DRB5*01	DRB5*01/02	14, 15
4A1 07/2016	DRB3*01	DRB3*01/02/03	14
4A1 08/2016	4A1 08/2016	4A1 09/2016	35
4A1 09/2016	4A1 09/2016 DRB3*02	4A1 08/2016 DRB3*01	35 25
4A1 10/2016	DRB1*07, 15 DRB5*01	DRB1*03, 15 DRB5*01/02	14 15

The majority of errors were due to incorrect 1st field (e.g. A*01, not A*02; n=9), followed by reports of multiple 1st field types – all for DRB3/4/5 (e.g. DRB5*01/02, n=5). There were 2 instances of missed alleles and a sample exchange involving 2 of the EQA samples in 2016 (4A1 08/2016 and 4A1 09/2016).

Scheme 4A2 – HLA Typing to 2nd Field

As a minimum requirement, participants must resolve all ambiguities resulting from polymorphisms within exon 2 and 3 for Class I loci, and exon 2 for Class II loci. 20-21 labs participated between 2013-2016.

25/830 HLA types were incorrect (error rate 3.01%). Errors were made by 12 labs. 7 labs made errors on >1 sample. The highest error rate was at HLA-C (1.04%, n=14), followed by DQA1 (0.4%, n=2), B (0.37%, n=5), DRB3/4/5 (0.28%, n=1), DPB1 (0.13%, n=2), A/DRB1/DQB1 (<0.1%, n=1). There were no errors for DPA1.

Table 3: Scheme 4A2 errors 2013-2016

Sample	Consensus Result	Error	Lab No.
4A2 03/2013	C*07:02	C*06:02	24
4A2 06/2013	C*07:18	C*07:01	9, 38
4A2 07/2013	DPB1*04:02	DPB1*04:02/82:01	24
4A2 08/2013	DQB1*02:01	DQB1*02:01/02:07	42
4A2 09/2013	DRB3*02:02	DRB4*02:02	62
4A2 06/2014	B*07:02 C*07:01 C*07:02	B*07:02/05/06/29/61 C*07:01/02/06/18/19/50 C*07:02/06/18/27/50	25
4A2 09/2014	C*03:03 C*03:04	C*03:03/04 C*03:04/20N	25
4A2 01/2015	B*57:01	BLANK	15
4A2 02/2015	DQA1*01:01 DPB1*04:01	DQA1*01:05 DPB1*04:02	34 42
4A2 04/2015	C*04:09N	C*04:01	20, 15
4A2 05/2015	B*07:02 B*38:01	B*07:01 B*37:01	24 48
4A2*06/2015 4A2*09/2015 4A2*10/2015	C*01:02	C*01:02/11/25	15
4A2 01/2016	C*07:18	C*07:01	9, 23
4A2 02/2016	A*03:01 C*05:01	A*03:01/03N C*05:01/07N/51Q/99N	20
4A2 05/2016	C*07:02	C*07:02/347N	20
4A2 08/2016	DRB4*01:01	DRB4*03:01N	9
4A2 09/2016	B*39:01 DRB1*01:01	B*39:01/02L BLANK	26 42

The errors could be grouped into four categories depending on the type of error made:

- 10 errors were due to reports not meeting the minimum typing requirements, i.e. reports of allele strings with alleles differing in exons 2 (class II) and exons 2 and 3 (Class I).
- 9 errors were due to reports with the incorrect 2nd field.
- 4 errors (6.1%) were at the 1st field.
- 2 errors were due to missed alleles

Comment

It is important that laboratories are able to perform accurate HLA typing. The low overall error rate (2.01%) is encouraging, however further work is required to eliminate errors that could impact on patient care.

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