UK NEQAS
International Quality Expertise

Histocompatibility & Immunogenetics

The accuracy of HLA typing to 2nd field resolution in UK NEQAS for H&I's samples 2013-2016

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Introduction

UK NEQAS for H&I's scheme 4A2 (HLA typing to 2nd field resolution) assesses participants' ability to HLA type samples to the 2nd field resolution.

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. 10 blood samples are distributed each year in 2 distributions of 5 samples. Participants can register for 2nd field result assessment for any combination of HLA loci; HLA-A, B, C, DRB1, DRB3/4/5, DQA1, DQB1, DPA1, DPB1.

Alleles reported by at least 75% of labs are taken as the consensus HLA type. Here we present the results from 2013-2016.

Participation

Between 2013-2016, 40 samples were distributed. During this time 69 labs participated, testing between 5-40 samples. 49 labs tested all 40 samples.

This resulted in 23,928 allele assignments over the 4 years. The most commonly typed loci were HLA-DRB1 (n=4,080) followed by DQB1 (4,033), A (3,547), B (3,682), C (3,539), DPB1 (2,438), DQA1 (1,299), DRB3/4/5 (1,125), and DPA1 (185).

Results

All alleles reached the 75% consensus level, and were therefore assessed. A total of 163/23,928 alleles were incorrect; thus the overall error rate was 0.68%.

The highest error rate was for DRB3/4/5 (2.13%, n=24), followed by C (1.10%, n=39) (Table 1). All other HLA loci had an error rate less than 1%, with DPA1 having no errors.

Table 1: Scheme 4A2 error rates

HLA Loci	Number of results	Number of errors	Error Rate
A	3547	12	**0.34%**
B	3682	11	**0.30%**
C	3539	39	**1.10%**
DRB1	4080	27	**0.66%**
DRB3/4/5	1125	24	**2.13%**
DQA1	1299	8	**0.62%**
DQB1	4033	28	**0.69%**
DPA1	185	0	**0.00%**
DPB1	2438	14	**0.57%**

58.0% (40/69) of labs reported an incorrect allele during the 4 years; 15 labs had 1 allele error, 25 had multiple incorrect alleles. Only 2 of the 40 samples distributed were reported correctly by all participants.

The errors could be grouped into four categories depending on the type of error made (Table 2):

- 80 errors (49.1%) 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).
- 59 errors (36.2%) were due to reports with the incorrect 2nd field.
- 14 errors (8.6%) were due to missed alleles
- 10 errors (6.1%) were at the 1st field

Table 2: Example Scheme 4A2 Errors

Error Type	Number of Errors	Example Error	
		Consensus Type	Error
Minimum typing requirements not met	80 (49.1%)	DQB1*02:01	DQB1*02:01/07
Incorrect 2nd field	59 (36.2%)	A*03:01, A*29:02	A*03:01, A*29:01
Missed alleles	14 (8.6%)	DRB1*01:01, DRB1*16:01	DRB1*16:01, blank
Incorrect 1st field	10 (6.1%)	B*07:02, 38:01	B*07:02, 37:01

There were 4 instances where multiple participants reported the same incorrect allele (table 3). These were all occasions where the incorrectly reported and consensus allele had the same exon 2/ exon 2 & 3 sequence. Labs who only reported the 'more common' allele in isolation were penalised, as their report implied the consensus allele had been excluded as a possible allele.

Table 3: Errors made by multiple participants

Sample	Consensus Allele	Incorrect Allele	Example Acceptable Report	Number of Labs
4A2 01/2016	C*07:18	C*07:01 only	C*07:01/06/18	6
4A2 10/2016	DRB1*14:54	DRB1*14:01 only	DRB1*14:01/54	4
4A2 09/2015	A*02:66	A*02:01 only	A*02:01/66	7
4A2 06/2013	C*07:18	C*07:01 only	C*07:01/06/18	8

Comment

It is important that laboratories are able to perform accurate HLA typing to the 2nd field level, especially in support of HSC transplantation. The low overall error rate is encouraging, however further work is required to eliminate errors that could impact on patient care.

Further Information

Full information on all UK NEQAS for H&I schemes is available at **www.neqashandi.org** or contact the Scheme Manager at **ukneqashandi@wales.nhs.uk**

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