UK NEQAS
International Quality Expertise

Histocompatibility & Immunogenetics

Interpretation of DNA-Based HLA Typing Assignments to Serological Specificities - Findings from a UK NEQAS for H&I Educational Exercise

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Introduction

Many H&I laboratories use DNA-based methods for HLA typing, but are often required to interpret and report the results at the serological 'split' specificity level.

For example:

- DQB1*03:01 allele group reported as DQ7
- B*40:01 allele group reported as B60
- C*03:02 allele group reported as Cw10

This is particularly relevant when relating HLA typing results for solid organ donors to patients' antibody specificity profiles. It may also occur when reporting typing results for HLA associated disease diagnosis.

Educational Exercise

UK NEQAS for H&I carried out a voluntary educational interpretive exercise to assess participants' ability to resolve specificities from DNA-based HLA types. This was done using 10 donor samples distributed for its 'DNA HLA Typing at 1st Field Resolution' scheme (Scheme 4A1).

Participants were invited to interpret the DNA based typing results of the 4A1 samples and report at the HLA specificity level.

Results

There were 100 participating laboratories in Scheme 4A1 in 2015 and 68 laboratories returned results for this interpretive exercise. The results are summarised in the table below:

HLA	Number of Interpretations	Number of Errors	Error Rate
A	1,188	3	0.3%
B	1,252	30	2.4%
Bw4/6	1,135	14	1.2%
C	1,083	38	3.5%
DR	1,051	50	4.8%
DR51/52/53	805	10	1.2%
DQ	1,074	40	3.7%
TOTAL	7,588	185	2.4%

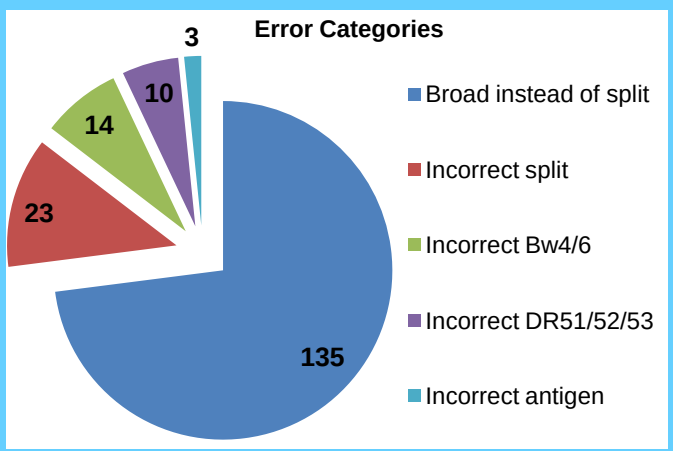
A total of a 7,588 'DNA to specificity' interpretations were made by the participating laboratories. 97.6% of these were correct based on a 75% consensus level.

The 185 incorrect assignments were reported by 32 labs (5 UK & Ireland laboratories) giving an overall error rate of 2.4%. This is relatively high compared to 33 incorrect assignments reported by 15 laboratories (3 UK & I) for the normal Scheme 4A1 (error rate = 0.2%) for the 10 samples.

The highest number of errors were reported for HLA-DR (n = 50, error rate = 4.8%), followed by DQ, C, B, Bw4/6 DR51/52/53. HLA-A had the lowest error rate (0.3%).

The 185 errors were categorised as follows:

- 135 reports of the broad instead of the split specificity *(e.g. Cw3 not Cw9)*
- 23 reports of the wrong split *(e.g. Cw10 instead of Cw9)*
- 14 incorrect Bw4/6 reports
- 10 incorrect DR51/52/53 reports
- 3 reports of the wrong antigen *(e.g. A2 instead of A1).*



Comment

These findings clearly indicate a need for further education in this area and a requirement to include 'DNA to specificity' interpretation as part of proficiency testing to reduce the occurrence of these worrying errors.

Further Information

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

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