# UK NEQAS FOR H&I'S EDUCATIONAL SCHEME FINDINGS IN 2012

Welsh Blood Service
Gwasanaeth Gwaed Cymru

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## Introduction

The UK National External Quality Assessment Service for Histocompatibility and Immunogenetics (UK NEQAS for H&I) has operated an 'Educational Scheme' for 10 years.

In this Scheme undisclosed whole blood or DNA samples with interesting HLA alleles/specificities are sent to its HLA Phenotyping and/or DNA HLA Typing scheme participants. Involvement is at the discretion of each laboratory. Findings are not assessed but participants can compare their results with some 30 other laboratories.

In 2012 four DNA extracts were provided with an HLA-A or -B allele of interest. Here we present our participants' findings on:

- ❑B*40:92
- ❑A*03:01:03
- ❑A*02:24:01
- ❑A*03:01:01:02N

### HLA-B*40:92

This allele differs from B*40:01:01 by 6 bases caused by a substitution motif of at least 60 nucleotides (*Int J Immunogenet* 2011, **32**, 161).

26 reports were made - 24 (92.3%) assigned B*40:92 and 1 each assigned B*40 and B*40:101/63. Thus, this allele was well defined.

### A*03:01:03

This allele differs from A*03:01:01:01 by a non-coding substitution (240G>T) (*Tissue Antigens* 2001, **57**, 546).

- ❑13 of the 30 laboratories (43.3%) reported A*03:01:03
- ❑1 lab reported A*03:01
- ❑16 labs principally assigned A*03 only (11 as A*03 and 5 as large A*03 allele groups containing A*03:01)

### A*02:24:01

A*02:24:01 differs from A*02:01:01:01 by 1 base (453A>C).

Importantly, this corresponds to the annealing site of a primer once commonly used in A*02-amplifying PCR-SSP mixtures (*Tissue Antigens* 1999, **53**, 190).

- ❑17 of the 30 participants (56.7%) reported A*02:24 (11 assigned A*02:24 and 6 A*02:24:01)
- ❑3 labs assigned A*02 allele groups of between 5 and 20 alleles
- ❑10 labs reported A*02 only

In UK NEQAS for H&I's 2002 Educational Scheme 29.2% (7 out of 24) of participants completely missed A*02/A*02:24 using DNA-based methods, possibly caused by using errant PCR-SSP primers. This, clearly, was not an issue a decade later.

### A*03:01:01:02N

The result of a point mutation in intron 4 (g1846G>A) causing incorrect splicing and a premature stop codon.

Of the 26 reports:

- ❑13 (50.0%) assigned an A*03:01 null (12 were A*03:01:01:02N and 1 was A*03:01N)
- ❑1 lab reported A*03:01:01:02N/01:18
- ❑8 labs reported A*03; 3 assigned A*03:01 and 1 reported A*03:01/02:01/05.

Therefore, disappointingly, 50.0% of laboratories failed to fully recognise this A*03 null allele.

## Further information

Full information on all UK NEQAS for H&I schemes is available at **www.neqashandi.org** or contact:

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