UK NEQAS

International Quality Expertise

Histocompatibility & Immunogenetics

UK NEQAS for H&I's External Quality Assessment Scheme for KIR Genotyping

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Introduction

UK NEQAS for H&I offers 19 external quality assessment (EQA) schemes to over 350 participants worldwide, including a scheme for Killer-cell immunoglobulin-like receptor (KIR) genotyping.

KIRs are present on NK cells and have an important role in regulating immune function. They are highly polymorphic and have been associated with outcomes in transplantation. Two kinds of KIR haplotype have been described based upon KIR gene content and are designated haplotype 'A' and haplotype 'B'.

UK NEQAS for H&I introduced a pilot external quality assessment (EQA) scheme for KIR genotyping in 2015 and since 2017 has been formally assessing KIR genotyping results.

EQA Scheme Design

10 undisclosed blood samples are distributed to participants each year (only 5 samples were distributed in 2015). Participants can register for assessment for the presence/absence of: KIR2DL1, KIR2DL2, KIR2DL3, KIR2DL4, KIR2DL5, KIR3DL1, KIR3DL2, KIR3DL3, KIR3DS1, KIR2DS1, KIR2DS2, KIR2DS3, KIR2DS4, KIR2DS5, KIR2DP1, KIR3DP1.

The consensus KIR genotype is determined by at least 75% of laboratories agreeing the presence/absence of each gene. Laboratories failing to report the consensus findings on more than one sample are considered as 'unacceptable performers'.

Participants can additionally report any other KIR polymorphisms, the KIR allele, or the KIR haplotype of the samples based upon the KIR gene content. This additional information is not assessed.

EQA Scheme Findings

The number of participant laboratories varied from 7-11 between 2015-2017. 25 samples have been distributed since 2015, with a total of 14 laboratories testing at lest 5 samples With the exception of one lab that did not report results for KIR2DP1 and KIR3DP1, all participating laboratories reported results for the presence/absence of all KIR genes.

The 25 samples distributed included 12 different KIR genotypes (Table 1)

The majority of laboratories tested using PCR-SSP (n=9), but some tested using SSO (n=4), with 1 lab reported using both techniques during the time period.

EQA Scheme Results

A total of 205 genotypes have been reported since the scheme was initiated. There have been 5 errors involving 2 labs, indicating an overall accuracy of 97.6%.

There was 1 error in 2015 where KIR2DL3 was reported as present (consensus absent), and 4 errors in 2016 where the same laboratory reported 4 samples as absent for KIR3DS1 (consensus present). There were no errors in 2017.

Table 2:	FQA sa	mple erro	ors 2015-20	117

	Lab Report	Consensus Result	No of Reports		
KIR2DL3	Present	Absent	1		
KIR3DS1	Absent	Present	4		

Overall 10/14 laboratories additionally reported information on the KIR haplotype for the 20 samples distributed in 2016 and 2017, although this information was not assessed.

For 8/20 samples all laboratories agreed on the haplotype assignment, but for 12/20 samples at least one laboratory reported a different haplotype assignment (13 differences, by 6 laboratories). 12/13 of these haplotype assignment differences involved reports of haplotype 'B' when the consensus result was 'AB'. The other difference was a report of haplotype 'AB' when the consensus result was haplotype 'A'.

The differences in the haplotype assignments could reflect the different criteria used to distinguish 'A' and 'B' haplotypes by various investigators.

Comment

The introduction of new EQA schemes in line with clinical developments is crucial to help ensure the accuracy of all laboratory test results that can affect patient care. The errors identified in KIR Genotyping in the past 3 years highlight the need for this EQA scheme.

Table 1: KIR genotypes in EQA samples 2015-2017																
2DL1	2DL2	2DL3	2DL4	2DL5	3DL1	3DL2	3DL3	3DS1	2DS1	2DS2	2DS3	2DS4	2DS5	2DP1	3DP1	No. of Samples
	Р		Ρ		Ρ	Ρ	Р			Ρ		Р			Р	3
Р		Р	Р		Р	Р	Р					Р		Р	Р	4
Р		Р	Р		Р	Р	Р					Р		Р	Р	3
Р		Р	Р	Р	Ρ	Р	Р	Р	Р			Р	Р	Р	Ρ	1
Р		Р	Р	Р	Р	Р	Р	Ρ	Р		Р	Р		Р	Ρ	1
Р	Р		Р	Р	Ρ	Р	Р	Р		Ρ	Ρ	Р		Р	Ρ	1
Р	Р	Ρ	Р		Р	Р	Р			Ρ		Р		Р	Р	2
Р	Р	Р	Р	Р		Р	Р	Р	Ρ	Ρ	Р		Р	Р	Р	1
Р	Р	Ρ	Р	Ρ	Ρ	Р	Р			Ρ	Ρ	Р		Ρ	Ρ	3
Р	Р	Ρ	Ρ	Р	Ρ	Р	Р	Р	Ρ	Ρ		Р	Р	Р	Р	3
Р	Р	Ρ	Р	Ρ	Ρ	Ρ	Ρ	Ρ	Ρ	Ρ	Ρ	Р		Ρ	Р	2
Р	Р	Р	Р	Р	Ρ	Ρ	Р	Р	Ρ	Ρ	Ρ	Р	Р	Р	Р	1
P= Pres	P= Presence of KIR gene															



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