UK NEQAS red cell genotyping pilot – how reliable is genotyping in practice?

Jenny White

UK NEQAS (BTLP)

UK NEQAS
Haematology and Transfusion

UK NEQAS pilot 2016 - date

Australia	Malaysia
Austria	New Zealand
Belgium	Portugal
Canada	Slovenia
Denmark	South Africa
Estonia	Spain
France	Sweden
Germany	Switzerland
Israel	Thailand
Italy	The Netherlands
Kuwait	USA

- 45 laboratories in 23 countries (**10 in the UK**)
- 4 exercises per year – with focus on routine testing

UK NEQAS
Haematology and Transfusion

UK NEQAS RCG pilot 2016- 2018

Haemoglobinopathy patient testing scenario

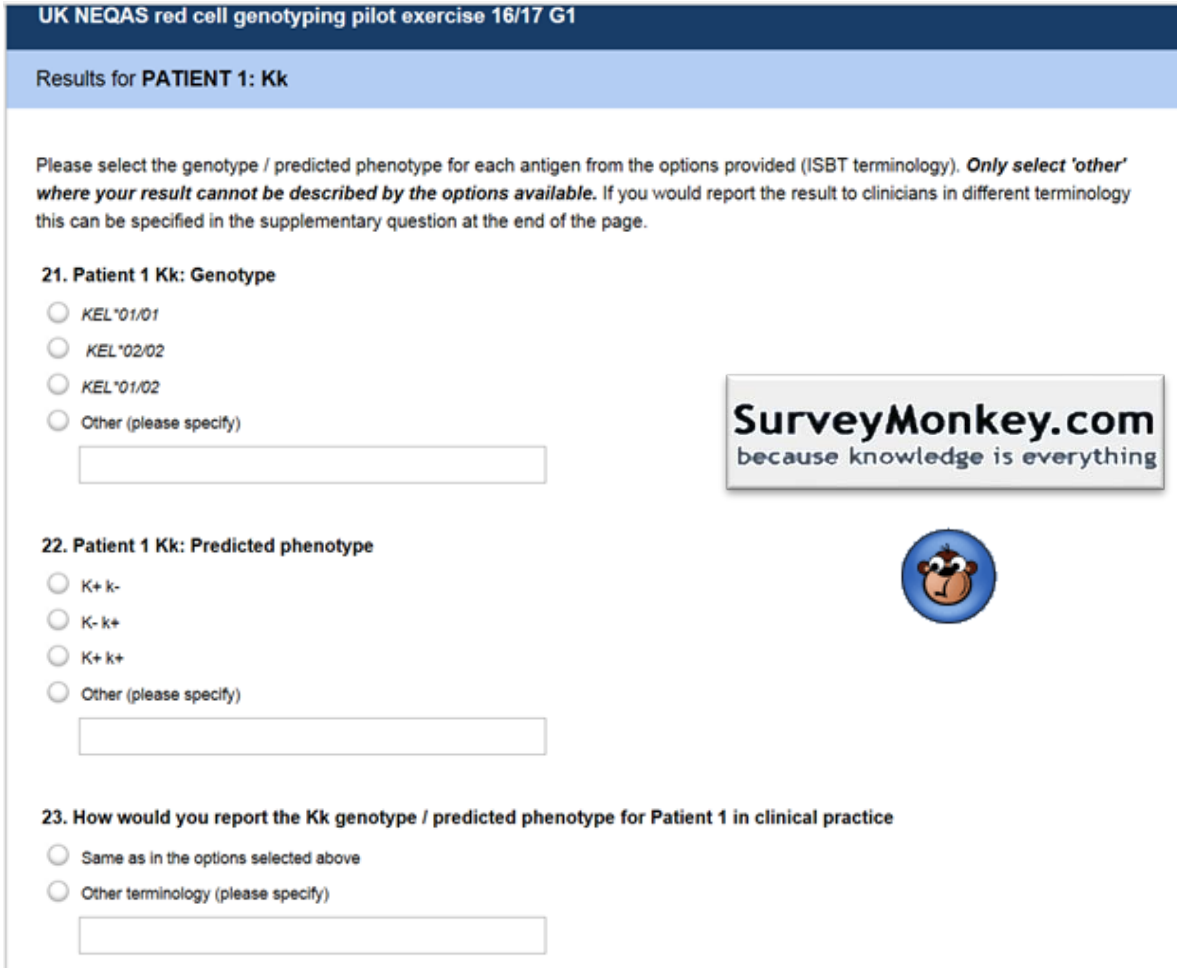
D, Cc, Ee, MN, Ss, Kk, Fy^a Fy^b Fy, Jk^a Jk^b, Do^a Do^b

- Genotype
- Predicted phenotype
- What is reported to clinicians
- Testing platform used
- How results are handled

UK NEQAS
Haematology and Transfusion

Data collection

- ISBT terminology dropdown options
- ‘Other’ only for when none of the ISBT options offered can describe what is found



UK NEQAS red cell genotyping pilot exercise 16/17 G1

Results for **PATIENT 1: Kk**

Please select the genotype / predicted phenotype for each antigen from the options provided (ISBT terminology). ***Only select 'other' where your result cannot be described by the options available.*** If you would report the result to clinicians in different terminology this can be specified in the supplementary question at the end of the page.

21. Patient 1 Kk: Genotype

- *KEL*01/01*
- *KEL*02/02*
- *KEL*01/02*
- Other (please specify)

22. Patient 1 Kk: Predicted phenotype

- K+ k-
- K- k+
- K+ k+
- Other (please specify)

23. How would you report the Kk genotype / predicted phenotype for Patient 1 in clinical practice

- Same as in the options selected above
- Other terminology (please specify)

Material

- 2 samples - whole blood donations
- Selected only for Rh (DCcEe) and Duffy phenotypes

16/17G1	1 x D variant, Fy(a-b-)
16/17 G2	no variants
16/17G3	no variants
16/17G4	1 x D DAU, Fy(a-b-)
17/18 G1	no variants
17/18 G2	no variants

- Reported variants did not contribute to the error rate
- Highest error rates for 16/17G2 and 17/18G2

2016/17 errors (G1,G2,G3)

2629 genotyping results

2376 predicted phenotypes

29 incorrect genotypes (1.1%)

24 incorrect phenotypes (1.0%)

13 laboratories with errors (2 with errors in 2 exercises)

18

geno/pheno 'pairs' with error(s)*

9

Both incorrect but matching

6

Genotype only

2

Predicted phenotype only

1

compound error

*Excludes errors due to transposition of 2 samples
No apparent correlation with platform used

Example - 16/17G2 errors

Excluding 1 laboratory that transposed samples / results (multiple errors)

Laboratories with errors	Patient sample	Consensus genotype	Reported genotype	Consensus predicted phenotype	Reported predicted phenotype
A	2	FY*02/02	FY*01/02	Fy(a-b+)	Fy(a+b+)
B	2	DO*01/01	DO*02/02	Do(a+b-)	Do(a-b+)
C	1	FY*01/02	FY*null01/FY*null01	Fy(a+b+)	Fy(a-b-)
D*	1	KEL*02/02	KEL1(K) KEL2(k)	K-k+	K-k-
E	2	RHD*01/01[1]	RHD*01/01N.01	D+	D+
F*	2	RHD*01/01[1]	RHD*01/01N.01	D+	D+
G*	1	DO*01/02	DO*01/02	Do(a+b+)	Do(a+b-)
H	1	FY*01/02, GATA mutation not present	FY*01/02, GATA mutation not present	Fy(a+b+)	Fy(a+b-)

* Report only genotypes in clinical practice

UK NEQAS
Haematology and Transfusion

Sources of error other than in testing

- Critical errors – could be interpretation or transcription
- Terminology -genotypes reported as phenotypes and *vice versa*
- Unclear reporting to clinicians

Whose responsibility it to interpret results?

Knowledge required

Is it safer to report genotype, phenotype or both?

Depends who you are reporting to?
Ref lab to hospital
Direct to clinicians

UK NEQAS
Haematology and Transfusion

Questionnaire data 2017 - Reporting

Format of results	Reporting to				
	Reference centre undertaking genotyping	Hospital transfusion lab	Clinician in haem / transfusion	Another clinician managing the patient	Other
Genotype & predicted phenotype	17	19	18	15	7
Genotype only	4	4	3	2	4
Predicted phenotype only	9	18	17	17	6
Do not report – n/a	8	2	3	7	8

- 12 report genotype and predicted phenotype
- 2 centres report the genotype only
- 14 centres report the predicted phenotype only
- 8 change what is reported according to report recipient; with increased reporting of predicted phenotype to hospital laboratories and clinicians

Questionnaire data 2017 - Interpretation

How are genotyping results routinely translated to predicted phenotypes?	
By the testing platform software[1]	20 (43%)
Manually	21 (46%)
Using other IT	3 (7%)
Never report a predicted phenotype	2 (4%)
Total	46 (100%)

[1] 5 Progenika IDCORE XT, 6 HEA Beadchip, 3 InnoTrain FluoGene, 6 >1 platform (including Progenika BLOODChip, BAGene and InnoTrain Ready-Gene)

For platforms where 'automatic' interpretation of the predicted phenotype is available, not all users report using this information

Questionnaire data 2017 – Transfer of results

In clinical practice, how do results routinely get transferred for reporting?	
Transcribed manually to paper report	6 (13%)
Transcribed manually to an IT system	24 (53%)
Electronically from testing platform to an IT system	15 (33%)
Total	45 (100%)

67% have a manual step in interpretation and / or reporting

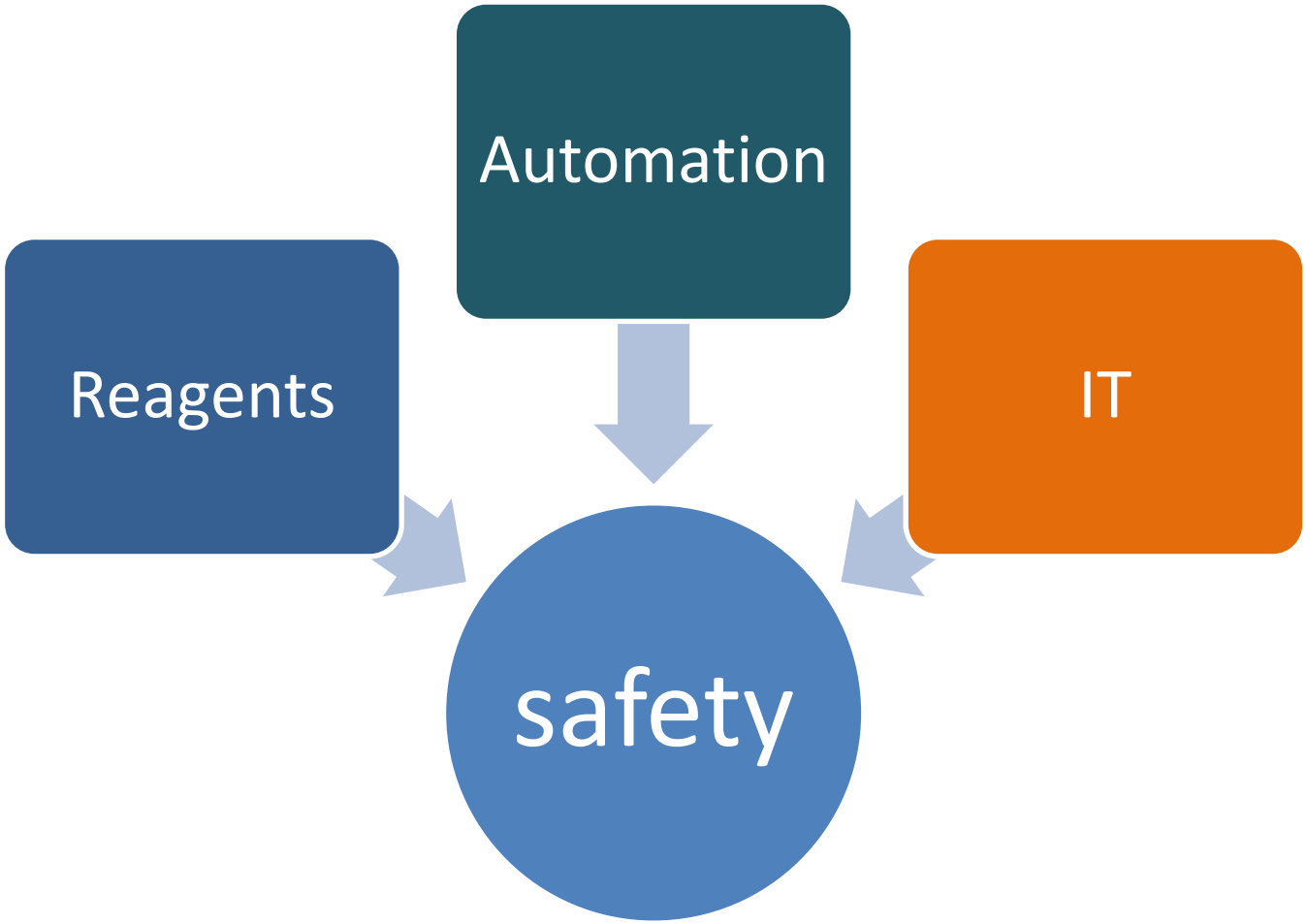
Genotyping and IT (UK) - Questions

How are genotyping results used in decision making on selection of blood for transfusion dependent patients, e.g. SCD, in the hospital laboratory?

- Can all LIMS receive results electronically?
- What is entered - genotype and / or predicted phenotype?
- Are results held in a field where they can be accessed by IT algorithms for selection of blood?

- *cffDNA results…as above, but limited to one pregnancy*

UK serological pre-transfusion testing…



Quality Systems

BSH guidelines

SHOT / EQA