When Valid Data Go Wrong: Detecting a Software Mapping Error in HLA Antigen Assignment

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Background

STAT HLA Typing was performed for deceased organ donor allocation purposes using RT-PCR (LinkSeq assay, ThermoFisher) and analyzed using SureTyper software (Thermo Fisher Scientific). The genotype and phenotype provided by the software were not in agreement for the DRB3/4/5 antigen (Table 1). The DRB3/4/5 assignment was incompatible with the observed DRB1 genotype, and a Haplocheck warning was not issued by the software.

Amplification results across the 384 wells were clean, interpretable results with no need for detailed melt curve review (Figure 1). A technologist initially entered the phenotype into UNET based on the incorrect software output. HLA associations were not manually reviewed despite the expected linkage pattern not aligning. The typing was corrected without impact to patient safety.

The laboratory performs documented validations on new versions of software, not new lot information upgrades. Notably, the laboratory upgraded the SureTyper software (from V6.1.8 R60-**139** to V6.1.8 R60-**141**) the day prior. Reanalysis of this case using the prior version (R60-139) produced the expected result, implicating the updated software version.

Vendor investigation identified a duplicated reaction pattern entry within the DRB345-V23 test matrix (DRB4*01:03:01:02N, DRB5*01:131N), leading to incorrect mapping of the reaction pattern and erroneous phenotype assignment. The issue was promptly corrected by the vendor (V6.1.8 R60-**142**).

Conclusion

This case highlights the critical role of technologist expertise in HLA interpretation. Reliance on software alone can introduce risk. Matrix-based interpretation systems are vulnerable to silent mapping errors, especially after version changes. Despite a vendor's coding error, the laboratory had the tools to detect this issue rather than solely relying upon software. Reviewing HLA associations would have flagged this discrepancy and prevented incorrect information from being entered into UNET. Expert review is needed to ensure accuracy, and technologists should not rely upon technology as being 100% absolute.

Table 1. SureTyper Assigned Genotype and Phenotype

Antigen	**Software Assigned R60-141**		HLA Associations Align	**Software Assigned R60-139/142**		HLA Associations Align
	Genotype	*Phenotype*		*Genotype*	*Phenotype*	
A	A*02 A*11	A2 A11	*n/a*	A*02 A*11	A2 A11	n/a
B	B*15 B*57	B62 B57	Yes	B*15 B*57	B62 B57	Yes
C	C*03 C*06	Cw9 Cw6	Yes	C*03 C*06	Cw9 Cw6	Yes
DRB1	DRB1*01 DRB1*07	DR1 DR7	**No for DRB3/4/5**	DRB1*01 DRB1*07	DR1 DR7	**Yes**
DRB345	**DRB4*01:03:01:02N DRB5*01:131N**	**DR53-Null DR51-Null**	**No for DRB1**	**DRB4*01:03:01:02N**	**DR53-Null**	**Yes**
DQA	DQA1*01 DQA1*02	DQA01 DQA02	n/a	DQA1*01 DQA1*02	DQA01 DQA02	n/a
DQB	DQB1*03 DQB1*05	DQ9 DQ5	Yes	DQB1*03 DQB1*05	DQ9 DQ5	Yes
DPA	DPA1*01 DPA1*01	DPA01 DPA01	n/a	DPA1*01 DPA1*01	DPA01 DPA01	n/a
DPB	DPB1*04:01:01:01 DPB1*04:01:01:01	DPB1*04:01 DPB1*04:01	n/a	DPB1*04:01:01:01 DPB1*04:01:01:01	DPB1*04:01 DPB1*04:01	n/a

Figure 1. Plate map for STAT organ case with Well Amplification

