Evaluation of LABType® CWD versus XR Beads for HLA Typing: Implications for Transition in Clinical Workflow

UAMS COLLEGE OF MEDICINE DEPARTMENT OF PATHOLOGY
UNIVERSITY OF ARKANSAS FOR MEDICAL SCIENCES

Juan Liu MD PhD S(ACHI), Soumya Pandey MD A(ACHI), Erin Fore BS MEd MLS(ASCP)CM, Terry O Harville MD PhD D(ABMLI) F(ACHI)
University of Arkansas for Medical Sciences, Little Rock, AR 72205

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UNIVERSITY OF ARKANSAS FOR MEDICAL SCIENCES

BACKGROUND

Human leukocyte antigen (HLA) typing plays a critical role in histocompatibility testing for organ and hematopoietic cell transplantation. Accurate HLA typing ensures optimal donor-recipient matching and reduces the risk of allograft rejection and other immune-mediated complications (such as GvHD). Our laboratory routinely employs OneLambda® LABType® sequence-specific oligonucleotide (SSO) assays for low to medium-resolution HLA typing, which are reported at the first-field level with serologic equivalents. For higher resolution needs, next-generation sequencing (NGS) is used via the CareDx AlloSeq® Tx17 platform.

To improve resolution within the SSO framework, our lab has historically relied on LABType® XR beads, which offer expanded exon coverage and greater bead diversity, enabling improved discrimination of alleles, particularly for the HLA-A, -B, -C, and -DRB1 loci. However, OneLambda® has announced the planned discontinuation of XR beads in 2025. In response, our laboratory initiated an evaluation of the LABType® CWD bead set as a potential replacement. CWD beads are designed to resolve alleles that are part of the Common and Well-Documented (CWD) allele catalog, which encompasses alleles most frequently encountered in the general population and considered as clinically significant.

This study aimed to assess the performance of LABType® CWD relative to the soon-to-be-discontinued XR beads and to determine whether the transition would maintain the accuracy and reliability of HLA typing within our existing clinical workflow.

METHODS

We performed a comparative analysis of ten patient samples typed at HLA-A, -B, -C, and -DRB1 loci using three platforms: LABType® XR (OneLambda® SSO), LABType® CWD (One Lambda SSO), and NGS-based typing with CareDx AlloSeq® Tx17. LABType® XR employs up to 500 beads with broader exon coverage (eg, exons 2–5 for HLA-A/-B and exons 2–7 for HLA-C) to achieve higher resolution, whereas LABType® CWD optimizes bead usage for population-relevant alleles listed in the CWD catalog. NGS (AlloSeq® Tx17) served as the gold standard, providing two-field resolution across all loci. Concordance was assessed at both first-field (eg, A*02 vs A*03, aligning with our laboratory's SSO reporting format) and two-field levels (eg, A*02:01 vs A*02:07) to evaluate agreement among platforms and determine whether LABType® CWD could feasibly replace XR beads without compromising clinical reporting accuracy.

RESULTS

Sample number	Locus	Methods	Allele 1	Allele 2
1	A	SSO (CWD)	A*03:01	A*29:02
		SSO (XR)	A*03:01	A*29:02
		NGS	A*03:01	A*29:02
	B	SSO (CWD)	B*07:02	B*44:03
		SSO (XR)	B*07:02	B*44:03
		NGS	B*07:02	B*44:03
	C	SSO (CWD)	C*07:02	C*16:01
		SSO (XR)	C*07:02	C*16:01
		NGS	C*07:02	C*16:01
	DRB1	SSO (CWD)	DRB1*07:01	DRB1*13:01
		SSO (XR)	DRB1*07:01	DRB1*13:01
		NGS	DRB1*07:01	DRB1*13:01
2	A	SSO (CWD)	A*03:01	A*66:01
		SSO (XR)	A*03:01	A*66:01
		NGS	A*03:01	A*66:01
	B	SSO (CWD)	B*53:01	B*57:04
		SSO (XR)	B*53:01	B*57:04
		NGS	B*53:01	B*57:04
	C	SSO (CWD)	C*04:01	C*18:02
		SSO (XR)	C*04:01	C*18:02
		NGS	C*04:01	C*18:02
	DRB1	SSO (CWD)	DRB1*08:04	DRB1*14:54
		SSO (XR)	DRB1*08:04	DRB1*14:54
		NGS	DRB1*08:04	DRB1*14:54
3	A	SSO (CWD)	A*24:02	A*24:02
		SSO (XR)	A*24:02	A*24:02
		NGS	A*24:02	A*24:02
	B	SSO (CWD)	B*39:06	B*40:02
		SSO (XR)	B*39:06	B*40:02
		NGS	B*39:06	B*40:02
	C	SSO (CWD)	C*03:05	C*07:02
		SSO (XR)	C*03:05	C*07:02
		NGS	C*03:05	C*07:02
	DRB1	SSO (CWD)	DRB1*04:07	DRB1*14:06
		SSO (XR)	DRB1*04:03	DRB1*14:06
		NGS	DRB1*04:07	DRB1*14:06
4	A	SSO (CWD)	A*33:01	A*68:01
		SSO (XR)	A*33:01	A*68:01
		NGS	A*33:01	A*68:01
	B	SSO (CWD)	B*58:02	B*78:01
		SSO (XR)	B*58:02	B*78:01
		NGS	B*58:02	B*78:01
	C	SSO (CWD)	C*06:02	C*16:01
		SSO (XR)	C*06:02	C*16:01
		NGS	C*06:02	C*16:01
	DRB1	SSO (CWD)	DRB1*07:01	DRB1*12:01
		SSO (XR)	DRB1*07:01	DRB1*12:01
		NGS	DRB1*07:01	DRB1*12:01
5	A	SSO (CWD)	A*03:01	A*68:01
		SSO (XR)	A*03:01	A*68:01
		NGS	A*03:01	A*68:01
	B	SSO (CWD)	B*27:05	B*35:01
		SSO (XR)	B*27:05	B*35:01
		NGS	B*27:05	B*35:01
	C	SSO (CWD)	C*02:02	C*04:01
		SSO (XR)	C*02:02	C*04:01
		NGS	C*02:02	C*04:01
	DRB1	SSO (CWD)	DRB1*01:01	DRB1*13:01
		SSO (XR)	DRB1*01:01	DRB1*13:01
		NGS	DRB1*01:01	DRB1*13:01

Sample number	Locus	Methods	Allele 1	Allele 2
6	A	SSO (CWD)	A*02:01	A*30:02
		SSO (XR)	A*02:01	A*30:02
		NGS	A*02:01	A*30:02
	B	SSO (CWD)	B*14:02	B*39:06
		SSO (XR)	B*14:02	B*39:06
		NGS	B*14:02	B*39:06
	C	SSO (CWD)	C*07:02	C*08:02
		SSO (XR)	C*07:02	C*08:02
		NGS	C*07:02	C*08:02
	DRB1	SSO (CWD)	DRB1*01:01	DRB1*14:06
		SSO (XR)	DRB1*01:01	DRB1*14:06
		NGS	DRB1*01:01	DRB1*14:06
7	A	SSO (CWD)	A*03:01	A*23:01
		SSO (XR)	A*03:01	A*23:01
		NGS	A*03:01	A*23:01
	B	SSO (CWD)	B*07:02	B*58:01
		SSO (XR)	B*07:02	B*58:01
		NGS	B*07:02	B*58:01
	C	SSO (CWD)	C*03:02	C*07:18
		SSO (XR)	C*03:02	C*07:18
		NGS	C*03:02	C*07:18
	DRB1	SSO (CWD)	DRB1*03:01	DRB1*11:01
		SSO (XR)	DRB1*03:01	DRB1*11:01
		NGS	DRB1*03:01	DRB1*11:01
8	A	SSO (CWD)	A*02:01	A*11:01
		SSO (XR)	A*02:01	A*11:01
		NGS	A*02:01	A*11:01
	B	SSO (CWD)	B*27:05	B*44:02
		SSO (XR)	B*27:05	B*44:02
		NGS	B*27:05	B*44:02
	C	SSO (CWD)	C*01:02	C*05:01
		SSO (XR)	C*01:02	C*05:01
		NGS	C*01:02	C*05:01
	DRB1	SSO (CWD)	DRB1*07:01	DRB1*07:01
		SSO (XR)	DRB1*07:01	DRB1*07:01
		NGS	DRB1*07:01	DRB1*07:01
9	A	SSO (CWD)	A*03:01	A*33:01
		SSO (XR)	A*03:01	A*33:01
		NGS	A*03:01	A*33:01
	B	SSO (CWD)	B*07:02	B*14:02
		SSO (XR)	B*07:02	B*14:02
		NGS	B*07:02	B*14:02
	C	SSO (CWD)	C*07:02	C*08:02
		SSO (XR)	C*07:02	C*08:02
		NGS	C*07:02	C*08:02
	DRB1	SSO (CWD)	DRB1*01:02	DRB1*14:01
		SSO (XR)	DRB1*01:02	DRB1*14:01
		NGS	DRB1*01:02	DRB1*14:01
10	A	SSO (CWD)	A*02:01	A*29:02
		SSO (XR)	A*02:01	A*29:02
		NGS	A*02:01	A*29:02
	B	SSO (CWD)	B*07:02	B*58:01
		SSO (XR)	B*07:02	B*58:01
		NGS	B*07:02	B*58:01
	C	SSO (CWD)	C*07:02	C*07:18:01
		SSO (XR)	C*07:02	C*07:18:01
		NGS	C*07:02	C*07:18:01
	DRB1	SSO (CWD)	DRB1*04:04	DRB1*15:01
		SSO (XR)	DRB1*04:04	DRB1*15:01
		NGS	DRB1*04:04	DRB1*15:01

- First-field comparison: LABType® CWD and XR yielded concordant results across all loci, fulfilling clinical reporting requirements.
- Two-field comparison: Concordance between XR and CWD was observed across loci except for one DRB1 assignment, where the CWD call aligned with NGS while the XR result did not, suggesting superior performance of CWD in this case.

DISCUSSION

The comparison between LABType® CWD and XR beads showed high concordance (100%) at the first-field level across all tested loci. Since our laboratory reports SSO-based typing results at the first-field level—with the exception of DPB1, which is reported at two-field resolution—this finding indicates that transitioning to CWD would not disrupt our current clinical workflow.

When examining two-field results, we found that CWD typing remained highly concordant with XR results, with one notable exception: a single DRB1 typing discrepancy where the CWD assignment matched the NGS result while the XR result did not. This isolated case suggests that, contrary to initial expectations, the CWD kit may offer equivalent or even superior resolution in certain situations—particularly where XR's additional exon coverage does not translate into improved discrimination.

It is important to note that the CWD kit's design—focused on alleles commonly encountered in the general population—makes it well-suited for routine clinical applications in settings where the subject population aligns with the population-based allele frequency of the CWD catalog. However, for patients with rare or underrepresented alleles, the limitations of the CWD kit in distinguishing less common HLA alleles may necessitate supplemental typing via NGS or other high-resolution platforms.

Overall, our findings support a smooth operational transition from XR to CWD reagents for HLA-A, -B, -C, and -DRB1 typing, with minimal impact on clinical reporting.

CONCLUSIONS

- Our evaluation demonstrated that LABType® CWD beads provide highly comparable HLA typing results to LABType® XR at the first-field level for the HLA-A, -B, -C, and -DRB1 loci. Given that our clinical reporting is based on first-field resolution with serologic equivalents, CWD reagents fully meet the current needs of our workflow.
- Moreover, two-field comparisons revealed that CWD results were concordant with XR and NGS typing, with one notable case at the DRB1 locus where CWD was more consistent with the NGS result than XR. This suggests that CWD may not only serve as a replacement for XR but could also offer improved allele discrimination in select contexts.
- These findings support the transition to LABType® CWD beads as a clinically appropriate and operationally feasible alternative to XR reagents, enabling continued high-quality HLA typing without compromising clinical accuracy.