

Addressing the hurdles in detecting alpha/beta-specific antibodies and the impact of limited bead coverage on accurate interpretation of the immunizing epitope

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ABSTRACT

Virtual crossmatch (vXM) is widely used as the final immunological risk assessment prior to solid organ transplantation. Accurate antibodies identification is critical to appropriate donor selection, and misinterpretation of alpha vs beta-specific antibodies can severely impact vXM results.

METHOD

Our lab routinely uses One Lambda LABScreen Single Antigen Assay (OL-SAB) and in certain cases LIFECODES Single Antigen Assay (LC-SAB). We reviewed a total of 1,714 patients whose sera has been tested by both OL-SAB and LC-SAB in our lab since 2019 to determine the patients that had antibodies to the alpha chain of the HLA-DQ protein which could not be resolved by the routine OL-SAB panel.

CONCLUSIONS

Although one SAB platform can provide an accurate assessment of a patient's antibodies profile in most cases, some patients may have ambiguous antibodies reactivity patterns which may result in misinterpretation and can potentially lead to transplantation with incompatible donors if not resolved.

These cases highlight the significant shortcoming of the limited SAB beads coverage that can impact epitope identification.

Case 1: A male patient with a prior kidney transplant was being evaluated for his second transplant. Based on the positive specificities, we determined that his class II antibodies were likely directed to the 84QL (DQ2/4/7/8/9) epitope (**Fig 1**).

Interestingly, LC-SAB demonstrated a single positive DQ6 bead (Fig 2).

LC-SAB contains one DQA1*02:01-DQB1*06:01 heterodimer bead, whereas OL-SAB DQ5/DQ6 beads only contain DQA1*01 alleles. Thus, the class II Antibodies were not directed to the DQ beta proteins but rather to the 61FT4 epitope in the DQ alpha chains. Of 1,714 patients analyzed by LC-SAB since 2019, 16 (0.93%) were confirmed to have antibodies to the 61FT4 epitope. While DQ5 and DQ6 are largely associated with DQA1*01 alleles, there are several populations in which DQ5 or DQ6 are associated with other DQA1 alleles.

Table 1 summarizes those haplotypes found just within the United States¹.

Figure 3.

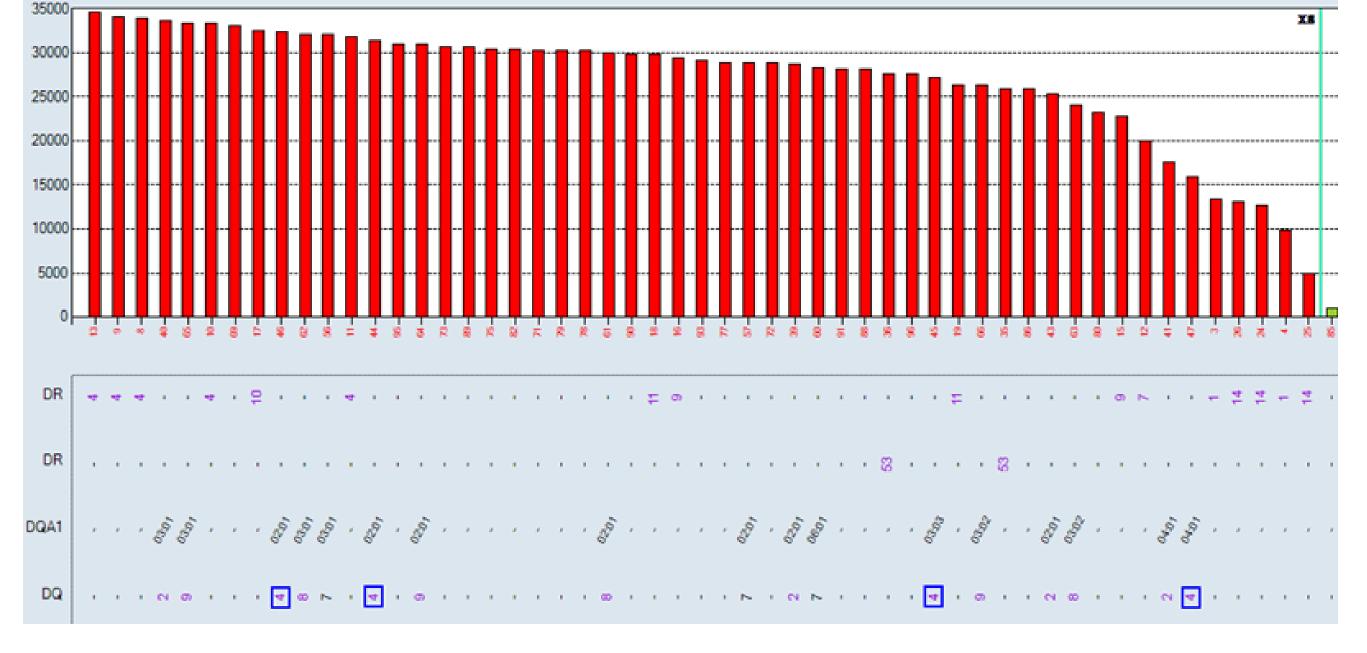


Figure 4.

| ssignment | BG Adjusted | AD-MFI | AD-BG Adjusted | DR/DR5x | DQA | DQB | DPA | DPB | DR Serology | DQ Serology | DP Serology | RAD | Epitopes |
|-----------|-------------|--------|-------------------|---------|------------|------------|-----|-----|----------------|----------------|----------------|--------|----------|
| Negative | 398 | 1168 | 535 | | DQA1*01:01 | DQB1*05:01 | | | | DQ5(1) | | 0.7440 | |
| Negative | 486 | 1010 | 523 | | DQA1*01:02 | DQB1*06:04 | | | | DQ6(1) | | 0.9300 | |
| Negative | 459 | 1038 | 567 | | DQA1*01:02 | DQB1*05:01 | | | | DQ5(1) | | 0.8080 | |
| Negative | 191 | 1029 | 307 | | DQA1*01:02 | DQB1*05:02 | | | | DQ5(1) | | 0.6220 | |
| Negative | 274 | 655 | 352 | | DQA1*01:02 | DQB1*06:02 | | | | DQ6(1) | | 0.7790 | |
| Negative | 696 | 1109 | 778 | | DQA1*01:03 | DQB1*06:01 | | | | DQ6(1) | | 0.8940 | |
| Negative | 209 | 1201 | 385 | | DQA1*01:03 | DQB1*06:03 | | | | DQ6(1) | | 0.5430 | |
| Negative | 322 | 1307 | 617 | | DQA1*01:04 | DQB1*05:03 | | | | DQ5(1) | | 0.5220 | |
| Negative | 404 | 820 | 528 | | DQA1*01:04 | DQB1*06:01 | | | | DQ6(1) | | 0.7650 | |
| Positive | 23933 | 27815 | 27446 | | DQA1*02:01 | DQB1*03:02 | | | | DQ8(3) | | 0.8720 | 175E |
| Positive | 23505 | 27413 | 27173 | | DQA1*02:01 | DQB1*04:01 | | | | DQ4 | | 0.8650 | 175E |
| Positive | 20467 | 23894 | 23471 | | DQA1*02:01 | DQB1*02:01 | | | | DQ2 | | 0.8720 | 175E |
| Positive | 19776 | 25311 | 24906 | | DQA1*02:01 | DQB1*02:02 | | | | DQ2 | | 0.7940 | 175E |
| Positive | 14846 | 19869 | 19407 | | DQA1*02:01 | DQB1*06:01 | | | | DQ6(1) | | 0.7650 | 175E |
| Positive | 32552 | 35874 | 35576 | | DQA1*03:01 | DQB1*03:01 | | | | DQ7(3) | | 0.9150 | 175E |
| Positive | 29884 | 36140 | 35704 | | DQA1*03:01 | DQB1*03:02 | | | | DQ8(3) | | 0.8370 | 175E |
| Positive | 27106 | 38891 | 38285 | | DQA1*03:01 | DQB1*04:02 | | | | DQ4 | | 0.7080 | 175E |
| Positive | 30016 | 36997 | 36515 | | DQA1*03:02 | DQB1*03:01 | | | | DQ7(3) | | 0.8220 | 175E |
| Positive | 29014 | 37006 | 36541 | | DQA1*03:02 | DQB1*02:02 | | | | DQ2 | | 0.7940 | 175E |
| Positive | 27510 | 37188 | 36631 | | DQA1*03:02 | DQB1*03:02 | | | | DQ8(3) | | 0.7510 | 175E |
| Positive | 27317 | 35105 | 34710 | | DQA1*03:02 | DQB1*03:03 | | | | DQ9(3) | | 0.7870 | 175E |
| Positive | 11142 | 14394 | 13790 | | DQA1*04:01 | DQB1*04:02 | | | | DQ4 | | 0.8080 | 175E |
| Positive | 10419 | 14132 | 13619 | | DQA1*04:01 | DQB1*03:03 | | | | DQ9(3) | | 0.7650 | 175E |
| Positive | 7650 | 11006 | 10596 | | DQA1*04:01 | DQB1*04:01 | | | | DQ4 | | 0.7220 | 175E |
| Negative | 651 | 1332 | 777 | | DQA1*05:01 | DQB1*03:01 | | | | DQ7(3) | | 0.8370 | |
| Negative | 226 | 670 | 316 | | DQA1*05:01 | DQB1*04:01 | | | | DQ4 | | 0.7150 | |
| Negative | 104 | 575 | 130 | | DQA1*05:01 | DQB1*02:02 | | | | DQ2 | | 0.7940 | |
| Negative | 12 | 513 | 15 | | DQA1*05:01 | DQB1*02:01 | | | | DQ2 | | 0.7790 | |
| Positive | 8919 | 11493 | 11038 | | DQA1*06:01 | DQB1*03:01 | | | | DQ7(3) | | 0.8080 | 175E |
| Positive | 8931 | 12461 | 12135 | | DQA1*06:01 | DQB1*03:03 | | | | DQ9(3) | | 0.7360 | 175E |
| Positive | 8190 | 11518 | 11127 | | DQA1*06:01 | DQB1*04:02 | | | | DQ4 | | 0.7360 | 175E |

RESULTS

Figure 1.

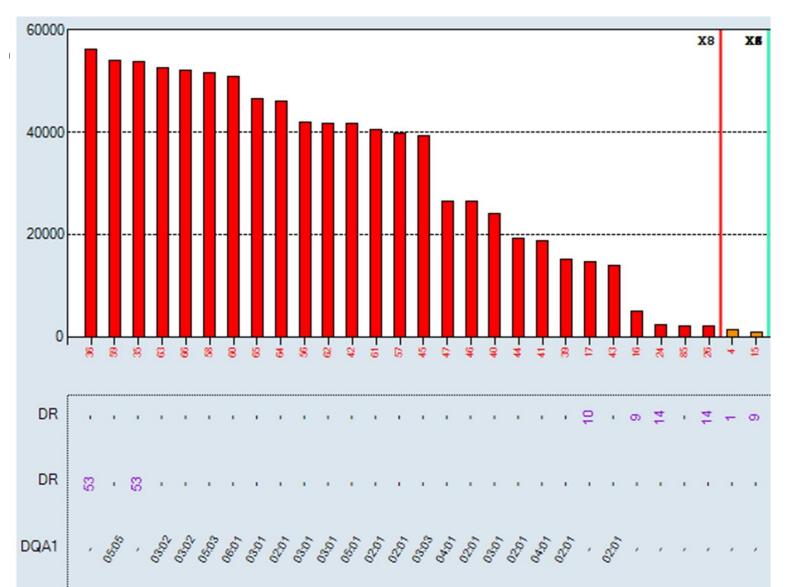


Figure 2.



Table 1.

| DQA1 allele | DQB1 allele | Frequency (%)* |
|-------------|-------------|----------------|
| DQA1*03:01 | DQB1*05:01 | 0.78 |
| DQA1*03:01 | DQB1*05:03 | 0.26 |
| DQA1*04:01 | DQB1*05:01 | 0.26 |
| DQA1*05:01 | DQB1*05:01 | 0.26 |
| DQA1*05:01 | DQB1*05:02 | 0.26 |
| DQA1*05:02 | DQB1*05:03 | 0.26 |
| DQA1*06:01 | DQB1*05:03 | 0.26 |
| DQA1*02:01 | DQB1*06:02 | 0.26 |
| DQA1*02:01 | DQB1*06:03 | 0.26 |
| DQA1*02:01 | DQB1*06:05 | 0.26 |
| DQA1*03:01 | DQB1*06:01 | 0.52 |
| DQA1*03:01 | DQB1*06:02 | 0.52 |
| DQA1*03:01 | DQB1*06:03 | 0.26 |
| DQA1*05:01 | DQB1*06:01 | 0.26 |
| DQA1*05:01 | DQB1*06:02 | 0.26 |
| DQA1*05:01 | DQB1*06:03 | 0.26 |
| DQA1*05:01 | DQB1*06:09 | 0.26 |

*Frequency: Total number of copies of the haplotype in the United States population sample (Haplotypes /2n) shown in percentages (%) per AlleleFrequencies.net

Case 2: A female patient with history of pregnancy and previous kidney transplant was being evaluated for her second transplant. She exhibited significant class II reactivity in OL-SAB (**Fig 3**).

However, while all the DQ4 beads were positive by OL-SAB, LC-SAB showed a single DQ4-DQA1*05:01 bead that was completely negative (**Fig 4**).

This confirmed that her antibodies were directed to the 175E epitope of the DQA1*02/03/04/06 chains and not to the DQ beta proteins. Two (0.12%) of 1,714 patients with LC-SAB testing have confirmed antibodies to the 175E epitope.

REFERENCES

Allele frequency net database (AFND) 2020 update: gold-standard data classification, open access genotype data and new query tools

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^{1.} Gonzalez-Galarza FF, McCabe A, Santos EJ, Jones J, Takeshita LY, Ortega-Rivera ND, Del Cid-Pavon GM, Ramsbottom K, Ghattaoraya GS, Alfirevic A, Middleton D and Jones AR