

HLA-DPB1 ALLELE FREQUENCIES ACROSS FOUR DONOR POPULATIONS

Luis Santiago¹, Stefan Stinnett², Jan J. Chew³, Nathan A. Lemp³, Sara Dionne¹. ¹Eurofins Donor & Product Testing, LLC, Centennial, CO, ²Honolulu, HI, ³Azusa, CA.



Donor & Product Testing

AIM

The update to the OPTN HLA Equivalency tables in 12/2024 brought substantial changes to the HLA-DPB1 Unacceptable Antigen Equivalences, including the addition of p-groups and many rare alleles. We performed an analysis of the DPB1 alleles identified in four of our laboratories serving distinct regional donor populations across the United States to examine allele frequencies among these populations and determine the impact of the updated HLA Equivalence tables.

METHODS

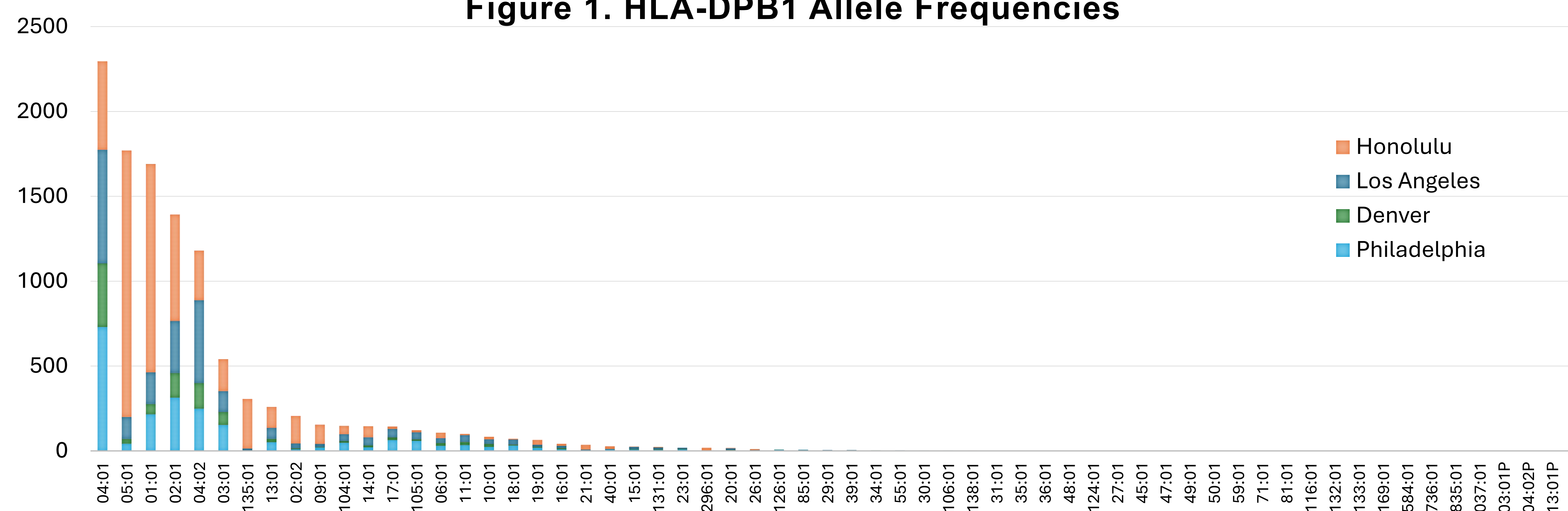
HLA typing was performed using LinkSeq HLA Typing Kits (One Lambda) as the primary method. To make rare (non-CWD 2.0) allele assignments, some specimens were additionally tested using Micro SSP (One Lambda), LABType SSO (One Lambda), and/or Olerup SSP (CareDx).

5,542 specimens tested between 01/2023 and 04/2025 at four Eurofins DPT laboratories (Honolulu (2,714), Los Angeles (1,218), Denver (502), and Philadelphia (1,108)) were included in the analysis (numbers in parentheses represent the volumes tested at each lab). Due to the lower numbers of deceased donors in Honolulu, living donor and transplant candidates were also included.

RESULTS

Over 5,000 HLA typings were reviewed. A total of 54 DPB1 alleles were identified (Figure 1). The five most frequently identified alleles (DPB1*04:01, 05:01, 01:01, 02:01, and 04:02) represented >75% of all alleles detected.

Figure 1. HLA-DPB1 Allele Frequencies



Using CWD 2.0, the frequency catalog utilized in the LinkSeq software, SureTyper, at the time of analysis, 30 Common, 6 Well-Documented (WD), and 18 non-CWD alleles were detected. However, using the CIWD 3.0.0 catalog, this became 48 Common, 1 Intermediate, 1 WD, and 4 non-CIWD alleles (Table 1). Each of the non-Common (CIWD 3.0.0) alleles was identified only once.

Of the 54 identified alleles, 8 were not included in OPTN Table 4-15: HLA DPB1 Unacceptable Antigen Equivalences (Table 2). However, all but two of these were only seen once, representing <0.1% of typed alleles. For two donors, a combination of rare alleles could not be resolved, and their DPB1 typings were reported using p-groups.

Table 1. Non-Common (CIWD 3.0.0) Alleles

DPB1 Allele	CIWD 3.0.0 Classification
116:01	Well-Documented
132:01	Indeterminate
169:01	Not classified
736:01	Not classified
835:01	Not classified
1037:01	Not classified

Table 2. Alleles Not in OPTN Table 4-15

DPB1 Allele	Number of Times Detected
36:01	2
48:01	2
47:01	1
49:01	1
50:01	1
71:01	1
116:01	1
169:01	1

CONCLUSIONS

The assignment of DPB1 typing and correlation to DPB1 unacceptable antigens (UA) in UNet continues to be complex. As evidenced by the absence of some alleles from the Antigen Equivalences table, the identification and utilization of Unacceptable Epitopes is more inclusive, although similarly complex. The option to use p-groups for reporting simplifies the resolution of rare ambiguities and will be particularly useful as the field moves toward high-resolution deceased donor typing.

