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Brief Communication

Balancing equity and human leukocyte antigen matching in deceased-donor kidney allocation with eplet mismatch

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ABSTRACT

Human leukocyte antigen-level matching in US kidney allocation has been deemphasized due to its role in elevating racial disparities. Molecular matching based on eplets might improve risk stratification compared to antigen matching, but the magnitude of racial disparities in molecular matching is not known. To assign eplets unambiguously, we utilized a cohort of 5193 individuals with high-resolution allele-level human leukocyte antigen genotypes from the National Kidney Registry. Using repeated random sampling to simulate donor-recipient genotype pairings based on the ethnic composition of the historical US deceased-donor pool, we profiled the percentage of well-matched donors available for candidates by ethnicity. The prevalence of well-matched donors with 0-DR/DQ eplet mismatch was 3-fold less racially disparate for Black and Asian candidates and 2-fold less for Latino candidates compared to 0-ABDR antigen mismatches. Compared to 0-DR antigen mismatch, 0-DR eplet mismatch was 1.33-fold more racially disparate for Asian and 1.28-fold more for Latino, with similar disparity for Black candidates, whereas 0-DQ eplet mismatch reduced disparities, showing 1.26-fold less disparity for Black, 1.14-fold less for Latino, but 1.26-fold higher for Asian candidates. The prevalence of well-matched donors for candidates of different ethnicities varied according to which molecules were chosen to define a low-risk match.

Abbreviations: agMM, antigen mismatch; dnDSA, de novo donor-specific antibody; epMM, eplet mismatch; HLA, human leukocyte antigen; NKR, National Kidney Registry; OPTN, Organ Procurement & Transplantation Network.

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1. Introduction

Closer donor-recipient human leukocyte antigen (HLA) matching is associated with improved posttransplant kidney graft survival.[1-3] However, prioritizing HLA matching comes with a tradeoff of increased transplant rates for candidates with more frequent HLA genotypes, which disadvantages underrepresented populations with greater HLA diversity. HLA matching priority has been reduced several times, by eliminating points for HLA-A matching in 1995,[4] and for HLA-B matching in 2003[5] with further deprioritization in 2014,[6] due to concerns of exacerbating racial disparities in transplant rates.[7] The 2014 change decreased the prevalence of 0-ABDR antigen mismatch (agMM) transplants from 8.2% to around 4%.[8] At present, only antigen-level 0-ABDR, 0-DR, and 1-DR mismatches are awarded points in the US deceased-donor kidney allocation, maintaining disparities in access to well-matched kidneys.[9] A prior study of the Organ Procurement & Transplantation Network (OPTN) database of recovered donors and waitlist registrations found that for the lowest-risk category of highly prioritized 0-ABDR agMMs, White candidates have 6 times as many 0-ABDR mismatched donors as African Americans have, and 9 times as many as Asians have.[10]

Advances in genotyping technology, such as next-generation sequencing, have enabled allele-level HLA compatibility assessment between donors and recipients.[11] Currently, reporting antigen-level typing is the standard practice, as unambiguous allele-level information is not usually available for deceased-donor kidney allocation. Antigen-level typing broadly categorizes HLA molecules based on serologic reactivity, concealing some clinically relevant differences between HLA proteins. Allele-level typing identifies the specific gene sequences, enabling eplet mismatch (epMM) to be directly computed from the HLA amino acid sequence of the alleles. Rapid long-read next-generation sequencing technology being tested in clinical HLA laboratories could soon provide allele-level genotyping of deceased donors routinely at the time of allocation.[12]

Eplet matching promises improved transplant outcomes by providing a more precise assessment of donor-recipient compatibility by examining critical amino acid motifs on HLA proteins that are predicted to influence the specificity of anti-HLA antibody binding. Several studies have demonstrated that higher levels of HLA-DR and DQ epMMs correlate with the formation of posttransplant de novo donor-specific antibody (dnDSA), which is associated with antibody-mediated rejection,[13-15] and that epMM is a prognostic biomarker for both T cell and antibody-mediated rejection.[16-18]

Because of the possible improvements in long-term graft survival, the idea of utilizing eplet matching in kidney allocation is gaining community attention.[19-21] Some living donation programs, such as the National Kidney Registry (NKR)[22] and Royal Children's Hospital Melbourne kidney transplant program have already adopted epMM in their allocation systems.[23] However, detailed studies on equity and utility of molecular mismatch in the context of allocation are needed, as the Sensitization in Transplantation: Assessment of Risk working group has advocated.[24] Bekbolsynov et al[21] showed in a simulation study that race-adjusted molecular matching can provide more opportunities for Black candidates to receive well-matched organs.

To model equity in access among candidate ethnic groups to well-matched deceased donors in the US, we utilized an NKR cohort of over 5000 individuals with the high-resolution HLA genotyping necessary to make unambiguous eplet assignments, as OPTN data sets lack the required HLA data. We compared the prevalence of low-risk eplet and antigen mismatch donors and differences in the availability of well-matched donors between 4 racial and ethnic groups.

2. Methods

2.1. Study population

This study used HLA genotyping and ethnicity data from the NKR, an organization that facilitates kidney paired donations for members of its clinical network in the United States. The NKR data set included 5193 recipients, and living donors who were all HLA genotyped at the allele-level enabling unambiguous assignment of eplets. Individual race/ethnicity (hereafter referred to more simply as "ethnicity") was self-reported.

Twenty distinct OPTN-representative donor pools of randomized 1000 individuals were sampled from the NKR cohort, each having the ethnic composition of the historical 5-year average (2016-2021) of the OPTN deceased-donor pool (Asian [2.5%], Black [14.5%], Hispanic/Latino [14.8%], White [66.8%], and Others [1.3%]); see Table 1. As a result, each of the 20 donor pools consisted of different sets of donors within each ethnic group to enhance results generalizability. Individuals identified as Hawaiian/Pacific Islander, Multiracial, Native American, and those with missing data and undisclosed ethnicity were combined into the "Other" category. After sampling each replicate donor pool, the percentage of well-matched donors was calculated for each of the remaining individuals (ie, 4193 individuals from the NKR pool who were not in the OPTN-representative donor pool). Creating 20 resampled 1000 donors/4193 candidates pools allowed us to generate a confidence interval in addition to a point estimate of our outcome and to capitalize on the larger sample size of the NKR data set while adjusting for the ethnic composition, reducing the impact of sampling error. We aggregated the percentages of well-matched donors with individuals by their ethnicity.

2.2. HLA genotyping and HLA epMM load

All 5193 individuals were fully genotyped at the allele-level for all 11 classical HLA loci (HLA-A, B, C, DRB1, DRB3/4/5, DQA1, DQB1, DPA1, DPB1). To assign agMM, each allele was mapped to corresponding HLA antigens according to the OPTN histocompatibility tables and guidance, using the ALLele to ANtigen[25] tool that incorporates population-specific allele frequencies, including race/ethnic data, to resolve ambiguous or undefined serologic assignments. For assigning epMM, we used the publicly available calculator from the NKR,[26] which is based on and has been verified against the calculator in the HLA Eplet Registry with

Table 1
Study population.

Population	NKR dataset		Resampled pools to reflect OPTN deceased donor pools	
	n	%	n	%
	5193		1000 (×20 replicates)	
Asian	214	4.1%	25	2.5%
Black	381	7.3%	145	14.5%
Latino	415	8.0%	148	14.8%
White	3309	63.7%	668	66.8%
Other	40	0.8%	14	1.4%
Hawaiian/Pacific Islander[a]	10	0.2%		
Multiracial[a]	44	0.8%		
Native American[a]	21	0.4%		
Not disclosed[a]	13	0.3%		
Missing data[a]	746	14.4%		

From a data set of 5193 individuals with high-resolution HLA typing data from NKR, we randomly sampled 20 replicate donor pools of 1000 individuals, each with pool reflecting the 5-year average (2016-2021) ethnic composition of the US deceased-donor pool (last column). Ethnic distributions of the NKR data set and the simulated donor pools are provided. HLA, human leukocyte antigen; NKR, National Kidney Registry; OPTN, Organ Procurement & Transplantation Network.

[a] Ethnicities that were grouped into the category "Other" in the simulation pools.

100% concordance.[27] For each candidate-donor pair, we calculated the following: (1) the sum of epMMs for HLA-DR (HLA-DRB1/3/4/5) and HLA-DQ (HLA-DQA1/HLA-DQB1), and (2) the number of A, B, DR, or DQ agMMs. We defined a low-risk epMM sum as a 1 to 10 DR mismatch and/or 1 to 10 DQ mismatch, on the strength of evidence from Wiebe et al.[28] We included both antibody-verified and nonverified eplets.

2.3. Simulation and statistical analysis

For each OPTN-representative donor pool, we calculated the percentage of well-matched donors for each candidate (also from NKR) in a resampled pool with the ethnic composition as the OPTN deceased-donor pool, using either the agMM or epMM risk categories. The percentage of well-matched donors is the percentage of donors with a given HLA mismatch level with a candidate. In our main analyses, candidates were matched solely based on HLA compatibility, not accounting for ABO blood group compatibility or any other allocation criteria.

The cohort resampling was programmed in Python 3.9 and the package Scipy 1.9.2 was used for statistical calculations. For each of the 20 simulation runs, the ratios of the percentage of well-matched donors between candidate ethnicities were calculated to obtain a 95% confidence interval.

3. Results

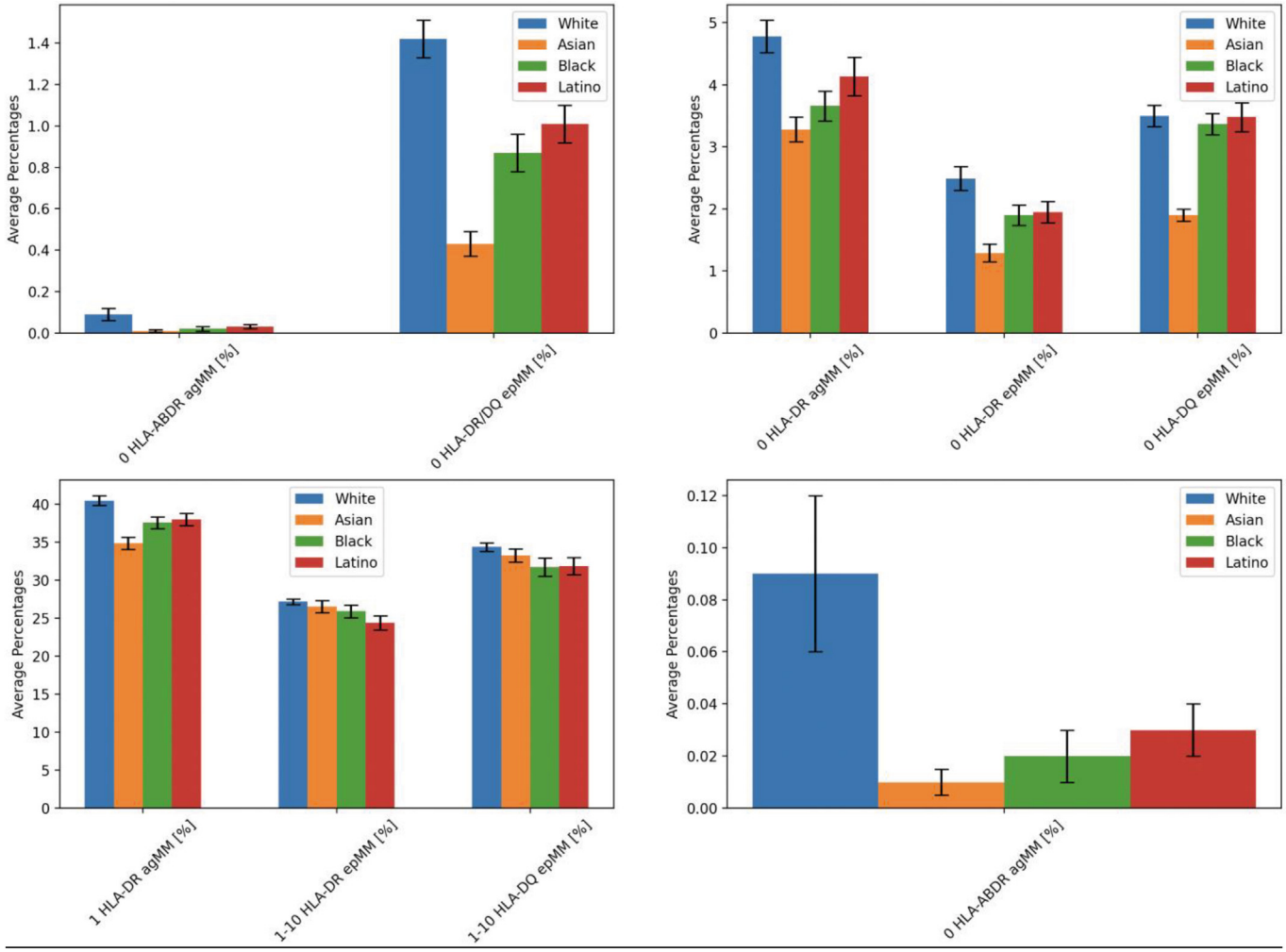
3.1. Comparing lowest-risk categories: 0-ABDR agMM and 0-DR/DQ epMM

Figure 1 shows the percentage of well-matched donors at the agMM or epMM level for candidates of each ethnic group. The average percentage of 0-ABDR agMM donors was 0.09% for White candidates, 0.01% for Asian candidates, 0.02% for Black candidates, and 0.03% for Hispanic/Latino candidates. The average percentage of 0-DR/DQ epMM donors was 1.42% for White candidates, 0.43% for Asian candidates, 0.87% for Black, and 1.01 % for Hispanic/Latino candidates.

Figure 2 illustrates the expected relative percentage of well-matched donors for White candidates vs Asian, Black, or Hispanic/Latino candidates across 20 simulated donor pools, each with the ethnic composition of OPTN deceased donors. The average percentage of 0-ABDR agMM donors for White candidates was 9.86 times higher than for Asian, 4.97 times higher than for Black, and 3.21 times higher than for Hispanic/Latino candidates. The average percentage of 0-DR/DQ epMM donors for White candidates was 3.26 times higher than for Asian, 1.63 times higher than for Black, and 1.41 times higher than for Hispanic/Latino candidates. Comparing the percentage of well-matched donors for 0-ABDR antigen vs 0-DR/DQ epMM, eplet matching was 3.01 times less racially disparate for Asian, 3.05 times less racially disparate for Black, and 2.21 times less racially disparate for Hispanic/Latino candidates compared to antigen-level matching. The 0-DR/DQ epMM risk category increased the percentage of well-matched donors compared to 0-ABDR agMM by 16 times for White, 43 times for Asian, 45 times for Black, and 34 times for Hispanic/Latino candidates.

3.2. Comparing 0-DR agMM, 0-DR epMM, and 0-DQ epMM

Among the 0-DR and 0-DQ risk categories, the 0-DQ epMM was the most equitable category for Black and Hispanic/Latino candidates, whereas 0-DR agMM and 0-DR epMM favored White candidates (Figs. 1 and 2). The average percentage of well-matched donors was 1.30 times higher for White than for Black



	White	Asian	Black	Hispanic / Latino
0 HLA-ABDR agMM [%]	0.09 (0.03)	0.01 (0.00)	0.02 (0.01)	0.03 (0.01)
0 HLA-DR/DQ epMM [%]	1.42 (0.09)	0.43 (0.06)	0.87 (0.09)	1.01 (0.09)
0 HLA-DR agMM [%]	4.78 (0.26)	3.28 (0.20)	3.66 (0.24)	4.14 (0.31)
0 HLA-DR epMM [%]	2.49 (0.19)	1.29 (0.14)	1.90 (0.16)	1.95 (0.17)
0 HLA-DQ epMM [%]	3.50 (0.17)	1.90 (0.10)	3.37 (0.17)	3.48 (0.23)
1 HLA-DR agMM [%]	40.53 (0.65)	34.91 (0.79)	37.60 (0.76)	38.01 (0.81)
1-10 HLA-DR epMM [%]	27.20 (0.37)	26.57 (0.79)	25.92 (0.83)	24.44 (0.93)
1-10 HLA-DQ epMM [%]	34.41 (0.57)	33.28 (0.85)	31.78 (1.21)	31.90 (1.14)
Low-Risk HLA-DR/DQ epMM* [%]	15.17 (0.30)	13.90 (0.64)	13.68 (0.83)	13.50 (0.67)

*1-10 DR and/or 1-10 DQ eplet mismatch

Figure 1. Expected percentages of well-matched donors by candidate ethnicity for various low-risk antigen and eplet mismatch (epMM) categories. Average percentages (and standard deviation) summarize the results across 20 replicate simulated donor pools. agMM, antigen mismatch; HLA, human leukocyte antigen.

candidates for 0-DR agMM, 1.31 times higher for White than for Black candidates for 0-DR epMM, and only 1.04 times higher for White than for Black candidates for 0-DQ epMM. The average percentage of well-matched donors was 1.16 times higher for White than for Hispanic/Latino candidates for 0-DR agMM, 1.28 times higher for White than for Hispanic/Latino candidates for 0-DR epMM, and only 1.01 times higher for White than for Hispanic/Latino candidates for 0-DQ epMM. Asian candidates were the most disfavored in all 0 mismatch risk categories due to having HLA alleles and antigens that are relatively rare in other populations and because Asians compose only a small percentage of donor pool (Supplementary Table and Supplementary Fig.).

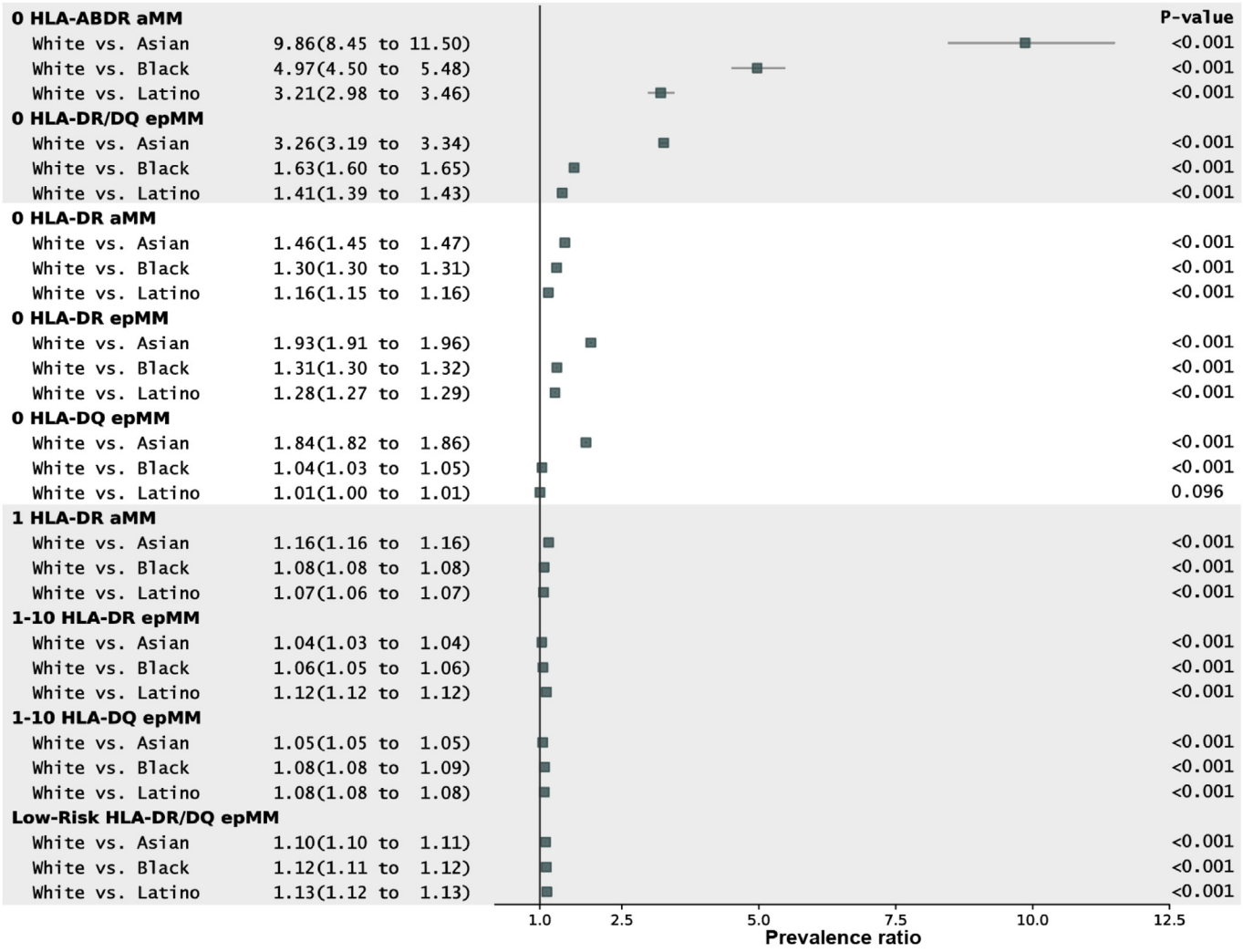


Figure 2. Ethnic disparity metrics for access to well-matched donors. Ratios of the average percentage of well-matched donors for White candidates relative to the average percentage of well-matched donors for Asian, Black, or Latino candidates, for each of 9 antigen and eplet risk categories. The larger the percentage ratio, the greater the ethnic disparity in access to well-matched donors (eg, White candidates had 9.86 more 0-ABDR antigen mismatch [agMM] donors than Asian candidates). Average point estimates for percentage ratios (and 95% confidence intervals) are provided for each candidate ethnicity comparison. epMM, eplet mismatch.

Table 2 shows the mean HLA eplet and antigen mismatches for candidates matched with donors from the same or different ethnic groups. The mismatches were generally higher when candidates were matched with donors from different ethnicities, particularly for ethnic groups other than White. For example, for Asian candidates, 0-DQ epMM were 12.34 for same ethnicity and 13.20 for different-ethnicity donors.

Figure 3 compares HLA-DR epMMs among pairs with 0-DR and 1-DR agMMs. For example, Black candidates matched at 0-DR HLA agMM had an average of 2.46 DR epMM, compared to White candidates with only 1.47 DR epMM.

3.3. Comparing 1-DR agMM, 1-10 HLA-DR epMM, 1-10 HLA-DQ epMM, and low-risk DR/DQ epMM

At the nonzero mismatch low-risk categories (1-DR antigen and 1-10 HLA-DR, 1-10 HLA-DQ, and low-risk DR/DQ epMM), well-matched donors were only 1.04 to 1.16 times more prevalent for White candidates than for ethnic underrepresented candidates (Figs. 1 and 2). The 1-DR agMM risk category had the largest average percentage of well-matched donors, ranging from 34.9% to 40.5% among racial and ethnic groups (Fig. 1). The 1 to 10 HLA-DR epMM risk category had an average percentage of 24.4% to 27.2% well-matched donors.

Although without a direct comparator, the 1 to 10 HLA-DQ epMM risk category was closely equitable in that the percentage of well-matched donors was similar across candidate ethnicities. There was also a similar percentage of well-matched donors for both the 1 HLA-DQ epMM risk category and the 1 HLA-DR agMM, ranging from 31.8% to 34.4% (Fig. 1). The percentage of well-matched donors in the low-risk DR/DQ epMM risk category ranged between 13.5% and 15.2% among candidate ethnicity.

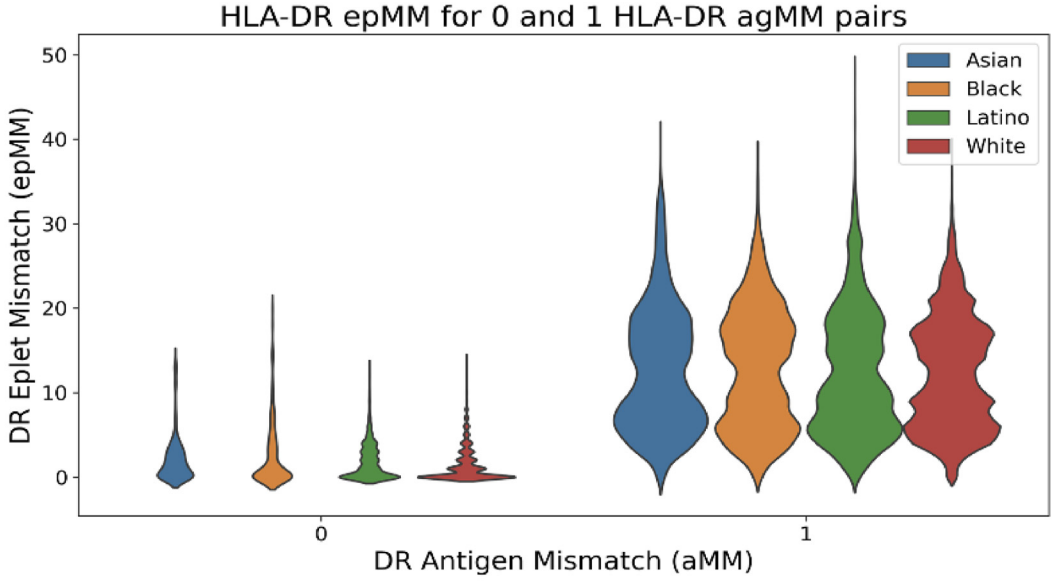
4. Discussion

HLA eplet matching has gained attention as having the potential for better stratification of primary allo-immune risk than antigen-level HLA matching.[28-30] Evidence supporting the

Table 2
Mean (standard deviation) HLA eplet and antigen mismatches (HLA-ABC epMM, HLA-DR epMM, HLA-DQ epMM, HLA-ABDR agMM, HLA-DR agMM) for simulated matching by candidate ethnicity.

	Donor ethnicity	HLA-ABC epMM	HLA-DR epMM	HLA-DQ epMM	HLA-ABDR agMM	HLA-DR agMM
Asian	Same	29.30 (11.89)	17.07 (10.28)	12.34 (6.92)	4.30 (1.28)	1.51 (0.60)
Asian	Different	35.53 (10.56)	17.34 (9.78)	13.20 (6.46)	4.95 (0.93)	1.60 (0.55)
Black	Same	32.60 (10.15)	15.56 (9.06)	12.18 (5.92)	4.83 (1.09)	1.54 (0.59)
Black	Different	34.78 (10.21)	17.37 (8.77)	12.79 (5.89)	4.90 (0.95)	1.58 (0.55)
Latino	Same	29.30 (9.88)	16.08 (11.28)	11.64 (6.54)	4.57 (1.21)	1.47 (0.61)
Latino	Different	32.89 (9.41)	17.10 (10.79)	13.18 (6.51)	4.72 (1.00)	1.56 (0.57)
White	Same	31.99 (10.88)	16.19 (8.81)	12.54 (6.41)	4.51 (1.11)	1.51 (0.58)
White	Different	31.17 (10.16)	15.94 (8.97)	12.43 (6.31)	4.69 (1.02)	1.52 (0.58)

The Table compares mismatch values between candidates matched with donors from the same ethnicity vs those from different ethnicities. agMM, antigen mismatch; epMM, eplet mismatch; HLA, human leukocyte antigen.



		HLA-DR epMM		
	HLA-DR agMM	mean (SD)	median	min/max
Asian	0	2.12 (2.83)	1	0/14
Black	0	2.47 (3.78)	1	0/20
Latino	0	1.71 (2.01)	1	0/13
White	0	1.47 (2.1)	1	0/14
Asian	1	12.59 (7.28)	11	0/40
Black	1	12.84 (7.06)	13	0/38
Latino	1	12.19 (7.35)	11	0/48
White	1	12.27 (6.64)	12	0/39

Figure 3. Comparison of HLA-DR eplet mismatch (epMM) and HLA-DR antigen mismatch (agMM). For pairs with HLA-DR agMM 0 or 1, we calculated mean (standard deviation [SD]), median, and min/max HLA-DR epMM. For instance, Asians with 0-DR agMM had a mean of 2.12 HLA-DR epMM. HLA, human leukocyte antigen.

deleterious effect of high epMM load at HLA-DR and HLA-DQ continues to increase. The possibility of redesigning allocation policy to engineer more transplants to be 0 or low HLA-DR and/or 0 or low HLA-DQ epMM is gaining traction in the transplant community because epMM appears to be more strongly associated with dnDSA formation and graft failure than antigen-level mismatch. However, because prioritizing antigen-level mismatch historically created ethnic disparities in kidney allocation, we designed a simulation study using allele-level HLA genotyping data to investigate the impact of prioritizing epMM on disparities. We calculated the percentage of well-matched donors for different ethnicities in replicate donor pools, each with a similar ethnic composition to the OPTN deceased-donor pool. To measure ethnic disparity, we calculated the relative prevalence of well-matched donors for Asian, Black, Hispanic/Latino, and White candidates using 9 different matching risk categories, comparing HLA antigen-level and HLA eplet-level matching. Our results indicate that giving priority to low HLA-DR and/or HLA-DQ epMM would not increase ethnic disparities among Black and Hispanic/Latino candidates (but might increase disparities for Asian candidates) compared to HLA-DR agMM. Low HLA-DR and/or HLA-DQ epMM would decrease disparities substantially compared to 0-ABDR agMM, which is now granted high priority in deceased-donor kidney allocation. Our results also support the transition toward HLA-DR antigen matching in the allocation system as being less racially disparate than 0-ABDR mismatch.

For Black and Hispanic/Latino populations, the most equitable risk category was 0-DQ epMM, eliminating the disparities almost completely. However, Asian candidates were the most deprived group across 0 antigen and eplet mismatches, likely due to the differential expression of HLA-DR and HLA-DQ alleles and the low prevalence of Asian donors in the OPTN deceased-donor pool. The HLA-DRB expressed most commonly by our Asian population was only expressed by about half of the other populations (Supplementary Table). Tran et al[19] found the HLA-DQ eplets to be the most shared among a heterogenous pool of 2000 kidney donors and recipients, which supports our finding that 0 HLA-DQ epMM has the potential to be the most equitable risk stratification method. With an increasing role for HLA-DQ and HLA-DR matching in kidney transplantation and the weight of evidence supporting the deleterious effect of HLA-DQ and HLA-DR dnDSA and graft rejection,[13,28,31] prioritizing 0-DQ epMM or 0-DR epMM donors might reduce allo-immune risk. Tambur et al[32] found that mismatches at HLA-DQ are not only correlated with rejection but that dnDSA targeting donor HLA-DQ antigens are the most common antibodies posttransplant.

Evidence has suggested that epMM analysis is a more precise method for primary allo-immune risk assessment.[28,30] Wiebe et al[28] found that a load of >10 HLA-DR and HLA-DQ mismatched eplet sums is a strong predictive biomarker for the development of HLA-DR and HLA-DQ dnDSA (AUC 0.72 for HLA-DR and DQ), outperforming traditional HLA-DR/DQ agMM (AUC 0.54 for HLA-DR and 0.58 for HLA-DQ). Sapir-Pichhadze et al[14] clearly demonstrated a significant correlation between the number of mismatched HLA-DR and HLA-DQ eplet and the likelihood of graft failure in an imputed Scientific Registry for Transplant Recipients data set. For every 10 mismatched HLA-DR and HLA-DQ eplets, the hazard ratio was 1.35 and 1.29, respectively, with 95% confidence intervals ranging from 1.01 to 1.81 and 1.01 to 1.67 ($P = .05$). In our simulation, 1 HLA-DR agMM identified an average of 35.0% to 40.5% matched donors among ethnic groups and improved disparities. However, only 24.4% to 27.2% of donors in the pool were low-risk HLA-DR epMM, 31.8% to 34.4% were low-risk HLA-DQ epMM, and 13.5% to 15.2% were low-risk HLA-DR/DQ epMM donors.

Prioritizing epMM in deceased-donor kidney allocation would require the implementation of rapid deceased-donor allele-level genotyping in clinical laboratories. However, the methods are still under evaluation. A key advantage of our study is that it utilized allele-level HLA genotypes determined by next-generation sequencing in the setting of organ transplantation. Continuing research in HLA mismatch and outcomes to build a strong evidence base to support policy changes is also necessary. Tambur et al[33] provided a comprehensive commentary on issues to address before using epMM in organ allocation, arguing that the immunogenicity of individual eplets should also be verified before assigning priority scores on the basis of the matched eplets.[34] Moreover, long-term outcomes research on low allo-immune risk donors remains necessary to refine optimal risk stratification paradigms and improve understanding of the immunologic mechanisms involved.

There are several limitations in our study. Although we resampled the donor population to match the racial/ethnic makeup of the OPTN deceased-donor pool, we analyzed only 4 of the most prevalent groups (Asian, Black, Hispanic/Latino, and White) from the NKR data set. We looked at the impact of eplet matching only on a crude aggregation into 4 broadly defined self-identified ethnic groups (Asian, Black, Hispanic/Latino, and White), which conceals population substructure and heterogeneity in match likelihoods for more detailed subpopulations. However, our simulation results are consistent with registry data analysis[8] showing that Asian, Black, and Hispanic/Latino candidates are less likely than White candidates to find a 0-ABDR agMM donor. It is a limitation that we have considered epMM risk categories as the sum of epMMs at a given locus. We included both antibody-verified and other eplets because there is no definitive proof yet that antibody-verified eplets are the only immunogenic eplets, with a large proportion of HLA eplets being theoretical, awaiting further verifications. Future studies could investigate the impact of other risk categories on equity by considering only antibody-verified eplets, single molecule epMM, or surface-exposed mismatched amino acid (HLA-EMMA[35]), or by the number of peptides derived from HLA mismatched donor proteins that are indirectly presented by recipient class II molecules to CD4+ T cells (PIRCHE-II).[36] Although Wiebe et al[37] have demonstrated that their different B cell molecular mismatch paradigms are highly correlated ($r^2 = 0.85$-0.96), these mismatch methods must be verified in a much more heterogeneous population. Optimal mismatch thresholds for risk stratification are still unknown. The association of epMM with graft failure has not been conclusively demonstrated in studies with high-resolution

typing data, though studies relying on imputation have shown this. Because our cohort comes from the living donation program, each potential recipient might be related to at most 1 donor, which could slightly inflate the likelihood of finding a well-matched donor. Our simulation did not account for other allocation priorities (like HLA sensitization, etc). The impact of epMM on transplant rates would depend on the details of the allocation scheme. We have not evaluated any particular allocation scheme; we only found the prevalence of well-matched donors.

Our study provides a new level of evidence for comparing ethnic disparity in the currently prioritized agMM risk categories to the ethnic disparity in potentially relevant epMM risk categories. The HLA-DQ epMM seems to be the most equitable for Black and Hispanic/Latino candidates; however, this may not be the case for Asian candidates.

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Declaration of competing interest

The authors of this manuscript have conflicts of interest to disclose as described by the American Journal of Transplantation. M.A. Mankowski and L. Gragert reports financial support from National Institute of Diabetes and Digestive and Kidney Diseases. B. Keating, B. Lonze, and D.L. Segev reports financial support from National Institute of Allergy and Infectious Diseases. The other authors of this manuscript have no conflicts of interest to disclose as described by the American Journal of Transplantation.

Data availability

The data are available from the National Kidney Registry (NKR) upon reasonable request.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ajt.2024.11.030.

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