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Citation

Osoegawa, K., Marsh, S. G. E., Holdsworth, R., Heidt, S., Fischer, G., Murphey, C., … Vina, M. A. F. (2022). A new strategy for systematically classifying HLA alleles into serological specificities. *Hla: Immune Response Genetics*, *100*(3), 193-231. doi:10.1111/tan.14662

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Note: To cite this publication please use the final published version (if applicable).

ORIGINAL ARTICLE

A new strategy for systematically classifying HLA alleles into serological specificities

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HLA serological specificities were defined by the reactivity of HLA molecules with sets of sera and monoclonal antibodies. Many recently identified alleles defined by molecular typing lack their serotype assignment. We surveyed the literature describing the correlation of the reactivity of serologic reagents with AA residues. 20 - 25 AA residues determining epitopes (DEP) that correlated with 82 WHO serologic specificities were identified for HLA class I loci. Thirteen DEP each located in the beta-1 domains that correlated with 24 WHO serologic specificities were identified for HLA-DRB1 and -DQB1 loci. The designation of possible HLA-DPB1, -DQA1, -DPA1, and additional serological specificities that result from epitopes defined by residues located at both -DQA1 and -DQB1 subunits were also examined. HATS software was developed for automated serotype assignments to HLA alleles in one of the three hierarchical matching criteria: (1) all DEP (FULL); (2) selected DEP specific to each serological specificity (SEROTYPE); (3) one AA mismatch with one or more SEROTYPES (INCOMPLETE). Results were validated by evaluating the alleles whose serotypes do not correspond to the first field of the allele name listed in the HLA dictionary. Additional 85 and 21 DEP patterns that do not correspond to any WHO serologic specificities for common HLA class I and DRB1 alleles

Abbreviations: AA, amino acids; CDQS, combinatorial DQ serotypes; CIDW, common, intermediate and well-documented; CREG, cross reactive group; CWD, common and well-documented; DEP, determining Epitope; DSA, donor-specific antibodies; HATS, HLA allele to serotype; HSCT, hematopoietic stem cell transplantation; IHIW, International HLA and Immunogenetics Workshops; IHW, International Histocompatibility Workshops; IMGT, ImMunoGeneTics; IPD, ImmunoPolymorphism database; mAb, monoclonal antibody; NSD, novel split designation; SAB, single antigen bead; SS, serologic specificities; UNA, UNASSIGNED; UNOS, United Network for Organ Sharing; WD, well documented; WHO, World Health Organization.

were identified, respectively. A comprehensive antibody identification panel would allow for accurate unacceptable antigen listing and compatibility predictions in solid organ transplantation. We propose that antibody-screening panels should include all serologic specificities identified in this study.

KEYWORDS

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antigen, common allele, epitope, eplet, residue, serotype

1 | INTRODUCTION

Identification of serological specificities is critical to assess whether anti-HLA humoral reactivity present in the patient's serum corresponds to donor-specific antibodies (DSA). Serological HLA specificities have been characterized during the International HLA and Immunogenetics Workshops (IHIW), previously known as Histocompatibility Workshops (IHW) through the correlation analyses of serological reactivity patterns defined by testing HLA typed cell panels with series of allo-antisera, monoclonal antibodies (mAbs), and specific amino acid (AA) residues of HLA alleles. $1-7$ The HLA serologically defined antigens had been officially recognized by the WHO Nomenclature Committee for Factors of the HLA System^{[8](#page-35-0)} following the extensive serologic testing exercises performed at previous $IHW²$ $IHW²$ $IHW²$. The report from Milford et al. $²$ $²$ $²$ illustrated how serologically defined</sup> specificities showed unique reactivity patterns as plotted in the so called "serograms." With the advent of molecular testing, serologic typing has virtually been discontinued and serologic exercises have been reduced or no longer performed after the 13th IHIW. $\frac{6}{5}$ $\frac{6}{5}$ $\frac{6}{5}$ As a result, many of the recently identified alleles lack the corresponding serotype designation. At IHIW, each recognized specificity was defined by its unique reactivity pattern with distinct clusters of allo-antisera; each serum cluster showed distinctive inclusion of serologic HLA specificities.^{[1](#page-35-0)} The elegant early experiments pioneered by van Rood and van Leeuwen demonstrated that some sera included in the same reactivity cluster recognized the same epitopes that could be confidently adjudicated as such by the preservation of the reactivity after performing absorption/ elution experiments. These tests were able to rule out that for some mono-specific sera, the positive reactions did not result from the occurrence of mixed populations of allo-antibodies.[9](#page-35-0) These investigators described the codominant bi-allelic system with the antigens $4a/4b$.^{[9](#page-35-0)} These mutually exclusive specificities are now officially designated as Bw4/Bw6 that behave as supertypic epitopes to nearly all currently named HLA-B antigens with a few exceptions in which the antigen/alleles are assigned neither as Bw4 nor Bw6. With the development of mAbs,

the processes for recognition and assignment of HLA serologic determinants became more straightforward obviating the need of performing additional characteriza-tion steps.^{[10](#page-35-0)–12} The evaluation of protein structures of HLA class I alleles and their correlation between mAbs further allowed identification of critical AA residues determining the epitopes recognized by the latter $12-15$ $12-15$; this work allowed identification of the dimorphism at residues 82 and 83 of HLA-B alleles as a necessary determinant of the Bw4 and Bw6 reactivity. The elegant work performed by Lutz and coworkers^{[15](#page-35-0)} examining single residue variants of HLA-B7 allowed mapping the reactivity of anti-Bw6 mAbs to specific residues and showed that, despite some overlap in the determining residues, substitutions at additional residues appear to further determine the antibody reactivity (DEP). Further identification of critical residues determining HLA- A^{16-18} A^{16-18} A^{16-18} and $-B^{19-29}$ serotypes and epitopes were readily identified by the direct comparison of the protein sequences of alleles that are structurally related that differ only by a few amino acids and have distinct serotypes. The evaluation of the reactivity of mAbs with different alleles allowed for the identification of residues possibly defining HLA class I epitopes to be mapped to residues shared by different alleles.^{10–[14,30](#page-35-0)–35} Critical residues defining serotypes or determining epitopes of HLA class II products were identified by similar approaches for HLA-DR, $36-43$ DO $43-45$ and DP.^{46–[48](#page-36-0)} Many of the epitopes defined in early studies were identified by non-human mAbs; additional work confirmed that these same epitopes were also identified by both, allo-antisera and mAbs of human origin.^{6,7,49,50}

The simultaneous application of molecular typing methods and serologic testing in IHIW exercises allowed inference of which amino acids at polymorphic positions in the HLA class I and class II proteins, may determine epitopes recognized by sets of mAbs or by clusters of alloantibody reagents evaluated in the $12th^{4,5}$ $12th^{4,5}$ $12th^{4,5}$ and $13th^{6,7}$ $13th^{6,7}$ $13th^{6,7}$ IHIW. In the 13th IHIW the systematic computational analyses for examination of the mAbs and allo-antisera reactivity allowed mapping the putative epitopes recog-nized by serologic reagents.^{[6](#page-35-0)} These analyses appeared to identify AA at specific positions that defined distinct epitopes when combined with substitutions at other AA positions. More recently, residues or eplets defining epitopes were further characterized or cataloged systematically.^{[51](#page-37-0)-59}

These studies identified residues that determine epitopes that in turn allow for the definition and distinction of the currently recognized WHO serological specificities. The majority of the residues mapped as defining serologic epitopes are located in the alpha-helical segments of the membrane distal domain, and these allo-antibodies react with HLA molecules regardless of peptide bound. However, some important residues defining epitopes, for example, those defining major DR serotypes and residue 45 of HLA-B, are located in positions that do not appear to be directly accessible to antibodies, and these are examples of allo-antibodies whose paratope may depend on the peptide bound. $60,61$ Similarly, the serologic splits of B14 are B64 and B65; the corresponding prototype alleles HLA-B*14:01 and HLA-B*14:02 differ only by one AA replacement at residue 11 that is located at the bottom of the groove. 29 29 29 With the current knowledge of residues determining serotypes, it can be proposed that HLA serotypes can be defined by the examination of the residues located at the principal serotype defining positions.

Names of previously recognized serological specificities were closely associated with the HLA allele name. For example, the HLA-A2 specificity corresponding to the allele HLA-A*02:10 were named as the associated antigen HLA-A210. Three HLA-A (A203, A210, and A2403), six HLA-B (B703, B3901, B3902, B4005, B5102, and B5103) and three DRB1 (DR103, DR1403, and DR1404) serological specificities were officially named as associated antigens by the WHO Nomenclature Committee for Factors of the HLA System in 1991, 62 and B2708 was named in 1996. 63 The serologic exercises performed in various IHIW identified possible serologic splits of HLA-A34, $64,65$ -A66 64 and $-DR4$,^{[66](#page-37-0)} however, these splits were not officially named. The examination of residues defining serotypes can, therefore, be used to name new splits corresponding to common prototype alleles. New serotypes of common alleles can also be assigned according to the AA substitutions in residues defining serologic epitopes.

All recently recognized HLA alleles are identified solely by molecular typing, and the number of alleles has been increasing in IPD-IMGT/HLA Database.^{[67](#page-37-0)} The most recent serologic information for some HLA alleles is available through HLA Dictionary 2008 in IPD-IMGT/ HLA Database, however, it contains information on only 1262 HLA class I and 336 class II alleles. 68 Therefore, many HLA alleles defined by molecular typing lack their serotype assignment.

HLA alleles follow a heavy tail distribution across all population/racial groups.^{[69](#page-37-0)} A small fraction of HLA alleles have been characterized as belonging to "common," "intermediate," and "well-documented" (CIWD) categories, $70-73$ $70-73$ with the majority of the HLA alleles in rare categories. It is not operationally feasible to have full representation of all HLA alleles in the antigen panel of solid phase antibody detection assays. In practice, it is valuable to have defined serotypes for all the common alleles that are often encountered in the routine clinical HLA tests, and to have common serotype representation in the antigen panel of solid phase assays.

Recently, serological specificities were predicted for $HLA-B*15$ alleles based on amino acid sequence patterns.⁷⁴ Using the information of the key AA residues that define serotypes, a computational tool that performs virtual serotype assignments for the HLA-A, -B, -C, -DRB1, -DRB3/4/5 and -DQB1 alleles that have little or no information about their serological specificities is designed in this study.

Serotypes for alleles at the HLA-DQA1, -DPA1, and -DPB1 loci have not been assigned with official WHO Nomenclature; there is a large body of evidence showing that serologic epitopes present in alleles at these loci can be identified using allo-antisera and mAbs. $53,75-78$ $53,75-78$ We propose to assign serotypes to alleles of these loci by selecting residues that appear to correlate well with the main epitopes of these loci. For HLA-C alleles that have no serologic antigen counterpart (blank), we propose to assign serotypes to the various groups of alleles at this locus based on the knowledge of a number of epitopes79–[81](#page-37-0) and including additional residue DEP that are important for the other homologous class I loci, HLA-A and -B. In this study, when HLA alleles that do not fit exactly in any existing serological groups were observed, new serological groups were created.

2 | MATERIALS AND METHODS

2.1 | IPD-IMGT/HLA database

IPD-IMGT/HLA Database release versions 3.38.0 and 3.44.0 were downloaded from GitHub [\(https://github.](https://github.com/ANHIG/IMGTHLA.git) [com/ANHIG/IMGTHLA.git\)](https://github.com/ANHIG/IMGTHLA.git).^{[67](#page-37-0)} hla_prot.fasta files were used to obtain the amino acid sequence for each allele. Nonitalicized two-field HLA allele name, e.g., HLA-B*14:01, is used to represent expressed protein product.^{[8](#page-35-0)}

2.2 | Residues for Public Epitopes, Bw4, Bw6, KIR C1, and KIR C2

WHO assigned HLA-B antigens are often distinguished using the differences in the presence of Bw4 and Bw6 epitopes, for example, B21 to B49 (Bw4) and B50 (Bw6), B12 to B44 (Bw4) and B45 (Bw6), B16 to B38 (Bw4) and B39

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Note: Table shows residues used to define Bw4-associated, Bw6-associated, KIR C1 and KIR C2 epitopes. The "Negative" category was added based on the presence of V instead of E at residue 76 in HLA-B and HLA-C alleles. The presence or absence of Bw4 and Bw6-associated residues was assessed in HLA-A and HLA-C alleles. Residues 76, 77 and 80 were assessed to distinguish HLA-C antigens from most HLA-B alleles, and to determine the KIR C1 and KIR C2 ligands and associated serologic epitopes. The majority of HLA alleles that are recognized as KIR C1 and KIR C2 that carry residues 76V77S80N and 76V77N80K, respectively. HLA-B73 that carries 76V77G80N is classified as KIR C1. "Two uncertain KIR ligand categories that carry 76V77N80N (e.g., HLA-C*14:04) and 76V77S80K (e.g., HLA-C*03:10) are included, but serotypes for these alleles were not proposed in this study.

(Bw6), respectively.^{[8,26](#page-35-0)} Residues 82L83R, 76E82R83G and 76V82R83G are used to identify Bw4, Bw6 and Bw4/Bw6 negative status (Table 1),^{[82](#page-38-0)} respectively. We also included these residues to screen Bw4- or Bw6-associated status for HLA-A and HLA-C (Table 1). The residues 76 V77S80N and 76V77N80K are known to determine the KIR C1 and KIR C2 ligands, respectively, 83 and they display different serological specificities, for example, HLA-C*16:01 and HLA-C*16:02, respectively.^{[80,120](#page-38-0)} HLA-B*73:01 that carries 76V77G80N is classified as KIR C1.^{[84,85](#page-38-0)} Two "Uncertain" KIR ligand categories were created for the alleles that a carry different substitution (76V77N80N and 76V77S80K) at residue 77 (Table 1).

2.3 | Key amino acid (AA) residues determining serologic epitopes and specificities

Prototype alleles that correspond to the WHO assigned antigens^{[8](#page-35-0)} and logical key residue positions based on the previously recognized AA residues that define specific serotypes were selected for proteins encoded at HLA-A, -B, -C, -DRB1/3/4/5 and -DQB1 loci (Tables [2A](#page-5-0)–E,

Supplemental Methods). Many key AA residues are shared across HLA class I antigens. Tables [3A](#page-11-0)–F show key AA residues for HLA-A, -B, -C, -DRB1/3/4/5 and -DQB1 loci. When HLA alleles that do not fit exactly in any existing serological groups corresponding to the WHO assigned antigens were observed, new serological groups were created and proposed (Tables [2A](#page-5-0)–E). Each proposed new serotype is associated to one of the WHO assigned antigens using the information described in the HLA Dictionary 2008 (Tables $2A-E$ $2A-E$).^{[68](#page-37-0)} With a few exceptions, the WHO antigen was systematically assigned to each allele based on the assigned serotype (Supplemental Tables 1–4). Supplemental Methods include detailed descriptions of the criteria applied to the identification and selection of key residues.

2.4 | Rules for novel split designation (NSD)

The serologic specificities for HLA-A, -B, -C and -DRB1 were designated using the locus name followed by the corresponding two-field allele name without colon (:) of the most common or lowest-digit prototype separated by

Proposed new serotype

TABLE 2 New serotypes, WHO assigned antigens and critical residue positions

A: HLA-A prope

(Continues)

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TABLE 2 (Continued)

A: HLA-A proposed new serotypes, WHO assigned antigens

B: HLA-B proposed new serotypes, WHO assigned antigens

TABLE 2 (Continued)

(Continues)

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TABLE 2 (Continued)

B: HLA-B proposed new serotypes, WHO assigned antigens

C: HLA-C proposed new serotypes, WHO assigned antigens

TABLE 2 (Continued)

C: HLA-C proposed new serotypes, WHO assigned antigens

D: HLA-DRB1/3/4/5 proposed new serotypes, WHO assigned antigens

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TABLE 2 (Continued)

D: HLA-DRB1/3/4/5 proposed new serotypes, WHO assigned antigens

Note: Tables [2A](#page-5-0)–E show "Proposed new serotype", "WHO assigned antigen", "Bw4/Bw6 associated" status, "Prototype" and "Critical residue positions" to define SEROTYPE assignments of HLA-A, -B, -C, -DRB1/3/4/5 and -DQB1. The "Associated", "Split," and "Broad" column indicates currently accepted antigens for HLA-A, -B, -C, -DRB1, -DRB3/4/5 and -DQB1 by WHO Nomenclature Committee for HLA factors, and the "Prototype" column shows the prototype two-field HLA alleles corresponding to the new proposed serotypes or WHO assigned antigens. The majority of the proposed new serotypes were assigned to one of the WHO-assigned Antigens according to the first field allele name, but some of these serotypes have not been experimentally confirmed yet. The serotype DR-1410 was assigned to DR4 based on residues 9–13. The alleles HLA-B*07:13 and HLA-B*67:02 with the proposed new serotypes B-0713 and B-6702, were not assigned to WHO-accepted antigens. These antigens may show a distinct serological reactivity, because the amino acid sequence in the alpha 1 domains are identical to those of some HLA-C alleles.

TABLE 3 Serotypes and residues used to define FULL and SEROTYPE assignments TABLE 3 Serotypes and residues used to define FULL and SEROTYPE assignments

(Continues)

(Continues)

TABLE 3 (Continued) TABLE 3 (Continued)

(Continues)

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(Continues)

TABLE 3 (Continued) TABLE 3 (Continued)

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assignments. Combined AA residues in the white, gray and black cells in each row define FULL assignments. The black shaded cells indicate AA residues that likely display different serological specificities from those Note: Tables 3A-1 show Amino Acid (AA) residues used to define FULL and SEROTYPE assignments of HLA-A, -B, -C, -DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1 and -DPA1. The "Serotype" column shows serotypes assignments. Combined AA residues in the white, gray and black cells in each row define FULL assignments. The black shaded cells indicate AA residues that likely display different serological specificities from those Note: Tables [3A](#page-11-0)–I show Amino Acid (AA) residues used to define FULL and SEROTYPE assignments of HLA-A, -B, -C, -DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1 and -DPA1. The "Serotype" column shows serotypes For HLA-DQA1 in Table 3G, the serotypes DQA-02, DQA-04, DQA-05, and DQA-06 carry a single AA deletion at residue position 56 in the AA alignment view in the IPD-IMGT/HLA Database. The
numbers in row 1 and 4 reflect the act e.g., HLA-C*02:23 and HLA-C*04:77. For HLA-A and HLA-B, residue 127 was included only to define FULL assignments. For HLA-C in Table 3C, residue 158 was used to distinguish C-1202 from B-6702. of the prototype serctypes. For HLA-A in Table 3A, residue 45 was included to eliminate HLA-C alleles. For HLA-B in Table 3B, residue 103V was used for the serctype B-713 to eliminate HLA-C proteins, e.g., HLA-C*02:23 and HLA-C*04:77. For HLA-A and HLA-B, residue 127 was included only to define FULL assignments. For HLA-C in Table [3C](#page-11-0), residue 158 was used to distinguish C-1202 from B-6702. numbers in row 1 and 4 reflect the actual AA residue position, and the numbers in the parenthesis in row 4 reflect the residue positions including the deletion in the AA alignment view. References were for each HLA locus, the numbers indicate residue positions, and the alphabetical characters indicates amino acids at each residue position. Combination of AA residues in the grav shaded cells define "SEROTYPE" for each HLA locus, the numbers indicate residue positions, and the alphabetical characters indicates amino acids at each residue position. Combination of AA residues in the gray shaded cells define "SEROTYPE" of the prototype serotypes. For HLA-A in Table [3A](#page-11-0), residue 45 was included to eliminate HLA-C alleles. For HLA-B in Table [3B](#page-11-0), residue 103V was used for the serotype B-713 to eliminate HLA-C proteins, For HLA-DQA1 in Table [3G](#page-11-0), the serotypes DQA-02, DQA-04, DQA-05, and DQA-06 carry a single AA deletion at residue position 56 in the AA alignment view in the IPD-IMGT/HLA Database. The shown in superscript numbers for each residue position. shown in superscript numbers for each residue position.

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dash $(-)$, for example, A-0201 for the HLA-A*02:01. The classical naming of the splits of B14, Cw3, DR3 and DQ3 are maintained in NSD to be consistent with previous naming of the broad antigens; their serologic split names differ from the first field of the corresponding prototype allele, for example, HLA-B*14:01 to be B64 and HLA-B*14:02 to be B65 (Tables [2B](#page-5-0) and [3B\)](#page-11-0).

2.5 | Serologic specificities for DQA1, DPA1, and DPB1

The serologic specificities for HLA-DQA1 and -DPA1 were designated using DQA and DPA followed by the common first-field allele name separated by dash $(-)$. Six serotypes, DQA-01, DQA-02, DQA-03, DQA-04, DQA-05, and DQA-06, were created for HLA-DQA1, and two serotypes, DPA-01 and DPA-02, were created for HLA-DPA1. For HLA-DPB1, analogous to DQ splits, the first field of the allele name is used to designate the serologic specificity separated by dash $(-)$. Initially eight serotypes DP-01, DP-0201, DP-03, DP-0401, DP-10, DP-15, DP-18, and DP-46 were defined using the residues 56–57 and 84–85 (Table $3H$).^{[75,77,78](#page-37-0)} Serotypes were further split using residue $69⁹⁹$ $69⁹⁹$ $69⁹⁹$ therefore, additional six serotypes DP-13, DP-0402, DP-06, DP-0202, DP-18, and DP-80 were defined. Tables [3G](#page-11-0)–I show AA residues that define specific serotypes for HLA-DQA1, HLA-DPB1, and HLA-DPA1.

2.6 | HLA allele to serotype (HATS) software and antigen assignments

A computational tool (HLA allele to serotype: HATS) was developed using Perl Programming Language to translate an HLA allele to a serotype. To create reference DEP patterns, HATS captures AA residues at predefined DEP positions (Table [3A](#page-11-0)–I) from full-length protein sequences of the prototype alleles in one hla_prot.fasta file. When leader peptide sequence that corresponds to exon 1 was missing for a certain HLA allele, the leader peptide sequences were filled with "X" to adjust these alleles to be full-length. HATS was originally optimized using IPD-IMGT/HLA Database release version 3.38.0, and tested using release version 3.44.0. HATS assigns HLA alleles to the predefined HLA serotypes in one of the following two criteria: key AA residues matched to a specific serotype either at (1) all positions defined in Table [3A](#page-11-0)–I (FULL) or (2) at only positions defining a serotype (SEROTYPE), (residues highlighted in gray in Table [3A](#page-11-0)–I).

In addition to the FULL and SEROTYPE assignments, the software defines INCOMPLETE assignments that implies alleles that carry a single mismatch with one or more SEROTYPES and UNASSIGNED (UNA). The INCOMPLETE assignments were further classified as TABLE 4 Proposed serologic Antigens defined by combinations of polymorphic subunits (DQ) observed in cis in the most common DQA1~DQB1 blocks

Note: "Prototype cis combination" column shows combinations of two-field HLA-DQA1 and HLA-DQB1 alleles separated by tilde (\sim) . The column represents the common $HLA-DQA1 \sim HLA-DQ1$ haplotypes containing the common alleles. CDQS column shows proposed combinational serotypes defined by DQA subunit, DQA02/03/04/05/06, and DQB1 subunit, DQ2/4/7/8/9.

SHORT that carries a single mismatch with a SERO-TYPE, and SHORT-CROSSREACTIVE assignment that implies alleles that carry a single mismatch with two or more SEROTYPES. HATS is available at [https://github.](https://github.com/kosoegawa/HATS) [com/kosoegawa/HATS](https://github.com/kosoegawa/HATS).

2.7 | Serologic DOA1 \sim DOB1 antigens defined by combinatorial DQ serotypes (CDQS)

Additional DQ serologic specificities were identified by mAbs and allo-antisera recognizing combinatorial epitopes defined by variations at the DQA1 and DQB1 subunits. 100 Allelespecific constraints were reported for formation of heterodimeric DQ α and DQ β on cell surface.^{[101](#page-38-0)} In this report, cis combinatorial HLA-DQA1 (DQA-02/03/04/05/06) and HLA-DQB1 (DQ2/4/7/8/9) serotypes using common $HLA-DQA1 \sim HLA-DQB1$ haplotypes containing the common alleles were proposed (Table 4).

2.8 | Common, intermediate, and welldocumented HLA alleles

The common and well-documented (CWD) and common, intermediate, and well-documented (CIWD) allele

'NN assigned," and "Comments" shows information listed in the HLA Note: The "Allele" column shows two-field HLA allele name used to created new serotypes. The columns "Expert assigned," "WHO Assigned," "NN assigned," and "Comments" shows information listed in the HLA *Note:* The "Allele" column shows two-field HLA allele name used to created new serotypes. The columns "Expert assigned," "WHO Assigned," and "Comments" shows information listed in the HL.
Dictionary 2008. The "Serotype" c Dictionary 2008. The "Serotype" column shows new proposed serotype name, and "Note" column includes brief description why the new serotype was proposed. The "C (Common)" category was assigned for the proposed new serotypes DR-5102, DR-5103 and DR-5202 using CWD2.0 catalogue, because only WD category was assigned for HLA-DRB3/4/5 loci in the CIWD3.0.[71](#page-37-0)

TABLE 5 (Continued)

TABLE 5 (Continued)

TABLE 6 Number of AA residue positions selected to define HLA serotypes, WHO assigned antigens and proposed new serotypes

Note: Locus column shows 11 HLA loci. "Residues" column shows the number of AA residues used to define FULL serotypes for each locus. "WHO Assigned Antigens" column shows the number of currently WHO assigned antigens. "Proposed New Serotypes" column shows the number of proposed new serotypes. "Total" column shows the total number of serotypes recognized in this study.

catalogs were published and became publicly available.^{[70](#page-37-0)–73} The CIWD3.0 catalogue was generated using HLA typing data originating from bone marrow registries around the world, but the CWD2.0 catalogue was not consid-ered.^{[71](#page-37-0)} Both CIWD3.0 and CWD2.0 allele catalogs were referenced to be comprehensive, and two-field allele name was used to represent protein level. All CWD HLA alleles identified in Europe and within European sub-regions were examined⁷³; the CIWD3.0 catalogue included all these alleles. It is clinically valuable if all common alleles are associated with specific serotypes. When common HLA alleles that fell INCOMPLETE or UNA categories, new serotypes were created. Table [5](#page-20-0) shows a list of new serotypes proposed in this study and includes information from the HLA Dictionary 2008^{68} 2008^{68} 2008^{68} and a brief descriptions why these serotypes were proposed in this study.

2.9 | Validation

HLA alleles whose serologic specificities were described to be discordant with the first field molecular designation in the previously published HLA Dictionary^{[68](#page-37-0)} were used for the validation of the serologic assignments. In addition, the AA sequences of the selected alleles were aligned with those of the prototype alleles corresponding to the assigned serotype using the Sequence Alignment Tool in IPD-IMGT/HLA Web site ([https://www.ebi.ac.](https://www.ebi.ac.uk/ipd/imgt/hla/alignment/) [uk/ipd/imgt/hla/alignment/\)](https://www.ebi.ac.uk/ipd/imgt/hla/alignment/). The AA sequence alignments were visually inspected for concordance with the HATS assignment.

3 | RESULTS

3.1 | HLA class I antigen assignments

3.1.1 | HLA-A

For the 24 WHO assigned HLA-A antigens, 5–9 AA residues were selected for SEROTYPE assignments (Table [2A\)](#page-5-0). The use of these residues resulted in the recognition of 29 additional serotypes (Tables [5](#page-20-0) and 6). Up to 11 AA residues were used to define the proposed new serotypes containing hybrid AA residue pattern, for example, A-0219, A-0244 and A-0323 (Table [2A\)](#page-5-0). When all residue positions were considered, 25 polymorphic residue positions were recognized for HLA-A (Table [3A](#page-11-0) and Figure $1A$), and these were used to make the new designate FULL assignments (Table 6). Supplemental Table 1 contains HLA-A two-field alleles and their serotypes. Thirty HLA-A proteins (two-field alleles) in which their first-field molecular designation does not correspond to the predicted WHO assigned HLA-A antigens were identified (Table [7](#page-25-0)), for example, HLA-A*02:55 was designated to A69 serologic specificity (Table [8\)](#page-26-0). In addition, 26 HLA-A proteins for which first-field molecular designation does not correspond to the newly defined HLA-A serotypes were identified (Table [7\)](#page-25-0), for example, HLA-A*26:09 was assigned to A-3402 serologic specificity (Table [8](#page-26-0)). Only 2 HLA-A alleles (HLA-A*11:271 and HLA-A*29:51) could not be assigned to specific antigens (marked as UNA in Supplemental Table 1), because these alleles had two or more mismatches to the DEP residues in any given serotypes.

FIGURE 1 Ribbon-taped crystal protein structures for HLA-A, HLA-B, HLA-C, HLA-DRA1~HLA-DRB1, HLA-DQA1~HLA-DQB1, and HLA-DPA1~HLA-DPB1 molecules. (A) HLA-A*02:01 molecule (PDB DOI: 10.2210/pdb7RTD/pdb)^{[124](#page-39-0)} and residues representing FULL $(RED+BLEU)$ and SEROTYPE (BLUE) for the serotype A-0201. (B) HLA-B*15:01 molecule (PDB DOI: 10.2210/pdb1XR8/pdb)^{[103](#page-38-0)} and residues representing FULL (RED+BLUE) and SEROTYPE (BLUE) for the serotype B-1501. (C) HLA-C molecule and residues representing FULL (RED+BLUE) and SEROTYPE (BLUE) for the WHO assigned antigen Cw9. HLA-C*06:02 (PDB DOI: 10.2210/pdb5W67/pdb)^{[125](#page-39-0)} is used to represent HLA-C molecule. (D) HLA-DRB1 molecule (light green) and residues representing FULL (RED+BLUE) and SEROTYPE (BLUE) for the serotype DR-1454. HLA-DRB1*04:01 (PDB DOI: 10.2210/pdb5NI9/pdb)^{[104](#page-38-0)} is used to represent HLA-DRB1 molecule. (E) HLA-DQA1*01:02~HLA-DQB1*06:02 molecule (PDB DOI: 10.2210/pdb1UVQ/pdb)^{[105](#page-38-0)} and residues representing FULL (RED+BLUE) and SEROTYPE (BLUE) for the serotypes DQA-01, DQ6 and combinatorial DQA-01~DQ6. (F) HLA-DPA1*01:03~HLA-DPB1*02:01 molecule (PDB DOI: 10.2210/pdb3LQZ/pdb)^{[106](#page-38-0)} and critical residues defining the serotypes for DPA-01, DP-0201 and combinatorial DPA-01 \sim DP-0201[.104-106](#page-38-0)

Note: Table shows the number of HLA alleles and proteins (two-field) with first-field names that are discrepant with the predicted WHO assigned antigens and proposed new serotypes.

3.1.2 | HLA-B

Currently, there are 49 WHO assigned HLA-B antigens not counting 10 broad specificities (B5, B12, B14, B15, B16, B17, B21, B22, B40, and B70). In all, 6–15 residues were selected to define WHO assigned HLA-B antigens for SEROTYPE assignments (Table [2B](#page-5-0)). When these residues were considered, 32 additional HLA-B antigens were defined (Table [6](#page-24-0)). When all residue positions were combined, 24 polymorphic positions were used to make

Two-field HI A alleles included in the HI A Dictionary 2008 used to validate the criteria for definition of HI A Antigens TABLE 8 Two-field HLA alleles included in the HLA Dictionary 2008 used to validate the criteria for definition of HLA Antigens TABLE 8

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Note: The "Allele" column shows two-field HLA allele with first field numbers that are discrepant with the predicted serotype. The columns "Expert assigned," "WHO assigned," "NN assigned," and "Comments" $\ddot{ }$ shows information listed in the HLA Dictionary 2008. The "Serotype" column shows assigned serotype using HATS. shows information listed in the HLA Dictionary 2008. The "Serotype" column shows assigned serotype using HATS. Response Genetics $-WILEY \perp$ 219

FULL assignments (Figure [1B](#page-25-0) and Table [6\)](#page-24-0). Supplemental Table 2 contains two-field HLA-B alleles and their serotypes. 145 HLA-B proteins (two-field alleles) in which their first-field molecular designation does not correspond to the WHO assigned HLA-B antigens were identified (Table [7\)](#page-25-0), for example, HLA-B*15:46 was assigned as HLA-B4005 serologic designation (Table [8](#page-26-0)). In addition, 50 HLA-B proteins in which their first-field molecular designation does not correspond to the newly defined HLA-B serotypes were identified (Table [6\)](#page-24-0), for example, HLA-B*13:03 was designated to the proposed new B-1524 serologic specificity (Table [8](#page-26-0)). Only 10 HLA-B proteins (two-field alleles), HLA-B*07:219, HLA-B*15:101, HLA-B*15:592, HLA-B*35:186, HLA-B*38:26, HLA-B*39:170, HLA-B*46:40, HLA-B*46:77, HLA-B*46:86, and HLA-B*55:34, were not assigned to specific serotypes, because these had two or more mismatches in the DEP residues that were used to define any given serotypes.

3.1.3 | HLA-C

Excluding HLA-Cw3, there are 9 WHO assigned HLA-C antigens including the splits Cw9 and Cw10. In addition, 6 possible HLA-C antigens corresponding HLA-C alleles with a blank HLA-C antigen were recognized when taking sequence homology into account (C-1202, C-1402, C-1502, C-1601, C-1701, and C-1801). These 15 possible HLA-C antigens account for the serologic specificities used in clinical practice. Additional 18 HLA-C antigens were recognized when examining 20 DEP residue positions for FULL assignments (Figure [1C](#page-25-0) and Table [6\)](#page-24-0). A range of 6 –14 selected residues were used for SEROTYPE assignments (Table [2C](#page-5-0)). Supplemental Table 3 contains HLA-C alleles and their antigens. Three HLA-C alleles (HLA-C*02:12, HLA-C*07:238, and HLA-C*16:85) were not assigned to specific serotypes.

3.2 | HLA class II antigen assignments

3.2.1 | HLA-DRB1 and -DRB3/4/5

For the assignment of all currently WHO assigned DR antigens, 5 –11 HLA-DRB1/3/4/5 residues were selected to make SEROTYPE assignments (Table [2D\)](#page-5-0); taking these residues into consideration, 21, 1 and 2 additional antigens were defined for HLA-DRB1, HLA-DRB3 and HLA-DRB5 alleles, respectively (Table [6\)](#page-24-0). When all polymorphic residue positions are combined, 13 positions were identified for making FULL assignments for HLA-DRB1 alleles (Figure [1D](#page-25-0)). Table [3D and E](#page-11-0) show the residues selected to designate FULL and SEROTYPE

antigens corresponding to the products of HLA-DRB1/3/4/5 genes. Supplemental Table 4 shows DR serotype information. Thirty DR proteins (two-field HLA-DRB1/3/5 alleles) for which their first-field allele name does not correspond to the currently WHO assigned HLA-DR antigens were identified (Table [7\)](#page-25-0). Of these, eight two-field HLA-DRB1 alleles (HLA-DRB1*03:42, HLA-DRB1*03:87, HLA-DRB1*11:30, HLA-DRB1*12:57, HLA-DRB1*13:67, HLA-DRB1*13:195, HLA-DRB1*14:46, and HLA-DRB1*14:141) were recognized carrying polymorphic residues associated with HLA-DR52 specificity corresponding to HLA-DRB3 alleles, and one HLA-DRB1 allele (HLA-DRB1*09:07) was recognized carrying residues associated with HLA-DR51 specificity corresponding to HLA-DRB5 alleles. The allele HLA-DRB3*01:14 was recognized carrying polymorphic residues associated with DR18 specificity (Supplemental Table 4). The proposed new serotype DR-0403 for the two-field allele HLA-DRB1*04:20 was assigned in silico, since the reference AA sequence of this allele does not include residues 9–13. Three HLA-DRB alleles (HLA-DRB1*04:66, HLA-DRB1*04:229, and HLA-DRB4*01:97) were not assigned to any of the currently known or newly proposed specific serotypes.

3.2.2 | HLA-DQB1

Table [3F](#page-11-0) shows residue positions used to define FULL or SEROTYPE assignment of HLA-DQB1 (Figure [1E\)](#page-25-0), and Supplemental Table 5 shows DQ serotype information for each HLA-DQB1 allele. Ten two-field HLA-DQB1 alleles in which their first-field allele name does not correspond to the WHO assigned HLA-DQ antigens were identified (Table [7](#page-25-0)).

3.2.3 | HLA-DQA1

Table [3G](#page-11-0) shows residue positions used to define FULL or SEROTYPE assignment of HLA-DQA1 (Figure [1E\)](#page-25-0), and Supplemental Table 6 shows DQA serotype information for each HLA-DQA1 allele identified to present. No discrepant assignments were identified when correlating the first field designation and the proposed DQA serotypes.

3.3 | Serologic DQA1/DQB1 antigens defined by combinations of polymorphic subunits

Table [4](#page-19-0) includes the serologic specificities defined by both subunits that are encoded in cis by common DQ haplotype blocks.

3.4 | HLA-DPB1 and HLA-DPA1

Table [3H](#page-11-0) shows residue positions used to make FULL assignment of HLA-DPB1 antigens (Figure [1F](#page-25-0)), and Supplemental Table 7 shows the proposed DP serotype information for each HLA-DPB1 allele. Residue 82 that is specific to HLA-DPB1 was included among the residues that define HLA-DP specificities. All 1653 expressed HLA-DPB1 alleles were assigned to the newly proposed HLA-DP serotypes (Supplemental Table 7).

Table [3I](#page-11-0) shows residue positions used to make FULL or SEROTYPE assignment corresponding to the product of the HLA-DPA1 alleles (Figure [1F\)](#page-25-0); Supplemental Table 8 shows DPA serotype information for each HLA-DPA1 allele. We assigned all 247 expressed HLA-DPA1 alleles to two serotypes (Supplemental Table 8).

3.5 | Distribution of FULL, SEROTYPE, SHORT (S), SHORT AND CROSS-REACTIVE (SC) serologic specificities among common, intermediate, welldocumented and rare alleles

Among the proposed 103 new serotypes for alleles at HLA-A, -B, -C, -DRB1, -DRB5 and -DRB3 loci, 55 were found among Common alleles, 22 were found in the group of Intermediate alleles, 24 of these serotypes were in the well-documented (WD) group. Only 2 alleles (HLA-A*02:65 and HLA-DRB1*13:43) of the proposed new serotypes were found in the rare allele category (Table [5\)](#page-20-0). The creation of serotypes for the rare alleles is an artifact using the lowest-digit allele names to represent the serotypes, because five WD group alleles (HLA-A*02:135, -A*02:149, -A*02:174, -A*02:190, and -A*29:48) were assigned to the serotype A-0265, and one Intermediate HLA-DRB1*14:16 allele was assigned to the serotype DR-1343. Therefore, these serotypes are virtually considered as WD and Intermediate group, respectively. Of 15,999 two-field alleles at five loci HLA (HLA-A, HLA-B, HLA-C, HLA-DQB1, and HLA-DRB1) that are assigned in one of the four categories, 3.3% (525) were common, 3.0% (474) were intermediate, 11.4% (1823) were WD and 82.3% (13,177) were rare categories in the CIWD 3.0. All common alleles were assigned in one of the serotypes as either FULL (84%) or SEROTYPE (16%) assignment. Figure [2A](#page-30-0)–D show the percentage of "C," "I," "WD," and "Rare" alleles assigned as either FULL, SEROTYPE, S or SC categories for each locus.

3.6 | Serotype validation

Table [7](#page-25-0) shows the number of HLA alleles and proteins with first-field names that are discrepant with the predicted serotype. Supplemental Table 9 contains list of HLA-A, -B, -C, -DRB1/3/5 and -DQB1 alleles in which their first-field allele name does not correspond to the WHO assigned antigens and proposed new serotypes. These outlier HLA alleles were used to validate the results if serotype information of HLA alleles is available in the HLA Dictionary 2008. Table [8](#page-26-0) summarizes the validation results. For example, HLA-A*02:55, HLA-B*78:04 and HLA-DRB1*14:15 were assigned to A69, B35 and DR8 being consistent with the report in the HLA Dictionary 2008, respectively. The proposed new serotypes were associated with WHO assigned antigens based on the information described in the HLA Dictionary as shown in Table [5](#page-20-0). Some discrepancies in WHO antigen assignments were found between the information provided in Supplemental Tables 1–5 and the information described in the HLA Dictionary for the alleles that were not used as prototype. For example, the alleles HLA-B*13:03 and -B*13:04 are reported in the present study as having the serotype B-1524, these were WHO assigned to the antigen B62 and Broad antigen B15 in Supplemental Table 2B. These alleles were, however, described as B49/B15 or B15x21-Bw4 in the HLA Dictionary (Table [8](#page-26-0)). The WHO assigned antigen B62 was associated with these alleles, because the prototype allele HLA-B*15:24 was described as B62 in the Dictionary.

3.7 | Bw4- and Bw6-associated residues

Table [9](#page-31-0) includes HLA alleles that most likely show different Bw4 or Bw6 reactivity from those of the prototype HLA alleles. The WHO assigned antigens A23, A24, A25, and A32 carry Bw4-associated residues. In addition to HLA-B alleles, Bw6-associated residues are found in the proposed new antigens A-3002, A-3007, and C-1212, Bw4-associated residues are found in A-6836. Of 6622 HLA-C alleles, we identified 16 HLA-C alleles carrying the Bw6-associated residues (Table [9\)](#page-31-0). The HLA class I alleles are noted as Bw4 or Bw6 in Supplemental Tables 1–3. Table [9](#page-31-0) includes HLA-B alleles that most likely lack Bw4 or Bw6 reactivity because of the substitutions at the key residue positions; these are noted as "Negative". For example, the allele HLA-B*57:08 carries residues 82L83P (Table [9](#page-31-0)), and the HLA Dictionary 2008 describes "Bw4 sera negative" (Table [7](#page-25-0)).

4 | DISCUSSION

With a few exceptions, the currently recognized antigens were defined by serum cluster analyses and reactivity patterns. Only a few studies correlating serologic testing with molecular typing have been performed to present. $68,74$ In addition, a small number of the serologic typing reagents have been characterized with novel and refined antibody screening technologies that include test-ing cells expressing a single expressed HLA antigen^{[107](#page-38-0)} or solid phase assays with single antigen preparations.^{[108](#page-38-0)} Therefore, the currently recognized HLA antigens do not identify the full extent of possible serotypes that can be defined by reagents detecting the most common immunogenic HLA epitopes, and do not include all specificities corresponding to some loci. In the solid organ transplantation setting, the assessment of humoral compatibility with a given donor is based on the evaluation of the patient's sensitization status and anti-HLA antibody reactivity and the precise knowledge of the donor's HLA mismatched alleles. The HLA allele to serotype conversion tables provided in this manuscript (Supplemental Tables 1–8) may prove to be clinically valuable in defining DSA. Informative antibody screening can be achieved by testing the patient's serum with a panel of antigen preparations that include the most common serotypes in a given population. The present study aimed to obtain a refined and likely more accurate characterization of serotypes defined in silico and to identify the common serotypes that can be found in most donors of allogeneic transplants based on the knowledge of the distribution of common alleles in world populations. Additional serotypes, which have been recognized in the course of several IHIW, but were not named officially, are proposed in the present study. The current study focused on wellrecognized residues located at the distal membrane domains that define common epitopes; all these residues are included in eplets located at these domains (Tables [3A](#page-11-0)–I). Supplemental Table 10 contains a list of these critical residues. Some residues that may determine less-recognized serologic splits and may not likely define distinct serologic epitopes in HLA antigens expressed on living cells were not considered as being relevant DEP in the present study; namely, residue 9 (distinguishing HLA-A*02:01 from HLA-A*02:06), residue 156 (distinguishing pairs of common alleles HLA-B*44:02/HLA- $B*44:03^{109}$ and HLA-B*35:01/HLA-B*35:08) of class I; residues 86 of HLA-DRB1 (distinguishing pairs of common alleles HLA-DRB1*11:01/HLA-DRB1*11:04 and HLA-DRB1*15:01/HLA-DRB1*15:02) and 112 (distinguishing a pair of HLA-DRB1*14:01/HLA-DRB1*14:54) and residue 160 of HLA-DQA1 (distinguishing pairs of

FIGURE 2 Representation of CIWD and Rare alleles in FULL, SEROTYPE, S, SC or UNA categories. (A) Common alleles. (B) Intermediate alleles. (C) Well-documented alleles. (D) Rare alleles. Each HLA-A, -B, -C, -DQB1 and -DRB1 two-field allele (protein level) was classified as "Common (C)," "Intermediate (I)," "Well-Documented (WD)," and "Rare" categories. HATS assigned serotypes for 4010 HLA-A, 4932 HLA-B, 3786 HLA-C, 1296 HLA-DQB1 and 2006 HLA-DRB1 two-field HLA alleles in one of the five (FULL, SEROTYPE, S, SC and UNA) categories. Null (N), Questionable (Q) alleles are excluded in these analyses. Figures 2A–D show the percentage of "C," "I," "WD," and "Rare" alleles assigned as either FULL, SEROTYPE, S, SC, or UNA categories. HLA-A, -B, -C, -DQB1, and -DRB1 loci are represented as A, B, C, DQB1, and DRB1 in these figures, respectively

HLA-DQA1*03:01/HLA-DQA1*03:03 and HLA-DQA1*05:03/HLA-DQA1*05:05) were not included among DEP. Residue 57 was not used to define HLA-DRB1 splits while this residue was conditionally considered in DQB1; the residues 57A (HLA-DQB1*03:04) and 57D (HLA-DQB1*03:01) do not split DQ7, but historically they are used to distinguish DQ8 (HLA-DQB1*03:02) from DQ9 (HLA-DQB1*03:03).

The classification of HLA alleles into previously assigned and proposed novel specificities is likely to enhance and increase precision in the assessment of DSA in allogeneic transplantation; for example, for the donor alleles assigned to the FULL category that carry identical replacements at common DEP residues, it is possible to use the prototype as surrogate in virtually all instances.

For instance, a donor who carries the HLA-B*35:03 allele may not be represented in the panel of single antigen beads, but the HLA-B*35:01 allele that is a prototype for the serotype B-3501 is represented. The HLA-B*35:01/ B*35:03 alleles share all residues defining major epitopes/ eplets for B-3501, therefore, the reactivity with B-3501 antigen preparation may serve as a precise surrogate to HLA-B*35:03. In this case, the donor's allele and the prototype differ by a single AA substitution at residue 116 (Phe for HLA-B*35:03 and Ser for HLA-B*35:01) located at the bottom of the groove, and this difference is not likely to determine major immunogenic serologic epitopes.

For alleles belonging to the same SEROTYPE category, it is possible to use the prototype as surrogate in TABLE 9 HLA class I alleles whose proteins will likely show differences in the serologic assessments associated with Bw4 or Bw6 serological specificities than those of the prototype serotypes

(Continues)

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TABLE 9 (Continued)

Note: The column "Allele" shows HLA class I two-field alleles. The "Serotype" column shows assigned serotypes for each allele by HATS, and the "COMMENT" column indicates the assignment category: FULL, SEROTYPE, S and SC. The column "Bw4/Bw6" shows expected Bw4 and Bw6 reactivity or Negative for these alleles. The "Prototype" column shows Bw4, Bw6 or Negative status of the corresponding prototype HLA serotypes. The "Note" column indicates substituted AA residues that affect the different Bw4 or Bw6 specificities from the prototype serotypes.

most instances, however, in order to perform more accurate DSA assessment, further epitope analyses in the corresponding serum antibody pattern may be needed to assign DSA. For example, the alleles HLA-A*24:373, HLA-A*29:98 and HLA-A*80:04 are assigned as serotypes A-2404, A29, and A80, respectively, in SEROTYPE category (Supplemental Table 1). Residue 76 is not required to assign these serotypes, thus an AA substitution at this position does not change the serotype assignment. However, these proteins carry the Bw6-associated residues, therefore, these may show reactivity with all

sera that define the SEROTYPE assignments and likely display additional reactivity with anti-Bw6 allo-antisera (Table [9\)](#page-31-0). The allele HLA-B*44:31 is assigned as the proposed new serotype B-4047 that resembles HLA-B60 being Bw4 positive in the SEROTYPE category but carries 167S that is an important residue to define the broad antigen HLA-B12 that includes both HLA-B44 and HLA-B45 (Tables [3B](#page-11-0) and [8](#page-26-0)). These cases exemplify the need of performing further epitope analyses to assess DSA when the donor carries an allele whose serologic assignment falls in the SEROTYPE category.

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With a few exceptions, designating new serotypes for the alleles that were not in CIWD categories in CWD2.0, CIWD3.0 or European CWD was avoided, and INCOMPLETE (SHORT and SHORT-CROSS-REACTIVE) category was used to classify the serotype of rare HLA alleles that present a single AA difference in the residues that define SEROTYPES. There are a few alleles whose serotype fall in the UNA category; these alleles present two or more AA differences in the residues that define any of the proposed SEROTYPES described in this study. Like the SEROTYPE category, performing the epitope analyses would be required to assess possible DSA for the alleles in INCOMPLETE and UNA categories.

A comprehensive evaluation of the splits corresponding to the HLA-B*15 alleles was performed in the present study; the results were concordant with those reported in a recent publication from Duygu and col-laborators.^{[74](#page-37-0)} In both studies, similar sets of residues were used to define the broad HLA-B15 and -B70 serotypes except for residues 24 and 77 that were used for HLA-C serotypes in the present study, and residue 163 that was not used by Duygu and collaborators (Table [3C\)](#page-11-0). Supplemental Table 11 contains 41 HLA-B*15 alleles that were discussed by Duygu and collabo-rators^{[74](#page-37-0)} and the serotype assignments in this study. The minor differences were because of the differences in these residues (Supplemental Table 11). The other differences were observed in outlier alleles. For example, the alleles HLA-B*15:46, -B*15:53, -B*15:106, -B*15:212, and -B*15:525 were not previously assigned to any broad HLA-B15 serotypes, 74 74 74 on the other hand, these alleles were assigned as B4005 in the present study. The allele HLA-B*15:46 was assigned as HLA-B72 in the HLA Dictionary 2008, but carries a mismatch at residue 45 K compared with the serotype HLA-B72 (45E). It has been described to show serological reactivity with allo-antisera specific for both HLA-B50 and -B72. 110

The serologic splits of HLA-DR4 that correlated well with HLA-D types were identified as early as $1984,^{1,66}$ $1984,^{1,66}$ $1984,^{1,66}$ and subsequently HLA-D types were correlated with alleles defined at the molecular level. Therefore, the residues determining serologic specificities identified readily, and the extended analyses of the substitutions at DEP led to identifying and proposing additional HLA-DR splits. These extensions were validated by the occurrence of previously defined splits in families of other HLA-DRB1 alleles (e.g., HLA-DR103 as an associated antigen of HLA-DR1) or hinted in other studies (e.g., HLA-DRB1*11:02 determining a split of HLA-DR11 99 99 99). The present study also defines several splits of the ill-defined HLA-DR14 serologic specificity; it is likely that the new

definition of these splits will allow for precise assessment of DSA directed against some HLA-DR14 associated specificities and not to others.

The present study defines serotypes for all loci assessed routinely for humoral compatibility in solid organ transplantation and HSCT; these loci include the products of HLA-DQA1, -DPA1 and -DPB1 (Supplemental Tables 6–8). It is important to note that the first field of HLA-DPB1 does not reflect the serotype. In addition to the serotypes of HLA-DQA1, -DPA1 and -DPB1 serotypes resulting from the combination of proteins encoded by HLA-DQA1 and -DQB1 are presented (Table [4\)](#page-19-0). Although additional splitting of HLA-DQA1, -DPA1, -DQB1 and -DPB1 encoded proteins has been suggested, no additional higher resolution specificities are proposed at this time. In the future, additional serologic specificities could be accepted by the general community, if significant evidence for further splitting the serological specificities corresponding to the products of these loci were to be demonstrated using cell-based assays. The combinatorial specificities associated with HLA-DQA1*01 alleles are not included in this study, because their proteins combine only with the product of HLA-DQB1*05 or -DQB1*06 alleles to form heterodimers because of restrictions in pairing, and splits of HLA-DQA01, -DQ5 and -DQ6 are not proposed yet.

A set of 240 serotypes (167 for HLA class I and 73 for HLA class II) representing all common alleles in all human populations has been presented in this report. Some of the newly proposed serotypes are virtually predicted in silico in this study; therefore, it will be valuable to conduct follow-up validation studies of the newly proposed serotypes with sera and/or mAbs in future studies. The information may be used in a rational design and antigen composition of anti-HLA antibody single antigen screening panels. The inclusion of at least one antigen preparation corresponding to the prototype alleles of each serotype will result in the representation of virtually all serotypes likely to be present in a given donor. The evaluation of the reactivity of the patient's serum with this panel and the patient's and donor's HLA genotypes obtained at a resolution that allows discriminating between alleles of the common serotypes will allow for precise predictions of cross-match results in silico. The use of antigen preparations including the proposed extended serotype coverage will result in a simple process for performing virtual cross-matches with enhanced resolution and increase prediction of physical cross-matches. In the United States, virtual cross-matching has become even more important given the new UNOS Kidney allocation system which has resulted in broader sharing of organs across larger geographical regions. Many transplant centers and HLA labs have been reticent to adopt virtual crossmatching or compatibility assessment in lieu of a physical

one because of the present limitations of coverage of the single antigen bead assays. The HATS tables provided as Supplemental 1–8 will allow for more accurate antibody profiling translating into better risk assessment of patients.

In summary, we developed logics for serotype assignments, and a computational tool (HATS) for systematically classifying HLA alleles into serological specificities. HATS can be implemented for systematic serotype assignment of all HLA alleles for every release of IPD-IMGT/HLA database version in the future. This manuscript proposes the designation of novel serological specificities presented in an organized manner that includes an addition to the previously recognized HLA antigens and an expansion to antigens of HLA loci that can be recognized at the serologic level. The lists of prototype and newly defined serotypes may serve for improvement of allele composition of single antigen panels for antibody screening. In order to facilitate their implementation in clinical Histocompatibility practice, we would like to propose to the WHO Nomenclature Committee for Factors of the HLA System that these newly defined serotypes become officially accepted having a new Antigen or Associated Antigen status.

AUTHOR CONTRIBUTIONS

This study was initially designed by Kazutoyo Osoegawa and Marcelo A. Fernández Viňa. Kazutoyo Osoegawa developed HATS, performed data validation. Kazutoyo Osoegawa and Marcelo A. Fernández Viňa were also involved in data interpretation and drafting the manuscript. Steven GE Marsh, Rhonda Holdsworth, Sebastiaan Heidt, Gottfried Fischer, Cathi Murphey, Martin Maiers contributed significantly to the refinement of the initial design and were responsible for reviewing HLA nomenclature including serotypes. All authors read and approved the final version of the manuscript.

ACKNOWLEDGMENTS

We thank Gonzalo Montero-Martin, Tamara Vayntrub, Debra D. Hiraki, Arianne Mankey, Megan Jeracki and Lielani Libiran for their advice and support, and Susan Twietmeyer and Felicia Marie Gonsalves for her administrative support. We also thank the Stanford Blood Center for the support.

CONFLICT OF INTEREST

The authors declared no conflicting interests.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in the Supporting Information of this article and will also be posted on the web site of the 18th International HLA & Immunogenetics Workshop ([https://www.ihiw18.org/serology-2022/\)](https://www.ihiw18.org/serology-2022/).

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REFERENCES

- 1. Albert ED, Barbalho T, Baur MP, et al. The Serological Analysis of the Data of the Ninth Histocompatibility Workshop. Springer-Verlag; 1984.
- 2. Milford ELPMS, Lalouel J-M, Kennedy L, Yunis EJ. Serologic Exercises of the Tenth Workshop. Vol 1. Springer-Verlag; 1989.
- 3. Juji T, Akaza T, Tokunaga K, Miyoshi H, Kashiwase K. The Serology Studies of the Eleventh International Histocompatibility Workshop: an Overview. Vol 1. Oxford University Press; 1992.
- 4. Tongio MM, Doxiadis II, Laforet M, et al. 12th International Histocompatibility Workshop HLA Class I Monoclonal Antibodies Study. Vol 1. EDK Medical and Scientific Publisher; 1997.
- 5. Navarrete C, Brown C, De Lange P, Schreuder GMT. 12th International Histocompatibility Workshop HLA Class II Monoclonal Antibodies Study. Vol 1. EDK Medical and Scientific Publisher; 1997.
- 6. Fernández-Viña MAMM, Gutierrez M, Mulder A, et al. Specificity of the Reagents Utilized in the Serology Component of the 13th IHWS. Vol 1. IHIWG Press; 2006.
- 7. Schreuder GMTHR, Tanaka H, Moraes ME, et al. The Serologic Specificity ofHLA-A, -B and -C Alleles Defined with Reagents of the13th International Histocompatibility Workshop. Vol 1. IHIWG Press; 2006.
- 8. Marsh SG, Albert ED, Bodmer WF, et al. Nomenclature for factors of the HLA system, 2010. Tissue Antigens. 2010;75(4): 291-455.
- 9. Van Rood JJ, Van Leeuwen A. Leukocyte grouping. A method and its application. J Clin Invest. 1963;42:1382-1390.
- 10. Ways JP, Rothbard JB, Parham P. Amino acid residues 56 to 69 of HLA-A2 specify an antigenic determinant shared by HLA-A2 and HLA-B17. J Immunol. 1986;137(1):217-222.
- 11. Ways JP, Lawlor DA, Wan AM, Parham P. A transposable epitope of HLA-B7, B40 molecules. Immunogenetics. 1987;25(5): 323-328.
- 12. Wan AM, Ennis P, Parham P, Holmes N. The primary structure of HLA-A32 suggests a region involved in formation of the Bw4/Bw6 epitopes. J Immunol. 1986;137(11):3671-3674.
- 13. Salter RD, Parham P. Mutually exclusive public epitopes of HLA-A,B,C molecules. Hum Immunol. 1989;26(2):85-89.
- 14. Takamiya Y, Sakaguchi T, Miwa K, Takiguchi M. Role of HLA-B*5101 binding nonamer peptides in formation of the HLA-Bw4 public epitope. Int Immunol. 1996;8(7):1027-1034.
- 15. Lutz CT, Smith KD, Greazel NS, et al. Bw4-reactive and Bw6-reactive antibodies recognize multiple distinct HLA structures that partially overlap in the alpha-1 helix. J Immunol. 1994;153(9):4099-4110.

228 WILEY-HLA OSOEGAWA ET AL. Response Genetics

- 16. Hogan KT, Clayberger C, Bernhard EJ, et al. A panel of unique HLA-A2 mutant molecules define epitopes recognized by HLA-A2-specific antibodies and cytotoxic T lymphocytes. J Immunol. 1989;142(6):2097-2104.
- 17. Little AM, Madrigal JA, Parham P. Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3. Immunogenetics. 1992;35(1):41-45.
- 18. Pistillo MP, Bini D, Pozzi S, Ferrara GB. A cytotoxic human monoclonal antibody that can discriminate HLA-A*3002 from HLA-A*3001 subtypes. Tissue Antigens. 1995;46(4):327-329.
- 19. Hayashi H, Ennis PD, Ariga H, et al. HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical region of the alpha 1 domain. *J Immunol*. $1989;142(1)$: 306-311.
- 20. Little AM, Parham P. The HLA-Bw75 subtype of B15: molecular characterization and comparison with crossreacting antigens. Tissue Antigens. 1991;38(4):186-190.
- 21. Hildebrand WH, Domena JD, Shen SY, et al. HLA-B15: a widespread and diverse family of HLA-B alleles. Tissue Antigens. 1994;43(4):209-218.
- 22. Domena JD, Little AM, Madrigal AJ, et al. Structural heterogeneity in HLA-B70, a high-frequency antigen of black populations. Tissue Antigens. 1993;42(5):509-517.
- 23. Little AM, Domena JD, Hildebrand WH, et al. HLA-B67: a member of the HLA-B16 family that expresses the ME1 epitope. Tissue Antigens. 1994;43(1):38-43.
- 24. Adams EJ, Martinez-Naves E, Arnett KL, Little AM, Tyan DB, Parham P. HLA-B16 antigens: sequence of the ST-16 antigen, further definition of two B38 subtypes and evidence for convergent evolution of B*3902. Tissue Antigens. 1995;45(1):18-26.
- 25. Hildebrand WH, Madrigal JA, Belich MP, et al. Serologic cross-reactivities poorly reflect allelic relationships in the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2 helix. J Immunol. 1992;149(11):3563-3568.
- 26. Hildebrand WH, Domena JD, Shen SY, et al. The HLA-B7Qui antigen is encoded by a new subtype of HLA-B27 (B*2708). Tissue Antigens. 1994;44(1):47-51.
- 27. Domena JD, Arnett KL, Marsh SG, Bodmer JG, Parham P. Alloantibodies can discriminate three populations of HLA-B40 molecules encoded by B*4002. Tissue Antigens. 1994; 44(1):57-58.
- 28. Domena JD, Johnston-Dow L, Parham P. The B*4002 allele encodes the B61 antigen: B40* is identical to B61. Tissue Antigens. 1992;40(5):254-256.
- 29. Domena JD, Azumi K, Bias WB, Parham P. B*1401 encodes the B64 antigen: the B64 and B65 splits of B14 differ only at residue 11, a buried amino acid. Tissue Antigens. 1993;41(2): 110-111.
- 30. Holmes N, Parham P. Exon shuffling in vivo can generate novel HLA class I molecules. EMBO J. 1985;4(11):2849-2854.
- 31. Arnett KL, Moses JH, Williams F, et al. HLA-A *2607: sequence of a novel $A*26$ subtype predicted by DNA typing which shares the MA2.1 epitope with $A*02$, $B*57$ and $B*58$. Tissue Antigens. 1996;47(5):422-425.
- 32. Hildebrand WH, Domena JD, Parham P. Primary structure shows HLA-B59 to be a hybrid of HLA-B55 and HLA-B51, and not a subtype of HLA-B8. Tissue Antigens. 1993;41(4): 190-195.
- 33. Parham P, Arnett KL, Adams EJ, et al. The HLA-B73 antigen has a most unusual structure that defines a second lineage of HLA-B alleles. Tissue Antigens. 1994;43(5):302-313.
- 34. Mulder A, Kardol M, Blom J, Jolley WB, Melief CJ, Bruning H. A human monoclonal antibody, produced following in vitro immunization, recognizing an epitope shared by HLA-A2 subtypes and HLA-A28. Tissue Antigens. 1993;42(1): 27-34.
- 35. Duquesnoy RJ, Marrari M, Mulder A, Claas FH, Mostecki J, Balazs I. Structural aspects of HLA class I epitopes detected by human monoclonal antibodies. Hum Immunol. 2012;73(3): 267-277.
- 36. Klohe EP, Watts R, Bahl M, et al. Analysis of the molecular specificities of anti-class II monoclonal antibodies by using L cell transfectants expressing HLA class II molecules. J Immunol. 1988;141(6):2158-2164.
- 37. Jakobsen BK, Platz P, Ryder LP, Svejgaard A. A new homozygous typing cell with HLA-D"H" (DB6) specificity. Evidence that the DN-1 monoclonal antibody 9w925 is specific for the HLA-D"H" determinant. Tissue Antigens. 1986;27(5):285-290.
- 38. Gorski J, Radka SF, Masewicz S, Mickelson EM. Mapping of distinct serologic and T cell recognition epitopes on an HLA-DR beta-chain. J Immunol. 1990;145(7):2020-2024.
- 39. Klohe E, Pistillo MP, Ferrara GB, Goeken NE, Greazel NS, Karr RW. Critical role of HLA-DR beta 1 residue 58 in multiple polymorphic epitopes recognized by xenogeneic and allogeneic antibodies. Hum Immunol. 1992;35(1):18-28.
- 40. Madrigal JA, Ikeda H, Marsh SG, et al. Epitope mapping of an HLA-DR-specific monoclonal antibody produced by using human-mouse transfectant cells. J Immunol. 1989;143(12): 4084-4089.
- 41. Fu XT, Klohe E, Alber C, et al. Diverse locations of amino acids in HLA-DRβ chains involved in polymorphic antibody binding epitopes on $DR(\alpha, \beta1*0101)$, $DR(\alpha, \beta1*1101)$, and DR (α,β3*0202) molecules. Hum Immunol. 1992;33(3):193-201.
- 42. Matsuyama T, Winchester R, Lee S, Shookster L, Nunez-Roldan A. Identification of the DRw10 DR beta 1-chain allele as encoding a polymorphic class II major histocompatibility complex epitope otherwise restricted to DR beta 2 molecules of the DRw53 type. J Immunol. 1988;140(2):537-543.
- 43. Marsh SG, Bodmer JG. HLA-DR and -DQ epitopes and monoclonal antibody specificity. Immunol Today. 1989;10(9): 305-312.
- 44. So AK, Lindsay J, Bodmer J, Trowsdale J. Molecular variation of human major histocompatibility complex DQw3 betachains. J Immunol. 1987;139(10):3506-3511.
- 45. Radka SF, Nelson KA, Johnston JV. HLA-DQw3-related determinants: analysis of subunit and spatial relationships. Hum Immunol. 1989;25(4):225-236.
- 46. Heyes J, Austin P, Bodmer J, et al. Monoclonal antibodies to HLA-DP-transfected mouse L cells. Proc Natl Acad Sci USA. 1986;83(10):3417-3421.
- 47. Pistillo MP, Mazzoleni O, Kun L, Falco M, Tazzari PL, Ferrara GB. Production of two human hybridomas secreting antibodies to HLA-DRw11 and -DRw8+w12 specificities. Hum Immunol. 1991;31(2):86-93.
- 48. Mazzoleni O, Longo A, Angelini G, et al. Human monoclonal antibody MP8 detects a supertypic determinant encoded by

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DPB alleles DPB2.1, DPB3, DPB4.2, DPB8, DPB9, DPB10, and DPB14. Immunogenetics. 1989;30(6):502-505.

- 49. Kramer CSM, Franke-van Dijk MEI, Bakker KH, et al. Generation and reactivity analysis of human recombinant monoclonal antibodies directed against epitopes on HLA-DR. Am J Transplant. 2020;20(12):3341-3353.
- 50. Bezstarosti S, Kramer CSM, Franke-van Dijk MEI, et al. HLA-DQ-specific recombinant human monoclonal antibodies allow for in-depth analysis of HLA-DQ epitopes. Front Immunol. 2021;12:761893.
- 51. El-Awar N, Lee JH, Tarsitani C, Terasaki PI. HLA class I epitopes: recognition of binding sites by mAbs or eluted alloantibody confirmed with single recombinant antigens. Hum Immunol. 2007;68(3):170-180.
- 52. Duquesnoy RJ, Askar M. HLAMatchmaker: a molecularly based algorithm for histocompatibility determination. V. Eplet matching for HLA-DR, HLA-DQ, and HLA-DP. Hum Immunol. 2007;68(1):12-25.
- 53. El-Awar N, Nguyen A, Almeshari K, et al. HLA class II DQA and DQB epitopes: recognition of the likely binding sites of HLA-DQ alloantibodies eluted from recombinant HLA-DQ single antigen cell lines. Hum Immunol. 2013;74(9):1141- 1152.
- 54. El-Awar N, Terasaki PI, Cai J, Deng CT, Ozawa M, Nguyen A. Epitopes of the HLA-A, B, C, DR, DQ and MICA antigens. Clin Transpl. 2007;18:175-194.
- 55. Duquesnoy RJ, Marrari M, Tambur AR, et al. First report on the antibody verification of HLA-DR, HLA-DQ and HLA-DP epitopes recorded in the HLA epitope registry. Hum Immunol. 2014;75(11):1097-1103.
- 56. Duquesnoy RJ, Marrari M, Mulder A, Sousa LC, da Silva AS, do Monte SJ. First report on the antibody verification of HLA-ABC epitopes recorded in the website-based HLA epitope registry. Tissue Antigens. 2014;83(6):391-400.
- 57. Duquesnoy RJ, Marrari M, da Mata Sousa LC, et al. 16th IHIW: a website for antibody-defined HLA epitope registry. Int J Immunogenet 2013;40(1):54–59.
- 58. Duquesnoy RJ, Mostecki J, Marrari M, da Silva AS, da Mata Sousa LC, do Monte SJ. First report on the antibody verification of MICA epitopes recorded in the HLA epitope registry. Int J Immunogenet. 2014;41(5):370-377.
- 59. Duquesnoy RJ, Marrari M, Marroquim MS, et al. Second update of the international registry of HLA epitopes. I. the HLA-ABC epitope database. Hum Immunol. 2019;80(2):103-106.
- 60. Mulder A, Eijsink C, Kester MG, et al. Impact of peptides on the recognition of HLA class I molecules by human HLA antibodies. J Immunol. 2005;175(9):5950-5957.
- 61. Wolpl A, Halder T, Kalbacher H, et al. Human monoclonal antibody with T-cell-like specificity recognizes MHC class I self-peptide presented by HLA-DR1 on activated cells. Tissue Antigens. 1998;51(3):258-269.
- 62. Bodmer JG, Marsh SG, Albert ED, et al. Nomenclature for factors of the HLA system, 1991. WHO nomenclature committee for factors of the HLA system. Tissue Antigens. 1992;39(4): 161-173.
- 63. Bodmer JG, Marsh SG, Albert ED, et al. Nomenclature for factors of the HLA system, 1996. Tissue Antigens. 1997;49(3 Pt 2): 297-321.
- 64. Madrigal JA, Hildebrand WH, Belich MP, et al. Structural diversity in the HLA-A10 family of alleles: correlations with serology. Tissue Antigens. 1993;41(2):72-80.
- 65. Ishikawa Y, Tokunaga K, Lin L, et al. Sequences of four splits of HLA-A10 group. Implications for serologic cross-reactivities and their evolution. Hum Immunol. 1994;39(3):220-224.
- 66. Williamson J, Tait B, Richiardi P, et al. Antigen Report: HLA-DR4. Springer; 1984.
- 67. Robinson J, Barker DJ, Georgiou X, Cooper MA, Flicek P, Marsh SGE. IPD-IMGT/HLA Database. Nucleic Acids Res. 2020;48(D1):D948-D955.
- 68. Holdsworth R, Hurley CK, Marsh SG, et al. The HLA dictionary 2008: a summary of HLA-A, -B, -C, -DRB1/3/4/5, and -DQB1 alleles and their association with serologically defined HLA-A, -B, -C, -DR, and -DQ antigens. Tissue Antigens. 2009;73(2):95-170.
- 69. Slater N, Louzoun Y, Gragert L, Maiers M, Chatterjee A, Albrecht M. Power laws for heavy-tailed distributions: modeling allele and haplotype diversity for the national marrow donor program. PLoS Comput Biol. 2015;11(4):e1004204.
- 70. Mack SJ, Cano P, Hollenbach JA, et al. Common and welldocumented HLA alleles: 2012 update to the CWD catalogue. Tissue Antigens. 2013;81(4):194-203.
- 71. Hurley CK, Kempenich J, Wadsworth K, et al. Common, intermediate and well-documented HLA alleles in world populations: CIWD version 3.0.0. HLA. 2020;95(6):516-531.
- 72. Cano P, Klitz W, Mack SJ, et al. Common and welldocumented HLA alleles: report of the ad-hoc committee of the american society for histocompatiblity and immunogenetics. Hum Immunol. 2007;68(5):392-417.
- 73. Sanchez-Mazas A, Nunes JM, Middleton D, et al. Common and well-documented HLA alleles over all of Europe and within European sub-regions: a catalogue from the European Federation for Immunogenetics. HLA. 2017;89(2):104-113.
- 74. Duygu B, Matern BM, Wieten L, Voorter CEM, Tilanus MGJ. Specific amino acid patterns define split specificities of HLA-B15 antigens enabling conversion from DNA-based typing to serological equivalents. Immunogenetics. 2020;72(6–7):339-346.
- 75. Cano P, Fernandez-Vina M. Two sequence dimorphisms of DPB1 define the immunodominant serologic epitopes of HLA-DP. Hum Immunol. 2009;70(10):836-843.
- 76. Bodmer J, Bodmer W, Heyes J, et al. Identification of HLA-DP polymorphism with DP alpha and DP beta probes and monoclonal antibodies: correlation with primed lymphocyte typing. Proc Natl Acad Sci U S A. 1987;84(13):4596-4600.
- 77. Yu WY, Watts R, Karr RW. Identification of amino acids in HLA-DPw4b beta and -DR5 beta 1 chains that are involved in antibody binding epitopes using site-directed mutagenesis and DNA-mediated gene transfer. Hum Immunol. 1990;27(2): 122-135.
- 78. Viken HD, Gaudernack G, Thorsby E. Characterization of a monoclonal antibody recognizing a polymorphic epitope mainly on HLA-DPw2 and DPw4 molecules. Tissue Antigens. 1989;34(4):250-259.
- 79. Vilches C, de Pablo R, Herrero MJ, Moreno ME, Kreisler M. Molecular cloning and polymerase chain reaction-sequencespecific oligonucleotide detection of the allele encoding the novel allospecificity HLA-Cw6.2 (Cw*1502) in Spanish gypsies. Hum Immunol. 1993;37(4):259-263.

230 WILEY-HLA OSOEGAWA ET AL.

80. Vilches C, Herrero MJ, de Pablo R, Moreno ME, Bunce M, Kreisler M. Molecular characterization of a novel, serologically detectable, HLA-C allele: Cw*1602. Hum Immunol. 1994; 41(2):167-170.

esponse Genetics

- 81. Herrero MJ, Bunce M, van Dam M, de Pablo R, Vilches C. On the nature of "HLA-B42" alloantibodies. Specific reagents for HLA-Cw*17? Tissue Antigens. 1998;52(1):92-95.
- 82. Hilton HG, McMurtrey CP, Han AS, et al. The intergenic recombinant HLA-B*46:01 has a distinctive Peptidome that includes KIR2DL3 ligands. Cell Rep. 2017;19(7):1394-1405.
- 83. Gwozdowicz S, Nestorowicz K, Graczyk-Pol E, et al. KIR specificity and avidity of standard and unusual C1, C2, Bw4, Bw6 and A3/11 amino acid motifs at entire HLA:KIR interface between NK and target cells, the functional and evolutionary classification of HLA class I molecules. Int J Immunogenet. 2019;46(4):217-231.
- 84. Moesta AK, Norman PJ, Yawata M, Yawata N, Gleimer M, Parham P. Synergistic polymorphism at two positions distal to the ligand-binding site makes KIR2DL2 a stronger receptor for HLA-C than KIR2DL3. J Immunol. 2008;180(6):3969- 3979.
- 85. Moesta AK, Abi-Rached L, Norman PJ, Parham P. Chimpanzees use more varied receptors and ligands than humans for inhibitory killer cell Ig-like receptor recognition of the MHC-C1 and MHC-C2 epitopes. J Immunol. 2009;182(6):3628-3637.
- 86. Gutierrez M, Stoddard J, Machan C, et al. Report of the Serologic Reactivity of Alleles Associated with the Specificity HLA-A2. Vol 1. IHWG Press; 2006.
- 87. El-Awar NR, Akaza T, Terasaki PI, Nguyen A. HLA class I epitopes: update to 103 total epitopes, including the C locus. Transplantation. 2007;84(4):532-540.
- 88. McMichael AJ, Parham P, Rust N, Brodsky F. A monoclonal antibody that recognizes an antigenic determinant shared by HLA A2 and B17. Hum Immunol. 1980;1(2):121-129.
- 89. Fuller AA, Trevithick JE, Rodey GE, Parham P, Fuller TC. Topographic map of the HLA-A2 CREG epitopes using human alloantibody probes. Hum Immunol. 1990;28(3): 284-305.
- 90. Duquesnoy RJ, Marrari M. Correlations between Terasaki's HLA class I epitopes and HLAMatchmaker-defined eplets on HLA-A, -B and -C antigens. Tissue Antigens. 2009;74(2): 117-133.
- 91. El-Awar N, Jucaud V, Nguyen A. HLA epitopes: the targets of monoclonal and alloantibodies defined. J Immunol Res. 2017; 2017:3406230.
- 92. El-Awar N, Terasaki PI, Nguyen A, et al. Epitopes of HLA class I antibodies found in sera of normal healthy males and cord blood. Hum Immunol. 2009;70(10):844-853.
- 93. De Vito LD, Mason BP, Jankowska-Gan E, et al. Epitope fine specificity of human anti-HLA-A2 antibodies. Identification of four epitopes including a haptenlike epitope on HLA-A2 at lysine 127. Hum Immunol. 1993;37(3):165-177.
- 94. Trapani JA, Mizuno S, Kang SH, Yang SY, Dupont B. Molecular mapping of a new public HLA class I epitope shared by all HLA-B and HLA-C antigens and defined by a monoclonal antibody. Immunogenetics. 1989;29(1):25-32.
- 95. LDA PP, Salter RD, Lomen CE, Bjorkman PJ, Ennis PD. HLA-A,B,C: patterns of polymorphism in peptide-binding proteins. Springer; 1989.
- 96. El-Awar N, Terasaki PI, Nguyen A, Lias M, Conger N. New HLA class I epitopes defined by murine monoclonal antibodies. Hum Immunol. 2010;71(5):456-461.
- 97. Kubo K, Tachino J, Yamaguchi H, et al. A human monoclonal antibody that detects HLA-A1, A23 and A24 antigens. Tissue Antigens. 1993;41(4):186-189.
- 98. Kato K, Trapani JA, Allopenna J, Dupont B, Yang SY. Molecular analysis of the serologically defined HLA-Aw19 antigens. A genetically distinct family of HLA-A antigens comprising A29, A31, A32, and Aw33, but probably not A30. J Immunol. 1989;143(10):3371-3378.
- 99. Callender CJ, Fernandez-Vina M, Leffell MS, Zachary AA. Frequency of HLA-DP-specific antibodies and a possible new cross-reacting group. Hum Immunol. 2012;73(2): 175-179.
- 100. Kwok WW, Schwarz D, Nepom BS, Hock RA, Thurtle PS, Nepom GT. HLA-DQ molecules form alpha-beta heterodimers of mixed allotype. J Immunol. 1988;141(9): 3123-3127.
- 101. Kwok WW, Kovats S, Thurtle P, Nepom GT. HLA-DQ allelic polymorphisms constrain patterns of class II heterodimer formation. J Immunol. 1993;150(6):2263-2272.
- 102. Kashiwase K, Tokunaga K, Ishikawa Y, et al. A new HLA-A9 subtype lacking the Bw4 epitope. Ancestral or revertant allele? Hum Immunol. 1995;42(3):221-226.
- 103. Roder G, Blicher T, Justesen S, et al. Crystal structures of two peptide-HLA-B*1501 complexes; structural characterization of the HLA-B62 supertype. Acta Crystallogr D Biol Crystallogr. 2006;62(Pt 11):1300-1310.
- 104. Pieper J, Dubnovitsky A, Gerstner C, et al. Memory T cells specific to citrullinated alpha-enolase are enriched in the rheumatic joint. J Autoimmun. 2018;92:47-56.
- 105. Siebold C, Hansen BE, Wyer JR, et al. Crystal structure of HLA-DQ0602 that protects against type 1 diabetes and confers strong susceptibility to narcolepsy. Proc Natl Acad Sci USA. 2004;101(7):1999-2004.
- 106. Dai S, Murphy GA, Crawford F, et al. Crystal structure of HLA-DP2 and implications for chronic beryllium disease. Proc Natl Acad Sci USA. 2010;107(16):7425-7430.
- 107. Zoet YM, Eijsink C, Kardol MJ, et al. The single antigen expressing lines (SALs) concept: an excellent tool for screening for HLA-specific antibodies. Hum Immunol. 2005;66(5):519-525.
- 108. Pei R, Lee JH, Shih NJ, Chen M, Terasaki PI. Single HLA flow cytometry beads for accurate identification of HLA antibody specificities. Transplantation. 2003;75(1):43-49.
- 109. Gutierrez M, Stoddard J, Machan C, et al. Report of the Serologic Reactivity of Alleles Associated with the B12 Antigen Group (B44, B45) and the B21 Antigen Group (B49 and B50). Vol 1. IHWG Press; 2006.
- 110. Elsner HA, Wolpl A, Goldmann SF, Blasczyk R. Identification of the novel allele HLA-B*1546 which belongs to the serological B72 type: implications for bone marrow transplantation. Tissue Antigens. 2000;55(1):83-85.
- 111. Bergmans AM, Tijssen H, Lardy N, Reekers P. Complete nucleotide sequence of HLA-B*0703, a B7 variant (BPOT). Hum Immunol. 1993;38(2):159-162.
- 112. Ge J, Hannestad K. A cytotoxic human hybridoma monoclonal antibody (TrJ5) specific for HLA-B38(16) and -B39(16). Hum Immunol. 1993;36(3):168-171.
- 113. Kikuchi A, Sakaguchi T, Miwa K, et al. Binding of nonamer peptides to three HLA-B51 molecules which differ by a single amino acid substitution in the A-pocket. Immunogenetics. 1996;43(5):268-276.
- 114. Wang H, Tokunaga K, Akaza T, Tadokoro K, Shibata Y, Juji T. Identification of HLA-C alleles using PCR-singlestrand-conformation polymorphism and direct sequencing. Tissue Antigens. 1997;49(2):134-140.
- 115. Campbell EM, Tongio MM, Urlacher A, Mayer S, Mayr WR. Antigen Report: HLA-Cw3. Springer-Verlag; 1984.
- 116. Fernandez-Vina MA, Wang T, Lee SJ, et al. Identification of a permissible HLA mismatch in hematopoietic stem cell transplantation. Blood. 2014;123(8):1270-1278.
- 117. Doxiadis I. H-RA detection of HLA-Cw3 Subtypes and a New HLA-C Antigen by One-Dimensional Isoelectric Focusing (1D-IEF). Vol 1. Springer-Verlag; 1989.
- 118. Duquesnoy RJ, Marrari M. Detection of antibodies against HLA-C epitopes in patients with rejected kidney transplants. Transpl Immunol. 2011;24(3):164-171.
- 119. Kenter MJ, Anholts JD, Schreuder GM, et al. Unambiguous typing for HLA-DQ TA10 and 2B3 specificities using specific oligonucleotide probes. Hum Immunol. 1989;24(1): 65-73.
- 120. Mandelboim O, Reyburn HT, Vales-Gomez M, et al. Protection from lysis by natural killer cells of group 1 and 2 specificity is mediated by residue 80 in human histocompatibility leukocyte antigen C alleles and also occurs with empty major histocompatibility complex molecules. J Exp Med. 1996; 184(3):913-922.
- 121. Fussell H, Thomas M, Street J, Darke C. HLA-A9 antibodies and epitopes. Tissue Antigens. 1996;47(4):307-312.
- 122. Starling GC, Witkowski JA, Speerbrecher LS, McKinney SK, Hansen JA, Choo SY. A novel HLA-A*8001 allele identified in an African-American population. Hum Immunol. 1994;39(3): 163-168.
- 123. Blasczyk R, Wehling J, Kubens BS, Hahn U, Huhn D, Salama A. A novel HLA-A24 allele (A*2405) identified by single-strand conformation polymorphism analysis and confirmed by solid-phase sequencing and isoelectric focusing. Tissue Antigens. 1995;46(1):54-58.
- 124. Szeto C, Nguyen AT, Lobos CA, et al. Molecular basis of a dominant SARSCoV-2 spike-derived epitope presented by HLA-A*02:01 recognised by a public TCR. Cells. 2021;10(10): 2646. <https://doi.org/10.3390/cells10102646>
- 125. Mobbs JI, Illing PT, Dudek NL, et al. The molecular basis for peptide repertoire selection in the human leukocyte antigen (HLA) C*06:02 molecule. J Biol Chem. 2017;292(42):17203- 17215. <https://doi.org/10.1074/jbc.m117.806976>

SUPPORTING INFORMATION

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How to cite this article: Osoegawa K, Marsh SGE, Holdsworth R, et al. A new strategy for systematically classifying HLA alleles into serological specificities. HLA. 2022;100(3):193-231. doi:[10.1111/tan.14662](info:doi/10.1111/tan.14662)