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Section editor: Fernando Duarte Barroso 

Received: Nov. 20, 2025 • Accepted: Feb. 17, 2026

ABSTRACT

This brief communication summarizes the joint session of the Brazilian Cellular Therapy and Bone Marrow Transplantation Society (SBTMO) and the Brazilian Histocompatibility and Immunogenetics Association (ABHI), held during the 2025 SBTMO Annual Meeting. The joint session focused on how post-transplant cyclophosphamide (PTCy) is redefining donor selection in contemporary allogeneic hematopoietic cell transplantation (HCT). In three lectures with experts in the field, several topics concerning PTCy were addressed, including the effectiveness of PTCy in overcoming the HLA barrier, the increased use of mismatched unrelated donors (MMUD) under PTCy, which significantly broadens HCT access for underserved ethnic minorities, and strategies for reducing the dose of PTCy. The impact of donor-specific HLA antibodies in allogeneic HCT, the importance of HLA serotypes (associated antigens) in improving the accuracy of virtual crossmatch during MMUD searches, and the utility of novel bioinformatics tools to enhance serotype evaluation for MMUD selection under PTCy were also discussed. Additionally, the present report outlines the discussions among the speakers, session chairs, and audience members.

Keywords: Donor selection; Hematopoietic cell transplantation; Post-transplant cyclophosphamide; Alternative donors; Virtual crossmatch; Donor-specific HLA antibodies.

The 2025 joint session of the Brazilian Cellular Therapy and Bone Marrow Transplantation Society (Sociedade Brasileira de Terapia Celular e Transplante de Medula Óssea [SBTMO]) and Brazilian Histocompatibility and Immunogenetics Association (Associação Brasileira de Histocompatibilidade e Imunogenética [ABHI]) was held on August 22 at the 2025 SBTMO Annual Meeting and focused on the impact of post-transplant cyclophosphamide (PTCy)-based graft-versus-host disease (GVHD) prophylaxis in allogeneic hematopoietic cell transplantation (allo-HCT) donor selection. It included Dr. Antonio Jimenez-Jimenez from the Sylvester Comprehensive Cancer Center at the University of Miami, Dr. Celso Arrais Rodrigues from Hospital 9 de Julho and Universidade Federal de São Paulo, and Dr. Alberto Cardoso Martins Lima from Instituto de Imunogenética (IGEN)/Associação Fundo de Incentivo à Pesquisa and Complexo Hospital de Clínicas/Universidade Federal do Paraná. Dr. Adriana Seber, the current vice-president of the SBTMO, Dr. Raquel Fabreti, the current president of the ABHI, and Dr. Margareth Torres chaired the joint session.

In the first presentation, Dr. Jimenez provided a comprehensive overview of how PTCy has revolutionized allo-HCT by mitigating the detrimental impact of the HLA barrier, thereby expanding transplant access to historically underserved ethnic minorities¹ and attenuating the disparity in outcomes between matched unrelated donor (MUD) and mismatched unrelated donor (MMUD).² In this context, Dr. Jimenez presented a large retrospective Center for International Blood and Marrow Transplant Research (CIBMTR) cohort analysis showing that PTCy transplants had better outcomes than those with standard GVHD prophylaxis. Within the PTCy arm, 8/8 MUD and 7/8 MMUD transplants yielded similar overall survival (OS) and GVHD-free/relapse-free survival results.² He also described two prospective studies from the National Marrow Donor Program (NMDP)/CIBMTR, which used only HLA-mismatched MMUD (HLA < 7/8), with either bone marrow (15-MMUD trial) or peripheral blood (ACCESS trial) as graft sources.^{3,4} Remarkably, both trials exhibited low rates of severe acute and chronic GVHD and excellent survival outcomes, despite using highly HLA-MMUD. Next, Dr. Jimenez briefly described the OPTIMIZE trial (NCT06001385), which will assess the effectiveness of a reduced dose of PTCy and the occurrence of infections in the first 100 days after transplant as the primary endpoint, and introduced the new ACCELERATE clinical trial (NCT06859424). Finally, he discussed that the classical “sequential” donor search should be replaced by a “concurrent” donor search strategy, in which all donors are evaluated simultaneously and guided by the search prognosis online tool (<https://search-prognosis.b12x.org/>).⁵

In the second presentation, Dr. Arrais shared his group’s experience with PTCy across various donor sources. The lecture began with a complex clinical case in which haploidentical HCT was ruled out due to very strong donor-specific HLA antibodies (DSAs) (mean fluorescence intensity [MFI] > 20,000), and the only available donors were MMUDs with several HLA mismatches. He presented data from several landmark studies showing the remarkable impact of PTCy in decreasing severe acute and chronic GVHD and improving non-relapse mortality (NRM).⁶⁻⁸ Next, Dr. Arrais presented his experience with PTCy’s dose reduction from the standard dose (100 mg/kg) to a reduced dose (80 mg/kg) of PTCy.⁹ In this retrospective analysis, 158 patients were assessed, and donors were haploidentical in most cases (72%). The standard PTCy dose was administered to 114 patients (72%). Remarkably, compared with the standard-dose group, the reduced-dose group showed higher OS, lower NRM, and similar relapse rates. A propensity score-matched analysis was conducted, confirming the superior outcomes observed in the reduced-dose group.⁹ Finally, Dr. Arrais revisited the clinical case, indicating that the patient found an 8/10 MMUD without DSA and underwent allo-HCT using PTCy, with satisfactory post-HCT results.

In the third lecture, Dr. Lima discussed how HLA serotypes can enhance the accuracy of virtual crossmatch and, ultimately, optimize the selection of unrelated donors in the PTCy era. Dr. Lima showed that DSA is strongly associated with higher risks of graft failure and lower survival.^{10,11} Thus, avoiding DSA is a primary selection criterion in the contemporary NMDP/CIBMTR donor selection guidelines.⁵ The DSA testing using Single Antigen Beads panels, however, has limitations that can lead to false-negative virtual crossmatch results.¹² Indeed, a key limitation discussed was the HLA antigen composition of the Single Antigen Beads panels, which is particularly relevant in the context of the highly admixed Brazilian population.¹³ Another drawback is that thousands of new HLA alleles identified by next-generation sequencing typing, many of which are non-common and well-documented, still lack defined serological equivalents,¹⁴ which can severely compromise virtual crossmatch

assessment. To address these issues, a new nomenclature of HLA serotypes has been recently proposed¹⁵ and validated.¹⁶ Then, Dr. Lima explained the “determining epitopes” concept, the HLA Allele To Serotype software, and the HLA serotype designation.^{15,16} He also presented two online tools (<https://www.igen.org.br/marco/> and <https://sorotipos18ws-v2.igen.org.br/en-US>) created by IGEN’s Bioinformatics Team to support the use of HLA serotypes in routine virtual crossmatch analysis for allo-HCT. Lastly, Dr. Lima presented two clinical cases of MMUD allo-HCT with PTCy, demonstrating that misleading virtual crossmatch results, with false-negative DSA assignment, can occur without detailed consideration of HLA serotypes and additional Single Antigen Beads testing.¹²

The chairs initiated the discussion with the audience, and the first question concerned the impact of B-leader matching on the selection of haploidentical donors.¹⁷ Both speakers agreed that B-leader matching could be used as a tie-breaker when multiple young, DSA-negative haploidentical donors are available.¹⁸ However, Dr. Lima cautioned that the B-leader model has been studied only in patients with acute leukemia and myelodysplastic syndrome, and its applicability should not be extended to other contexts (e.g., nonmalignant diseases).¹⁷ Additionally, it was mentioned that a multicenter European Society for Blood and Marrow Transplantation (EBMT) study, involving patients with acute myeloid leukemia receiving peripheral blood stem cell grafts, failed to validate the B-leader utility.¹⁹

Likewise, it was asked whether non-inherited maternal antigens (NIMA) play a role in the selection of haploidentical donors. Dr. Lima and Dr. Torres emphasized that there is a paucity of data regarding NIMA in haploidentical transplants with PTCy¹⁸; therefore, this parameter should not be used for donor prioritization. In the context of haploidentical HCT with PTCy for nonmalignant diseases, specific donor characteristics may be more important depending on the patient’s diagnosis (e.g., ABO matching is prioritized in sickle cell disease).²⁰

The utility of C1q testing in allo-HCT was questioned,²¹ and Dr. Lima highlighted that the literature shows that DSAs with MFI > 10,126 are highly predictive of C1q positivity, with an area under the curve of 0.99, 100% sensitivity, and 99% specificity.²² He also mentioned that the high cost of this test limits its widespread use in Brazil. Subsequently, Dr. Jimenez mentioned that he uses C1q in his routine DSA assessment but avoids DSA whenever possible, regardless of whether the DSA is C1q-negative but still presents moderate to high MFIs (e.g., MFI ≈ 8,000). Dr. Lima and Dr. Torres stated their preference for using flow cytometry crossmatch with serial dilutions (titration) over C1q testing for DSA risk stratification in their HLA laboratories.²³

Next, Dr. Arrais raised an interesting discussion about choosing a highly mismatched MMUD (< 5/8) with PTCy versus selecting a well-matched, high-dose umbilical cord blood unit (CBU). In response, Dr. Jimenez stated that he would prefer a highly mismatched MMUD rather than a CBU, citing his center’s experience with MMUDs under PTCy. However, all speakers and panelists agreed that HLA-mismatched sources are helpful and that their use should be tailored to the patient’s specific needs and the center’s experience.⁵ Dr. Arrais also asked Dr. Jimenez about the lowest HLA-mismatch degree used in his practice with MMUD with PTCy. Dr. Jimenez mentioned that a 4/8 MMUD had been employed with PTCy, resulting in positive post-HCT outcomes.^{3,4} Of note, Dr. Adriana Seber highlighted that evidence on highly mismatched MMUD transplantation with PTCy in the pediatric setting remains scarce,²⁴ and MMUD cases are assessed on a case-by-case basis.²⁵

Continuing the MMUD topic, Dr. Lima asked Dr. Jimenez about his perspective on the conflicting results between recent CIBMTR and EBMT registry studies evaluating HLA mismatching under PTCy-based prophylaxis.^{2,26} Dr. Jimenez replied that the U.S. and European cohorts differed in several relevant characteristics (e.g., use of anti-thymocyte globulin, types of malignancies included, chronic GVHD definitions, etc.), which limit direct comparisons of the studies’ findings. In addition, Dr. Lima inquired whether the impact of the peptide-binding motif (PBM) model would be studied in the ACCESS trial,^{26,27} and Dr. Jimenez stated that details on HLA mismatching, including the PBM model, will be evaluated and provided in the ACCESS final trial report.

Dr. Torres emphasized that several common HLA alleles in the Brazilian population are not covered by the three commercially available Single Antigen Beads panels.¹³ In her comment, she emphasized the necessity of 11-loci, high-resolution donor HLA typing when performing virtual crossmatch analysis in allo-HCT. She

also provided examples demonstrating how virtual crossmatch can be compromised if only HLA-A, -B, -DRB1, and -DQB1 at medium resolution are available.¹² Dr. Daniele Oliveira from REDOME Registry stated that providing DSA results for REDOME's requests can expedite the search process,⁵ especially for patients who have experienced graft failure and are undergoing a MUD/MMUD search for a salvage transplant.

Concluding this discussion, Dr. Lima emphasized the importance of organizing a future webinar between ABHI, SBTMO, REDOME, and the General Coordination of the National Transplantation System to address the current challenges of virtual crossmatch in allo-HCT. This joint webinar is expected to discuss the shared responsibilities, required qualifications, and practical procedures to implement an effective virtual crossmatch strategy for MUD/MMUD selection in Brazil. Lastly, the chairs thanked the audience for their attendance and adjourned the joint session.

CONFLICTS OF INTEREST

Nothing to declare.

DECLARATION OF USE OF ARTIFICIAL INTELLIGENCE TOOLS

The authors declare that generative artificial intelligence tools were not used in the creation of the present manuscript.

FUNDING

Not applicable.

DATA AVAILABILITY STATEMENT

Not applicable.

AUTHORS CONTRIBUTION

Conceptualization: Lima ACM, Jimenez-Jimenez AM, Silva CAR, Seber A, Oliveira RASF, Torres MA, Bonfim C. **Writing:** Lima ACM, Seber A. **Supervision:** Bonfim C. **Final Approval:** Lima ACM, Jimenez-Jimenez AM, Silva CAR, Seber A, Oliveira RASF, Torres MA, Bonfim C.

ACKNOWLEDGEMENTS

Dr. Andresa Melo and Dr. Fernando Barroso Duarte are acknowledged for the initial discussion on the topic of the SBTMO/ABHI joint session. We also thank Tatiana Almeida, Igor Dias, and Valeria Duarte for organizing the logistics with the speakers.

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