OPTN Histocompatibility Committee
Meeting Summary
March 9, 2021
Conference Call

Peter Lalli, Ph.D., D(ABHI), Chair
John Lunz, Ph.D., D(ABHI), Vice Chair

Introduction

The Histocompatibility Committee met via Citrix GoToMeeting teleconference on 03/09/2021 to discuss the following agenda items:

1. Refusal Codes Feedback
2. Kidney/Pancreas Continuous Distribution and HLA Matching Data Request
3. HLA Tables Update Strategy

The following is a summary of the Committee's discussions.

1. Refusal Codes Feedback

The Committee chair brought forward the current refusal codes project open for public feedback. He recommended changing "No donor serum available for crossmatching" to "no donor cells available for crossmatching", as it would be more accurate. The committee was in consensus.

The UNOS liaison asked if the committee had a preference as to whether all of the histocompatibility codes be grouped together or not. The committee had no preference, and deferred to what works best for OPO and transplant coordinators, as they would be the ones utilizing the codes.

2. Kidney/Pancreas Continuous Distribution and HLA Matching Data Request

UNOS staff presented on the current use of HLA matching in kidney/pancreas allocation, the transition to continuous distribution, and requested feedback from the committee on the following questions:

- Which HLA matches should get more points than others?
- Should we emulate the current system and assign points to 0 ABDR mismatches and DR mismatches?
- Do we want to have a rating scale for individual loci?
- Should we be considering other options?

Summary of discussion:

Committee members were in agreement that Class II alleles are far more immunologically significant than Class I, and proposed that the data request focus on DR/DQ matching. They proposed that limitations of current knowledge include that current data is available from small 1 or 2 center studies, but no large scale studies on antigenic matching and long term outcomes for Class II matching, and especially with DQ matching.

The committee would be interested in evaluating the level of mismatch at each locus, weight them separately, and look at the hazard ratio of mismatches by locus. They would also be interested in seeing how the mismatch at each locus interacts with the others, as there may be an interactive effect. However, they felt that this might not be feasible to analyze at this time, and wanted to focus on a more

practical approach for the shorter term. Other areas of interest were the direction of mismatch with recipient vs. donor and whether the donor or recipient is homozygous.

Next steps:

Committee leadership and UNOS staff will take this feedback to the kidney and pancreas continuous distribution workgroup.

3. HLA Tables Update Strategy

The committee Vice Chair presented on the current work of the HLA equivalency tables update subcommittee and requested feedback from the committee on the following questions:

- Should we expand the possible alleles available in the equivalency tables, both for matching and unacceptable antigen assignment?
- Is there any overt benefit or detriment to expanding the alleles?
- If we expand the alleles using CIWD3.0 definitions, should we expand only to common alleles, to common and intermediate alleles, or to all frequencies of alleles covered by the study?

Summary of discussion:

The committee was split on the benefit of increased allelic data vs. the functionality of matching and unacceptable antigen screening.

Reasons posed to add all common or common/intermediate alleles:

- Would allow for allele-level specificities to be implemented prior to single antibody bead testing, instead of having a 1-2 year delay and be added piecemeal as vendors increase available testing
- Some labs are already using NGS typing, and these will be needed in the future

Reasons posed not to all common or common/intermediate alleles:

- People may think that allele-specific antibodies are fully accounted for in the current matching algorithm and not effectively evaluate potential donors

One member proposed that labs be allowed to enter ambiguous allele string typings, but other members were concerned that it would completely change how the matching and unacceptable algorithms work. Another member brought up that it may mislead programs into thinking they have more information than they truly do, and that it won't necessarily capture the true alleles like high-resolution typing would.

Next steps:

The committee will continue this discussion at a future meeting.

Upcoming Meetings

- April 13, 2021, 11 AM EST, teleconference
- May 11, 2021, 12 PM EST, teleconference

Attendance

- **Committee Members**
  - Bill Goggins
  - Cathi Murphey
  - Evan Kransdorf
  - Idoia Gimferrer
  - Jennifer Schiller
  - Jerry Morris
  - John Lunz
  - Karl Schillinger
  - Marcelo Pando
  - Pete Lalli
  - Phyllis Weech
  - Reut Hod Dvorai
  - Tracy McRacken
  - Valia Bravo-Egana
  - Vikram Pattanayak
  - Yvette Chapman
- **HRSA Representatives**
  - Marilyn Levi
  - Raelene Skerda
- **SRTR Staff**
  - Katie Audette
  - Nick Salkowski
- **UNOS Staff**
  - Abby Fox
  - Adel Husayni
  - Amanda Robinson
  - Chad Waller
  - Courtney Jett
  - Kelsi Lindblad
  - Leah Slife
  - Nicole Benjamin
  - Susan Tlusty
- **Other Attendees**
  - Loren Gragert