



IHIWS CONNECTS

Issue No 2



NGS of full length HLA genes: New Projects

NGS HLA Component:

Under the NGS-HLA component, participants may choose to engage in one or multiple of the following projects: Human Genetic Diversity, Disease Association, Study of unrelated subjects by NGS HLA, Study of haplotypes in families by NGS HLA, Characteristics and distribution of unusual haplotypes by NGS HLA, Study of Rare & Novel HLA Alleles by NGS HLA. Each project has a project leader and a set of study group specimens' criteria and data requirements.

Reference Cell Line Typing Panels for Proficiency and Validation:

In addition to the projects listed, participants may choose to participate in the Reference Cell Lines HLA typing by NGS project. This project provides the opportunity for participants to perform Full-length HLA genes typing of a reference panel of Cell Lines (collected historically by the previous workshops). We have available a total of 5 panels of 24 DNA each which will serve as an unambiguous reference for the evaluation of each reagent/platform used. It may also be used for performance validation, or for accreditation by the various certification boards.

Uploading data in IHWIS Database

At a high level, the process of uploading HLA typing by NGS to the database involve the following steps:

1. Create a dataset (this task is performed by the Project leader or Component Chair). There could be multiple datasets associated to a project, depending on the analysis to be performed, but in general, one dataset per project will be created. When preparing to upload the typing results, the user selects from the available datasets, the appropriate one to upload the results for a specific project.

... Read more: ihiws.org/participation-guides

Event Dates & Locations

The 17th International HLA & Immunogenetics Workshop

September 6–10, 2017
Asilomar Conference Grounds
800 Asilomar Ave
Pacific Grove, California 93950

43rd Annual ASHI Meeting

September 11-15, 2017
Hilton San Francisco Union Square
333 O'Farrell Street
San Francisco, California 94102

Steering Committee

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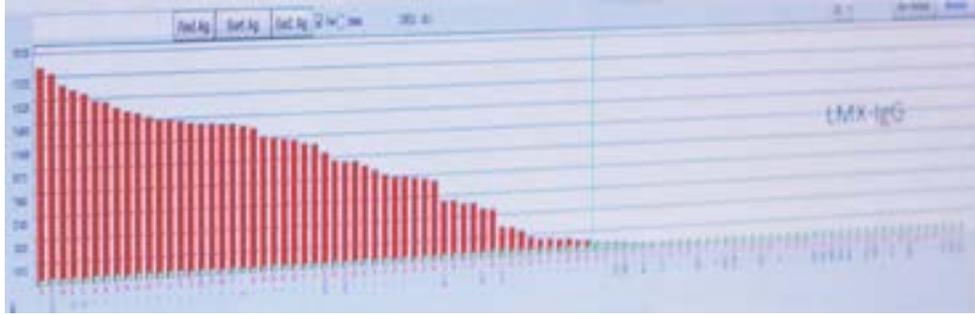
About The Host

The Stanford Histocompatibility, Immunogenetics, and Disease Profiling Laboratory (HIDPL) performs state of the art and cutting edge histocompatibility and genetic testing for solid organ and bone marrow transplantation as well as for disease associations and drug resistance/susceptibility. The HIDPL offers a wide selection of testing services, has an active research and development program and houses and curates a bio-repository of patient specimens. It primarily services the Stanford Hospital and Clinics and the Lucile Packard Children's Hospital but also performs services for outside centers (e.g., Kaiser). It is accredited by the American Society for Histocompatibility and Immunogenetics (ASHI), CLIA, and the state of CA for high complexity testing. The HIDPL performs greater than 60,000 tests per year and employs a staff of more than 50 full-time employees.

Histocompatibility,
Immunogenetics & Disease
Profiling Laboratory



Mapping of Serologic Epitopes: Projects Underway



Characterization of serologic HLA epitopes

Mapping serologic epitopes using NGS, and single antigen bead technologies is one of the components of the 17th IHIWS. Its main goal is to define HLA serologic epitopes contributing to antibody mediated rejection in renal and cardiac transplant recipients. To analyze the data generated by the projects under this component, it is important that we eliminate variables related to technique and reagents by using uniform methods, strict protocols and standardized reagents. To evaluate the performance of same technique and sample/reagents tested by different laboratories, we have launched an Epitopes Pilot project in which 13 international labs perform IgG SAB I, IgG SAB II, Bio-C1q SAB I, Bio-C1q SAB II on the same set of samples. Samples, custom and commercial reagents and SOPs will be provided by the Workshop organizers. The Epitopes Pilot Project is currently in progress, we hope to be able to share the results in the next edition of *IHIWS Connects*.

Under the Mapping of Serological Epitopes component, participants may select from the following projects:

- Analysis of DSA epitopes from donor/recipient transplant pairs: Analysis will be performed based on the results obtained using standardized solid phase procedures/reagents, NGS HLA typing combined with analysis on multiple available programs to translate into serological epitopes. The analysis will focus primarily on mapping serologically reactive epitopes, identify “acceptable” epitopes (NGS HLA defined epitopes to which highly sensitized patients failed to make antibodies) and study the different HLA-DQ epitopes to define the crucial amino acids for antibody reactivity to DQ molecule.
- Analysis of DSA epitopes and transplant outcomes from donor/recipient transplant pairs: Analysis will evaluate the benefit of adopting strategies for matching transplant recipients with potential donors, from HLA allele to HLA epitope matching by analyzing DSA epitopes and transplant outcomes. Analysis will evaluate the contribution of individual vs cumulative DSA epitope mismatches, immunodominance and immunogenicity of epitopes, as well as the clinical relevance of IgG-binding versus complement fixing DSA antibodies.
- Analysis of DSA epitopes and FXM: DSA-FXM is a flow cytometry based DSA detection assay combining cellular flow cytometric crossmatch (FCXM) with microbeads array technology to selectively detect DSA in the recipient serum. One common obstacle to predicting graft outcome with the results of the crossmatch is the lack of standardization of FXM techniques as well as the lack of predictable correlation between MFI values and crossmatch results by any method. This project will evaluate the correlation between DSA-FXM, other XM techniques and SAB results with transplant outcome data.

Learn more on our website: ihiws.org
Register to participate on our database: workshop.ihiws.org



Dear Colleagues,

As we move forward with the 17th International HLA and Histocompatibility workshop, there is much progress to report in the HLA NGS and Mapping of Serological Epitopes components. We also want to share with all of you recent updates to the database.

Contributors to the IHIWS may participate in any of five components, as well as in numerous projects that fall under several of the components listed below.

- NGS of Full-length HLA genes
- NGS of Full-length KIR Genes
- Mapping of Serologic Epitopes
- Informatics of Genomic Data
- Hematopoietic Cell Transplantation (HCT)

To date, we have greater than 90 individual principal investigators/laboratories enrolled in the workshop. Multiple projects under the Serologic Epitopes and NGS of Full-length HLA genes components have been listed for participants to choose from.

To facilitate and streamline participation, we have surveys that allow participants to identify their laboratory/organization capabilities, availability of samples and preferences which in turn allows project leaders to more effectively organize the groups participating in each project.

We urge you to complete the surveys by clicking on the following links (also available from our website):

NGS HLA Survey:
<http://goo.gl/forms/oKL9nQ1gbi>

Mapping Serologic Epitopes Survey:
<http://goo.gl/forms/4S3xNdf0YK>

Yours Sincerely,
Marcelo Fernandez-Viña

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