14th ihiws newsletter

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14th International HLA and Immunogenetics Workshop

29th November –
3rd December, 2005
Melbourne, Australia

www.microbiol.unimelb.edu.au/14ihiws/

14th International HLA and Immunogenetics Workshop and Conference

29th November – 6th December, 2005

Sidney Myer Asia Centre
Melbourne University
Melbourne, Victoria, AUSTRALIA

Email:14ihiws@arcbs.redcross.org.au
Web:
www.microbiol.unimelb.edu.au/14ihiws

Cover photo: Tony Miller

Message from Editor

This is the second of the 14th Workshop Newsletters and contains information on the established workshop components and special interest groups. We will be adding additional projects as more details become available from the relevant chairpersons. We plan to complete this list over the next month. With only 19 months left to the 14th IHIWS meeting the next few weeks is a critical time during which projects should become active, participation confirmed and workshop activities commence.

The newsletters will be a critical component of the 14th IHIWS communication network. We plan to produce a newsletter on a three monthly basis and we will have the 3rd newsletter prepared well in advance of the ASHI meeting early in October. The Newsletters will contain updated information on the progress of individual workshop components in addition to other news regarding workshop activities and the meeting.

We also intend to initiate website discussion fora attached to each project to allow continuous ongoing dialogue between component participants to be recorded and made available to anyone with an interest in the project. As with previous workshops, effective communication between all participants during the active phase of the workshop will be a critical ingredient of success.

If you have any suggestions or information you would like to add to the newsletter, please contact the newsletter editor on the e-mail address shown below.

Brian Tait
14th IHIWS Newsletter Editor
bdtait@arcbs.redcross.org.au

Update from Chairman

We are delighted to host the 14th HLA and Immunogenetics Workshop Conference in Melbourne Australia. This will be the first time that such a workshop is being held in the Southern Hemisphere. This recognises the internationalisation of HLA and immunogenetics and the increasing involvement of the research community in the Asia Pacific region.

The plan for the 14th IHIWS is that we will primarily act as host for existing projects occurring under different umbrellas. Among the projects already active are those programs within the International Histocompatibility Working Group which represent an extension of 13th IHIWS activities. This component is chaired by John Hanson and is led by scientists with a long standing involvement in international HLA workshops.

Importantly however the 14th Workshop will include project areas from many other laboratories not directly associated with IHWG. These include exciting initiatives looking at the structural basis of HLA compatibility, laboratory and clinical investigation of the highly sensitised transplant patient, development of virtual cross match techniques, definition of epitopes using single antigen beads, sequence based typing studies, topics surrounding bone marrow and cord blood donor registry, HLA micro satellite working group, HLA and genomic diversity in southern India, host genetics in hepatitis C infection and comparative MHC studies in non primate species.

The meeting will be held on the campus of The University of Melbourne just outside the central business district of Melbourne. The Workshop will have a presentations and discussions on workshop components and in addition, a number of keynote addresses from distinguished scientists. The campus is a beautiful area and within a few hundred yards there are many cafes, restaurants, shops and bars. Melbourne boasts some of the most beautiful parks and gardens in Australia and is only a one hour drive from some of the loveliest coastline and wineries in the world.

We hope that anyone with an interest in HLA and immunogenetics will see the Workshop as an opportunity to present their findings. Participants need not be directly involved in any projects and can come along just to hear cutting edge information in the field. We expect many of the projects might be small, local initiatives or involve bilateral or multilateral collaborative arrangements that lie outside any existing frameworks. The major goal of the 14th IHIWS is to bring together the community interested in HLA and immunogenetics to hear the latest and most important findings in the area, to share experience and research in this field.

Following the workshop there will be a Tumour Immunology Workshop and a formal scientific meeting in collaboration with the Australasian Society for Immunology held in Melbourne from December 5 to 8. This gives participants the opportunity to attend all or part of the Workshop as well as all or part of the subsequent scientific meeting without changing venues or cities as has been the case in the previous workshop and conference meetings.

The theme of the scientific meeting is "Genetics and the Immune Response" and will feature many distinguished international experts. Thus the meeting will complement the activities of the workshop and provide delegates with an outstanding opportunity to hear the cutting edge of scientific discovery in the field.

We warmly invite you to attend the workshop and meeting in Melbourne in November/December 2005. Please pencil in these dates and examine the various workshop projects to see in which way you would like to participate.

Yours sincerely,

James McCluskey
14th IHIWS Chairman
jamesm1@unimelb.edu.au

How to participate in the 14th IHIWS

The workshop will provide a forum for the presentation of collaborative studies, scientific reports and symposia in the field of HLA and immunogenetics. Many of the reports will involve feedback on international collaborations that have been active over the last three to five years. However we also expect there will be many reports from smaller bilateral and single centre studies that we hope will also be presented at the workshop. Accordingly registrants can participate as an audience or through involvement in any of the projects that comprise the background activities of the workshop. These projects comprise research carried out under the umbrella of the IHWG and representing an extension of the 13th IHIW but also include many projects and studies that are independent of IHWG and are being carried out through different collaborators around the world.

If potential registrants would like to participate in specific projects they are invited to contact either the organisers of the workshop or the project leaders for these projects as outlined on the website under the heading Projects. Funding of projects must come from local participants as there is no central funding of this activity other than that made available through the NIH grant to the IHWG.

Lastly, participants in the workshop need not be involved in any project and are welcome simply as audience if they wish to be brought up to date in the field of HLA and immunogenetics. We invite you to examine the workshop website for a list of project areas in which you may be interested.

In summary you can participate through
(i) just attending
(ii) contributing to a multi-centre project through IHWG
(ii) contributing to a project through any bilateral or multilateral collaboration
(iv) contributing to a project through a single centre study or scientific presentation
(v) participating in any of the special interest group discussions eg. minor antigens, registry issues, Sequence based typing etc.

Workshop Projects and Interest Groups

The following is a brief description of all currently registered projects. We have summarised the original project descriptions in the interest of space. We hope we have captured the essential essence of each project but suggest that you access the website for a full description of each project and instructions on how to participate.

Anthropology

Contact:

Steve Mack	steve.mack@roche.com
Heather Dron	heather.dron@roche.com

We are currently in the process of determining the organizational structure and plans for the next round of project activity, culminating in the 14th Workshop in 2005. We plan to support continued high-resolution genotyping at the class I loci using the RLS typing reagents and intend to offer class II RLS genotyping reagents for use. In offering class II reagents, it is our hope that the population samples that were genotyped at class I loci as part of the 13th Workshop can be more completely typed. In addition, we hope that some populations that were genotyped at intermediate resolution as part of the 12th Workshop will be genotyped at higher resolution in this round of the project.

In addition, we are eager to include new population samples in the Anthro project, with a focus on demographic groups that were poorly represented in the 13th Workshop (e.g., central African, Australian Aboriginal, Siberian, central Asian, North and South Native American, and Polynesian groups). If you

have access to new population samples, or know of investigators with new population samples who might be interested in joining the Anthro project, please contact either Steve Mack or Alicia Sanchez-Mazas.

Some datasets were submitted for analysis in the 13th Workshop reporting serological –level polymorphism or reporting high-resolution data in non-standard formats, and it was not possible to include these datasets in the 13th Workshop analyses. The inclusion and analysis of these datasets for the 14th Workshop will be a high priority, along with serological-level analyses of all datasets.

One of the obstacles to rapid and efficient data review and analysis has been the requirement to handle data transactions manually via email. We are pleased to announce that the IHWG will be implementing a web-based interface, which will permit web-based data submission and on-demand data review by submitting laboratories. We hope that this new interface will make the Anthro project (and other IHWG projects) more accessible to all participants.

Finally, we are actively seeking to recruit new project participants. In particular, we are hoping to increase participation from Africa, East Asia, Australia and South America. If you have any colleagues who are interested in participating in the IHWG Anthro project as part of the 14th workshop, or have suggestions for investigators that we should recruit, please contact Steve Mack or Alicia Sanchez-Mazas.

Bone Marrow Registry -Special Interest Group

Contact:

Dr Carolyn Hurley hurleyc@georgetown.edu

This special interest group with input from the World Marrow Donor Association is interested in discussions on scientific and technical issues surrounding bone marrow and cord blood registries. Registries today are facing many challenges, from technological change to nomenclature variation, all of which impact on data collection, data management, search algorithms and speed of results.
Technologies to type stem cells are ever changing but can result in significant differences that need to be compared to historical data.
High resolution typing is very expensive and resources for searching are limited. Discussions are needed on strategies to achieve a cost effective and timely search.
Topics to be covered include:

Typing methods for registries. What techniques, kits, automation, high throughput options.
Resolution for registry typing. Which loci, how to resolve alleles, ambiguous combinations, new alleles and historical data.
Search determinants. How do we link various HLA types in the match algorithm? How do we deal with a mismatch algorithm? Is it possible to standardise this process?
Quality control of typing. What should be the standard for results?
HLA data collection, storage, and analysis. Current and future methods. Approaches for optimizing matched donor search.
Ethnic diversity of registries. How we can evaluate the degree of diversity in registries? Strategies for recruitment of minority groups
This group would value the input of all involved in the typing and searching process.

Comparative MHC Studies in the Dog

Bill Ollier, Lorna Kennedy, Annette Barnes, Wendy Thomson & Stuart Carter

Contact:

Dr Lorna Kennedy or Professor Bill Ollier
Centre for Integrated Genomic Medical Research,Stopford Building,
Oxford Road, Manchester, M13 9PT, UK
Tel: +44 161 275 7316/5622
Fax: +44 161 275 1617
E-mail: Lorna.Kennedy@man.ac.uk or CIGMR@man.ac.uk

Comparative genomic studies are increasingly recognised as being a powerful approach to making inroads into understanding human disease aetiopathogenesis. Whilst so far this has largely focussed on spontaneous and experimentally induced diseases in rodents, more recently attention has turned to genetic studies in dogs. Canine veterinary medicine has much to offer clinical research of the human conditions in that:

* Dogs spontaneously develop many disease conditions that represent homologues of human disease
* Canine diseases are in most cases carefully and rigorously clinically phenotyped with a high level of imaging and laboratory investigation.
* The dog genome has already been sequenced (Celera) and is currently being sequenced through an NIH funded initiative. The latter will be completed in 2004.
* A large number of dog breeds have been established and in many ways these mirror closed human populations.

The MHC of the dog (DLA) is likely to be of major

importance in understanding both healthy immune function and disease susceptibility in canine medicine and contribute to comparative disease studies. DLA genes have already been relatively well characterised and there is an increasing body of information relating to class I and II polymorphisms, ancestral haplotypes and breed frequency distributions.

This Workshop component aims to:
* Determine more accurately the extent of polymorphism at DLA class I, II and III loci in dogs (and possibly other canids) and assign appropriate nomenclature.
* Establish DLA allele and haplotype frequencies in a defined number of dog breeds.
* Determine the phylogenetic relationship between DLA alleles.
* Examine the relationship between DLA and susceptibility to a small number of well defined canine disease phenotypes (perhaps diabetes and/or leishmaniasis).

We would like to ask whether any laboratories performing HLA SBT are interested in collaborating with their local Veterinary Faculty on this project. We will be happy to help make links between HLA labs and Veterinary Schools.

Haematopoietic Cell Transplantation -KIR Component

Contact:

Effie Petersdorf epetersd@fhcrc.org
Katharine Hsu
Mari Malkki
Bo Dupont

Summary of HCT-KIR Component Goals:

The purpose of the study is to perform typing for the killer Ig-like receptor (KIR) genes for patients and donors undergoing matched unrelated transplants for AML, MDS, CML, and ALL. KIR typing will be correlated with HLA typing for these individuals and will also be evaluated for correlation to transplant outcome. The clinical outcomes of interest include: survival, infection, graft-versus-host disease, and relapse.

A collective effort between international transplant registries and immunogenetics laboratories will be the most reliable way to identify the influence of KIR on transplant outcome. Transplant centers and typing laboratories are asked to provide clinical data, HLA typing, and KIR typing for the patients and donors on a standardized data submission form. Because KIR genotyping is a relatively new technology, there can be wide variation in typing results, depending on the methods used. To minimize method-related discrepancies, we require that all participating laboratories first complete genotyping of a reference panel of genomic DNA. The DNA samples are available free of charge from IHWG (laboratories pay only the shipping charge) and can be ordered through the IHWG website: http://www.ihwg.org/forms/NKKIRWebOrderForm.doc.

For questions on obtaining the reference panel, please contact Eric Mickelson (emickels@fhcrc.org).

Typing results can be submitted to database@ihwg.org. Your typing results will be evaluated and feedback provided on the reliability of your typing method.

HLA & Genomic Diversity in Southern India

Contact:

Dr. RM. Pitchappan
Senior Professor & Head, Dept. of Immunology
Centre for Advanced Studies in Functional Genomics - School of Biological Sciences
Centre for Excellence in Genomic Sciences -
Madurai Kamaraj University
MADURAI, Tamil Nadu, 625 021, INDIA
Email: pitchappanrm@yahoo.co.uk
Fax: +(91 452) 2459181 or 2459139
Tel: + (91 452) 2458269 (off);2569889 ®

Fifteen different ‘populations’ (breeding isolates = castes) from the state of Tamil Nadu and nearby Kerala, the southern most part of India will be studied. The available ethnographic notes indicate many of them to be very ancient and isolated populations. An at random blood sample of 200 individuals from each population will be collected, DNA extracted, quality controlled and stored at –70C. All relevant background population information will be obtained in a precoded questionaire, for analysis.

These samples will be made available to those interested in studying any genetic / genomic polymorphisms in these populations. This will include HLA genes, non HLA genes, STR/SNP loci, microsatellite markers, MHC haplotypes and other various polymorphic loci of MHC and other gene regions, NRY, mitochondrial DNA, etc. The same set of coded samples of two populations will first be provided to all the participating laboratories and the results will be submitted to the 14th ihwc central data processing and analysis laboratory: the sample id will be decoded at the time of analysis and interpreted. Based on this preliminary exercise on two populations, the rest of the populations will then be studied in the workshop.

HLA Expression and Cancer

Contact:

Brian Tait bdtait@arcbs.redcross.org.au

The HLA expression and cancer component of the workshop aims to evaluate the importance of class 1 expression in both disease course and response to immunotherapy in a limited range of 5-6 tumour types. The 14th Workshop study is a continuation and extension of the of the 13th Workshop study, one of its aims being the development of monoclonal reagents for use in immunohistochemistry for detection of class 1 expression, and which addressed some of the technical issues related to this technology.

There are several aims of the 14th Workshop study which are summarised below:

- Initiate exchange of tissue sections between laboratories to attempt standardisation in the reading of immunohistochemically stained tissue sections.
- Investigation of the molecular mechanisms underlying loss of class 1 expression using a range of molecular techniques
- By studying patients undergoing vaccination using either whole tumour antigen or peptide fragments a correlation will be sought between HLA class 1 expression and clinical response.

The workshop will be organised by a group including Soldano Ferrone, Federico Garrido , Marcel Tilanus and Brian Tait. An HLA and Cancer Newsletter will be available for distribution soon.

Host Interaction in Hepatitis C Infection

Contact:

Dr. Silvana Guadieri
Silvana.guadieri@health.wa.gov.au

The purpose of this study is to examine the effect of host (HLA and other immunogenetic markers) and viral genetic diversity on hepatitis C infection. Particular attention will be paid to the role of HLA genetic markers on clinical outcomes in racially homogeneous infected cohorts. The objectives are to establish a clinical data and patient sample database of racially homogeneous cohorts infected with Hepatitis C. These will be examined for HLA alleles and the evolution of population adapted consensus hepatitis C virus sequence.

The selection of CTL and possibly T helper cell escape mechanisms in acute and chronic infections, will be studied at a population level using known in vivo targets of immune responses as index epitopes. Knowledge of contemporary and primordial selection affects associated with HLA restricted immune responses can be used to construct highly predictive models of hepatitis C virus infection outcome and disease progress in individuals given the HLA type and hepatitis C virus sequence.

The Laboratory and Clinical Management of the Highly Sensitised Transplant Patient

Contact:

Solomon Cohney solomon.cohney@mh.org.au
Brian Tait bdtait@arcbs.redcross.org.au

Although renal transplant graft and patient survival has improved remarkably over the last two decades the issue of the management of the highly sensitised patient remains a significant laboratory and clinical issue. Despite reduction in the use of blood transfusion as a therapy over this period there is still a significant proportion of patients who have an HLA panel reactive antibody (PRA) of >50% (approximately 10-15%). Many of these patients are multiparous or regraft patients. The main impact of high levels of sensitisation in these patients is an increase in the incidence of positive crossmatches, hence a delay in time to grafting, resulting in a longer waiting time on dialysis. In addition there is a group of patients who while not necessarily having a high PRA, have HLA antibodies which precludes them from a specifically targeted living related, or living unrelated transplant.

Several strategies have been employed designed to immunomodulate the highly sensitised patient in order to reduce PRA level and increase the chance of receiving a successful graft. The strategies include the use of plasmapheresis, intravenous immunoglobulin, splenectomy and Rituximab (a B cell specific monoclonal antibody),either alone or in combination.

This special interest study will bring together groups utilising different laboratory and clinical protocols in dealing with highly sensitised patients, with the aim of devising optimal protocols and increasing understanding of the mechanisms involved. Groups with an interest in other forms of solid organ transplantation, such as cardiac, lung and liver, are also encouraged to participate and share experience.

Please contact the project co-ordinators for further details. Electronic Newsletters will be prepared to keep all participants informed.

MHC and Infection

Chair : Narinder Mehra
Secretary: Gurvinder Kaur

Contact:

Narinder Mehra
Prof and Head Department of Transplant Immunology & Immunogenetics
All India Institute of Medical Sciences, Ansari Nagar, New Delhi-110029, INDIA
Tel (91 11) 26588588, 26594638
Fax (91 11) 26588663
Email narin98@hotmail.com

Following the successful completion of the Mycobacterial Disease Study of the 13IHWC, it is apt to extend the study to the role of MHC in infectious diseases. Accordingly, it has been planned to include 'MHC and Infection' as a major component of the 14IHIWS. The study has been designed to include the following infections:
Mycobacterium tuberculosis,
HIV infection, with and without tuberculosis, and
Mycobacterium leprae infection.
With the availability of advanced molecular biology tools, bioinformatics and immunoinformatics, the following important issues would be addressed:

- identification of specific HLA motifs and supertypes responsible for restricting T cell responses in infectious diseases,
- identification of mycobacterial epitopes bound by select MHC motifs or supertypes in different populations,
- role of non HLA genes residing within MHC, e.g MICA, TNF and others.
- investigation of functional polymorphism in non MHC genes like the KIRs, NK cell stimulatory ligands e.g RAET1 family on 6q24.2-q25.3, Toll receptor genes, cytokines and others, and dual interaction between HIV and the opportunistic TB infections.

Minor Histocompatibility Antigen Nomenclature

Collaborative study in the 14th IHIWC
Special interest group

Contact:

Els Goulmy ihbsecr@euronet.nl

The field of minor Histocompatibility (H) antigens is clearly moving. Chemical characterization became feasible especially for the MHC class I associated minor H antigens and the first minor H antigens have found their route into clinical application. So far, the only clear distinction of minor H antigens can be made on their encoding genes i.e.Y-genes and autosomal genes. The growing identification of minor H antigens and their putative impact for the development for immunotherapeutical strategies demand the availability of a minor H antigen nomenclature. This is of first importance and cannot early enough be agreed upon.

Therefore the goal of this collaborative study is : formation of an international nomenclature committee aiming at the creation of an international accepted nomenclature for human minor H antigens.

Name References
HA-1 (den Haan 1998) (Mommaas 2002)
HA-2 (Pierce 2001b)
HA-3 (Spierings 2003a)
HA-8 (Brickner 2001)
HB-1 (Dolstra 1999)
BCL2A1 (Akatsuka 2003)
UGT2B17 (Murata 2003)
SMCY (Meadows 1997) (Wang 1995)
UTY (Warren 2000) (Vogt 2000b)
DFFRY (Vogt 2000a) (Pierce 2001a)
DBY (Vogt 2002)
RPS4Y (Spierings 2003b)

Reproductive Immunology

Contact:

Dr Marighoula Varla-Leftherioti
Department of Immunobiology,
Helena Venizelou Maternity Hospital
2 Helens Venizelou sq., Athens 11521, Greece
Fax: 30-210-6402149,
Tel: 30-210-6453759,
e-mail: gr1bmdr@hol.gr

The association of HLA with recurrent spontaneous abortions (RSA) is a long lasting story, which remains controversial. Since 1977, when Komlos et al reported increased HLA sharing between spouses in couples with RSA appeared, many studies have investigated this hypothesis as well as the possibility of specific HLA antigens or HLA haplotypes to be markers of RSAs, but their results are still conflicting. Discrepancies between studies are complicated by the inconsistent definitions of recurrent miscarriage and of control groups, the small numbers of populations sampled, the different tissue typing methodologies used and the exclusion of possibly relevant but still unknown loci.

The 14thIHIW will build on the results presented at the 13th Workshop with the following goals to investigate whether:
a) Increased HLA sharing or HLA allele homozygosity between partners predispose to immune-mediated abortions and repeated IVF/ET

failures.
b) The aborters HLA phenotype is associated with repeated pregnancy losses/failures.
c) Maternal KIR / trophoblastic HLA-C epitope matching is involved in the maintenance of pregnancy.

Research plan:

Subjects:
a. Childless couples with 3 or more RSA
b. Couples with no more than one successful pregnancy and 2 or more consecutive RSAs
c. Women with <3 abortions, where histology / immunohistology of the products of the abortions has revealed immune abnormalities.
d. Couples with repeated IVF/ET failures (women younger than 35 years of age, >5 E/T failures).
e. Controls: Fertile couples with no history of abortions (ethnically matched).
Exclusions: In all cases, other than immune aetiology of pregnancy failures, ought to be excluded:

Stage I:
In the initial stage of the study the centers and laboratories interested in participation will be identified. As it is essential to have well defined groups of immunological abortions, participants have to ensure that they can follow the protocol that will be given to them for the identification and the investigation of the couples.

Stage II:
After the selection of couples, DNA samples will be collected from all partners for HLA-A, -B, -C, -G, -E, -DRB1, -DQA1, -DQB1, -DPA1, -DPB1 allele typing by PCR-SSO. All individuals will be also typed for NKR polymorphisms following the protocol of the ³NK Receptors and HLA polymorphisms² component of the Workshop.
Typing results will be accepted from ASHI or EFI accredited laboratories. Laboratories with no accreditation will be accepted after successful typing of control DNA samples.
Laboratories can use their own reagents or those of the workshop (upon request and payment).

Stage III:
According to the results of the protocol immunological tests, couples will be divided to subgroups (cases with alloimmune, autoimmune, thrombophilic abnormalities) for final analysis (sharing, homozygosity, associations).

Sequence based typing of HLA-DQA1: A study to determine the level of molecular heterogeneity of HLA-DQA1 and its haplotypes

Contact:

Dr C Voorter
Tissue Typing Laboratory,
University Hospital Maastricht,
P.O. Box 5800, 6202 AZ Maastricht.
E-mail cvoo@lwee.azm.nl;
phone: +31 43 3874680, fax: +31 43 3874678.

Project proposal within the Sequence Based Typing workshop

The project will be a collaboration between different laboratories. All data will be submitted to the IHWG database.
Those laboratories already having experience with SBT of DQA1 are invited to participate in the project. Also laboratories with experience in SBT of other HLA genes, but not DQA1, are welcome to join. Laboratories with interesting samples (i.e. peculiar SSP or SSO patterns for DQA1 or rare DQB1 alleles) and not prepared to perform SBT of DQA1 are invited to make these samples available for the project.

The aims of the project comprises the following:
1 Selection of the most efficient and validated protocol:
2 Polymorphism: filling in gaps that exist in currently described alleles.
3 Sequence determination of HLA-DQA1 alleles in samples with:
3a. Unusual SSO or SSP profiles for DQA1 typing
3b. Unusual DRB1 - DQB1 associations
4 Comparison of the sequences of reported alleles from different ethnic groups, to study the presence of intra-allelic polymorphism.

Those laboratories interested in participation can send a letter or e-mail to the coordinator, giving their name, affiliation and information on the SBT experience.

Structural Basis of HLA Compatibility

Contact:

Rene J. Duquesnoy, Ph.D.
Division of Transplantation Pathology,
University of Pittsburgh Medical Center
Biomedical Science Tower, Room W1552 ,
Pittsburgh, PA, 15261, USA
Phone: ++1-412-647-6148 or ++1-412-624-1075
Fax: ++1-412-647-1755
E-mail: Duquesnoyr@msx.upmc.edu

Frans H. J. Claas, Ph.D.
Department of Immunohematology and Blood Transfusion, Leiden University Medical Center
P.O. Box 9600, 2300 RC Leiden, The Netherlands
Phone: ++31-71-526-3800 Fax: ++31-71-521-6751
E-mail: F.H.J.Claas@lumc.nl

The goal of this workshop project is to develop structurally based approaches to determine HLA compatibility. These studies focus on humoral immune responses to HLA because HLA-specific alloantibodies represent important risk factors for transplant failure and platelet transfusion refractoriness. Structural HLA matching considers amino acid sequence polymorphisms as potential epitopes for alloantibodies and several matching algorithms have been reported. The studies have been designed to increase our understanding of the antigenicity and immunogenicity of structurally defined polymorphisms and their clinical significance in HLA compatibility. There are three projects:

1. Determine the structural basis of epitopes recognised by HLA specific human monoclonal antibodies.
2. Determine the relative immunogenicity of structurally defined HLA mismatches following kidney transplantation
3. Determine the role of structurally defined HLA polymorphisms in platelet transfusion support of aloimmunised thrombocytopenic patients.

This project will be guided by the Structural HLA Compatibility (SHC) Project Steering Committee:
Rene Duquesnoy (Pittsburgh), Chair
Frans Claas (Leiden, The Netherlands), Co-Chair
Rhonda Holdsworth (Melbourne, Australia)
Howard Gebel (Atlanta, GA),
Andrew Lobashevsky (Birmingham, AL),
Cristina Navarette (London, UK),
Steve Takemoto (Los Angeles, CA)
Ralf Wassmuth (Duesseldorf, Germany)

The website outlines fully the requirements for participation in this component.

Sequence Based Typing:

Contact:

Dr. Marcel G.J. Tilanus
UMC-Utrecht, Heidelberglaan 100,
Postbus P.O. Box 85500
HP H04.312,. GA UTRECHT, the Netherlands
phone ++ 31 30 2506487/7665,
fax ++ 31 30 2544990,
email M.Tilanus@lab.azu.nl

Dr. David Sayer
Royal Perth Hospital
Dept of Clinical Immunology,
Wellington Street, Perth 6000, Australia,
phone ++61 8 92242899, fax ++618 92242920
email david.sayer@health.wa.gov.au

The goals of the SBT component are as follows;

1. To collate and assess current SBT protocols for HLA typing with particular reference to the resolution of typing ambiguities.
2. To identify reference SBT labs that are able to provide limited sequencing of potential new alleles and reference sequences.
3. To complete exon 2 sequencing for incomplete HLA class II alleles and exon 2 and 3 sequencing for incomplete HLA class I alleles.
4. To collate additional HLA allele sequence information.

Sub-committees will be set up to oversee

1) Quality – review of local QA data e.g. UCLA , provision of QA panel in absence of local QA data.
2) Bioinformatics – collation and provision of available analysis and data submission tools. Liase with IMGT to incorporate all sequence data into IMGT.
3) Sub-committees will be set up for each HLA locus that will have a similar focus to the allele/haplotype groups used in previous workshops. The chairpersons would collate protocols, have input to the QA group, request cells/DNA for missing alleles, liase with bioinformatics & SIGs and steer data analysis. A communication forum will be set up using the website (http://www.microbiol.unimelb.edu.au/micro/14ihiws/).
4) Special Interest groups e.g. mutation analysis in blasts, correlation of exon and promoter sequences and RNA-SBT will be listed on the website.

Please contact the chairpersons directly or register your interest directly through the website

Workshop Analytical Tools

Biostatistical analyses of population level data for the 14th IHIWS

Glenys Thomson, Richard Single, Diogo Meyer, Alex Lancaster

We have implemented an analysis package (PyPop) for comprehensive analyses of MHC multi-locus population genetic variation. We applied this package in analyses of data from the 13th IHW for the following projects: Anthropology/Human Diversity, HLA and Disease, and Hematopoietic Cell Transplantation (HCT). The PyPop program is available for analyses of data from the 14th IHIWS.

PyPop is in an object-oriented framework that allows us to implement individual analysis modules which can be inserted or removed without affecting other modules. The following PyPop modules are in place:
1. population summary data,
2. locus specific information,
3. Hardy Weinberg (HW) testing using:
(a) the chi-square test statistic with genotypes with an expected value less than 5 combined together in a lumped class, and
(b) the exact overall test of Guo and Thompson,
4. Ewens Watterson homozygosity test of neutrality,
5. haplotype frequency estimation using the Expectation-Maximization (EM) algorithm, for all pairwise combinations, and specified 3, 4, etc. locus combinations,
6. individual allele pair and locus measures of linkage disequilibrium (LD) and significance testing of LD using a likelihood approach.

For more information on PyPop go to:
http://allele5.biol.berkeley.edu/pypop/
and for details on statistical tests etc. or help in running your data contact
Glenys Thomson glenys@allele5.biol.berkeley.edu

14th IHIWS Workshop Meeting

The 14th IHIWS workshop meeting will be held in the Sidney Myer Asia Centre at the University of Melbourne. The 14th IHIWS will commence on Tuesday, the 29th November, 2005, with a welcome reception and conclude on Saturday the 3rd December. On Friday night there will be a workshop dinner for all delegates. We are currently negotiating to hold the dinner at a riverside venue in the heart of Melbourne. As with previous workshops we intend to make this a memorable night.

There will be a common structure to each days scientific programme. The day will commence at 8.30am with some keynote speakers addressing a defined theme. For example the Wednesday theme will be stem cell transplantation. After morning tea at 11:00am workshop groups can convene in the breakout rooms and initiate or continue discussions on individual workshop components. We plan to have a plenary lecture immediately prior to lunch on each of the three days (Wednesday, Thursday, Friday) to be given by three distinguished world renowned scientists. After lunch there will be an additional workshop component session and on Wednesday and Thursday a second session of keynote speakers. It is essential that there is sufficient time for each component participants to meet and discuss data and findings. Under the programme structure there will be approximately 8 hours available to each component chairperson for project meetings and summaries. If additional time is required for group meetings this can be accommodated after the formal conclusion to each day.

14th IHIWS Timetable

	Tues: Nov. 29	Wed: Nov. 30	Thu: Dec. 1	Fri: Dec. 2	Sat: Dec. 3
08:30 10:30		Symposia: Stem Cell Transplantation	Symposia: Infection and Immunity	Symposia: Immunogenetics HLA and Disease	Tool Box for the 21st Century
10:30 - 11:00		Coffee Break	Coffee Break	Coffee Break	
11:00 12:10		Workshop Activity	Workshop Activity	Workshop Activity	
12:15 13:00	Registration	Plenary Lecture	Plenary Lecture	Plenary Lecture	
13:00 - 14:00		Lunch	Lunch	Lunch	
14:00 15:30		Workshop Activity	Workshop Activity	Workshop Summary Component	Conference Outing
15:30 - 16:00		Coffee Break	Coffee Break	Coffee Break	
16:00 17:30	Welcome and Opening Lecture	Symposia: Stem Cell Transplantation	Symposia: Infection and Immunity	Workshop Summary Component	
18:00+	Welcome Reception	Wine Tasting	Council Dinner	Workshop Dinner	

Joint 14th IHIWS/ASI Conference

Genetics and the Immune Response

A joint conference of the ASI and the 14th IHIWS will be held from Monday, December 5th, 2005, to Thursday, December 8th. The meeting will be structured to include plenary sessions, symposia and workshops. Details concerning abstract submission will be announced later this year. A Tumour Immunology workshop is also planned in conjunction with the ASI at a time yet to be decided.

Invited speakers to the joint scientific conference will include Rafi Ahmed, Mike Bevan, Grant Gallagher, Katia Georgopoulos, Marc Jenkins, Peter Parham, Steve Porcelli, Klaus Rajewsky, Jeff Ravetch, Maria Grazia Roncarolo, Sasha Rudensky, Edward Wakeland and Bruce Walker.

We are pleased to announce the Burnet Oration in 2005 will be given by Professor Ian McKenzie.

Mon: Dec. 5	Tue: Dec. 6	Wed: Dec. 7	Thu: Dec. 8
Plenary Session	Plenary Session	Plenary Session	Plenary Session
Symposia	Symposia	Symposia	Symposia
Lunch	Lunch	Lunch	
Symposia	Symposia	Symposia	
Workshop	Workshop	Workshop	

14th IHIWS Contacts

James McCluskey
Chairman
jamesm1@unimelb.edu.au

Brian Tait
Co-chairman
bdtait@arcbs.redcross.org.au

John Hansen
Co-chairman and Convener IHWG
email: jhansen@fhcrc.org

Frank Christiansen
Co-chairman
ftchrist@cyllene.uwa.edu.au

Rhonda Holdsworth
Co-chairman
rholdsworth@arcbs.redcross.org.au

email: 14ihiws@arcbs.redcross.org.au

www.microbiol.unimelb.edu.au/micro/14ihiws