



CONFERENCE 2016, Salt Lake City, USA

Comparative MHC Workshop

Organised by a standing committee yes

Date and meeting time: Monday July 25th 08.30-12.00

Chair, name and contact email: Keith Ballingall (keith.ballingall@moreun.ac.uk) and Sam Ho (SHo@giftoflifemichigan.org)

Agenda / programme attached

Number of participants at meeting: Between 40 and 60

Summary of the meeting including votes, decisions taken and plans for future conferences

The Comparative MHC nomenclature committee is a standing committee of both ISAG and the International Union of Immunological Societies (IUIS). Its role is to provide official allelic nomenclature for MHC loci in non-human species and to organize workshops for discussion of comparative MHC genetics and associated biology. The workshop at the 35th ISAG meeting in Salt Lake City consisted of nine oral presentations of 12-15 minutes followed by questions from the audience. Professor Steven Marsh provided the workshop plenary presentation on the “Development of the IPD-MHC Database”. Following the presentations a general discussion on how the species specific nomenclature committees and the IPD-MHC database deals with next generation sequence data. This was followed by the committee business meeting.

1. Summary of the workshop presentations.

- (i) The Chairs introduced the workshop and welcomed the speakers and audience.
- (ii) The first presentation was provided by **Kei Hanzawa** (Tokyo University of Agriculture, Japan) who presented an update on “Diversity analysis of transcribed MHC class II β loci in Japanese quail” using amplicon sequencing and RNAseq.
- (iii) The second presentation was provided by **Minh Thong Lee**, (Konkuk University, South Korea) who presented “Revealing the importance of SLA-DRB1 to post-weaning piglet survivability by a case-control analysis and subsequent validation using in silico epitope binding analysis and molecular structural modelling”.
- (iv) The third presentation was from **Danial Goszczynski** (Universidad Nacional de La Plata, Argentina) who described the “Differential proportion of ancestral MHC haplotypes in Brangus breed”.

(v) The fourth presentation was from **Sam Ho** (Gift of Life, Michigan, USA) who presented an update from the Swine MHC nomenclature committee “The Swine Leukocyte Antigen (SLA) Nomenclature System of the International Society for Animal Genetics (ISAG) and the International Union of Immunological Societies (IUIS): Update 2016.

(vi) The fifth presentation was from **Mehmet Cinar** (Washington State University, USA) who described the Ovar-DRB1 *0404 haplotype and its association with growth and lifetime prolificacy traits in ewes.

(vii) In the sixth and last presentation before the coffee break **Keith Ballingall** (Moredun Research Institute, Edinburgh, UK) presented an analysis of class II MHC DRB diversity in the endangered Red squirrels of the UK and compared levels of diversity with those animals from Continental Europe.

(viii) The invited plenary presentation was provided by Professor **Steven Marsh**, Director of Bioinformatics at the Anthony Nolan Research Institute, London where he leads the HLA-informatics group. He is also Professor of Immunology at University College London and Chair of the WHO nomenclature committee for HLA and KIR. Professor Marsh described the origins and latest developments with the immunopolymorphism database (IPD-MHC). This public resource provides a centralized repository for validated sequences of the MHC from a large number of different species. IPD-MHC has recently benefited from significant BBSRC funding which will allow its capabilities to be updated, improved and expanded to include additional species. The rebuilt website (<http://www.ebi.ac.uk/ipd/mhc/index.html>) will become publically available by the end of 2016.

(ix) The seventh presentation was provided by **Chankyu Park**, (Konkuk University Seoul, South Korea) in which he described the duplication of the beta-2 microglobulin gene in arteodactyla and the maintenance of this functional duplication only in pigs.

(x) In the eighth presentation **Bonnie Mallard** (University of Guelph, Canada) described the accuracy of imputation in the highly polymorphic MHC region of the cattle genome. The results showed a low prediction rate of imputation for the MHC compared with other loci within the bovine genome.

(xi) In the final presentation **Keith Ballingall** (Moredun Research Institute, Edinburgh, UK) presented an overview of the degree of functional allelic diversity at the class I loci in sheep using a combination of RT-PCR, cloning and Sanger sequence analysis.

2. General discussion on how the IPD-MHC database deals with next generation sequence data.

Background: with the power of next generation sequence based MHC genotyping approaches to produce large amounts of novel allelic data the question is how do the nomenclature committees and the IPD-MHC database deal with it.

Discussion: The HLA nomenclature committees deal with similar problems. A single validated sequence is required rather than splicing small fragments together. PAC Bio

sequencing technology which produces longer single sequences is preferred. While the final requirements are the responsibility of individual species curators, small fragments of single exons are unlikely to be sufficient to provide an official nomenclature. When longer sequence is provided there are no reasons why an official name cannot be assigned.

3. The committee business meeting was attended amongst others by Keith Ballingall, (Chair), Joan Lunney (Treasurer of VIC), Chris Davies (committee member and former Chair), Claire Rogel-Gaillard, Steven Marsh, Sam Ho, Tomas Bergstrom, Dirk Werling, and Sabine Hammer.
 - The contribution of John Hammond, (The Pirbright Institute, UK) in leading the successful application to BBSRC to fund the development of the IPD-MHC database is gratefully acknowledged.
 - KB to draft a comparative MHC committee report for publication detailing changes to IPD-MHC, nomenclature updates and species reports.
 - Sam Ho and Chris Davies to act as ISAG contacts in addition to the Chair.

Election of new committee members

- Keith Ballingall agreed to continue as Chair of the Comparative MHC Nomenclature committee until 2019
- Tomas Bergström, (Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden), was nominated, seconded and duly elected to serve on the committee.

Committee members (the new committee)

Chair Keith Ballingall term of service to 2019, E mail, keith.ballingall@moredun.ac.uk

The committee composition remains essentially the same with rolling appointments for species specific IPD-MHC curators along with a number of new members.

Keith Ballingall Chair & Ovine
Term of service rolling until 2019
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Other members / IPD-MHC curators

Chak-Sum (Sam) Ho, Chair of the SLA nomenclature committee
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New member

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