ISAG Conference 2004, Tokyo

Comparative MHC Nomenclature Committee

Report on ISAG Comparative MHC Nomenclature Committee workshop held at the International Veterinary Immunology Symposium, July 2004

The aims of this workshop were to give a brief overview of the committee, including a description of the new IPD/MHC database, and to provide a forum for discussion of issues relating to MHC nomenclature, including methods for discriminating MHC alleles in a range of species. The workshop was chaired by Shirley Ellis (Institute for Animal Health, Compton, UK) and Lorna Kennedy (Centre for Integrated Genomic Medical Research, Manchester, UK). It was announced that this ISAG committee is now also affiliated to the Veterinary Immunology Committee (VIC) of the International Union of Immunological Societies (IUIS).

The first presentation was a report from the committee, given by S. Ellis and L. Kennedy. Current membership of the committee is: S. Ellis, L. Kennedy, C. Davies, D. Smith, J. Kaufman, S. Marsh. Species currently included are dog, cat, pig, cattle, horse and chicken. The aims of the committee were briefly described: to establish a common 'framework' and guidelines for MHC nomenclature in any species; to demonstrate this in the form of a database that will ensure that in the future researchers can easily access a source of validated MHC sequences for any species; to facilitate discussion on this area between existing groups / nomenclature committees.

Some time was spent describing the new Immuno Polymorphism Database (IPD). This was established in 2003 to provide a centralised system for the study of polymorphism in genes of the immune system. It was set up by individuals at the Anthony Nolan Research Institute and the European Bioinformatics Institute. The MHC section of the database operates by publishing the work of established MHC nomenclature committees in a standardised format, allowing many related species to be grouped together. 'Validation' and naming of new alleles will be carried out by an individual / committee for each species, who will also be responsible for submitting the sequences to the database. The database currently includes MHC sequences from canines, felines, cattle and non-human primates. Pigs will be added in the near future.

Establishment of rules for naming alleles was discussed, and while it was generally accepted that each species committee could act independently, it was felt that some level of standardisation would be helpful. Human MHC nomenclature rules were being followed up to a point – the main difficulty was in deciding how to 'group' alleles, in order to assign the allele name. There were clearly a number of options, for example each allele can be given a unique number, alleles can be considered different if there are any changes in the peptide-binding region, or alleles can be grouped according to serological specificity. It seems likely that each species committee will reach their own conclusions regarding this issue, and it was felt that this was acceptable, as long as the rules being followed were clearly described in the appropriate species section of the IPD MHC database.

Locus assignment of alleles is clearly a common problem, most often within class I. This may be due to a number of features such as variable MHC haplotype configurations, interlocus recombination, and insufficient sequence / mapping data. It was agreed that this need not delay official naming of alleles, which was seen to be a priority for alleles placed on IPD, and that the best option would be to name in a single series, as was done for human MHC prior to allocation of alleles to HLA-A, B or C. In addition, this would allow some alleles to be assigned to a locus, and others to remain unassigned.

The remainder of the workshop was taken up with brief presentations from invited speakers on the subject of MHC typing methods in use or under development.

C. Davies: development of a microarray system for MHC typing of cattle.
Doug Smith: use of PCR-SSP to MHC type pigs
D. Miltiadou: use of PCR / sequencing to analyse MHC class I in sheep
M. Stear: use of microsatellite typing and sequencing to analyse class II in sheep
L. Kennedy: development of RSCA to type MHC class II in dog and cat
S. Ellis: development of RSCA to MHC class I type cattle
P. Lunn: use of IEF to study MHC class I in horses
B. Tallmadge: study of MHC genes in the horse by genome analysis

The committee have agreed to maintain contact primarily by e-mail. Efforts will be made to create more IPD sections to include additional species by approaching key workers in the relevant fields e.g. fish MHC. The committee will encourage individual species representatives to continue to work on their IPD section by, for example, adding text explaining nomenclature, review articles, reference lists and links to other sites. In addition it is considered a priority to replace local allele names as soon as possible, to make full use of the site less problematic. The committee will continue to discuss the possibility of publishing a paper publicising the IPD resource.

Shirley Ellis - September 6th 2004