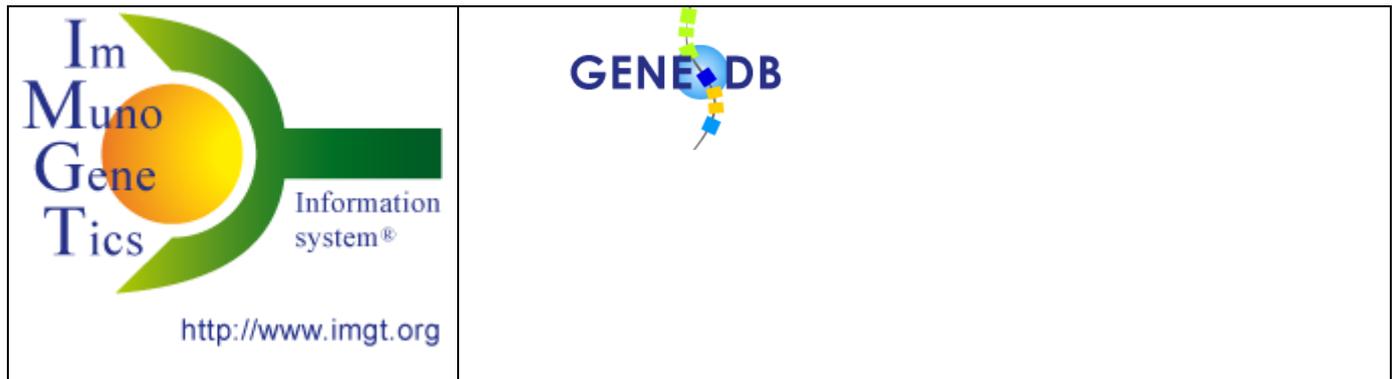


## 2013- Report for the 61<sup>st</sup> IUIS Council Meeting, August 22, Milan, Italy



### **Immunoglobulins (IG), T cell Receptors (TR) and Major Histocompatibility (MH) Nomenclature Sub-Committee**

Chair: Marie-Paule Lefranc (Marie-Paule.Lefranc@igh.cnrs.fr)

Université Montpellier 2

Web page: [www.imgt.org](http://www.imgt.org)

The goal of this Sub-Committee and IMGT-NC is the standardization of the immunoglobulins (IG), T cell receptors (TR) and major histocompatibility (MH) genes and alleles from any vertebrates from fish to humans.

1) Three new members, Felix Breden and Jamie Scott both from Vancouver (Canada) and Corey T. Watson from New York (USA) joined the Sub-Committee during the year. The other members remained unchanged.

2) In June 2013, IMGT/GENE-DB, the IMGT® gene database contained 3,081 IMGT genes and 4,687 alleles from 17 species.

- 694 IG and TR genes and 1,420 alleles for *Homo sapiens*
- 868 IG and TR genes and 1,1318 alleles for *Mus musculus*.

Standardized rules for the description of MH class I (MH1) and MH class II (MH2) from any vertebrate from fish to mammals were established last year and used for creating the nomenclature of MH1 and MH2 genes of *Onchorhynchus mykiss*. Seven MH genes and 237 alleles were entered in IMGT/GENE-DB (4 MH1 genes and 91 alleles and 3 MH2 genes and 146 alleles). This nomenclature proves its usefulness, it is highly standardized and easy to

apply and can be used for any species. It considerably simplifies the field as MH1 and MH2 are used systematically in the gene names and replaces ‘MHC class I’ and MHC class II’ when referring to the sequences, genes and tridimensional structures. MH-like genes are not included in the MH nomenclature, instead they are part of the related proteins of the immune system (RPI) in the RPI-MH1Like group.

Genes and alleles (and subgroups for IG and TR) are systematically associated to a species, for example *Homo sapiens* IGHV1 subgroup, *Homo sapiens* IGHV1-2 gene, *Homo sapiens* IGHV1-2\*01 allele, *Oncorhynchus mykiss* MH1-A gene, *Oncorhynchus mykiss* MH2-DB1\*01 allele. When abbreviated names are necessary (e.g., in tables or figures, the 6-letter format (3 first letters from the genus name and 3 first letters from the species name) is used: Homsap (for *Homo sapiens*), Oncmyk (for *Oncorhynchus mykiss*) with the full name indicated in the legend.

3) The IMGT booklet (11 papers, 144 pages) edited by Cold Spring Harbor Protocols (CSHP) has been largely publicized by the Sub-Committee (the content of this booklet was detailed in the 2012 Sub-Committee report). CSHP specifically edited the IMGT booklet for educational purposes and authorized IMGT® to have it freely available on the IMGT® site <http://www.imgt.org> (available in 'IMGT References'). CSHP also authorized that the IMGT booklet be printed and distributed freely. IMGT® databases and tools described in these chapters use the WHO/IUIS/IMGT nomenclature approved by Human Genome Organization (HUGO) Nomenclature Committee (HGNC).

4) IMGT/HighV-QUEST, a web portal created in October/November 2010, is currently the only online tool freely available for academics for the analysis of Next Generation Sequencing (NGS) data for the study of repertoires of immunoglobulins and T cell receptors in normal and pathological situations (150.000 sequences per batch; statistical analysis up to 450.000 sequence results). IMGT/HighV-QUEST promotes the use of the WHO/IUIS/IMGT IG and TR nomenclature for genes and alleles.

5) Perspectives for next year: 2014 will mark the 25 years of IMGT®, the international ImMunoGeneTics information system® (<http://www.imgt.org>), creation of which in New Haven in 1989, was at the origin of immunoinformatics.

Celebrations and events will be organized to promote IMGT® standardization, based on the IMGT-ONTOLOGY concepts of identification (standardized keywords), description (standardized labels), classification (gene and allele nomenclature) and numerotation (IMGT unique numbering and IMGT Collier de Perles). These concepts have been crucial in the development of immunoinformatics which are more necessary than ever in immune repertoire NGS studies.

Montpellier, July 07, 2013