

2014- 62nd IUIS Council Meeting, November 30, 2014, Nairobi, Kenya

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

Chair: Marie-Paule Lefranc (Marie-Paule.Lefranc@igh.cnrs.fr)
Université de Montpellier (France)
Institut de Génétique Humaine IGH, UPR CNRS 1142
Web page: www.imgt.org

List of subcommittee members

Donald Capra (USA)
Max Cooper (USA)
Tasuku Honjo (Japan)
Leroy Hood (USA)
Gérard Lefranc (France)
Marie-Paule Lefranc (France)
Fumihiko Matsuda (Japan)
Hans Zachau (Germany)
Cynthia L. Baldwin (USA)
Eva Bengtén (USA)
Pierre Boudinot (France)
Felix Breden (Canada)
Salvatrice Ciccarese (Italy)
Deborah Dunn-Walters (UK)
Jean-Pol Fripiat (France)
Véronique Giudicelli (France) +
Evelyne Jouvin-Marche (France)
Sophia Kossida (Greece) +
Véronique Laurens (France)
Serge Muyldermans (Belgium)
Jamie Scott (Canada)
Bettina Wagner (USA)
Corey T. Watson (USA)

+ new members. Two new members, Véronique Giudicelli (France) and Sophia Kossida (Greece) joined the Sub-Committee during the year. The other members remained unchanged.

I. Objective

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.

II. Recent Accomplishments

1) In August 2014, IMGT/GENE-DB, the IMGT® gene database contained 3,279 IMGT genes and 4,902 alleles from 21 species.

- 710 IG and TR genes and 1,438 alleles for *Homo sapiens*,
- 321 IG and TR genes and 368 alleles for *Macaca* (312 genes and 353 alleles for *Macaca mulatta*),
- 889 IG and TR genes and 1,342 alleles for *Mus* (868 genes and 1318 alleles for *Mus musculus*),
- 560 IG and TR genes and 564 alleles for *Rattus norvegicus*.

Other statistics are available at <http://www.imgt.org/genedb/stats>.

2) 2014 marks 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. A publication in *Frontiers in Immunology*, invited by the WHO/IUIS Nomenclature Committee, retraces the development on the immunoglobulin and T cell receptor genes
<http://journal.frontiersin.org/Journal/10.3389/fimmu.2014.00022/abstract>

III. Ongoing Projects

1) Collaboration with HGNC, Vega, Ensembl, NCBI.

- 2) Addition of reciprocal links to IUPHAR-DB and to IEDB.
- 3) Diffusion of the IMGT booklet (11 papers, 144 pages) edited by Cold Spring Harbor Protocols (CSHP). 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, the web portal created in October/November 2010, and 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 now accept 500.000 sequences per batch. IMGT/HighV-QUEST promotes the use of the WHO/IUIS/IMGT IG and TR nomenclature for genes and alleles.

III. Future directions

IG, TR and MH standardized nomenclature 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) have been crucial in the development of immunoinformatics.

These concepts are more necessary than ever in large scale genome sequencing, immune repertoire NGS studies and antigen receptor biotechnology for immunotherapy. Future directions consist in promoting WHO/IUIS/IMGT nomenclature for new data originating from genome analysis, repertoire next generation sequencing and antibody engineering.

Montpellier, September 01, 2014