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Nomenclature Committee on the Immunoglobulins (IG), T cell Receptors (TR) and Major Histocompatibility (MH)

Chair

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List of members of the committee

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Previous member

Donald Capra (USA) Founding member (died on February 24, 2015)

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 with jaws (*gnathostomata*) from fishes to humans.

II. Recent Accomplishments

1) In September 2015, IMGT/GENE-DB, the IMGT® gene database contained 3,570 IMGT genes and 5,267 alleles from 22 species.

- 718 IG and TR genes and 1,478 alleles for *Homo sapiens*,
- 487 IG and TR genes and 544 alleles for *Macaca* (478 genes and 529 alleles for *Macaca mulatta*),
- 890 IG and TR genes and 1,343 alleles for *Mus* (869 genes and 1319 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 marked 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> (3,214 views in September 2015).

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, accepts 500.000 sequences per batch and one million sequences for statistical analysis. A novel functionality 'identification and characterization of IMGT clonotypes (AA)' is based on the IG and TR gene and allele names. 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. We are currently developing the concept of localization to annotate and manage the copy number variations (CNV) and polymorphisms by insertion/deletion in the *Homo sapiens* IG and TR loci.

These concepts are necessary more 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 28, 2015