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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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Sofia Kossida (France)
Véronique Laurens (France)
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Bettina Wagner (USA)
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Previous member

Donald Capra (USA) Founding member (1937-2015)

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) On August 10, 2016, IMGT/GENE-DB, the IMGT® gene database contained 3,925 IMGT genes and 5,267 alleles from 23 species.

- 462 IG and 249 TR genes and 1,474 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) The publication in Frontiers in Immunology, invited by the WHO/IUIS Nomenclature Committee, Lefranc M-P. Immunoglobulin (IG) and T cell receptor genes (TR): IMGT® and the birth and rise of immunoinformatics. *Front Immunol.* 2014 Feb 05;5:22.

<http://journal.frontiersin.org/Journal/10.3389/fimmu.2014.00022/abstract> has reached 4,732 views on August 10, 2016.

III. Ongoing Projects

- 1) Collaboration with HGNC, Vega, Ensembl, NCBI.
- 2) 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).

IV. Challenges and opportunities in 2016

1) IMGT/HighV-QUEST and IMGT/StatClonotype for NGS

IMGT/HighV-QUEST, <http://www.imgt.org/HighV-QUEST/login.action> 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/StatClonotype, <http://www.imgt.org/StatClonotype/> is an IMGT® tool for statistical analysis of sets from IMGT/HighV-QUEST output, on the Web since June 2016. IMGT/StatClonotype uses a generic statistical procedure for identifying significant changes in IG and TR differences of proportions of IMGT clonotypes (AA) diversity and expression..

IMGT/HighV-QUEST and IMGT/StatClonotype use the IUIS/IMGT/HGNC IG and TR nomenclature for genes and alleles, based on IMGT-ONTOLOGY and the IMGT standards in immunoinformatics.

2) Large scale genome sequencing

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 IUIS/IMGT/HGNC nomenclature for new data originating from genome analysis, repertoire next generation sequencing and antibody engineering.

V. Selected recent publications derived from the work of the committee

Yu GY, Mate S, Garcia K, Ward MD, Brueggemann E, Hall M, Kenny T, Sanchez-Lockhart M, Lefranc M-P, Palacios G.

Cynomolgus macaque (*Macaca fascicularis*) immunoglobulin heavy chain locus description. Immunogenetics. 2016 Jul;68(6-7):417-28. doi: 10.1007/s00251-016-0921-2. Epub 2016 May 27. [PMID: 27233955](#) LIGM:453

Boudinot P, Mondot S, Jouneau L, Teyton L, Lefranc M-P, Lantz O.

Restricting nonclassical MHC genes coevolve with TRAV genes used by innate-like T cells in mammals. Proc Natl Acad Sci U S A. 2016 May 24;113(21):E2983-92. doi: 10.1073/pnas.1600674113. Epub 2016 May 11. [PMID: 27170188](#) LIGM:452

Aouinti S, Malouche D, Giudicelli V, Kossida S, Lefranc M-P.

IMGT/HighV-QUEST statistical significance of IMGT clonotype (AA) diversity per gene for standardized comparisons of next generation sequencing immunoprofiles of immunoglobulins and T cell receptors. PLoS ONE. 2015 Nov 5;10(11):e0142353. doi: 10.1371/journal.pone.0142353. eCollection 2015. [Free Article](#) PMID: [26540440](#) Correction: PLoS ONE 2016 Jan 5;11(1): e0146702. doi: 10.1371/journal.pone.0146702 [View correction](#). PMID: [26731095](#). LIGM:450

Piccinni B, Massari S, Caputi Jambrenghi A, Giannico F, Lefranc M-P, Ciccarese S, Antonacci R. Sheep (*Ovis aries*) T cell receptor alpha (TRA) and delta (TRD) genes and genomic organization of the TRA/TRD locus. BMC Genomics. 2015 Sep 18;16(1):709. doi: 10.1186/s12864-015-1790-z. [Open access](#). PMID: [26383271](#) LIGM:449

Lefranc M-P.
Antibody informatics: IMGT®, the international ImMunoGeneTics information system®, the international ImMunoGeneTics information system®
Microbiol Spectrum 2014, 2(2):AID-0001-2012. doi:10.1128/microbiolspec.AID-0001-2012. LIGM:430

Lefranc M-P.
Immunoglobulin (IG) and T cell receptor genes (TR): IMGT® and the birth and rise of immunoinformatics.
Front Immunol. 2014 Feb 05;5:22. doi: 10.3389/fimmu.2014.00022. [Open access](#). PMID: [24600447](#)
LIGM:429

Ciccarese S, Vaccarelli G, Lefranc M-P, Tasco G, Consiglio A, Casadio R, Linguiti G, Antonacci R. Characteristics of the somatic hypermutation in the *Camelus dromedarius* T cell receptor gamma (TRG) and delta (TRD) variable domains.
Dev Comp Immunol. 2014 May Oct;46(2):300-313. doi: 10.1016/j.dci.2014.05.001. Epub 2014 May 13. PMID: [24836674](#) LIGM:432

Giudicelli V, Duroux P, Lavoie A, Aouinti S, Lefranc M-P, Kossida S.
From IMGT-ONTOLOGY to IMGT/HighV-QUEST for NGS immunoglobulin (IG) and T cell receptor (TR) repertoires in autoimmune and infectious diseases.
Autoimmun Infect Dis. 2015 Aug 10. 1(1): doi: 10.16966/aidoa.103. [Free Article](#). LIGM:448

Xochelli A, Agathangelidis A, Kavakiotis I, Minga E, Sutton LA, Baliakas P, Chouvarda I, Giudicelli V, Vlahavas I, Maglaveras N, Bonello L, Trentin L, Tedeschi A, Panagiotidis P, Geisler C, Langerak AW, Pospisilova S, Jelinek DF, Oscier D, Chiorazzi N, Darzentas N, Davi F, Ghia P, Rosenquist R, Hadzidimitriou A, Belessi C, Lefranc M-P, Stamatopoulos K.
Immunoglobulin heavy variable (IGHV) genes and alleles: new entities, new names and implications for research and prognostication in chronic lymphocytic leukemia.
Immunogenetics. 2015 67(1):61-6.doi: 10.1007/s00251-014-0812-3. Epub 2014 Nov 12. PMID: [25388851](#) LIGM:442

Lefranc M-P.
Immunoglobulins: 25 years of Immunoinformatics and IMGT-ONTOLOGY.
Biomolecules. 2014, 4(4), 1102-1139; doi:10.3390/biom4041102 [Open access](#). PMID: [25521638](#)
LIGM:440

Lefranc M-P.
IMGT® immunoglobulin repertoire analysis and antibody humanization.
In: Alt, F.W, Honjo, T, Radbruch A. and Reth, M. (Eds.), Molecular Biology of B cells, Second edition, Academic Press, Elsevier Ltd, London, UK, Chapter 26, 2014, pp. 481-514. [dx.doi.org](#), ISBN : 978-0-12-397933-9. LIGM:438

Montpellier, August 10, 2016