IMGT[®] genomic annotation of the dog (*Canis lupus familiaris*) seven immunoglobulin (IG) or antibody and T cell receptor (TR) loci

Imène Chentli*, Perrine Pégorier*, Saida Saljoqi*, Géraldine Folch, Joumana Jabado-Michaloud, Véronique Giudicelli, Patrice Duroux, Sofia Kossida and Marie-Paule Lefranc *Equal contribution

IMGT[®], the international ImMunoGeneTics information system[®], Laboratoire d'ImmunoGénétique Moléculaire (LIGM), Institut de Génétique Humaine (IGH), UMR 9002 CNRS-UM, Université de Montpellier (UM), Montpellier (France)

IMGT[®], the international ImMunoGeneTics information system[®], http://www.imgt.org [1], is the global reference in immunoinformatics [2], founded in 1989 by Marie-Paule Lefranc at Montpellier (Université de Montpellier and CNRS). IMGT[®] is a high-quality integrated knowledge resource specialized in the immunoglobulins (IG) or antibodies, T cell receptors (TR), major histocompatibility (MH) of human and other vertebrate species, and in the immunoglobulin superfamily (IgSF), MH superfamily (MhSF) and related proteins of the immune system (RPI) of vertebrates and invertebrates.

The genome of the vertebrates with jaws (Gnathostomata), which appeared in the evolution about 450 million years ago, includes the IG, TR and MH genes characteristic of the adaptive immune repertoires. Currently, there are 244 annotated vertebrate genomes including 112 from mammals at NCBI.

In humans and other mammals, there are seven main loci for IG and TR: three for IG (IGH, IGK and IGL) and four for TR (TRA, TRB, TRD and TRG). IMGT[®] genomic annotated data are classically displayed in IMGT Repertoire Web Resources (Locus description, Locus representation, Gene tables, Alignments of alleles). So far the number of species present in the IMGT Web Resources reaches 40, however only two species, Homo sapiens and Mus musculus, have been fully annotated for their seven antigen receptor loci. The seven IG and TR loci of the dog (Canis lupus familiaris) were recently described [3]. The dog represents the first species for which the seven antigen receptor (IG and TR) loci are annotated simultaneously in IMGT[®]. The biocuration was performed on the loci extracted from genome assembly. Six hundred thirty-three genes (413 IG and 220 TR genes were identified in the seven loci spanning more than 6.15 megabases (Mb) and were fully annotated. This biocuration has been perfomed manually and the standardized annotation has allowed data entry in IMGT/UEST [6], IMGT/HighV-QUEST [7] and IMGT/DomainGapAlign [8]).

[1] Lefranc M.-P. et *al*. Nucl. Acids Res. 43:D413-422 (2015) PMID: 25378316 [5] Giudicelli V. et al. Nucl. Acids Res. 33:D256-261 (2005) PMID: 15608191

[2] Lefranc M.-P. Front. Immunol. 5:22 (2014) PMID: 24600447 [6] Brochet X. et al. Nucl. Acids Res. 36:W503-508 (2008) PMID: 18503082

[3] Martin J. et al. Immunogenetics. 70(4):223-336 (2018) PMID: 28924718 [7] Alamyar E. et al. Immunome Res. 8:1:2 (2012) PMID: 22647994

[4] Giudicelli, V. et al., Nucl. Acids Res. 34:D781-D784 (2006) PMID: 16381979 [8] Ehrenmann F. et al. Nucl. Acids Res. 38:D301-307 (2010) PMID: 19900967

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Information

system®

http://www.imgt.org





Each locus sequence is





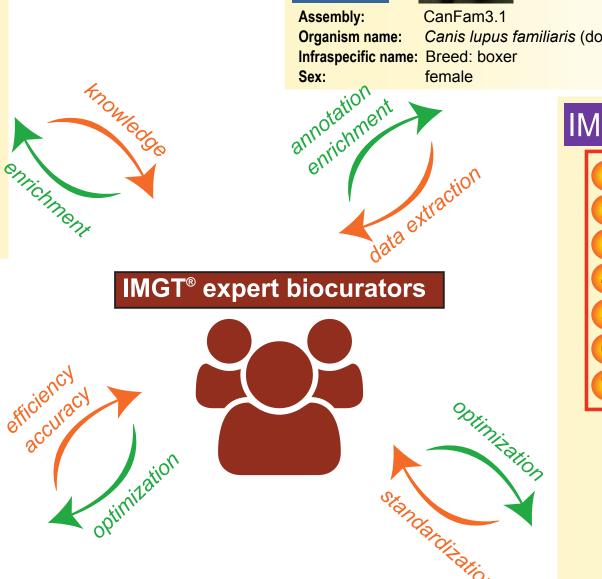
- MGT/LIGM-DB: IMGT[®] nucleotide database that includes 179,171 genomic and cDNA sequences of IG and TR from 351 species (June 2018).
- IMGT/GENE-DB: IMGT[®] genome database that includes 5,120 IG and TR genes and 7,070 alleles from 26 species (June 2018).
- IMGT/V-QUEST: is an integrated system for IG and TR standardized V-J and V-D-J rearranged sequence analysis.

etc, ...

Internal tools

Internally developed, proprietary IMGT[®] research tools:

- IMGT/LIGMotif: annotation of genomic sequences of IG and TR loci.
- IMGT/Automat: annotation of cDNA sequences of IG and TR loci.
- IMGT/NtiToVald: automatical control of data for consistency and relevance.



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NCBI

	localized on the corresponding							
P/	chromosome	and	extracted					
0.	from NCBI.							
am3.1								
s lupus f	<i>amiliaris</i> (dog)							

IMGT-ONTOLOGY

IMGT-ONTOLOGY axioms and concepts, 1 IDENTIFICATION bridge the gap between genes, sequences 2 DESCRIPTION and three-dimensional structures. 3 CLASSIFICATION IMGT-ONTOLOGY includes a controlled vocabulary and annotation rules which are 4 NUMEROTATION indispensable to ensure accuracy, 5 LOCALIZATION consistency and coherence in IMGT[®]. 6 ORIENTATION Prototypes

7 OBTENTION V-GENE L-V-GENE-UNIT V-EXON V-RS V-REGION -INTRON 3'V-REGION V-SPACE CDR2-IMGT CDR1-IMGT CDR3-IMGT IMGT[®] standardized labels for the description of V-GENE.

IMGT[®] unique accession number

The orientation of the locus on the chromosome can be either forward (FWD) or reverse (REV). The REV locus sequences were placed in the 5' to 3' locus orientation. Each locus sequence was asigned to a unique IMGT[®] accession number and is available in IMGT/LIGM-DB.

IMGT000001	1	Canis lupus familiaris	Canis lupus familiaris (dog), taxon:9615, breed: boxer, assembly CanFam3.1, GenBank assembly ID: GCA_000002285.2, chromosome 8: CM000008.3 (72847279-74272075, complement), IGH locus.
IMGT000002	1	Canis lupus familiaris	Canis lupus familiaris (dog), taxon:9615, breed: boxer, assembly CanFam3.1, GenBank assembly ID: GCA_000002285.2, chromosome 17: CM000017.3 (37492784-37841916, complement), IGK locus.
IMGT000003	1	Canis lupus familiaris	Canis lupus familiaris (dog), taxon:9615, breed: boxer, assembly CanFam3.1, GenBank assembly ID: GCA_000002285.2, chromosome 26: CM000026.3 (25049458-27632798), IGL locus.
IMGT000004	1	Canis lupus familiaris	Canis lupus familiaris (dog), taxon:9615, breed: boxer, assembly CanFam3.1, GenBank assembly ID: GCA_000002285.2, chromosome 8: CM000008.3 (2209873-2953167), TRA/TRD locus.
IMGT000005	1	Canis lupus familiaris	Canis lupus familiaris (dog), taxon:9615, breed: boxer, assembly CanFam3.1, GenBank assembly ID: GCA_000002285.2, chromosome 16: CM000016.3 (6753902-7016410, complement), TRB locus.
IMGT000006	1	Canis lupus familiaris	Canis lupus familiaris (dog), taxon:9615, breed: boxer, assembly CanFam3.1 GenBank assembly ID: GCA_000002285.2, chromosome 18: CM000018.3 (11282571-11730442), TRG locus.

Immunoglobulins (IG): IGH, IGK & IGL

Locus description

The **413** dog IG genes are distributed on 3 loci, among 3 chromosomes: - IGH locus in REV orientation on chromosome 8 - IGK locus in REV orientation on chromosome 17 - IGL locus in FWD orientation on chromosome 26

- 89 IGHV genes belonging to 4 IGHV subgroups, 6 IGHD genes, 6 IGHJ genes and 5 IGHC genes on 1,425 kilobases (kb).
- ICK 22 IGKV genes belonging to 5 IGKV subgroups, 5 IGKJ genes

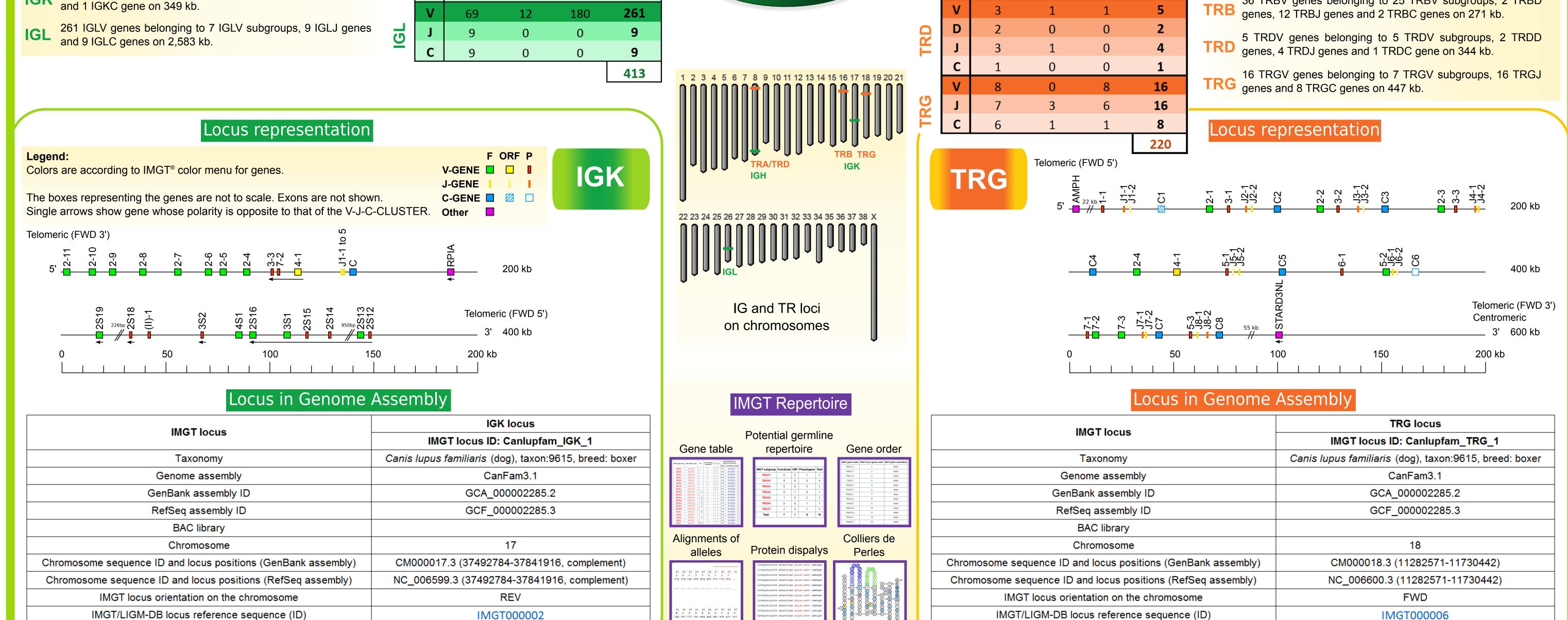
		F	ORF	Ρ	Total	Genes: 413
	V	36	2	51	89	Alleles: 416
IGH	D	5	1	0	6	
Y	J	5	1	0	6	
	С	4	1	0	5	IG 413
	V	13	1	8	22	413
IGK	J	4	1	0	5	
_	С	1	0	0	1	

T cell receptor (TR): TRA, TRB, TRD & TRG

Genes: 220			F	ORF	Р	Total
Alleles: 221	RA	V	34	0	22	56
		J	40	12	7	59
TR 220	- E	С	1	0	0	1
220		V	22	1	13	36
	TRB	D	2	0	0	2
		J	9	2	1	12
		С	2	0	0	2

Locus description

The **220** dog TR genes are distributed on 4 loci, among 3 chromosomes: - TRA/TRD loci in FWD orientation on chromosome 8 - TRB locus in REV orientation on chromosome 16 - TRG locus in FWD orientation on chromosome 18 56 TRAV genes belonging to 30 TRAV subgroups, 59 TRAJ TRA genes and 1 TRAC gene on 743 kilobases (kb). 36 TRBV genes belonging to 25 TRBV subgroups, 2 TRBD

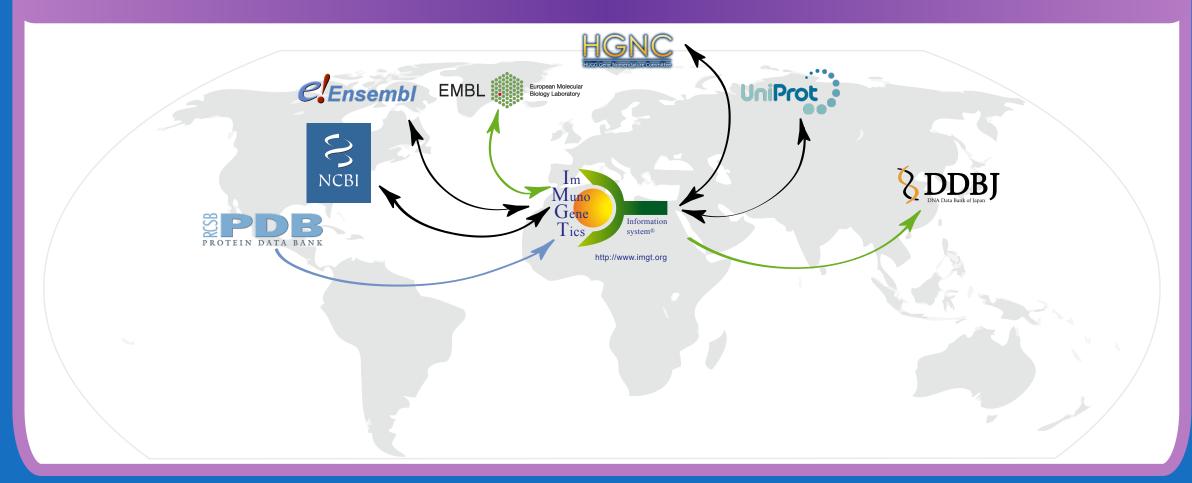


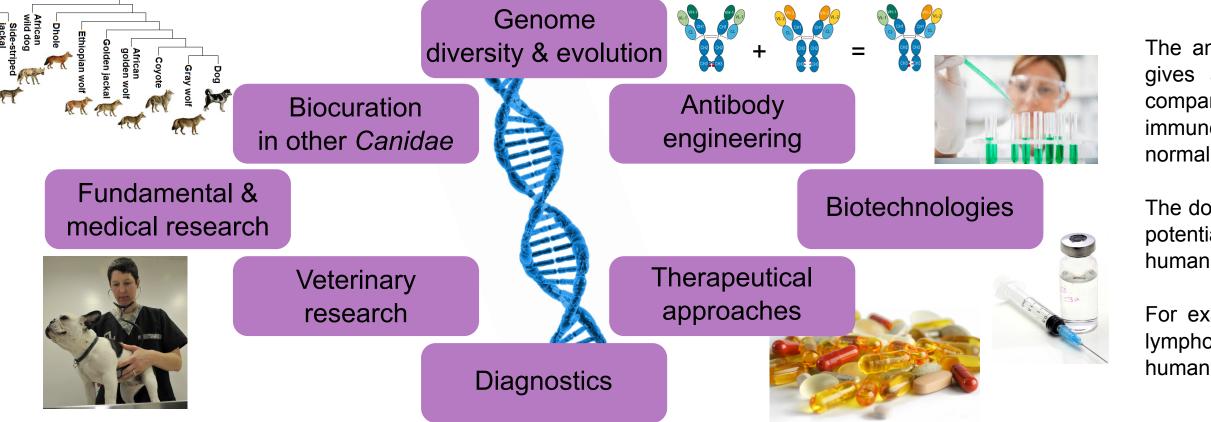


Dog repertoire: a model for veterinary and human medicine

External links

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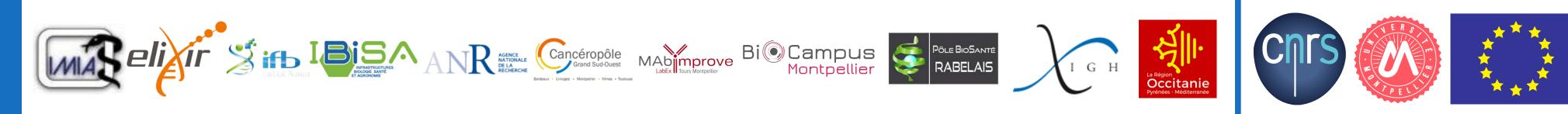


The annotation of the seven dog loci gives access to the study and the comparison of the expressed adaptive immune repertoires in veterinary normal and pathological situations.

The dog offers a unique opportunity for potential applications in veterinary and human medicine.

For example, the treatment of canine lymphoma has been predictive of the human response to that treatment

IMGT[®] founder and executive director emeritus: Marie-Paule Lefranc (Marie-Paule.Lefranc@igh.cnrs.fr) **IMGT**[®] **director**: Sofia Kossida (Sofia Kossida@igh.cnrs.fr) **Bioinformatics manager:** Véronique Giudicelli (Veronique.Giudicelli@igh.cnrs.fr) **Computer manager:** Patrice Duroux (Patrice.Duroux@igh.cnrs.fr) Corresponding authors: Imène Chentli (Imene.Chentli@igh.cnrs.fr), Perrine Pégorier (Perrine.Pegorier@igh.cnrs.fr) & Saïda Saljoqi (Saida.Saljoqi@igh.cnrs.fr)



Dog

Human

220 244

TR

IG