Capra hircus and Ovis aries IGK loci: simultaneous annotation in IMGT®

Viviane Nguefack Nguene*, Morgane Bertignac*, Jourmana Jabado-Michaloud, Géraldine Folch, Sofia Kossida, Marie-Paule Lefranc

*Corresponding author

IMGT®: the international IMmunoGeneTics information system®, Laboratoire d'Immunogénétique Moléculaire (IGSM), Institut de Génétique Humaine (IGH), UMR 3002 CNRS-UM, Université de Montpellier (UM), Montpellier (France)

IMGT®, the international IMmunoGeneTics information system®, http://www.imgt.org® (1), is the global reference in immunogenetics and 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 (Gnathostoma), which appeared in the evolution about 450 million years ago, includes the IG, TR, and MH genes characteristic of the adaptive immune repertoires (2). In humans and other mammals, there are seven main loci for IG and TR: three for IG (IGH, IGL 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, Alignment of alleles).

The IG are B cell antigen receptors, expressed at the membrane of the B cells or secreted by plasma cells, and characterized by the high diversity of their binding specificities. Classically IG proteins comprise two identical heavy chains (H) associated with two identical light chains (L) which belong, in higher vertebrates, to two chain types, kappa (IGK) or lambda (IGL). Several variable (V), diversity (D) (only present in the IGK locus), joining (J) and constant (C) genes compose the IGK, IGD and IGL loci. The IGK biosynthesis requires the recombination of these genes (2) and is the result of these complex mechanisms of V(D)J rearrangements and functional N-diversity and, for the IGK somatic mutations which creates the IGK high diversity.

The IG loci have so far been explored in only a limited number of species. Indeed these loci are difficult to annotate owing to their multigene organization of highly similar genes and their biocuration requires a reliable and high quality locus assembly. The genomes of different ruminant species start becoming available, and among them, those of the domestic goat (Capra hircus) (3) and of the sheep (Ovis aries).

IMGT® Capra hircus and Ovis aries IGK loci annotation pipeline

Data acquistion

IMGT®-ONTOLOGY & Prototypes

IMGT databases

IGK locus representation of Capra hircus and Ovis aries: a unique and common nomenclature

Protein display of IGKV genes: Capra hircus & Ovis aries

IMGT Collier de Perles: Caphir IGKV2-8 Oviar IGKV2-8

Hydrophobic amino acids and tryptophan (W), blue. Proline (P): yellow. The CDR-IMGT are limited by amino acids shown in squares, which belong to the neighbouring FR-IMGT. Arrows indicate the direction of the beta sheets and their different conformations in 3D structures. CDRI- IMGT (blue), CDRII-IMGT (green), CDRIII-IMGT (greenblue). C at position 23 (1st-CYS), W at position 41 (CONSERVED TRIP), letter of the conserved hydrophobic amino acid at position 89, and C at position 104 (2nd-CYS) are in red. Missing positions: hatched circles or squares

Interest of this study

Copyright 1998-2018 IMGT, the international IMmunoGeneTics information system®