

# A Report on Major Histocompatibility Complex

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## BRIEF REPORT

The Major Histocompatibility Complex (MHC) is a huge gene cluster on vertebrate DNA that codes for cell surface proteins required by the adaptive immune system. MHC molecules are the name for these cell surface proteins.

Because it was discovered through the investigation of transplanted tissue compatibility, this locus was given its name. Later research demonstrated that tissue rejection due to incompatibility is an experimental artefact obscuring the true function of MHC molecules, which is to bind an antigen originating from self-proteins or pathogens and bring it to the cell surface for detection by T-cells. MHC molecules regulate how leukocytes, commonly known as White Blood Cells (WBCs), interact with other leukocytes and body cells. The MHC determines organ donor compatibility as well as autoimmune disease risk through cross-reacting immunisation.

Protein molecules from the host's phenotype or from other biologic entities are constantly generated and destroyed in a cell. A tiny peptide (a molecular portion of a protein) called an epitope is displayed on the cell surface by each MHC molecule. Self-antigens are proteins that inhibit an organism's immune system from attacking its own cells. When pathogen-derived proteins are presented to the immune system, the infected cell is eliminated.

MHC self-antigens mediate diversity of self-antigen presentation in individuals in at least three ways: an organism's MHC repertoire is polygenic (through several, interacting genes); MHC expression is codominant (from both sets of inherited alleles). MHC gene variations are quite varied (diversely varying from organism to organism within a species). Male mice have been observed selecting females with various MHCs as mates, indicating sexual selection. There has also been evidence of antigenic peptide splicing, which can join peptides from different proteins, significantly expanding antigen diversity, at least for MHC I presentation.

All jawed vertebrates have the MHC locus, which is thought to have evolved around 450 million years ago. Despite the fact that the number of genes included in the MHC of different species varies, the overall structure of the locus is rather consistent. There are around a hundred genes and pseudogenes in a typical MHC, but not all of them are engaged in immunity. The MHC area is located on chromosome 6 between the flanking genetic markers MOG and COL11A2 (from 6 p 22.1 to 6 p 21.3 on the hg38 assembly, about

29 Mb to 33 Mb), and comprises 224 genes covering 3.6 mega base pairs (36,00,000 bases). About half of them have immunological roles that are known.

The HLA (human leukocyte antigen) complex is another name for the human MHC (often just the HLA). SLA (Swine Leukocyte Antigens), BLA (Bovine Leukocyte Antigens), DLA (Dog Leukocyte Antigens) and so forth. Historically, the MHC in mice has been referred to as the Histocompatibility System 2 (H-2), RT1 in rats and B-locus in chickens. All nucleated cells, as well as platelets, express MHC class I molecules—in other words, all cells except red blood cells. Killer T cells, also known as cytotoxic T lymphocytes, are presented with epitopes (CTLs). CD8 receptors, as well as T-cell Receptors (TCRs), are expressed by CTLs. When a CTL's CD8 receptor binds to an MHC class I molecule, and the CTL's TCR matches the epitope within the MHC class I molecule, the cell is programmed to die by apoptosis.

As a result, MHC class I contributes to cellular immunity, which is a key mechanism for combating intracellular pathogens such as viruses and bacteria like bacterial L forms, Mycoplasma, and Rickettsia. HLA-A, HLA-B, and HLA-C molecules make up MHC class I in humans.

Human HLA-A2, the first crystal structure of a Class I MHC protein, was reported in 1989. MHC-I molecules are heterodimers, with a polymorphic heavy-subunit whose gene is found inside the MHC locus and a tiny invariant 2 microglobulin subunit whose gene is normally found outside of it, according to the structure. The N-terminal extracellular portion of the polymorphic heavy chain of the MHC-I molecule is composed of three domains, 1, 2, and 3, a transmembrane helix to retain the MHC-I molecule on the cell surface, and a short cytoplasmic tail.

Two domains, 1 and 2, form a deep peptide-binding groove between two long  $\alpha$ -helices and an eight-stranded groove floor. The interaction with the CD8 co-receptor is mediated by the immunoglobulin-like domain 3. 2 microglobulin contributes to the stability of the complex and helps the CD8 co-receptor recognise the peptide-MHC class I complex. The peptide is kept by numerous pockets on the floor of the peptide-binding groove and is non-covalently attached to MHC-I. The central and largest region of the binding groove is filled with amino acid side chains that are most polymorphic in human alleles, whereas conserved side chains are grouped at the narrower ends.

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**Received:** September 06, 2021; **Accepted:** September 20, 2021; **Published:** September 27, 2021

**Citation:** Thirunahari A (2021) A Report on Major Histocompatibility Complex. J Biol Syst Open Access. 10:206.

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