Abstract

The major role of MHC class I molecules in adaptive system is to present antigen peptides derived from intracellular environment on the cell surface. These peptides are recognized by $CD8^+$ T-lymphocytes and they can also interact with NK cells via *trans*-interaction.

MHC class I molecules are composed of a heavy chain, β2-microglobulin (β2m, light chain) and peptide, forming a closed conformation. The heavy chain is non-covalently associated with the light chain and is folded into extracellular domain (α1, α2, α3 subunits), transmembrane domain and cytoplasmic domain (with conserved motifs). Upon active metabolism, the β2m and peptide may dissociate from the MHC I heavy chain what leads to the formation of open conformations of MHC I. This conformational change causes the subunit to unfold and allow its interaction with various receptors and molecules.

Open conformers of MHC I may form *cis*-interactions with themselves creating homodimers involved in immunological functions or they can associate with different receptors on the cell surface creating heterodimers responsible for non-immunological functions. Soluble forms of free heavy chains also exist outside of the cell surface. *Cis*-associations are very important as they influence signaling pathways of the cell, inhibition or activation of T-lymphocytes and NK cells or tumor escape from the immune system. However, the exact mechanism of the formation, expression, and function of open MHC I conformers is not completely understood. They can be detected in several oncological, autoimmune, and viral infectious diseases. They can be used as prognostic factors and the studying and understanding of their biological functions could contribute to understanding the origins of several diseases.

Key words: MHC I, open and closed conformations of MHC I, *cis*-interaction, $CD8^+$ T-lymphocytes, NK-cells