MS03-1-5 Structural insight into the salivary serpins of Ixodes ricinus
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Abstract
Serine protease inhibitors – serpins are one of the largest superfamilies of structurally conserved proteins that are widely distributed in nature [1]. They have many regulatory functions that make them one of the most studied protein families. Many serpins lost their inhibitory function during their evolution and work as chaperons or storage proteins. Serpins with protease inhibition function form covalent complexes with target protease [2]. This process leads to a suicide mechanism that inactivates the protease as well as serpin. The serpin inhibitory activity requires rearrangement of the conformation. The typical secondary structure is made of 3 β-barrels, 9 α-helices and an exposed, flexible reactive centre loop (RCL) that contains a proteinase recognition site. During crystallographic attempts, different types of conformation were solved and each of these structural rearrangements was important to understanding the inhibitory pathway. The successful process of serine proteinase inhibition results in an irreversible suicide substrate mechanism, by which serpin is covalently bound to the target protease [3].
Here are presented results of the X-ray structural analysis of four *Ixodes ricinus* serpins named Iripin-3, Iripin-5, Iripin-4, and Iripin-1. All of them help the tick in different ways to stay attached to the host for sufficient time for feeding necessary for reproduction and distribution of ticks by inhibiting the proteases involved in host immune defense responses to a tick bite. These serpins are mainly expressed in salivary glands and thus are present at the site of first contact with a host. This group of proteins has primarily immunological and haemostatic functions, but their functions can vary according to their specificity. The tick serpins act as modulators of immune responses by using their anti-coagulation, and anti-complementary functions and play role in immunosuppression [4]. Serpins are good candidates for drug development in combination with protein engineering.

References
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