

## Poster Presentation

BM.P26

### *Stacking Interactions mediate Recognition in Ribosome Inactivating Protein*

P. Kaur<sup>1</sup>, S. Yamini<sup>1</sup>, G. Kushwaha<sup>1</sup>, M. Sinha<sup>1</sup>, S. Sharma<sup>1</sup>, T. Singh<sup>1</sup>

<sup>1</sup>Department of Biophysics, All India Institute of Medical Sciences, New Delhi, India

Ribosome Inactivating Proteins (RIPs) are capable of inhibiting protein synthesis by catalytically hydrolyzing at specific purine residues from the sarcin / ricin loop of large ribosomal RNA. There are two types of RIPs: type 1 - RIPs (RIP-1) are single polypeptide chain proteins while type 2 - RIPs contain two polypeptide chains which are covalently linked by a disulphide bond. Studies have indicated that stacking interactions play a dominant role in the ligand binding to RIPs. However, the structural basis of these interactions with RIPs as well as the nature of stack pairing and associated molecular mechanisms are not clearly understood. In order to examine the significance of these stacking interactions and the role of various aromatic residues involved, we have carried out the structural analysis of the complexes of RIP-1 from *Momordica balsamina* (MbRIP-1) and crystallized it with six different sugar molecules, ribose, fucose, glucose, fructose, maltose and lactose. The crystals belong to hexagonal space group H3 with approximate cell dimension of  $a = b = 130 \text{ \AA}$ ,  $c = 40.5 \text{ \AA}$ . The r.m.s. deviation for the C $\alpha$  atoms in the complexed structures was found to be in the range of  $0.5 \text{ \AA}$  to  $0.9 \text{ \AA}$ . The aromatic rings of sugars are seen to be involved in stacking with aromatic rings of Tyr 70 and Tyr 111. The side chain torsion angles  $\chi_1$  and  $\chi_2$  of Tyr 70 in the complexes with ribose, fucose, glucose, fructose, maltose and lactose were found to be  $64^\circ / 161^\circ$ ,  $166^\circ / 86^\circ$ ,  $6^\circ / 172^\circ$ ,  $70^\circ / 167^\circ$ ,  $64^\circ / 161^\circ$  and  $-75^\circ / 178^\circ$  respectively. The sugars are held firmly in the binding site of RIP-1 with the help of stacking interactions and hydrogen bonds. The results presented here have revealed the significance of aromatic stack pairing and delineated the stabilizing role of tyrosine residue in these interactions.

**Keywords:** Ribosome Inactivating Protein, Stacking Interactions, sugars