

MS06-P06 | STRUCTURE AND FUNCTION OF *S. AUREUS* YABJ AS A NOVEL CHLORINATION-INDUCED RIBONUCLEASE

Kwon, Ae-Ran (Daegu Haany University, Gyungsan-City, KOR)

The characteristic fold of a protein is the decisive factor for its biological function. However, small structural changes to amino acids can also affect their function, for example in the case of post-translational modification (PTM). Many different types of PTMs are known, but for some, including chlorination, studies elucidating their importance are limited. A recent study revealed that the YjgF/YER057c/UK114 family (YjgF family) member RidA from *Escherichia coli* shows chaperone activity after chlorination. Thus, to identify the functional and structural differences of RidA upon chlorination, we studied an RidA homolog from *Staphylococcus aureus*: YabJ. The overall structure of *S. aureus* YabJ was similar to other members of the YjgF family, showing deep pockets on its surface, and the residues composing the pockets were well conserved. *S. aureus* YabJ was highly stable after chlorination, and the chlorinated state is reversible by treatment with DTT. However, it shows no chaperone activity after chlorination. Instead, YabJ from *S. aureus* shows chlorination-induced ribonuclease activity, and the activity is diminished after subsequent reduction. Even though the yabJ genes from *Staphylococcus* and *Bacillus* are clustered with regulators that are expected to code nucleic acid-interacting proteins, the nucleic acid-related activity of bacterial RidA has not been identified before. From our study, we revealed the structure and function of *S. aureus* YabJ as a novel chlorination-activated ribonuclease. The present study will contribute to an in-depth understanding of chlorination as a PTM.