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POSTER ABSTRACT PRESENTATIONS

SESSION TITLE: STRUCTURE OF VIRUSES AND CHAPERONINS

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Abstract P-32: Viral Chaperonins – New and Intriguing Group

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Background: Chaperones can bind nascent or misfolded proteins and assist them in properly attaining their functional conformations to maintain the cellular protein homeostasis (Skjærven *et al.*, 2015). According to gene family and structure, chaperonins are classified in two distantly related structural groups: Group I, found in bacteria and eukaryotic organelles, and Group II, expressed in Archaea and in eukaryotic cytosol.

Recently, putative GroEL-like chaperonins have been predicted in viruses of bacteria (bacteriophages). We have obtained, and characterized by various methods, including cryo-EM, two of the members of this group of proteins: gp (gene product) 146 from bacteriophage EL *Pseudomonas aeruginosa* (Kurochkina *et al.*, 2012) and gp246 from bacteriophage OBP *Pseudomonas fluorescens* (Semenyuk *et al.*, 2016).

All viral chaperonins are strikingly different in their architecture. While EL chaperonin acts as a double-ring structure, separating into two closed rings only in ADP-bound form (Molugu *et al.*, 2016), the recombinant OBP chaperonin represents a single heptameric ring. In this form, it can adopt various conformational states, representing different steps in its ATPase cycle. It is not excluded that the OBP chaperonin acts as a heptamer, which is consistent with previous findings that the single-ring mutant of GroEL represents an independent folding unit (Erbse *et al.*, 1999; Chatellier *et al.*, 2000).

Most recently described by us the new viral chaperonin, gp228 from bacteriophage AR9 *Bacillus subtilis*, was investigated by single particle EM. To our surprise, it seems to possess the structural features of both, OBP and EL, viral chaperonins. The AR9 chaperonin particles were distributed into two subpopulations, representing open single-ring and closed double-ring structures. These features may suggest the new mechanism of viral chaperonins functioning.

Conclusion: Unique and diverse structural and functional features of viral chaperonins imply that they might be considered as the new group.

Key Words: single particle cryo-electron microscopy • structure • viral chaperonin

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