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New insights on the feature and function of tail tubular protein B and tail fiber protein of the lytic bacteriophage φYeO3-12 specific for *Yersinia enterocolitica* serotype O:3.

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Streszczenie

For the first time, we are introducing TTPBgp12 and TFPgp17 as new members of the tail tubular proteins B (TTPB) and tail fiber proteins (TFP) family, respectively. These proteins originate from Yersinia enterocolitica phage φYeO3-12. It was originally thought that these were structural proteins. However, our results show that they also inhibit bacterial growth and biofilm formation. According to the bioinformatic analysis, TTPBgp12 is functionally and structurally similar to the TTP of Enterobacteria phage T7 and adopts a β-structure. TFPgp17 contains an intramolecular chaperone domain at its C-terminal end. The N-terminus of TFPgp17 is similar to other representatives of the TFP family. Interestingly, the predicted 3D structure of TFPgp17 is similar to other bacterial S-layer proteins. Based on the thermal unfolding experiment, TTPBgp12 seems to be a two-domain protein that aggregates in the presence of sugars such as maltose and N-acetylglucosamine (GlcNAc). These sugars cause two unfolding events to transition into one global event. TFPgp17 is a one-domain protein. Maltose and GlcNAc decrease the aggregation temperature of TFPgp17, while the presence of N-acetylgalactosamine (GalNAc) increases the temperature of its aggregation. The thermal unfolding analysis of the concentration gradient of TTPBgp12 and TFPgp17 indicates that with decreasing concentrations, both proteins increase in stability. However, a decrease in the protein concentration also causes an increase in its aggregation, for both TTPBgp12 and TFPgp17.

Słowa kluczowe

tail tubular proteins, tail fiber proteins, biofilm

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