

Screening of *Salmonella enteritidis* and *Bacillus thuringiensis* proteomes for potentially amyloidogenic proteins

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Motivation and aims: *Salmonella enteritidis* and *Bacillus thuringiensis* are pathogens in different groups of organisms. *S. enteritidis* causes intestinal infections of rodents and *B. thuringiensis* is insecticidal pathogen used to control pests. Recently it was shown that bacterial factors of virulence might form amyloids and it might play an important role in infection [1]. The aim of this study was to find potentially amyloidogenic proteins in the proteomes of *S. enteritidis* and *B. thuringiensis*.

Methods: To find amyloidogenic regions in proteins we used Waltz tool [2], which was developed to predict amyloid-forming regions; Aggrescan [3], which finds aggregation-prone regions; and SARP algorithm [4], which was designed to find compositionally biased regions. All protein sequences and their annotations were downloaded from Uniprot database (uniprot.org).

Results: We found that about 30 % of all proteins of *S. enteritidis* and *B. thuringiensis*, harbored regions predicted with Waltz, up to 1 % of proteins were enriched with amyloidogenic amino acids asparagine and glutamine (QN-rich) and more than 80 % of proteins contained regions found with Aggrescan. Proteins with Waltz-predicted regions are mostly membrane-associated and participate in transport or biosynthesis. The group of flagellar proteins were significantly enriched with QN-rich proteins, found with SARP. The flagellum proteins participate in host-pathogen interactions. All proteins attributed to the process of pathogenesis by GeneOntology database, contained regions found with Aggrescan.

Conclusion: We have found that various factors of virulence of the phylogenetically distant pathogenic bacteria *Salmonella enteritidis* and *Bacillus thuringiensis* are rich in amyloidogenic regions. Thus, amyloid formation by the factors of virulence might represent evolutionary conservative molecular mechanism underlying pathogenesis of different bacterial infections.

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References

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