Host-Endolysins interactions

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Abstract

(Bacterio)phages are viruses that specifically infect bacteria. They are tremendously diverse and the most abundant living entities on Earth with an estimated total population size of 1031 phage particles. During infection they inject their DNA in the host bacteria and drive the cell machinery to produce new progeny phages. At the end of the infection cycle, phages (with the exception of a few known filamentous phages) produce enzymes called (endo)lysins that degrade the peptidoglycan (PG) leading to bacterial lysis and death in order to release the progeny virions. PG is a heteropolymer that protects the bacterial cell against osmotic pressure. The ability of endolysins to degrade PG causing the death of the bacterial cell makes these enzymes a very interesting biocontrol agent against problematic antibiotic resistant pathogenic bacteria.

Considering that the muralytic activity of endolysins is directed to different bonds of the PG, which differs from species to species, it is conceivable that there is a relation between the endolysins and the bacteria that they target. This work is based on the *oligonucleotide-stickiness* method1, where the *stickiness* (σ) – the binding analysis (or hybridization) stability of an oligo-nucleotide/peptide or protein – is used against a genome or proteome sequence of interest as follow:

$$\sigma = \frac{1}{n} \sum_{i=l_0+1}^{l_0+n} \delta(p, T(i)) \quad , \qquad (0 \leq \sigma \leq 1)$$

where *l*0 + 1 and n are the model positions at which the sampling region begins and the sampling size for *stickiness* respectively, and δ is a determinant that takes the value of 1 when the sequence (*p*) binds stably to the *i-th* local sequence of the model (T (*i*)), that is, a fragmental sequence that has a fixed end at the sequence position *i*, or the value of 0 when there is no binding. In this formula, the p-T binding is determined based on the thermodynamic stability of the *p-T* complex under physiological conditions [1,2]. Therefore, we developed a network of bacteria-endolysin relationships making use of the 723 putative endolysins identified in 890 available completed sequenced phage genomes. For this, we calculated the stickiness between hosts models (bacterial wall models) and putative/known endolysin sequences. A proteomic vs. genomic model approach is discussed. Our study allows us to highlight evolutionary relationships between Gram-positive and Gram-negative phage endolysins and develop a model for lytic spectrum prediction of the endolysin based on its sequence.

References

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