

Establishment of the staphylococcal bacteriophage collection characterized by a reticulate classification system in the Czech Collection of Microorganisms (CCM)

Author(s) Roman Pantucek¹, Jana Kahankova¹, Pavel Benda², Ivo Sedlacek², Pavla Holochova^{2,1}, Vladislava Ruzickova¹, Lucie Kuntova¹, Pavel Svec², Ivana Nepejchalova¹, Jiri Doskar¹

Institution(s) 1. MU-UEB, Masaryk University, Faculty of Science, Institute of Experimental Biology, Kotlarska 2, 61137 Brno, Czech Republic 2. MU-CCM, Masaryk University, Faculty of Science, Czech Collection of Microorganisms, Tvrdého 14, 60200 Brno, Czech Republic

Abstract:

Staphylococcal bacteriophages of the family *Siphoviridae* have been widely used in phage typing of human strains of *Staphylococcus aureus* subsp. *aureus* as well as in fundamental genetic studies of this species. Prophages are the most widespread mobile genetic elements playing an important role in pathogenicity of *S. aureus*, changing its phenotype as a result of lysogenic conversion associated with production of enterotoxins, exfoliative toxin A (ETA), Panton-Valentine leukocidin (PVL) and immune evasion factors and/or mediate generalized transduction. The bacteriophage genes are organized into functional genomic modules showing remarkable degree of mosaicism. In the recent work we have designed a multiplex PCR strategy for typing the major modules of the staphylococcal siphophage genome. The nine PCR assays designed for the sequences distinctive for 50 module types were shown to be capable to identify the bacteriophage gene pool present in phage genomes. Here we propose updating the phage classification describing reticulate relationships among phages to better reflect the modular structure and extensive mosaic pattern of their genomes. Given the great biological and clinical importance of staphylococcal siphoviruses, the staphylococcal bacteriophage collection was established in 2010 by extending the CCM in the Czech Republic. About 40 *S. aureus* siphophage strains coding for ETA or PVL, phages exhibiting transducing properties or applicable for phage typing were characterized in detail up to now and being maintained. A database for computer storage and handling bacteriophage strain data has been developed on the basis of standardized format for plasmids, viruses and transposons (PVT) published previously (Vincente *et al.*, World J. Microbiol. Biotechnol. 8:519) and extended by fields concerning phage genome module properties. The database is designed to allow storage a variety of data and cross-reference with that concerning propagating, selection, host and lysogenic bacterial strains records in MINE (Microbial Information Network Europe). The database will be available to the public on the Web at <http://www.sci.muni.cz/ccm/> from January 2011. Acknowledgements: Supported by the Czech Science Foundation (310/09/0459) and the Ministry of Education of the Czech Republic (MSM0021622415 and MSM0021622416).

Key words: Staphylococcus, bacteriophage, Siphoviridae, collection, reticulate evolution