Genome sequence of the broad host range *Salmonella* bacteriophage phi PVP-SE1

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Salmonella is an important zoonotic pathogen and remains the primary cause of reported food poisoning worldwide with massive outbreaks. The increased resistance of *Salmonella* to antibiotics and other biocides has encouraged the development of alternatives to chemotherapy such as phage therapy. Phage phi PVP-SE1 is a *Salmonella* phage isolated from a Germany (Regensburg) wastewater plant. This phage is characterized by having a broad lytic spectrum, even broader than Felix 01, being able to infect different *Salmonella* serotypes of different countries and different origins (food, environmental and clinical). TEM analysis showed a *Myoviridae* phage having an icosahedral head (84 nm) attached to a contractile tail (120x18 nm) by a connector and presents short fibres. Genome sequencing is of enormous importance for classification of bacteriophages and for understanding their evolution. A full knowledge of phage genome sequences would be helpful to evaluate phage safety for therapy. Moreover, it might allow the identification of useful phage proteins against pathogenic bacteria. Phage PVP-SE1 was sequenced and the genome was found to be terminally redundant and circularly permuted with a size of 145,964 bp. The GC content of this phage genome is 45.6% which is lower than its hosts (50%-54%). A total of 244 ORFs were found representing 91.6% (excluding tRNAs) of the full genome. Approximately 46% of encoded proteins are hypothetical and present no homology with any other proteins. Only a few of them (22.1%) exhibited homology with known proteins. As with other large members of the *Myoviridae* its genome contained a large number of genes coding for tRNA (24). Furthermore, 9 promoters and 7 rho-independent terminators were identified. The genome sequence presents a high homology (145 gene encoding proteins) with the *Escherichia coli* bacteriophage rV5. Both phages are unrelated to any other known phage, which might suggest that they belong to a new phage genetic group.