

Isolation and characterization of novel *Staphylococcus aureus* bacteriophage Hesat from dairy origin

Barbara Turchi^{a,*,#}, Claudia Campobasso^{b, c,#}, Arianna Nardinocchi^b, Jeroen Wagemans^c, Beatrice Torracca^a, Cédric Lood^{c,d}, Graziano Di Giuseppe^b, Paola Nieri^c, Fabrizio Bertelloni^a, Luca Turini^a, Valeria Ruffo^a, Rob Lavigne^c, Mariagrazia Di Luca^b

^aDepartment of Veterinary Science, University of Pisa, Viale Delle Piagge 2, 56124 Pisa, Italy

^bDepartment of Biology, University of Pisa, Via San Zeno 37, 56127 Pisa, Italy

^cDepartment of Biosystems, KU Leuven, Kasteelpark Arenberg 21, box 2462, 3001 Leuven, Belgium

^dDepartment of Microbial and Molecular Systems, Centre for Microbial and Plant Genetics, KU Leuven, Kasteelpark Arenberg 20, box 2460, 3001 Leuven, Belgium^e

Department of Pharmacy, University of Pisa, Via Bonanno Pisano 6, 56126 Pisa, Italy

*Corresponding author: mariagrazia.diluca@unipi.it, Department of Biology, Via San Zeno 37, 56127 (Pisa), Italy, phone: +390502213697

Equally contributed

Supplementary figures

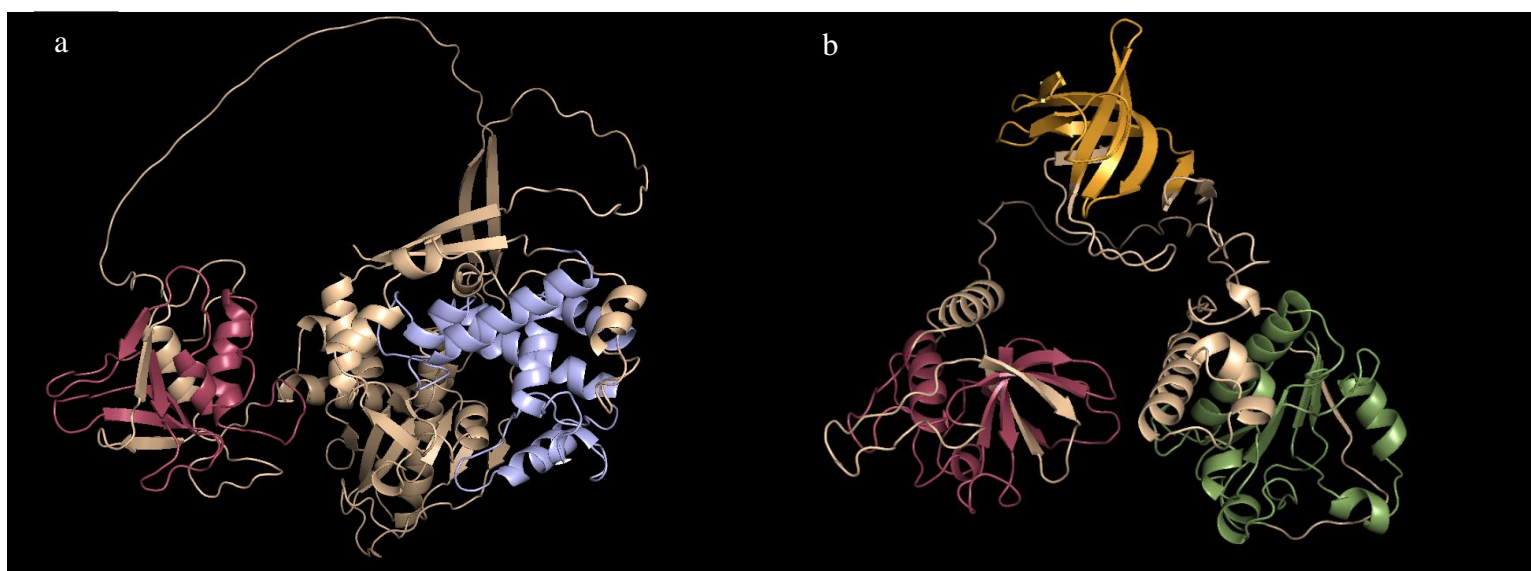


Fig. S1 Tridimensional structure of the endolysins a) *gp67* and b) *gp71*, predicted by ColabFold. The backbones are displayed in beige while the functional domains are highlighted as follows: in pink the CHAP domains, in purple the glucosamidase, in green the amidase and in yellow the SH3_5 domain.

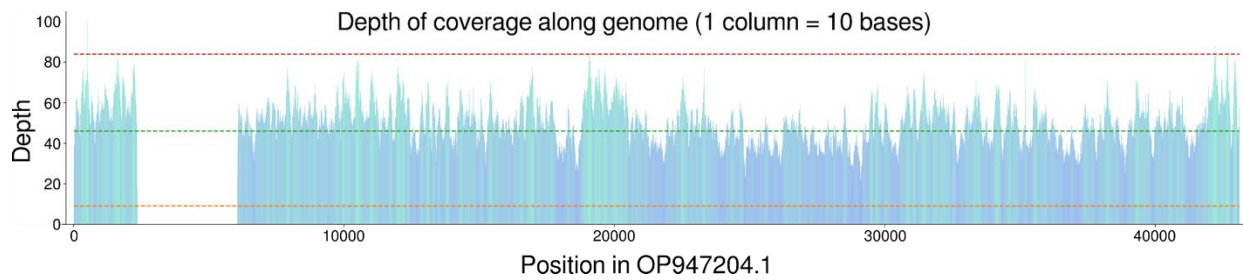


Fig. S2 Mapping of the reads from the *S. aureus* 916 strain sequencing against the phage Hesat genome reveals a coverage of about 40× all along the phage genome, besides the 3.7 kbp recombined region that is uniquely found in the temperate phage

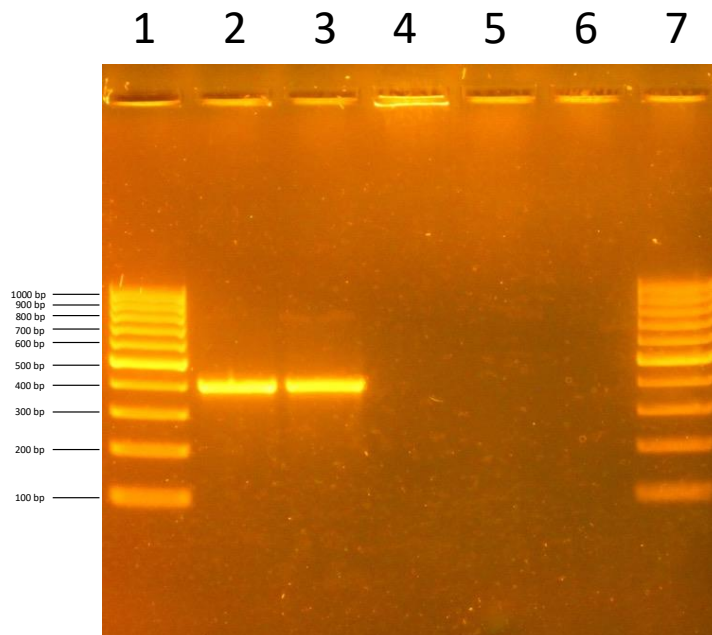


Fig. S3 Agarose gel electrophoresis (2% agarose) of the PCR product of the 405 bp fragment amplification: lane 2 and 3, two samples of phage Hesat lysate, lane 4 *S. aureus* 916 strain glycerol stock, lanes 5 and 6 two samples of the bacterial genome DNA. In the lanes 1 and 7 the GeneRuler 1kb DNA ladder