

**Table S3.** Features of annotated bacteriophages genomes in this study by RAST, Virulence Finder, Res Finder 3.1 and ToxFinder.

Bacteriophage			
Feature	φMA11	φMA12	φMA13
GC content (%) <sup>a</sup>	48.9	51.6	53.4
L50 <sup>a</sup>	1	1	1
Number of contigs (with PEGs) <sup>a</sup>	1	1	1
Number of subsystems (genes) <sup>a</sup>	5	5	1
Number of coding sequences <sup>a</sup>	52	55	55
Number of RNAs <sup>a</sup>	0	0	0
Shiga-toxins <sup>b</sup>	0	0	0
Virulence genes <sup>b</sup>	0	0	0
Antibiotic resistance genes <sup>c</sup>	0	0	0
Mycotoxins <sup>d</sup>	0	0	0

<sup>a</sup> Features determinate by RAST; <sup>b</sup>Features determinate by Virulence Finder; <sup>c</sup>Features determinate by ResFinder 3.1 at threshold 90% for identifying genes encoding resistance for: Aminoglycoside, Beta-lactam, Colistin, Fluoroquinolone, Fosfomycin, Glycopeptide, MLS – Macrolide, Lincosamide, Streptogramin B, Nitroimidazole, Oxazolidione, Phenicol, Rifampicin, Sulphonamide, Tetracycline and Trimethoprim; <sup>d</sup>Features identified by ToxFinder.