

## Supplementary Information

### **Identification of *Mammaliicoccus fleurettii* as the source of a methicillin-resistance gene in a First Nation reserve lake in Manitoba, Canada**

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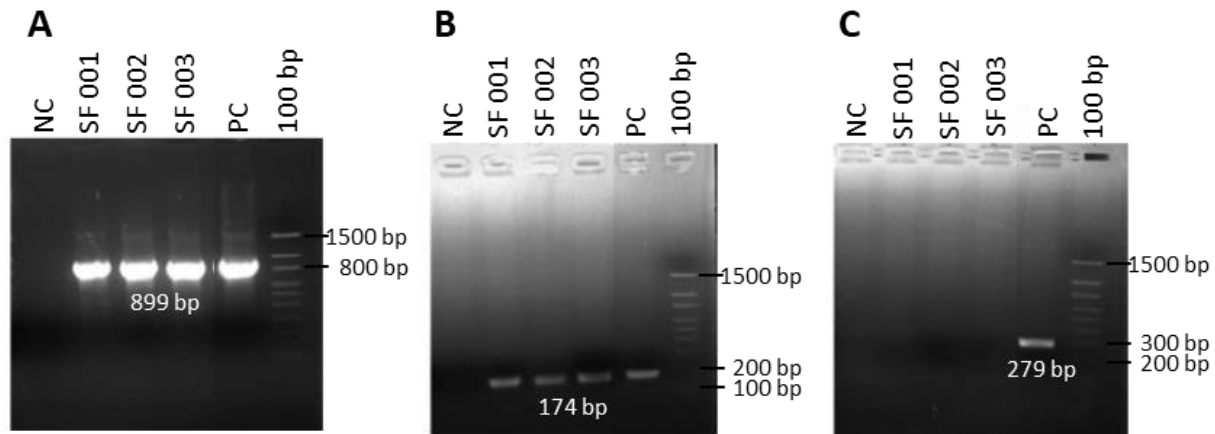
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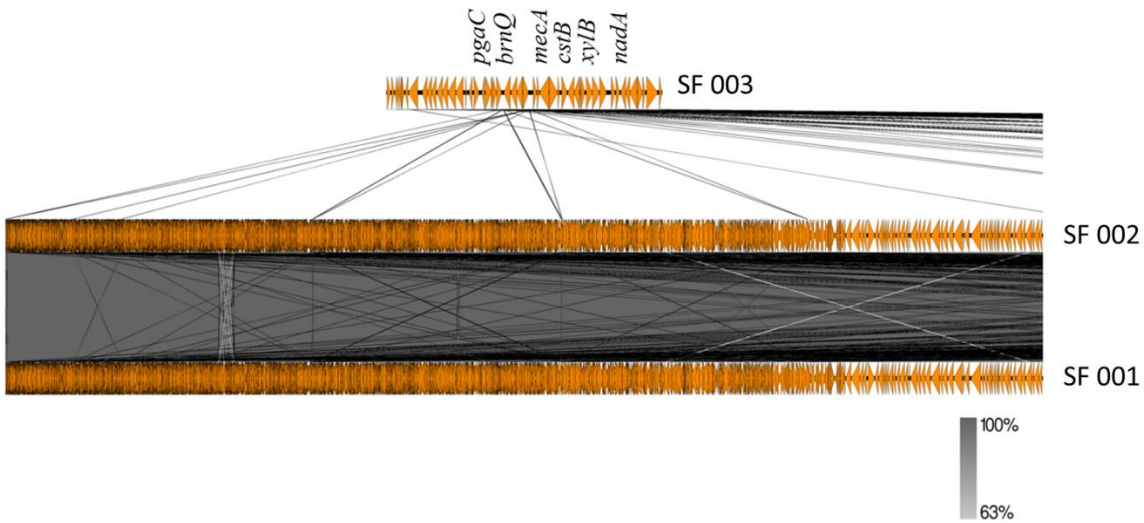
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**Table S1:** PCR primers used in this study.

Primer	Sequence (5'-3')	Reference
<b>rpoB forward</b>	CAATTCATGGACCAAGC	1
<b>rpoB reverse</b>	CCGTCCCAAGTCATGAAAC	
<b>mecA forward</b>	AACAGGTGAATTATTAGCACTTGTAAG	2
<b>mecA reverse</b>	ATTGCTGTTAATATTTTTTGAGTTGAA	
<b>nuc forward</b>	GCGATTGATGGTGATACGGTT	3
<b>nuc reverse</b>	AGCCAAGCCTTGACGAACTAAAGC	



**Figure S1:** Agarose gel electrophoresis of PCR amplicons for genotypic analysis of bacterial isolates SF 001, SF 002, and SF 003. **(A)** *Staphylococcus* species-specific *rpoB* (RNA polymerase  $\beta$  subunit); **(B)** methicillin-resistance *mecA* (penicillin binding protein 2a); **(C)** *S. aureus*-specific *nuc* (thermonuclease). All gels from left to right: NC - negative control (no DNA template); SF 001; SF 002; SF 003; PC - positive control (*S. aureus* HA-MRSA 100697 genomic DNA); 100-base pair (bp) molecular marker (Biobasic).



**Figure S2:** Genomic organization of the *mecA* gene locus of each *Mammaliicoccus fleuretii* isolate (SF001, SF002, and SF003) in this study and comparison of the locus-containing *mecA* gene complex among the isolates. Arrows indicate the translation orientation of the coding genes (EasyFig (4)).

## References

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4. Sullivan MJ, Petty NK, Beatson SA. Easyfig: a genome comparison visualizer. *Bioinformatics*. 2011; 27(7): 1009-1010. doi: [10.1093/bioinformatics/btr039](https://doi.org/10.1093/bioinformatics/btr039)