

### ***Comparison of antimicrobial resistance and virulence genes***

Protein sequences of predicted ORFs were searched for ARGs against the IARDB using BLASTP with an E-value  $\leq 10^{-5}$ . An ORF was designated as an ARG sequence if the best BLASTP alignment to ARG reference sequences was at least 80% similar to a query coverage of at least 70%. Secretory proteins were detected on the genome assembly by SignalP (1). Type I-VII secretion system-related proteins were extracted from all annotation results. Type III secretion system effector proteins were detected by EffectiveT3 (2), and secondary metabolite gene clusters were predicted by antiSMASH (3,4).

### **References**

1. Petersen TN, Brunak S, von Heijne G et al. 2011. SignalP 4.0: discriminating signal peptides from transmembrane regions. *Nat Methods* 8: 785-6.
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3. Blin K, Medema MH, Kazempour D et al. 2013. antiSMASH 2.0--a versatile platform for genome mining of secondary metabolite producers. *Nucleic Acids Res* 41: W204-12.
4. Medema MH, Blin K, Cimermancic P et al. 2011. antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. *Nucleic Acids Res* 39: W339-46.