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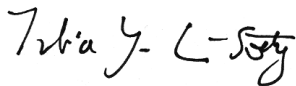Spirit | Intellect | Purpose

Department of Biology

May 22, 2015

Dear Colleagues,

Thank you for your review of **Arthrobacter phage Tank**. I did not format the second "minimalistic" Final dnam5 file since the collection of Arthrobacter phages is not quite as vast as those for Mycobacteriophages and the functions of many gene features are still unknown.

The 67592 bp genome of Tank contained 589 bp overlap at the 5' and 3' ends. One gene feature at the ends that was partially duplicated was deleted. (**1**) Gene feature with 10257 start showed a possible frame shift with the following feature; the slippery sequence was GGAAA, rather than GGAAA. (**2**) Gene feature with 35553 start showed a possible frame shift with the following feature; the following feature (starts at 36088) has really weak SD scores, but no obvious slippery sequences were found. (**3**) GeneMark had called a forward gene starting at position 46458 (amongst reverse genes) with weak coding potential. This feature was deleted since we also deleted the comparable feature in phage Wilde in the same cluster; there, the coding potential is even weaker. (4) Large gaps were left upstream of starts 50435, 60400, and 66077; no or very weak coding potentials were predicted by GeneMark or Glimmer.

Best,

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