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**Reviewers Comments**

**Hoppin’ Out of the Metagenome: De Novo Genome Assembly of the Obligate Leafhopper Endosymbiont *Candidatus Sulcia muelleri***

Authors proposed cleverly- titled whole genome analysis of *Candidatus Sulcia muelleri****,*** bacteria symbiotic with sharphopper *Kolla Paulula* and another bacteria *Xylella fastidiosa*, involved in disease of grapevines with a goal to delineate symbiotic strategies of *Sulcia*.

Theexplaining the reasons and steps of their **innovative** methods, using the newest versions of available software Abyss, BWA, FastQC and they emphasized the role and clearly specified the criteria of quality control. The **investigator** were clearly defined The laboratory and computing **environment** at WVU are sufficient to be supportive of this project.

The two areas that may require some attention are the background and order of steps in the **approach pipeline.** Background didn’t flow well, lacked clear direction, there were some details that were included that didn’t seem pertinent to the story (*Dalbulus*). For instance, is the *Xylella fastidiosa* a secondary partner complementing *Sulcia*; is the sharpshooter the vector or the *Xylella fastidiosa* is a vector of the disease; or perhaps, just the word ‘of’ is missing in row 13 of Background in …and efficient vector **of** *Xylella…?* Thus, the **significance** of the study was lost and not clearly defined. Is the overall goal to find out how the vector is more efficient (therefore may cause more damage to the edible plants), or would it be goal to find what would make the vector less efficient (thus the plant damage may be prevented)? The second area that may be easily modified is the pipeline for assembly: quality control and trimming should be the first step completed to remove row quality reads regardless of species purity, then the BWA used to separate reads by species of origin as the second step.