

3-30-2016

16S rDNA Pyrosequencing Indicates Pseudomonas sp as the Predominant Bacteria in Gut Microbiome of Soybean Thrips, *Neohydathothrips variabilis*

Min Jung Kim

Indiana University - Purdue University Fort Wayne

Follow this and additional works at: http://opus.ipfw.edu/stu_symp2016

Recommended Citation

Kim, Min Jung, "16S rDNA Pyrosequencing Indicates Pseudomonas sp as the Predominant Bacteria in Gut Microbiome of Soybean Thrips, *Neohydathothrips variabilis*" (2016). *2016 IPFW Student Research and Creative Endeavor Symposium*. Book 36.
http://opus.ipfw.edu/stu_symp2016/36

This Book is brought to you for free and open access by the IPFW Student Research and Creative Endeavor Symposium at Opus: Research & Creativity at IPFW. It has been accepted for inclusion in 2016 IPFW Student Research and Creative Endeavor Symposium by an authorized administrator of Opus: Research & Creativity at IPFW. For more information, please contact admin@lib.ipfw.edu.

I. BACKGROUND

Soybean Thrips

- The soybean thrips, *Neohydatothrips variabilis*, are the major vector of Soybean Vein Necrosis Virus. (Fig. 1) [1, 2].



Figure.1. Soybean thrips

Insect Endosymbionts

- Endosymbionts are bacteria that live in the body or cells of another organism forming a mutualistic relationship [3].
- These bacteria play an important role such as providing essential amino acid and recycling of waste in the insects.
- There is no report on the endosymbionts of thrips.

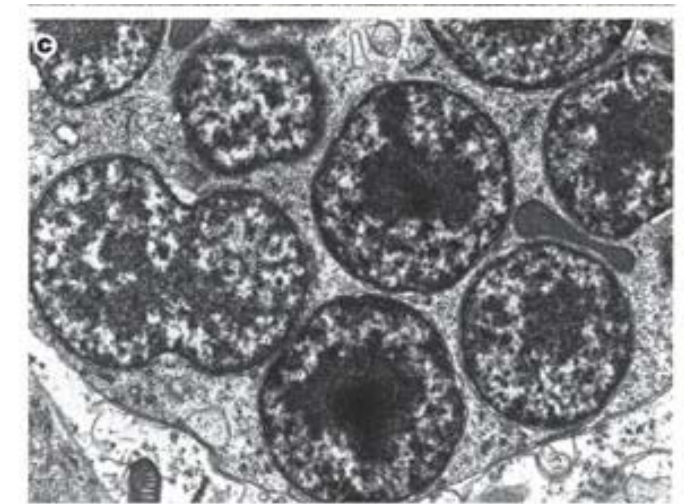


Figure.2. Endosymbiotic bacteria in insects

The objective of our research was to determine the abundance and diversity of endosymbionts in soybean thrips

II. METHODS

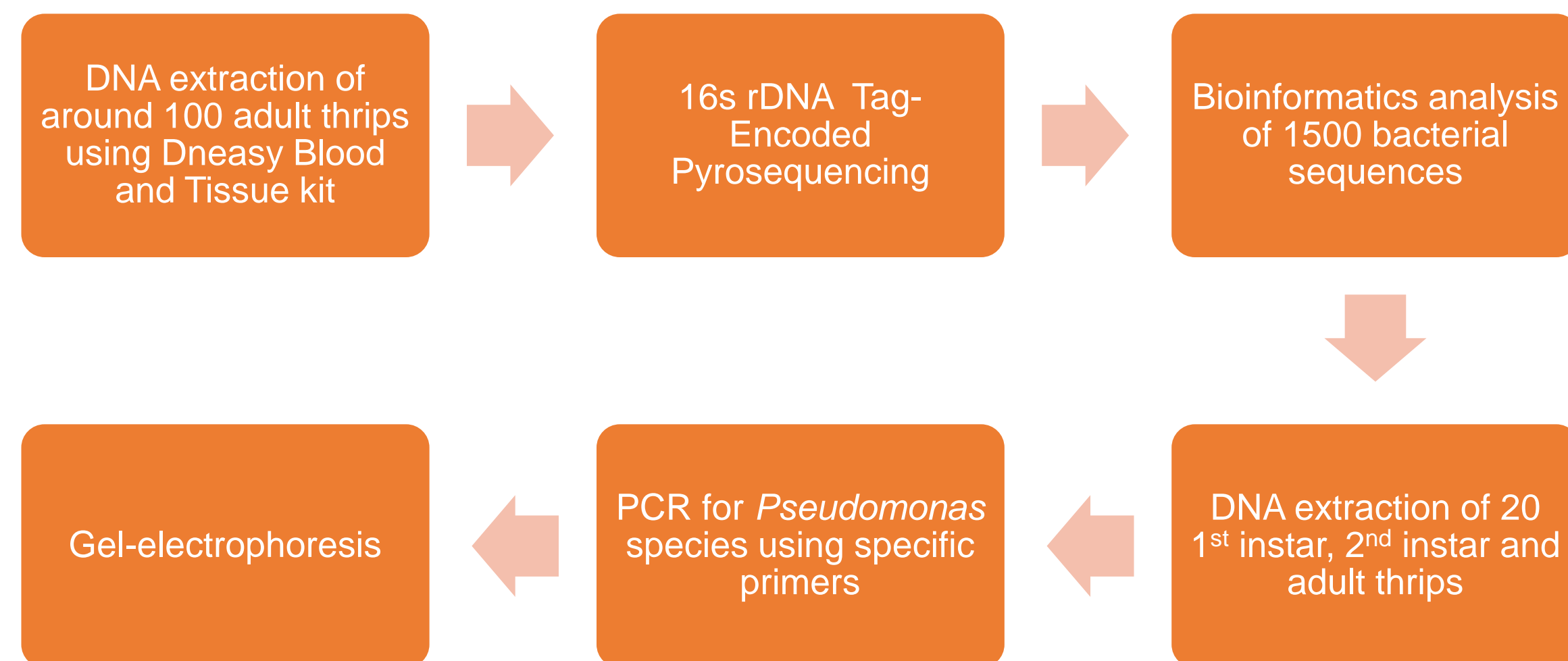


Figure 3. Experimental workflow

III. RESULTS

16S ribosomal DNA Pyrosequencing Results

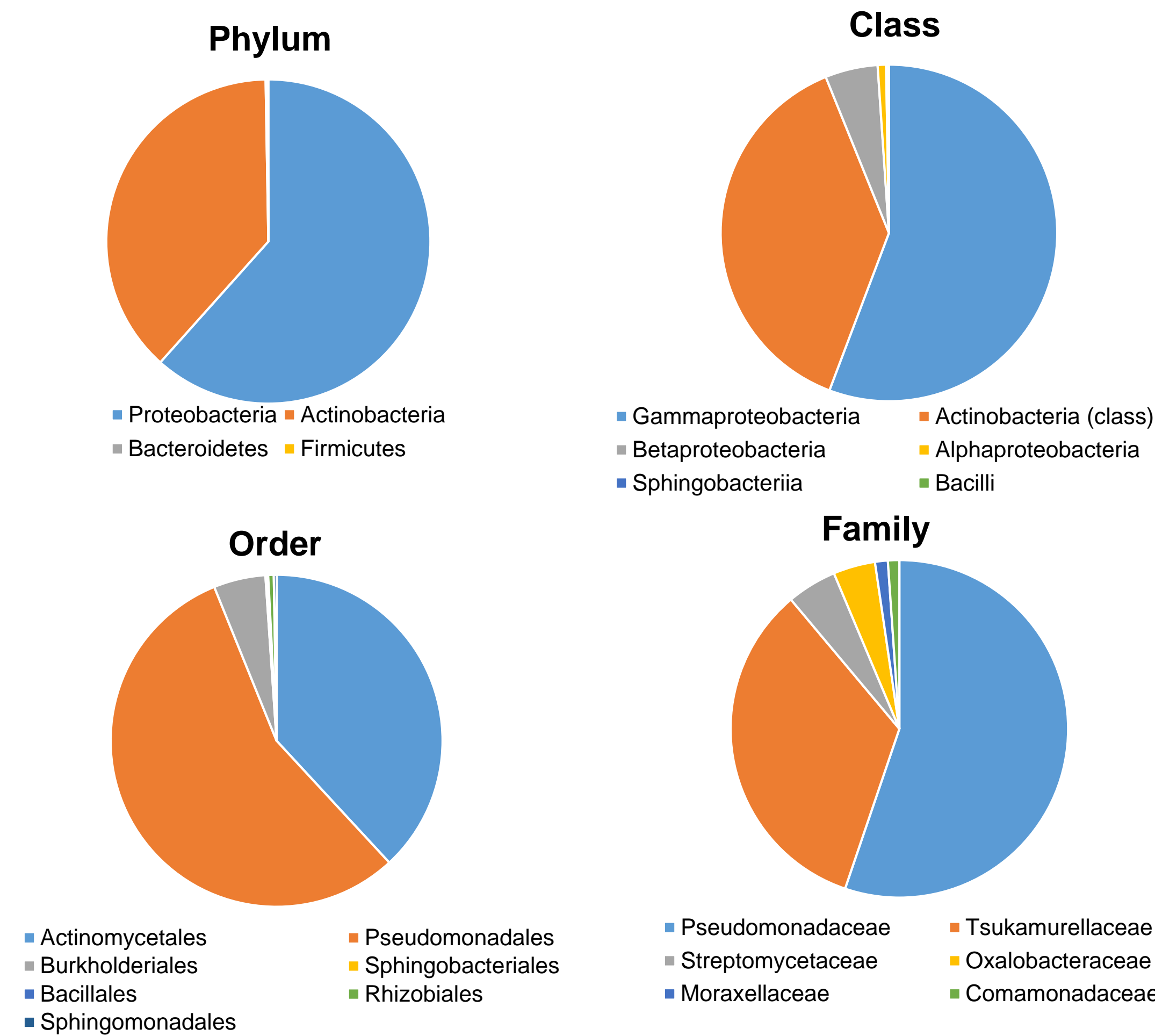


Figure 4. Percentage of bacterial species in adult soybean thrips

Table 1. Percentage composition of bacterial species in adult soybean thrips identified using 16S rDNA pyrosequencing

Bacterial species	Percentage
<i>Pseudomonas sp</i>	49.70
<i>Tsukamurella strandjordii</i>	31.58
<i>Streptomyces sp</i>	4.71
<i>Herbaspirillum sp</i>	2.56
<i>Pseudomonas trivialis</i>	2.36
<i>Herbaspirillum huttiense</i>	1.41
<i>Pseudomonas marginalis</i>	1.28
<i>Acinetobacter sp</i>	1.08
<i>Acidovorax sp</i>	0.94
Other	4.37

III. RESULTS (CONTD.)

Confirmation of *Pseudomonas sp.* in thrips life-stages using PCR

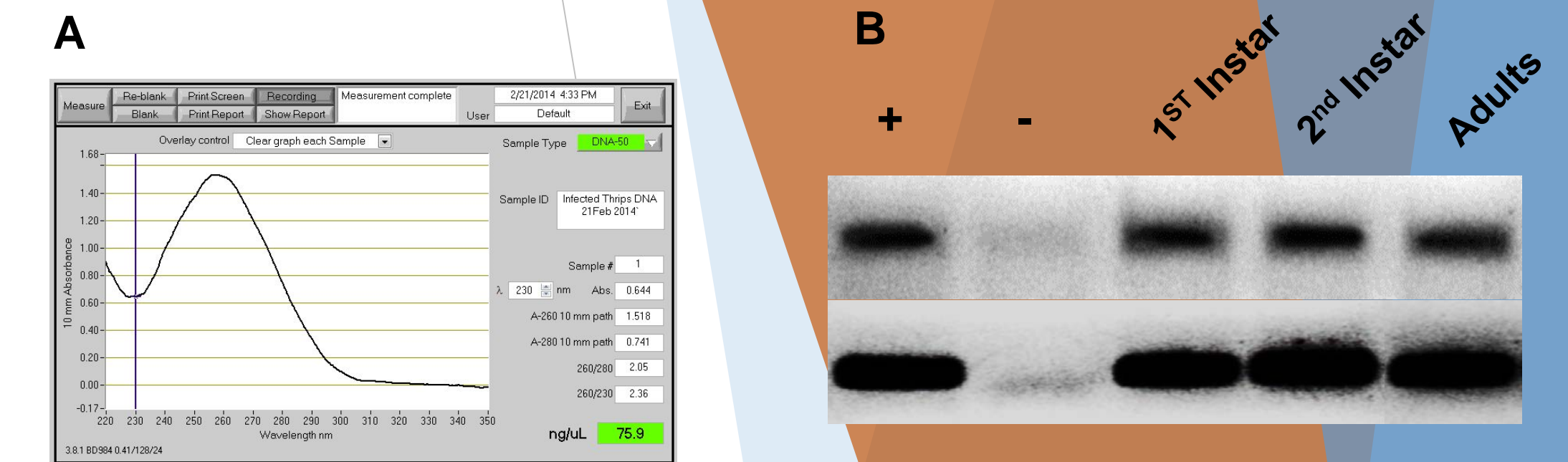


Figure 5. A) Quality of DNA extraction. B) PCR analysis of *Pseudomonas sp.* in thrips life-stages.

IV. CONCLUSIONS AND FUTURE RESEARCH

- 16S rDNA pyrosequencing showed that *Pseudomonas sp* was the most abundant bacteria in adults.
- Confirmatory PCR showed same levels of *Pseudomonas sp.* even in all thrips life-stages.
- Future research will be aimed at understanding the source of *Pseudomonas sp* in thrips and their role in thrips biology.

V. REFERENCES

- Zhou et al. (2011). Molecular characterization of a new tospovirus infecting soybean. *Virus Genes* 43: 289-295.
- Irwin et al. (1979). Spatial and seasonal patterns of phytophagous thrips in soybean fields with comments on sampling techniques. *Environ. Entomol.* 8: 131-140
- Baumann P (2005). Biology bacteriocyte-associated endosymbionts of plant sap-sucking insects. *Annu Rev Entomol* 59:155-189.

VI. ACKNOWLEDGEMENTS

This research is funded by grants from the Indiana Soybean Alliance and USDA National Institute of Food and Agriculture-Agriculture and Food Research Initiative (USDA NIFA-AFRI) grant to Dr. Nachappa.