# Analysis of Beneficial Bacterial Populations from Chinese Longbeans Scott Holt\*, Alexis Zaide, Jeff Hillyer, Western Illinois University, Biology, Macomb, IL **RESULTS: Identification of Methylobacterium & Rhizobia**

#### ABSTRACT

unguiculate (L.) Chinese Longbean (Vigna Walp. Ssp. Sesquipedalis (L.) Verdc.) is a crop plant that originated in the southern Asia region from domestication of Cowpea. Longbeans are now grown in Asia, Europe, and North America as a food source and for ornamental applications. Longbean pods, leaves, and stems are edible and the violet-blue flowers with draping pods are a useful ornamental. Despite their popularity, little information is known about the beneficial bacteria associated with this productive alternative food crop. The objectives of this project were to detect, enumerate, and identify beneficial Methylobacterium spp. on the leaves and symbiotic rhizobia spp. in the root nodules. The beneficial bacterial species isolated from productive longbeans can be used to develop natural microbial inoculants that support the growth of other crop plants.







#### METHODS

Longbean plants were divided into two groups and cultivated in a garden setting (summer 2018) and a greenhouse setting (fall 2018). For Methylobacterium detection, macerated leaves were plated on selective agar containing methanol and incubated for seven days at 25°C. Pink colonies typical for *Methylobacterium* spp. were counted identified using cultural, microscopic, and molecular and identification. Leaf samples were also plated on Plate Count Agar to determine total bacterial count. For rhizobia detection, root nodules were surface sterilized, crushed, plated on Congo Red Yeast Extract Mannitol Agar (CRYMA), and incubated for fourteen days at 25°C. Suspected rhizobia colonies were counted and identified using cultural, microscopic, and molecular identification.



Table 1. Identification of Rhizobia from root no		
Cultural Characteristics	cream or pinkish, mucoid	
	14 days incubation on *C	
Cellular Characteristics	Gram negative, rod-shap granules of poly-B-hydro	
	granules of poly-B-hydro	
Molecular (16S V4 region)	"Bradyrhizobium" typical	
	"Bradyrhizobium" atypica	
	(B. japonicum or B. radio	

\*CRYMA, congo red yeast extract mannitol agar.

## **RESULTS: Longbean Microbial Counts**





**Total Bacterial Count** 





Greenhouse



Greenhouse



Methylobacterium Count

**Bradyrhizobium Count** 

### CONCLUSIONS

100 85.76 90 80 106 70  $\boldsymbol{\times}$ 60 /nodule 50 40 FU 30 20  $\mathbf{O}$ 10

Greenhouse

This is the first report on detection and identification of beneficial *Methylobacterium* and *Bradyrhizobium* spp. associated with the productive alternative food crop Chinese Longbeans. It is also unusual to find two different rhizobia species form a symbiosis with the same crop plant. The beneficial bacterial species isolated from productive longbeans can be used to develop natural microbial inoculants that support the growth of other crop plants.

odules d colonies CRYMA ped oxybutyrate (B. elkanii)

obacter)

	Table 2. Identification of	Methylobacteriur
	Cultural Characteristics	pink-pigmented co
		5-7 days grown on
		Gram negative, ro
		lipid inclusions or
	Molecular (16S V4 region)	"Methylobacterium
		(extorquens or pop

\*AMS = Ammonium Mineral Salts Medium supplemented w/ 0.5% methanol

Fig. 1 Total Aerobic Bacterial Viable Count From Leaves



## **RESULTS SUMMARY**

Table 1. Two types of Bradyrhizobium spp. were isolated from nodules but only one sp. type per nodule. Bradyrhizobium "typical" (elkanii) was found in a majority of nodules. Bradyrhizobium "atypical" (japonicum) was found in an occasional nodule.

Fig 1. Heterotrophic bacterial counts for greenhouse longbeans were slightly higher (43 CFU /g leaf x 10<sup>6</sup>) vs garden setting (36 CFU /g leaf x  $10^6$ ).

Garden

Garden



Fig 2. The *Methylobacterium* counts for greenhouse-grown longbeans (8.7 CFU /g leaf x 10<sup>4</sup>) were much lower versus the garden longbean plants 1230 CFU /g leaf x  $10^4$ ).

> Although none of the bacterial count comparisons were statistically significant due to variability, there was clearly a trend that growth conditions impact *Methylobacterium* counts on longbeans.

#### Fig. 3. Rhizobia Viable Count from Root Nodules



Fig 3. The root-nodule rhizobia bacterial count for greenhouse longbeans was slightly lower (9.8 CFU / nodule x 10<sup>6</sup>) than the garden longbeans plants (16.0 CFU/ nodule x

Garden



