



### Introduction

Consumer demand for organically produced crops is on the rise. As a result, organic vegetable production in Indiana has steadily expanded in acreage and number of producers recently. These growers generally rely on fertilizers that are not readily available to plants. Such amendments must be mineralized and transformed by soil microorganisms before being taken up by the crop. We seek to determine the impact of commonly used alternative fertility practices on soil microbial ecology and plant productivity. Assessing how alternative fertility practices influence ecological functioning and plant productivity will broaden the understanding of the scientific community on how alternative fertility practices impact soil microbial ecology and lead to improved fertility management for organic and low input growers.

### Experimental Design

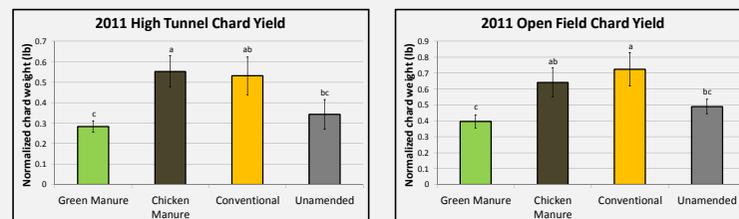
Four fertility treatments (unamended control, green manure, composted chicken manure & conventional fertilizers) are applied in a RCBD with four replicates in open field and high tunnel settings over the course of three growing seasons.



### Objectives

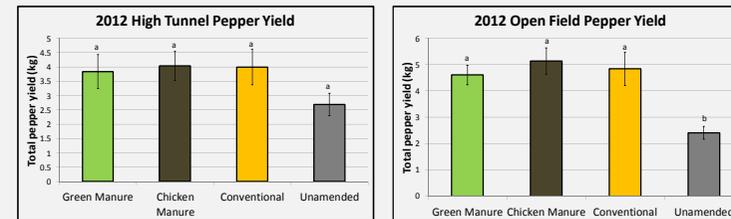
- Quantify the long-term impact of fertility management options on soil quality, nitrogen availability and plant productivity in common market vegetables
- Determine how fertility management options influence functional communities involved in the nitrogen cycle and link this to the efficient use of nitrogen in an open field vegetable production system
- Evaluate the relationship between fertility management options and microbial community composition in the pepper rhizosphere on nutrient uptake, plant health and yield in an open field vegetable production system

### Preliminary Results



**Figures 1 & 2:** Yield of swiss chard during the 2011 growing season in the high tunnel and open field settings, respectively. As indicated by the letters, statistically significant differences were seen between treatments. Significance levels based on t-test using the least significant difference.

### Preliminary Results cont.



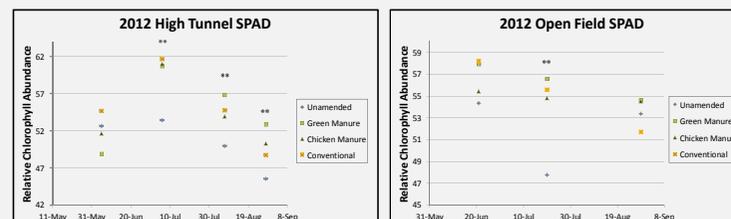
**Figures 3 & 4:** Total yield of peppers during the 2012 growing season in the high tunnel and open field settings, respectively. Significance levels based on t-test using the least significant difference.

High Tunnel FDA Activity							
	Green Manure	Chicken Manure	Conventional	Unamended	Anova		
	mg fluorescein released / g dry soil				df	F	p
2011 Baseline	0.109	0.109	0.109	0.109			
2011 Day 63	0.132 a	0.111 ab	0.123 ab	0.119 b	3, 28	1.75	0.1804
2012 Day 70	0.155 a	0.118 b	0.109 b	0.119 b	3, 28	3.64	0.0246

Open Field FDA Activity							
	Green Manure	Chicken Manure	Conventional	Unamended	Anova		
	mg fluorescein released / g dry soil				df	F	p
2011 Baseline	0.096	0.096	0.096	0.1			
2011 Day 63	0.131 a	0.127 a	0.133 a	0.129 a	3, 28	0.13	0.9424
2012 Day 70	0.13 b	0.138 ab	0.156 a	0.127 b	3, 28	3.82	0.0204

**Tables 1 & 2:** Overall microbial activity in the high tunnel (above) and open field (below) settings as indicated by the hydrolysis of FDA. Activity is greatest in fertilized treatments and tends to increase over time in organic fertility treatments. Significance levels based on t-test using the least significant difference.



**Figures 5 & 6:** SPAD measurements taken during the 2012 growing season in the high tunnel and open field settings, respectively, as an indication of plant uptake and use of nitrogen. In general, significant differences were seen across the treatments, particularly in the high tunnel setting. Statistically significant differences are indicated by (\*\*) at a specific sampling date.

### On-going Research

Field trials will be carried out at Meigs Horticulture Farm during the 2013 growing season in the same open field and high tunnel plots. During this time, bell peppers will be the main vegetable crop. Concomitantly, efforts to optimize molecular techniques will be made. Soil biological and chemical analyses for samples collected in 2011 and 2012 are underway. We plan to use qPCR to monitor N cycling gene abundances. Further, we plan to estimate the diversity of N cycling genes using T-RFLP.