

# Black soldier fly frass as a biofertiliser for Chinese Cabbage Growth: Impact on Soil Microbiome and Plant Performance

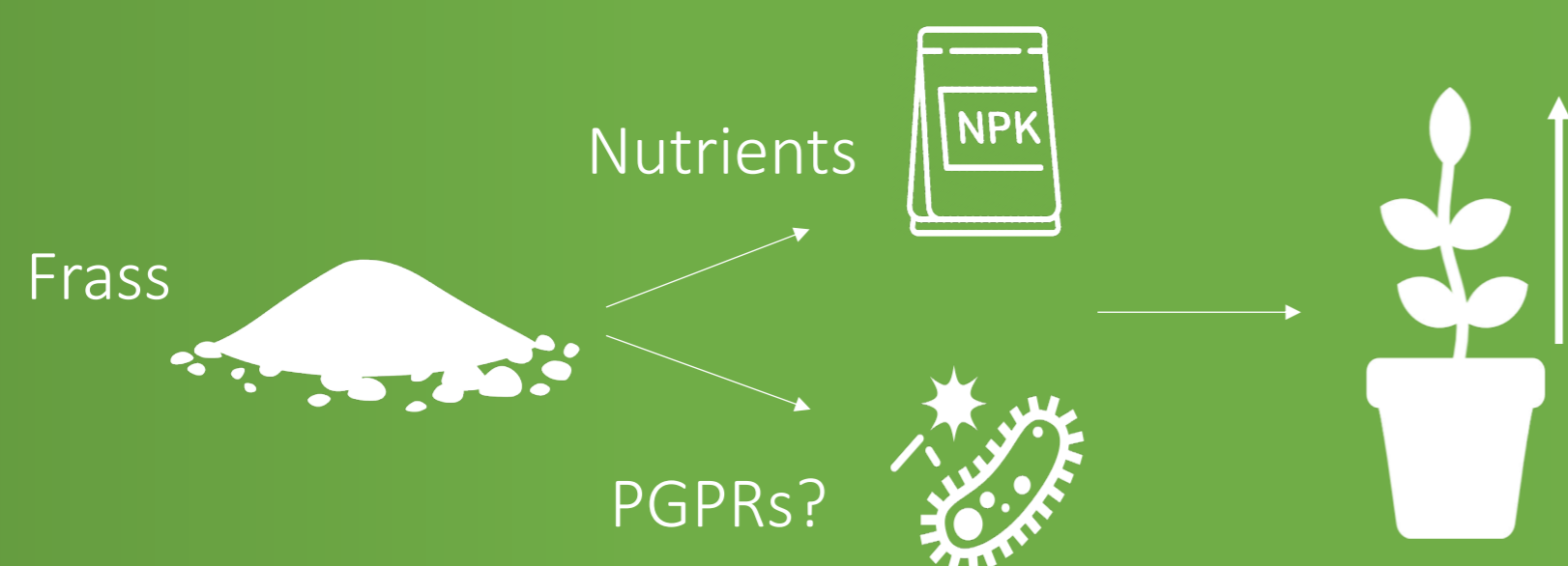
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## 1. Motivation

Black soldier fly (BSF) farming produces large volumes of frass which is composed of insect excrement, shed exoskeletons, and undigested decomposing substrate.

Frass contains microbes and micro and macro nutrients that are beneficial to plants when added to soil popularising frass as an alternative to chemical fertilizers.

However, there has been limited research conducted to determine the effectiveness of frass as a biofertiliser.

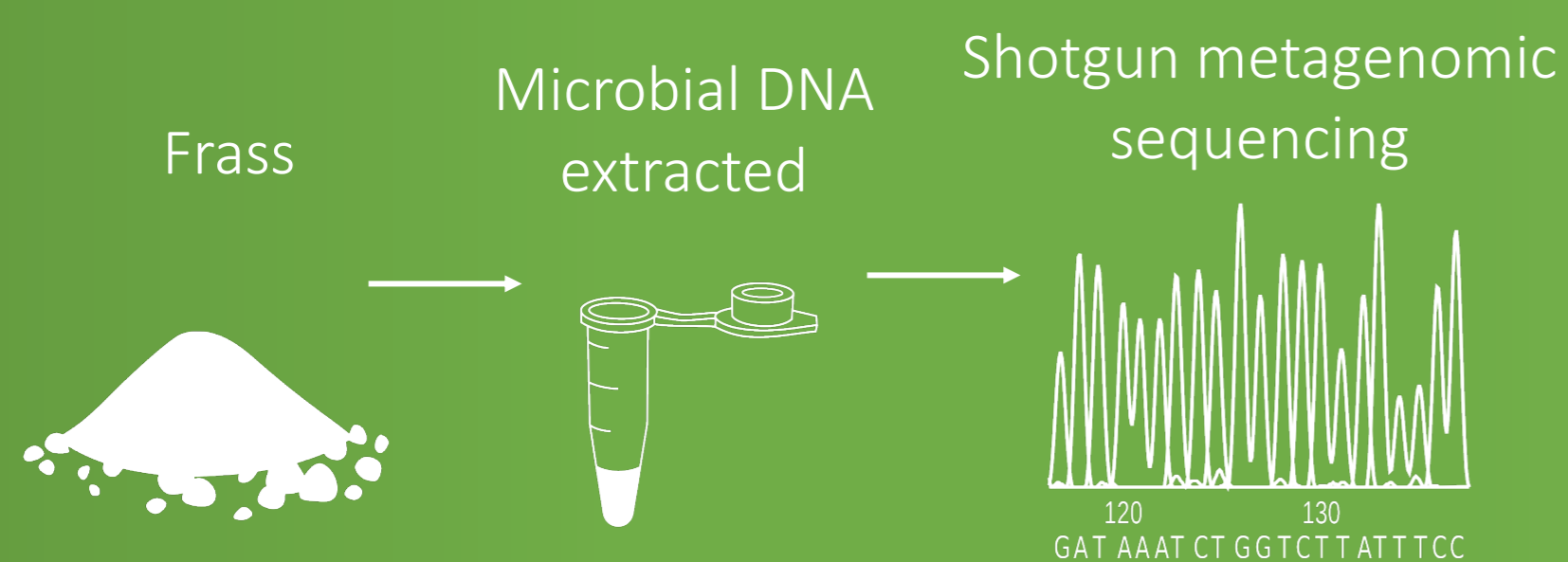


## 2. Aim

- Conduct pot trials with fresh and sterile frass to determine if the frass microbiome is aiding cabbage growth.
- Analyse the microbial community present in frass.

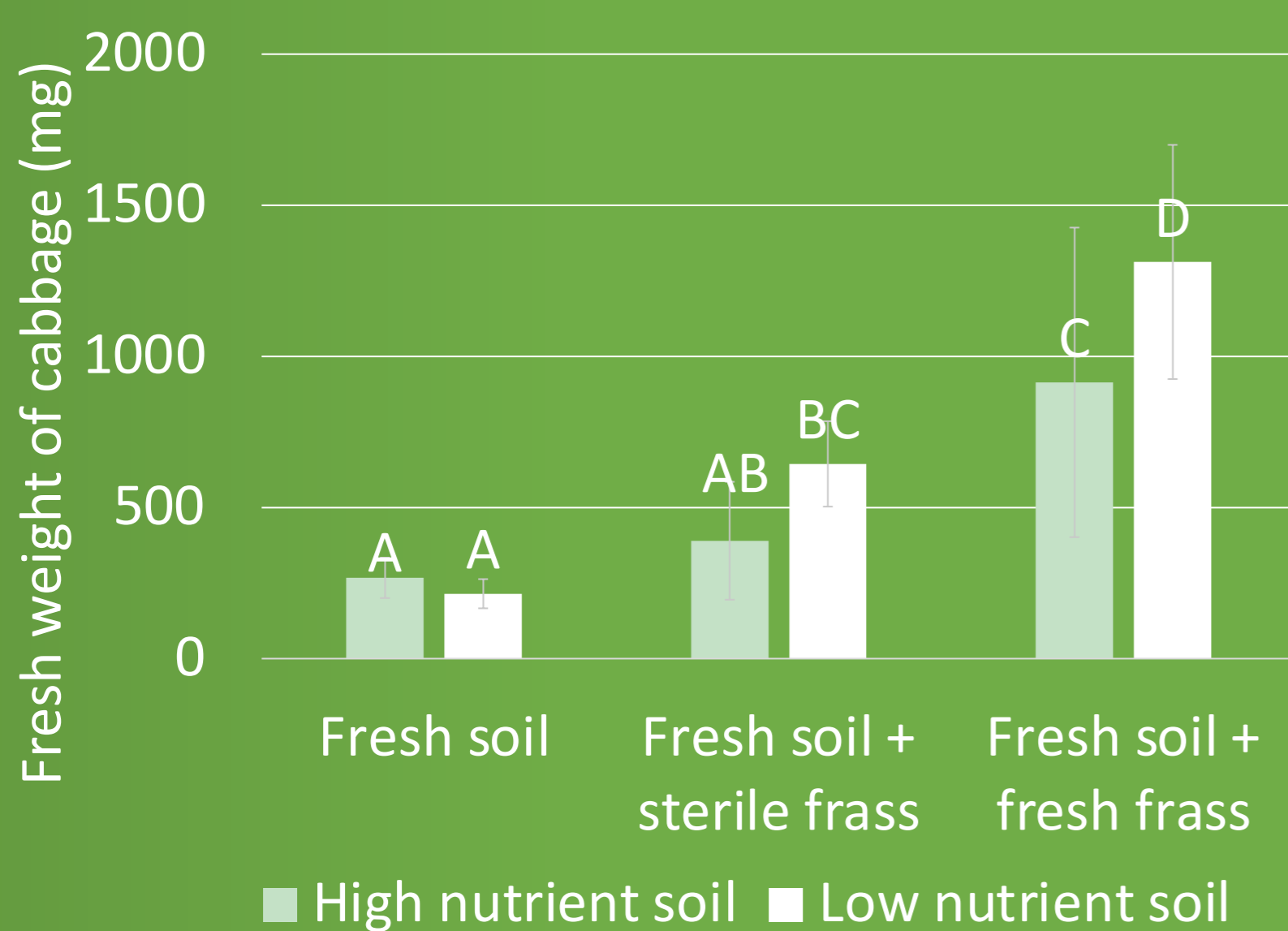
## 3. Methods

Conducted pot trials using 2.5% sterile or fresh frass mixed on a dry matter basis with high or low nutrient soil. Measured the aboveground cabbage biomass to determine plant growth promoting properties of the microbes in frass.



Extract frass microbial DNA and sequence using metagenomic shotgun sequencing.

## 4. Pot trials



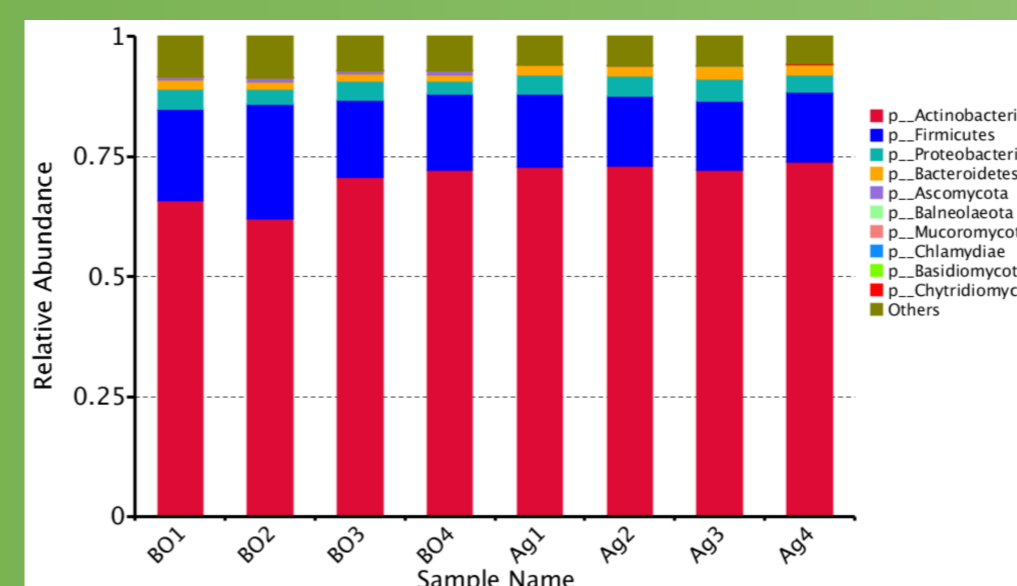
Frass addition to soil greatly increases the biomass of cabbage plants, compared to soil controls. Fresh frass results in significantly greater cabbage biomass than sterile frass, suggesting the frass microbiome is further increasing plant growth in addition to the nutrients.



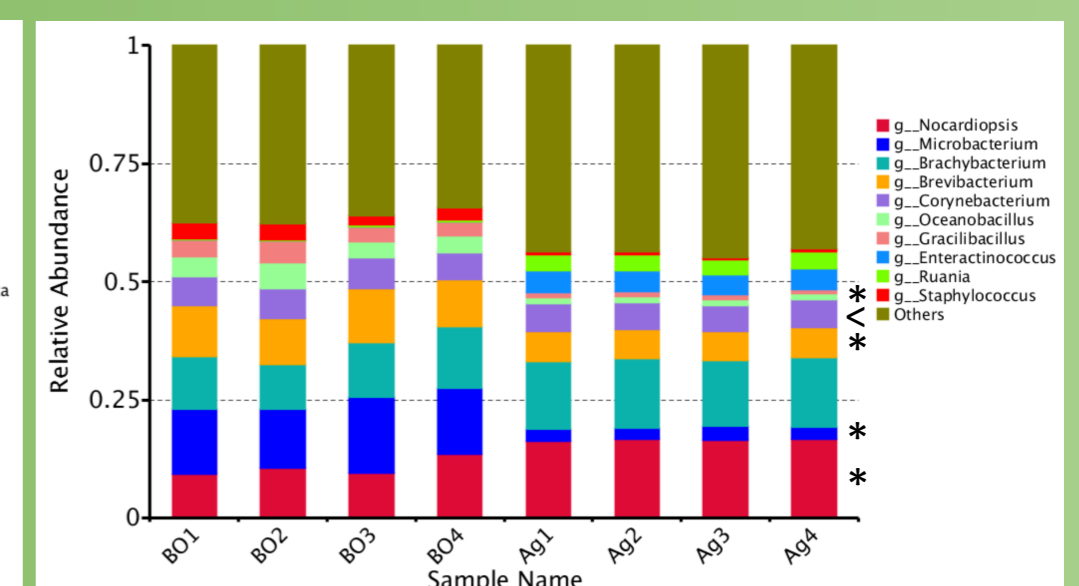
## 5. Microbial taxonomy

**BO** From BSF  
Reared on fruit/vegetable mix  
4 replicates analysed  
Stored in shed for 7 months

**Ag** From BSF  
Reared on fruit/vegetable mix  
4 replicates analysed  
Stored in shed for 5 months



The top 10 most abundant phyla present in each sample.

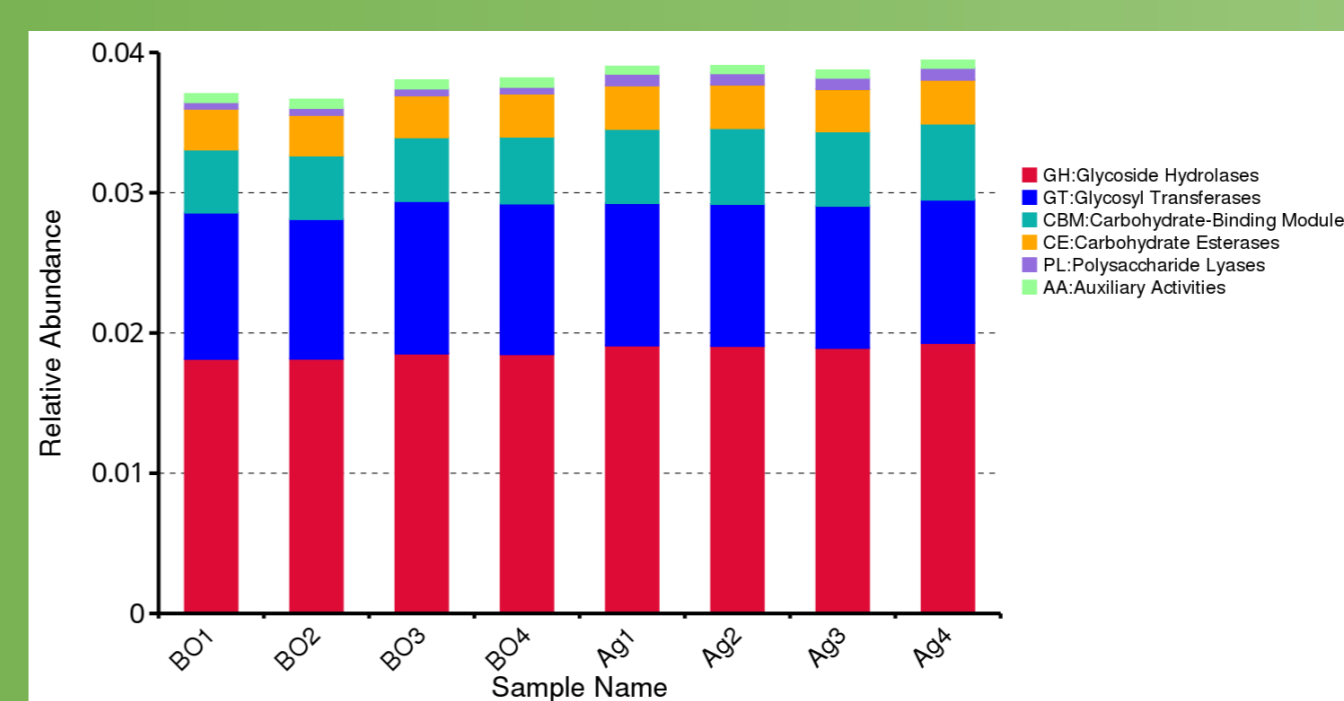


The top 10 most abundant genera present in each sample.

The most abundant phyla is actinobacteria, which is associated with organic matter decomposition.

\* Indicates genera contains known PGPRs (plant growth promoting rhizosphere).  
> Indicates genera contains known pathogens.

## 6. Functional annotation

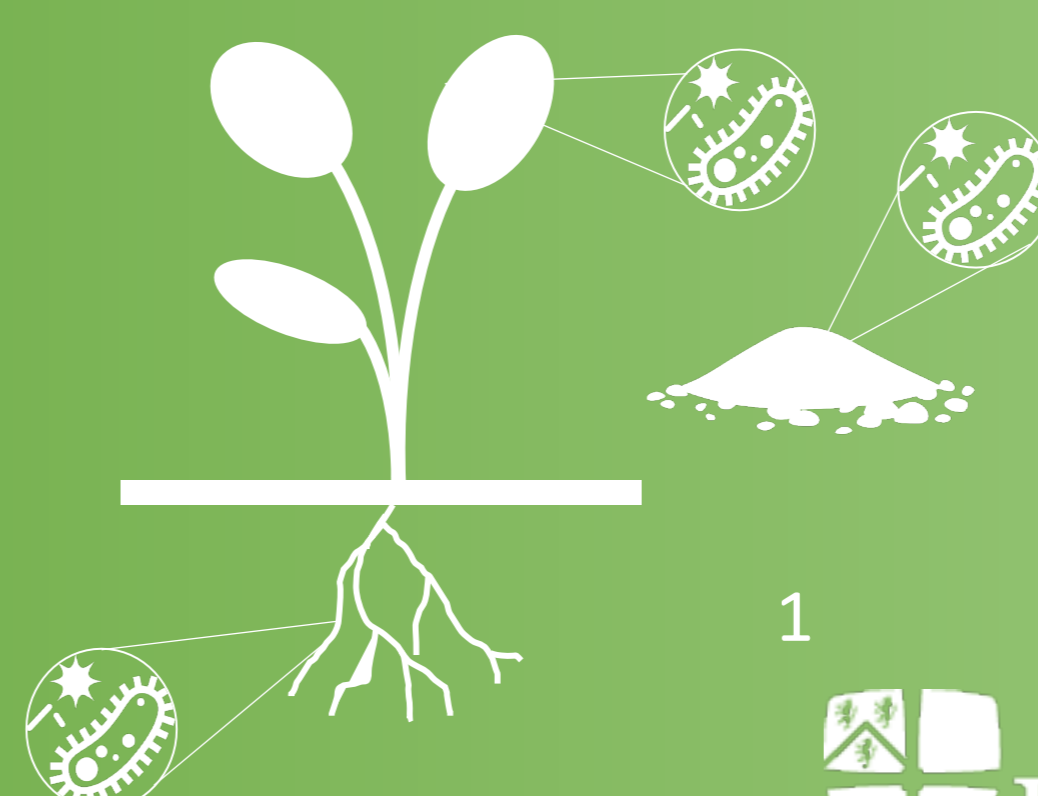


Relative abundance of CAZY genes

The most abundant enzyme is glycoside hydrolases, which can be associated with chitin degradation.

## 7. Conclusion and future work

- The pot trials suggest the frass microbiome increases cabbage biomass.
- Shotgun metagenomic sequencing suggests PGPRs are present in frass that may aid plant growth



The next experiments will determine if PGPRs are colonising cabbage roots by extracting and sequencing microbial DNA from bulk soil, cabbage roots and leaves.