

# IDENTIFICATION OF MICROBIAL INDICATORS OF SOIL POTATO PRODUCTIVITY BASED ON SOIL MICROBIOME ANALYSIS

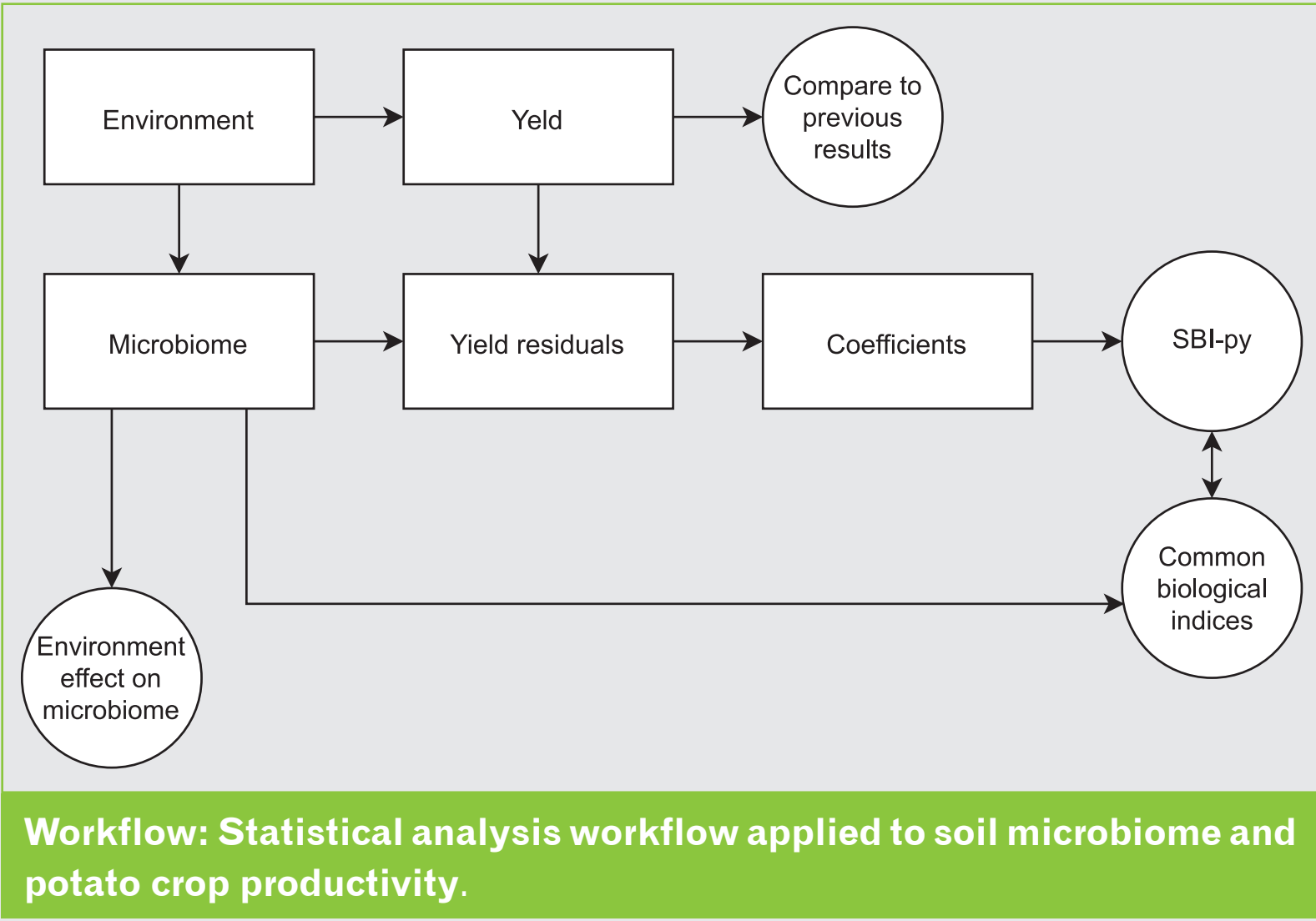
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## INTRODUCTION

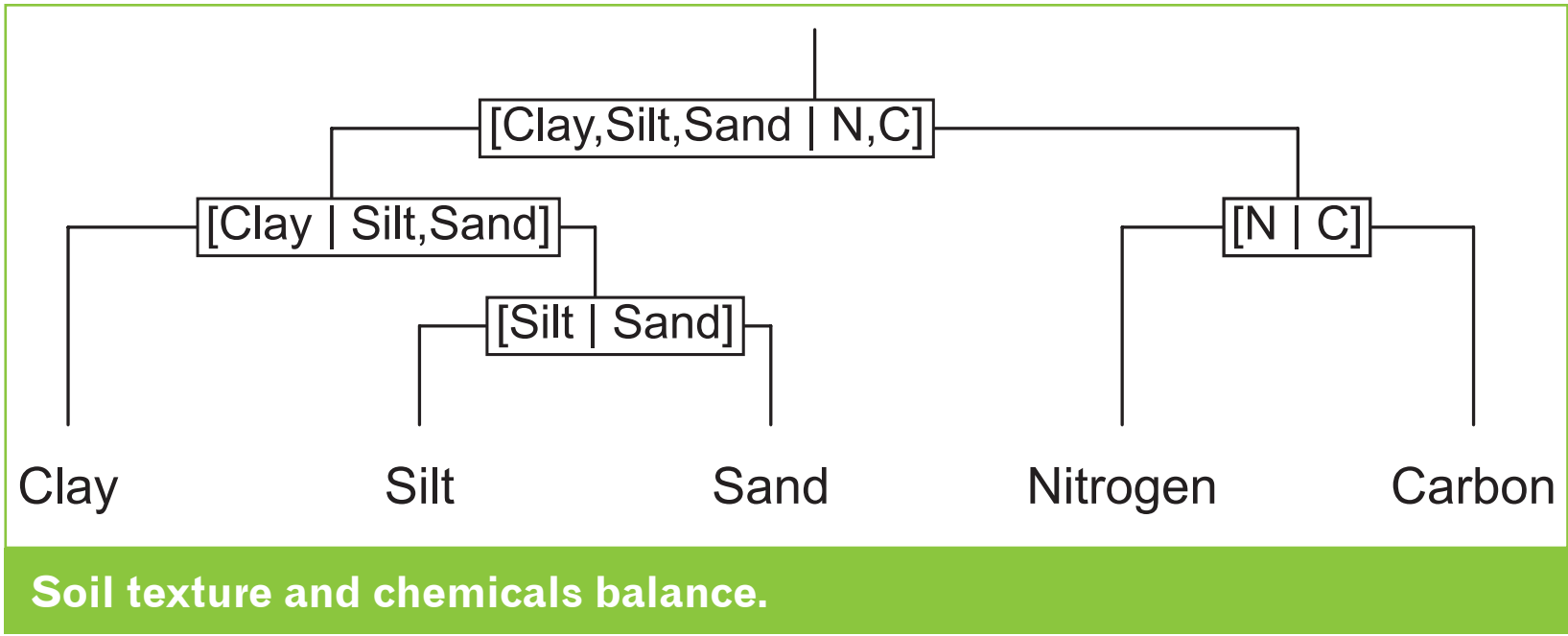
The development of ‘molecular-omic’ tools and computing analysis platforms have greatly enhanced our ability to assess the impacts of agricultural practices and crop management protocols on soil microbial diversity. The use of the notion of Amplicon Sequence Variants (ASV) has improved our ability to define the basis of bacterial soil composition.

We aim to apply an innovative selection procedure using physicochemical, climatic and biological indicators to select ASV that correlate with potato yields; and to develop an integrative approach using a species balance index linked to potato productivity.



## MATERIALS & METHODS

- 52 geo-localized (GPS coordinates) sampling plots in the Province of Quebec in Canada.
- Four (6 cm x 20 cm) soil cores sampled in 2013 and 2014 during the potato flowering period (2500 m<sup>2</sup> area) from each plot and manually homogenized.
- Soil DNA extracted using FastDNA Spin kit for Soil (MPBiomedicals).
- Bacterial diversity assessment targeting 16S rRNA (V4 region) [1,2]. Fungal diversity was also evaluated using ITS region (Data not shown).
- Bio-informatic treatment: QIIME platform [3] and R with DADA2 [4] for filtration.
- Abiotic variables: Meteorological with Cumulative precipitation (PPT), Shannon Diversity Index for rainfall (SDI), Growing degree-days (GDD) and physicochemical (Texture, total nitrogen and total carbon, C/N, pH).



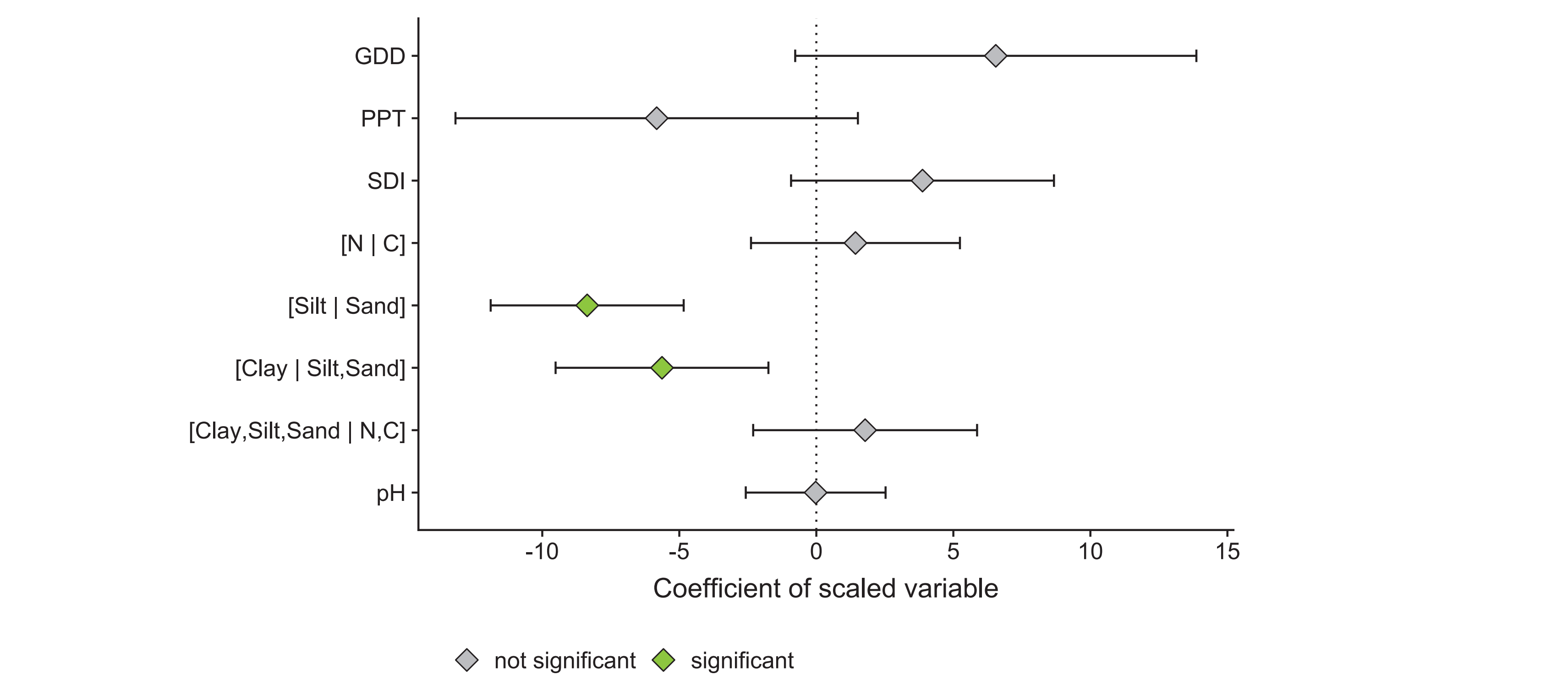
- Alpha diversity metrics: Shannon, Chao1, Pielou
- Isometric log-ratios (ilr) transformation and identification of the residual yield (Y-res):

$$ilr_k = \sqrt{\frac{r_k s_k}{r_k + s_k}} \ln \frac{(x_{i_1} x_{i_2} \dots x_{i_{r_k}})^{\frac{1}{r_k}}}{(x_{j_1} x_{j_2} \dots x_{j_{s_k}})^{\frac{1}{s_k}}}$$

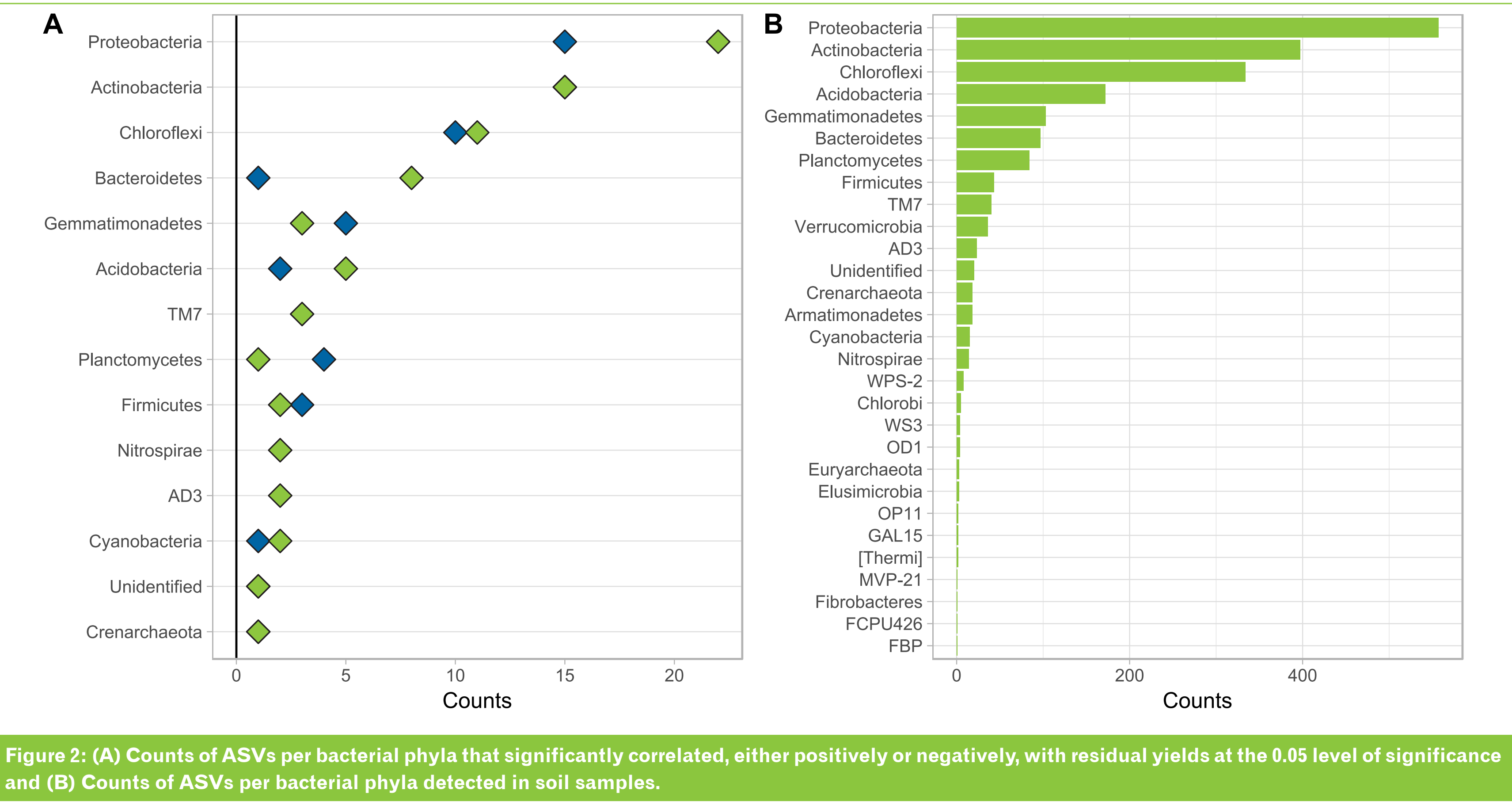
- Centered log-ratios (clr) transformation of ASVs :

$$clr_k = \log \left( \frac{x_k}{(x_1 \times x_2 \times \dots \times x_k)^{1/k}} \right)$$

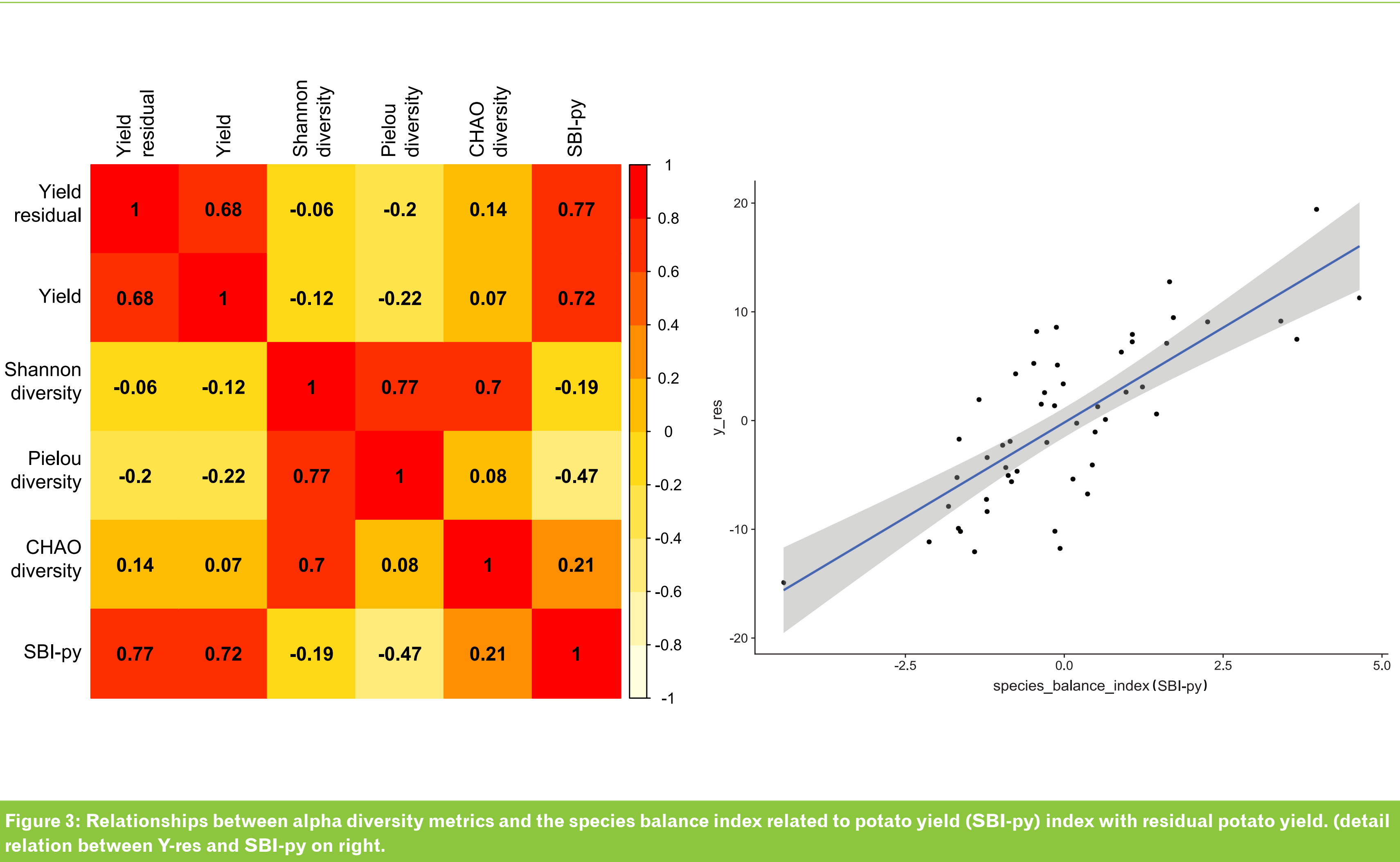
## RESULTS



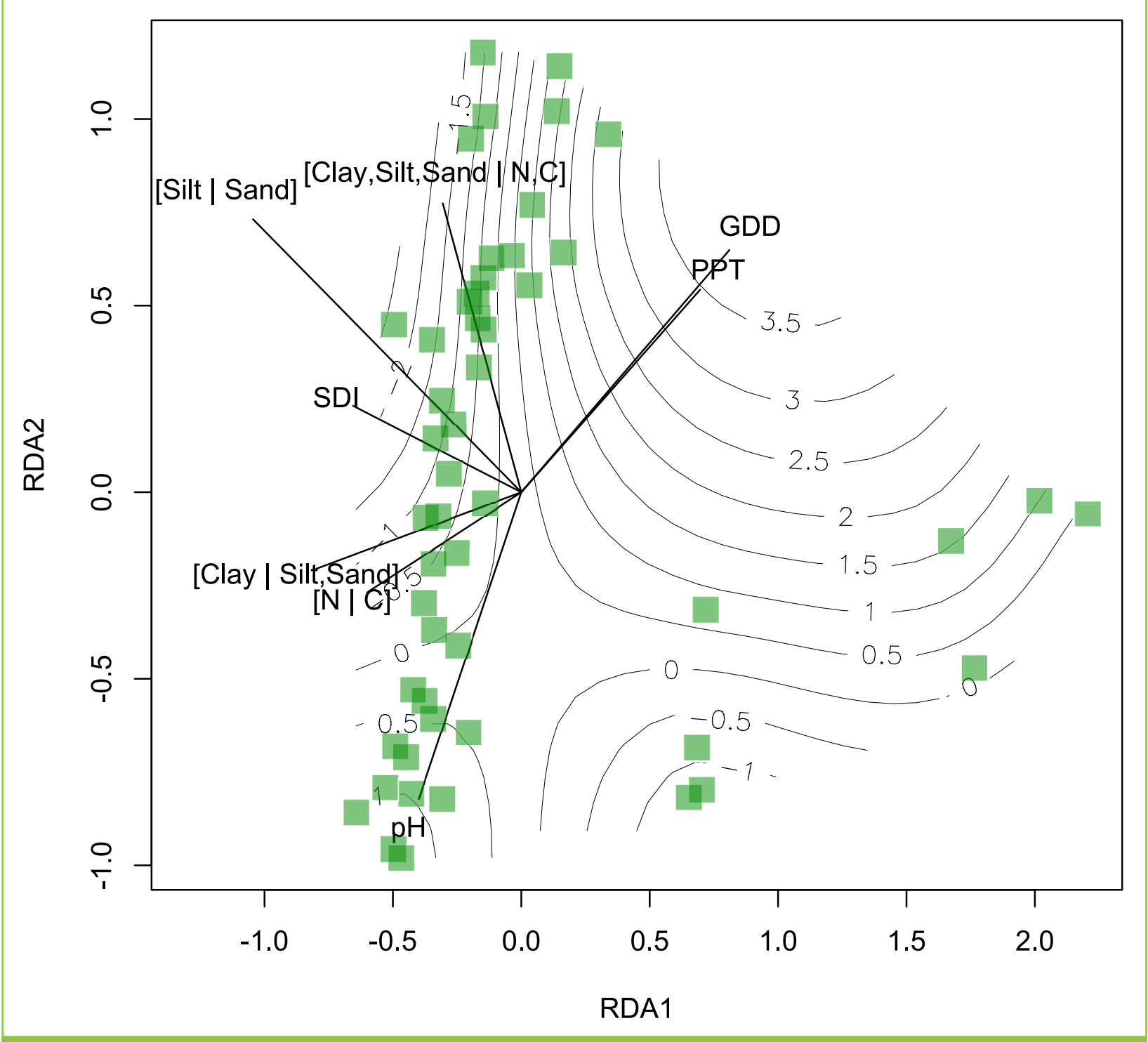
The two textural balances, [Clay | Silt, Sand] and [Silt | Sand] displayed significant negative slope coefficients at the 0.05 level.



The most of retained ASVs were from the Proteobacteria, Actinobacteria, Chloroflexi, Bacteroidetes, Gemmatimonadetes and Acidobacteria phyla. In the case of Proteobacteria, Bacteroidetes and Acidobacteria, there was a higher number of retained ASVs that positively correlated with residual potato yield.



The SBI-py was computed as the log-ratio between the ASV counts associated with positive (numerator) and negative (denominator) significant correlations (at the 0.05 level) between ASV clrs and potato residual yields. Alpha diversity metrics were barely correlated with potato yield and Y-res while SBI-py was well correlated.



## CONCLUSION

Our results highlight the importance of using soil bacterial composition as a biological index of soil quality and, more specifically, of crop productivity. We developed the SBI-py index based on the evidence that specific components of the soil bacterial microbiome can explain aspects of potato productivity. The approach we employed to develop the SBI-py index could be further validated using a larger sample size combined with machine learning techniques.



## REFERENCES

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