## Supplemental material for

## Establishment limitation constrains the abundance of lactic acid bacteria in the Napa cabbage phyllosphere

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## **Supplemental Figures**

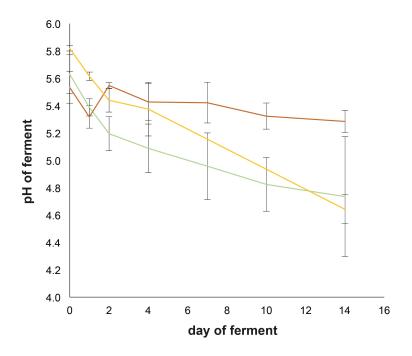
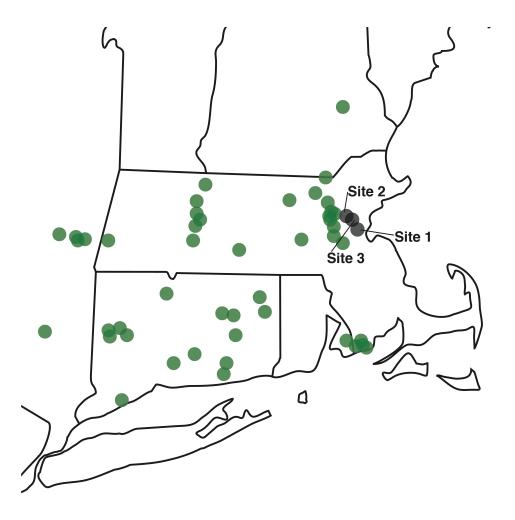
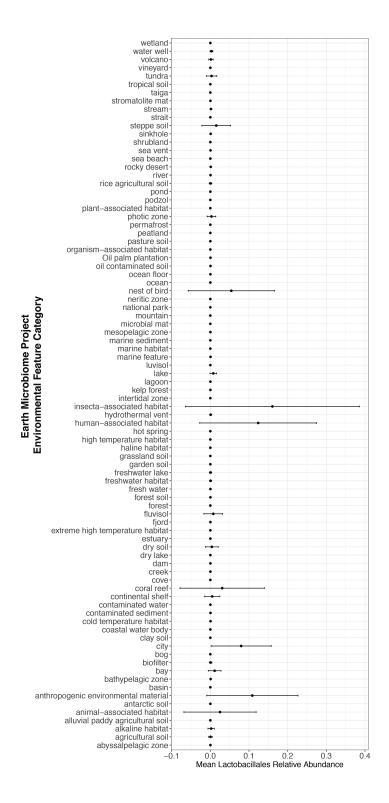


Figure S1. pH of cabbage ferments made with Napa cabbage phyllospheres from three different sites. Points represent replicate ferments (n = 4) sampled at each time point. Error bars represent one standard deviation.



**Figure S2.** Locations of the 51 sites sampled in this study. Sites 1-3 used to generate data in Figure 1 are indicated. All sites were used to generate leaf and soil species pool data in Figure 3.



**Figure S3. LAB abundance in Earth Microbiome Project database.** Data show the relative abundance of OTUs assigned to the Lactobacillales from various environments defined by the Earth Microbiome Project. These data include more categories than the soil and leaf categories presented in Figure 3. Error bars represent one standard deviation.

## Supplemental Tables (all tables provided in supplemental Excel data file):

**Table S1.** Genera of lactic acid bacteria detected in amplicon sequencing of the Napa cabbage phyllosphere from three sites, Napa cabbages purchased at five supermarkets, and soil and leaf species pools

**Table S2.** Summary of all OTUs identified in the Napa cabbage (*Brassica rapa* subsp. *pekinensis*) microbiome grown in the lab (before transplanted to field), after growing at three sites, and after fermentation

**Table S3.** Summary of all OTUs identified in the Napa cabbage (*Brassica rapa* subsp. *pekinensis*) purchased from a supermarket in the Boston, Massachusetts (USA) area

Table S4. Average abundance of OTUs identified in the species pools of soils and leaves