Mapping the Microbiome of Malted Barley and Wort Soured Using Malted Barley

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Background

• Naturally occurring bacteria, wild yeast, and molds (referred to as the microbiome) can be found on grains.
• Grains have been used historically to acidify (sour) wort.
Questions

• What is the native microbiome on various grains?
• What portion(s) of the microbiome thrive during “wort-souring” conditions?
• What is the resulting organic acid profile from the various grains?
Experiment: Sample Set

• Grains determined to be best suited for wort-souring tend to be very lightly malted barley.
• Germination of barley produces large increase in resident microbiome.
• Processing, handling, and packaging can alter microbiome.
Experiment: Sample Set

- 2016 vs 2015
- 4 maltster
- 5 regions
- 6 Varietals
- Pale/Pilsner
- Similar vs Unique Malt Houses

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<th>Harvest Year</th>
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<th>Varietal</th>
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<td>Pale</td>
<td>Endeavor</td>
<td>Texas</td>
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</table>
Experiment: Sample Preparation
(NRBS/Wort Microbiome)

• NRBS (nutrient-rich buffered starter) containing:
  • malt extract,
  • yeast nutrient,
  • CaCO₃,
  • 20g malted barley.
• T=0, 24hr
• NOTE: All studies conducted at 109F and stirred 1000RPM
Experiment: Sample Preparation
(NRBS/Wort Microbiome)

• Wort: 10P wort,
• pH = 4.7,
• 25 mL of NRBS.
• T=0, 24, 48hr
• NOTE: All studies conducted at 109F and stirred 1000RPM
Experiment: Sample Preparation
(Wort NMR)

• Wort: 10P wort,
• pH = 4.7,
• 25 mL of NRBS.
• T=0, 24, 48hr
• NOTE: All studies conducted at 109F and stirred 1000RPM
Experiment: Method

• Malt/Wort Microbiome: Bacterial 16S ribosomal RNA gene targeted sequencing.

• NMR: qNMR Spectroscopy.
Results: Malted Barley Microbiome
Results: Malted Barley Microbiome

- Acinetobacter johnsonii (not much information)
- Corynebacterium glutamicum (typical in soil and plants, helps decompose)
- Proteobacterium symbiont (g=arthrobacter, found in soil)
- Clavibacter michiganesis (tomato rot!)
Results: Soured-Wort Microbiome (t=0)
Results: Soured-Wort Microbiome (t=0)

- *Weisella cibaria*
- *Lactococcus lactic* (used in dairy)
- *Enterobacter aerogenes* (found in GI of humans, generally safe)
Results: Soured-Wort Microbiome (t=24)
Results: Soured-Wort Microbiome (t=24)

- *Weisella cibaria*
- *Lactococcus lactic* (used in dairy)
- *Pediococcus pentosaceous*
- *Lactobacillus reuteri, fermentum, helveticus, delbruekii*
- *Enterobacter aerogenes* (0.3%)
Results: Soured-Wort Microbiome (t=48)
Results: Soured-Wort Microbiome (t=48)

- *Weisella cibaria*
- *Pediococcus pentosaceus* (0.7%)
- *Enterobacter* (2.5%)
Results: Soured-Wort NMR (organic acids)
Results: Soured-Wort NMR (alcohols)
Discussion

• *Weissella cibaria*: first described in 2002 originating from Thai fermented foods (originally called *W. kimchii*) and European sourdough, closely related to *W. confusa*.

• Gram-positive, catalase-negative, non-endospore forming cells with coccoid or rod-shaped morphology. Family *Lueconostocaceae*.

• Obligately heterofermentative

• 59F-113F

• Hydrolyse Arginine

• Produces D and L lactic acid, acetic acid, CO2,

• Does not metabolize lactose, galactose

• Dextran (non-digestable polysaccharide) produced from sucrose

• [https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4362408/](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4362408/)
Further Experiments

• Different conditions: Temperature!
• Nutrition: Amino acids?
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