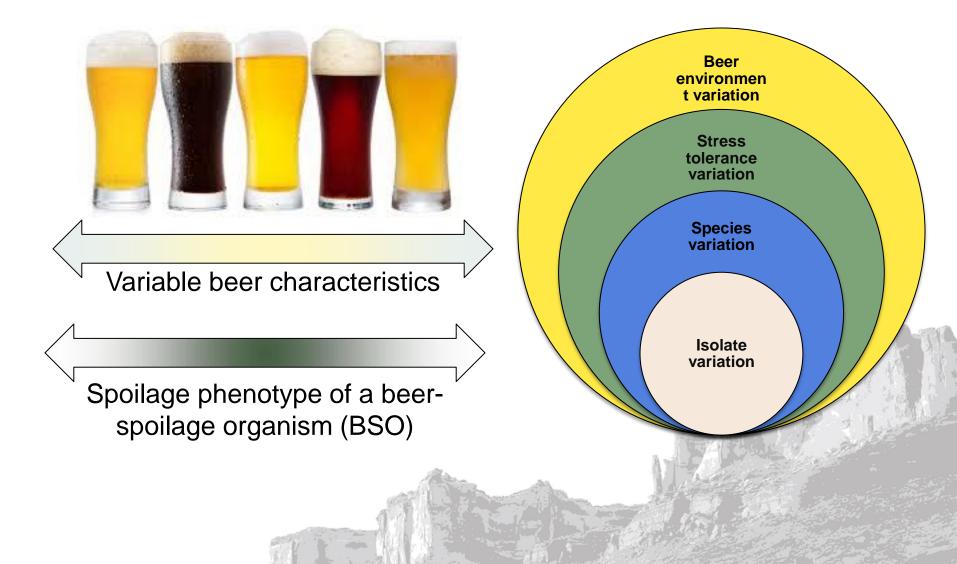


Genome comparisons of *Lactobacillus* and *Pediococcus* reveal genetic markers of brewery adaptation.

Barry Ziola, Jordyn Bergsveinson, Ilkka Kajala August 14th, 2016



Beer-Spoilage ≠ Binary Phenotype

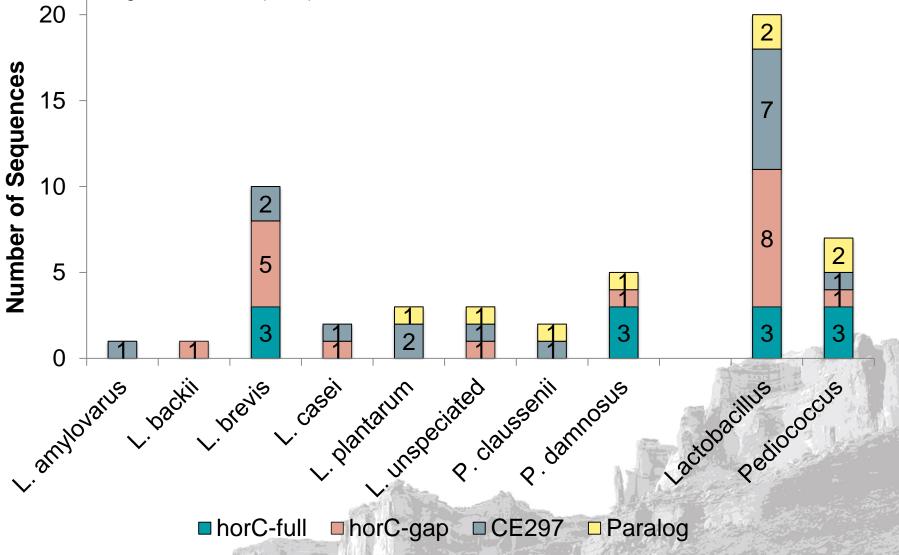




- hitA, horA, horB, horC, bsrA genes
 - not universal false (+) and false (-)
 - detection does not guarantee function
 - plasmid-harbored...but assumed
- 3-4 genes to describe all of LAB BSOs!?

horC variability

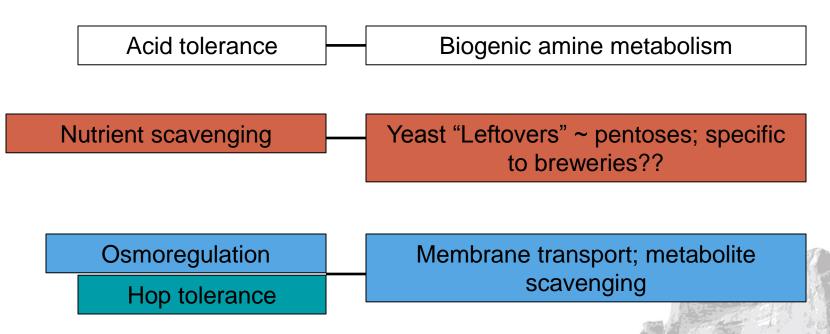
Genetic Variability in the Hop-Tolerance horC Gene of Beer-Spoiling Lactic Acid Bacteria Bergsveinson et al. (2016) J Am Soc Brew Chem 74:173-182





What activities are important during growth in beer?

Transcriptome analysis of Lactobacillus brevis BSO 464^{*} and Pediococcus claussenii ATCC BAA-344^{+**}



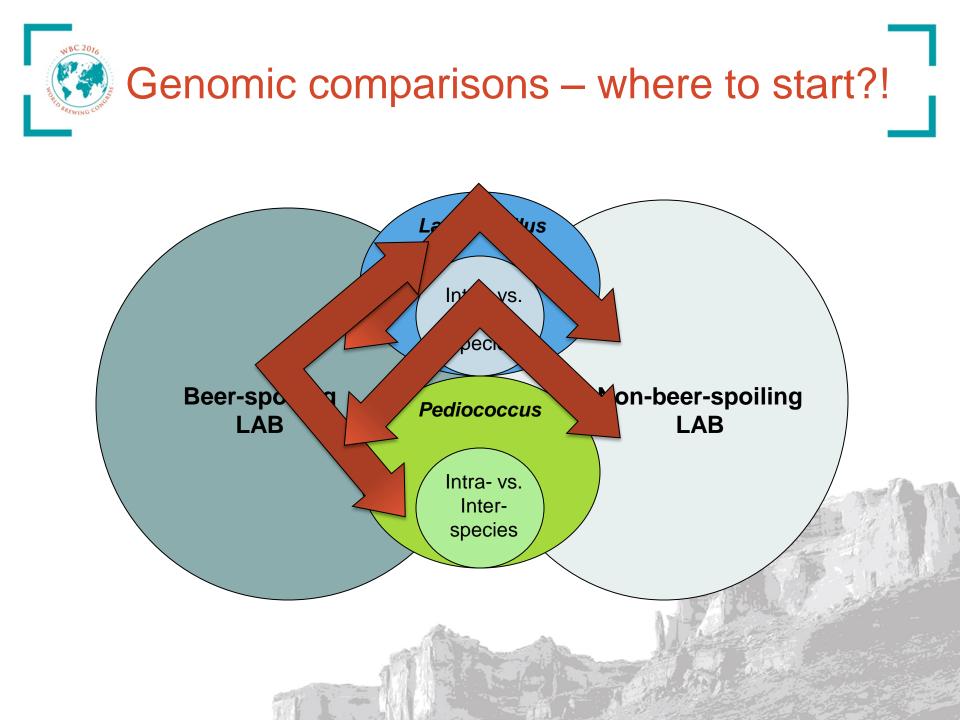
^{*}Transcriptome analysis of beer-spoiling Lactobacillus brevis BSO 464 during growth in degassed and gassed beer. Bergsveinson et al. (2016) **Int J Food Microbiol 235:28-35** ^{**}Transcriptome Sequence and Plasmid Copy Number Analysis of the Brewery Isolate Pediococcus claussenii ATCC BAA-344T during Growth in Beer. Pittet et al. (2013) **PLOS ONE 8(9):e73627**

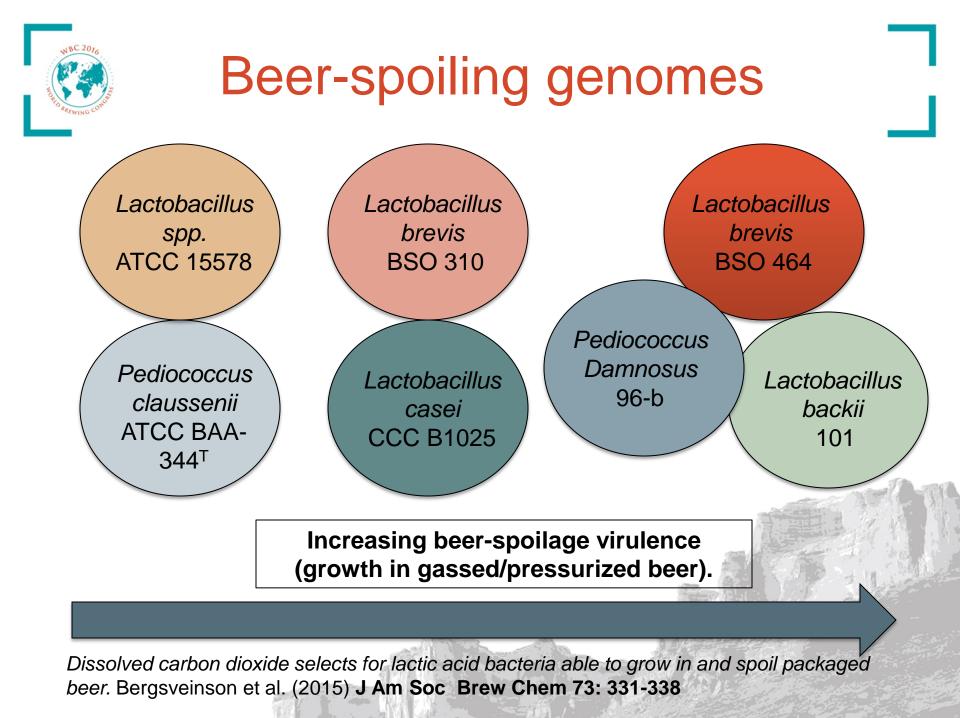


Mining meta-data for utility...

But where to start!?

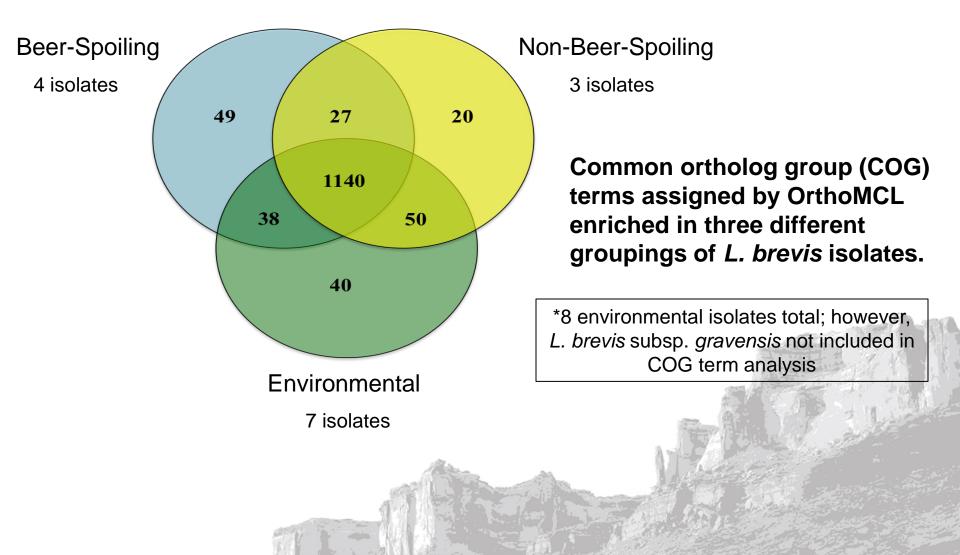
- Limited # of complete genomes of beerspoilage-related LAB
- Quality of genetic data publically available?
- Confounding role of plasmids/mobile genetic elements







To get anywhere, had to start at intra-species = *L. brevis* level





The leads...

Previous analysis of *L. brevis* beerspoiling organisms vs. non-beerspoilage isolates for "eco-type" specific markers (Behr et al., 2015. Food Microbiol, 51).

Beer-spoilage isolates isolated from one geographical location.

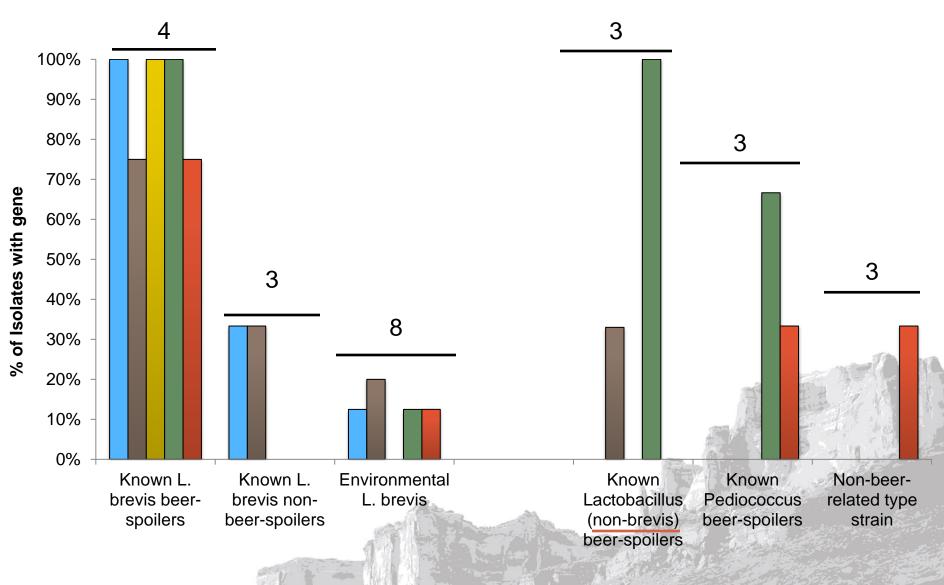
- histidine kinase
- specific transcriptional regulator arsR and cinA
- polygalacturonase (enzyme related to plant-degradation)

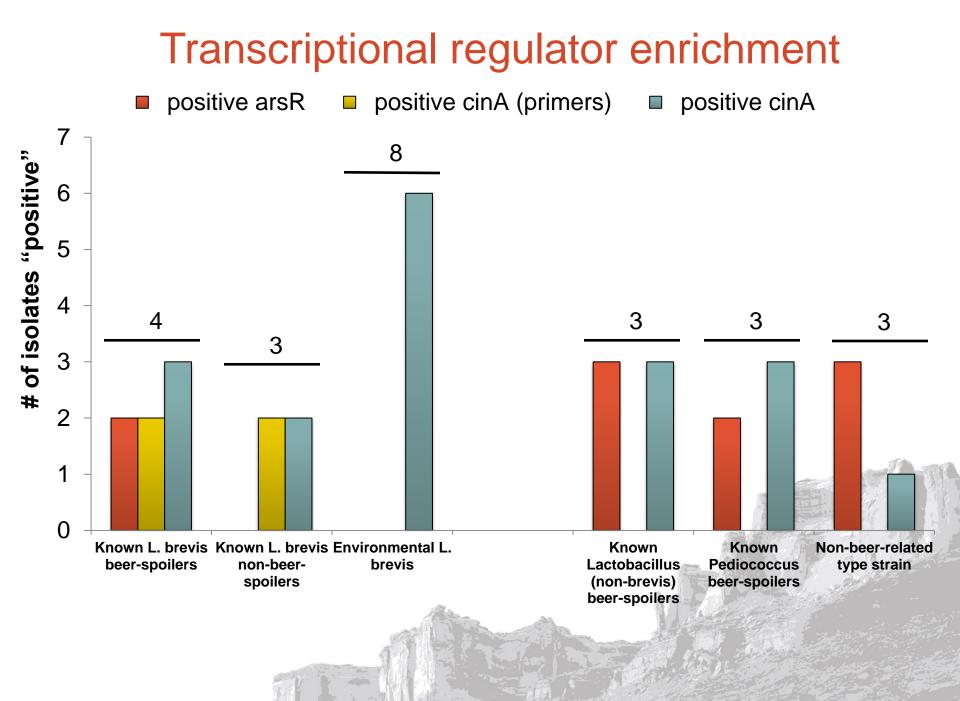
Transcriptional analysis during growth in beer:

- Nutrient ABC transporters
 - Specific transcriptional regulators
- enzymes related to plantdegradation

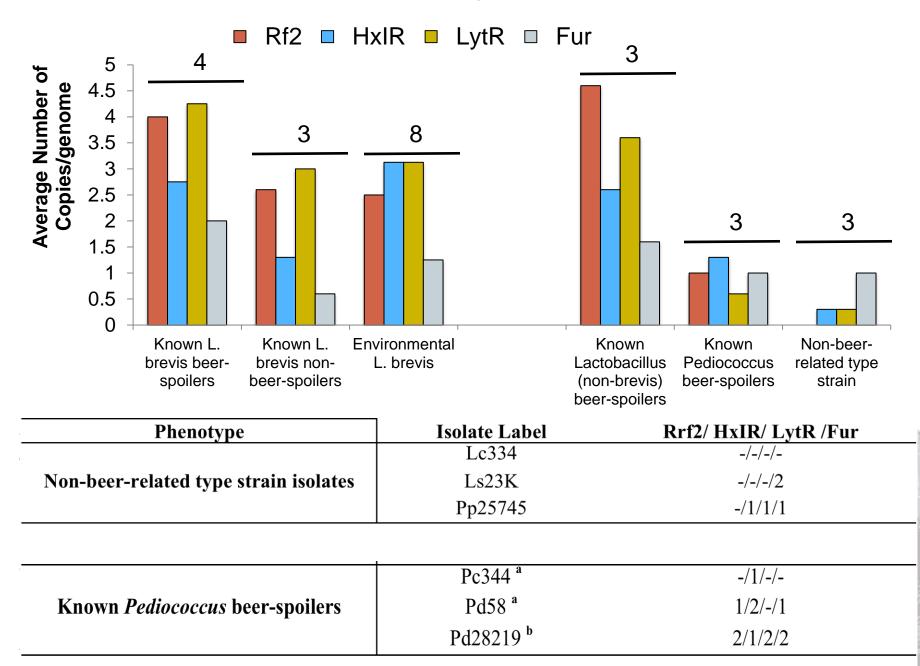
- Arabinose ABC permease
- Polygalacturonase
- Signal transduction histidine kinase

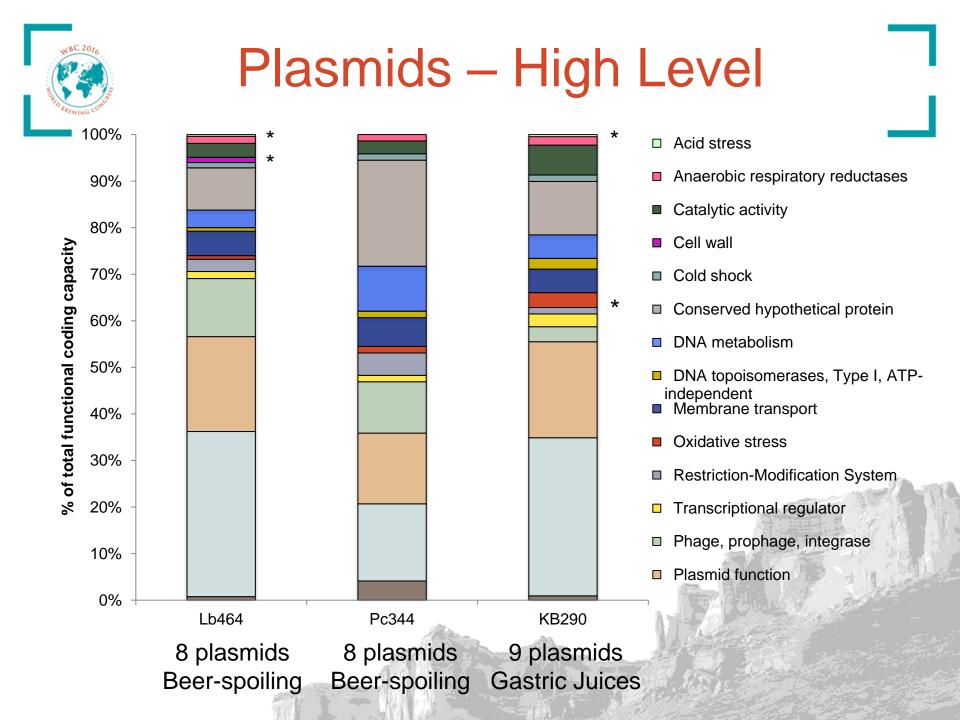
- Coniferyl Aldehyde Dehydrogenase
- PTS Sorbose-specific IIC Component



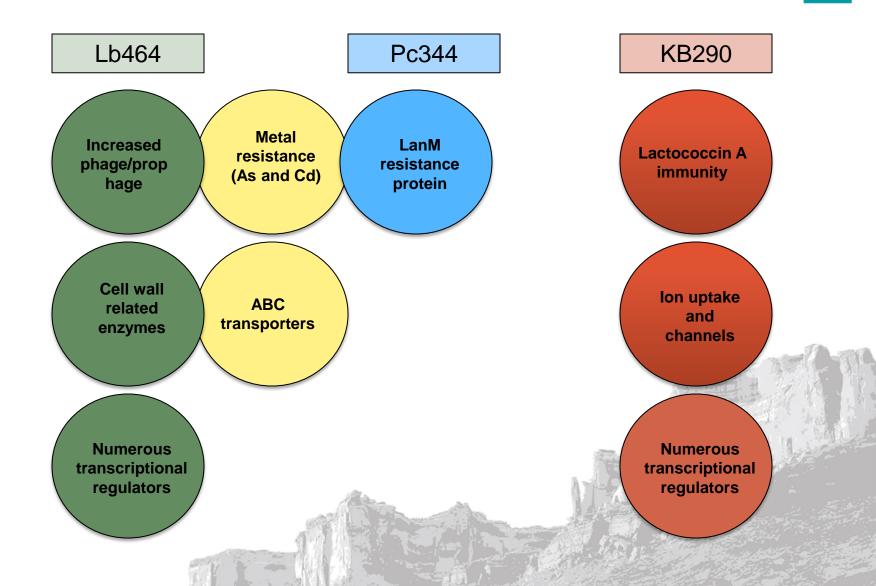


Transcriptional regulator enrichment



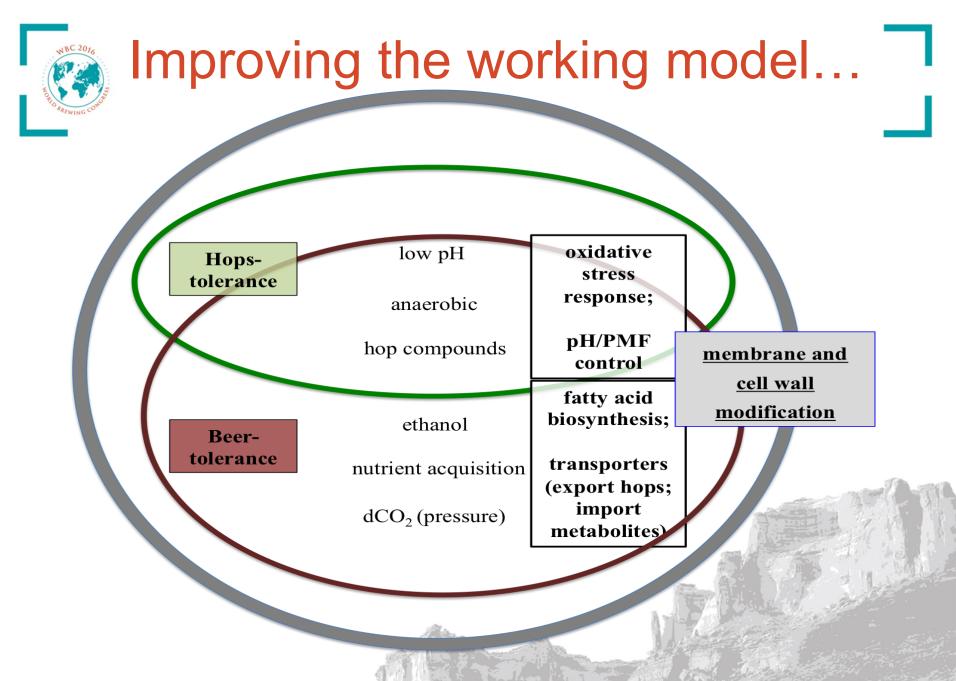








- Enzymes related to cell wall modifications and nutrient scavenging
- Plasmids confer very specific adaptations
- Can't underestimate the influence of selection environment (location~brewery)
- Increased need for quality, publicly available beer-spoilage-related LAB genomes
- Further "omics" studies!!



Bergsveinson, J. (2015). Chapter 9, PhD Thesis. University of Saskatchewan

Acknowledgements









The Science of Beer

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- Ilkka Kajala