

High amylose wheat starch structures display unique fermentability characteristics, microbial community shifts and enzyme degradation profiles

Alexander T. Bui¹, Barbara A. Williams¹, Emily C. Hoedt^{2,3}, Mark Morrison², Deirdre Mikkelsen¹, Michael J. Gidley¹

¹Centre for Nutrition and Food Sciences, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Brisbane, Australia

²Diamantina Institute, Faculty of Medicine, Translational Research Institute, The University of Queensland, Woolloongabba, Brisbane, Australia

³Department of Microbiology and APC Microbiome Institute, University College Cork, Ireland

Supplementary material

Table S1: SCFA production of HAWS over 72h fermentation from wheat starch substrates.

Substrate	Ac	Pr	Bu	Total	% AcTot	% PrTot	% BuTot	BrChPpn
W37	3.84 ^a	2.59 ^a	0.87 ^a	7.71 ^a	52.21 ^c	31.22 ^a	10.56 ^{bc}	0.20 ^b
W47	3.54 ^{ab}	2.19 ^b	0.82 ^a	6.94 ^{ab}	53.95 ^{ab}	29.12 ^b	10.48 ^{bc}	0.20 ^b
W85	3.44 ^{ab}	2.07 ^b	0.94 ^a	6.85 ^{ab}	52.58 ^{bc}	28.51 ^{bc}	11.85 ^{ab}	0.21 ^{ab}
W86	3.34 ^{ab}	1.89 ^{bc}	0.94 ^a	6.57 ^{ab}	52.67 ^{bc}	28.20 ^{bcd}	12.36 ^a	0.21 ^{ab}
W87	3.19 ^{ab}	1.88 ^{bc}	0.86 ^a	6.35 ^b	52.23 ^c	28.74 ^b	11.67 ^{ab}	0.22 ^{ab}
W93	2.93 ^b	1.63 ^c	0.81 ^a	5.78 ^b	52.53 ^{bc}	26.72 ^d	12.41 ^a	0.26 ^a
Prob. Starch	0.0001	<0.001	0.0277	0.0002	<0.001	<0.001	<0.001	0.0005
MSD*	0.656	0.397	0.253	1.292	1.595	1.738	1.439	0.054
Native	3.33 ^A	1.73 ^B	1.01 ^A	6.50 ^B	53.37 ^A	25.57 ^B	12.97 ^A	0.25 ^A
Cooked	3.45 ^A	2.27 ^A	0.78 ^B	6.88 ^A	52.08 ^B	31.08 ^A	10.48 ^B	0.19 ^B
Prob. Cook	0.1901	<0.001	<0.001	0.0374	<0.001	<0.001	<0.001	<0.001
MSD*	0.181	0.109	0.069	0.355	0.439	0.478	0.396	0.015
Prob. Starch x Cook	0.0091	<0.001	0.3994	0.0115	0.1601	<0.001	<0.001	0.0238

^{a,b,c,d} Superscripts in the same column for HAW starches which differ, are significantly different with a p-value (<0.05).

^{A,B} Superscripts in the same column for “Cook” which differ, are significantly different with a p-value (<0.05).

*MSD is the minimum significant difference.

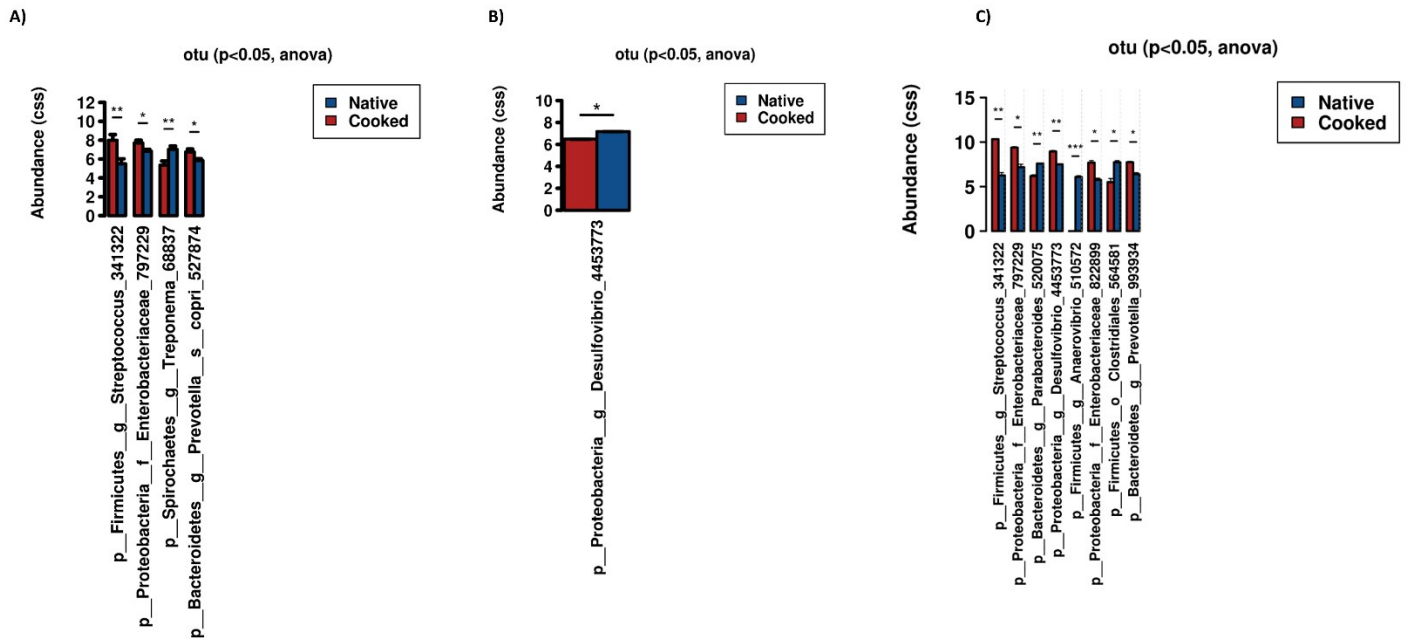


Fig. S1: One-way ANOVA test for relative abundance as a result of cooking treatment of A) W37 low amylose at 72h, B) W93 high amylose at 72h and C) Comparing both W37 and W93 over the fermentation time course. Parameters were set to the top 20 OTUs using Calypso.

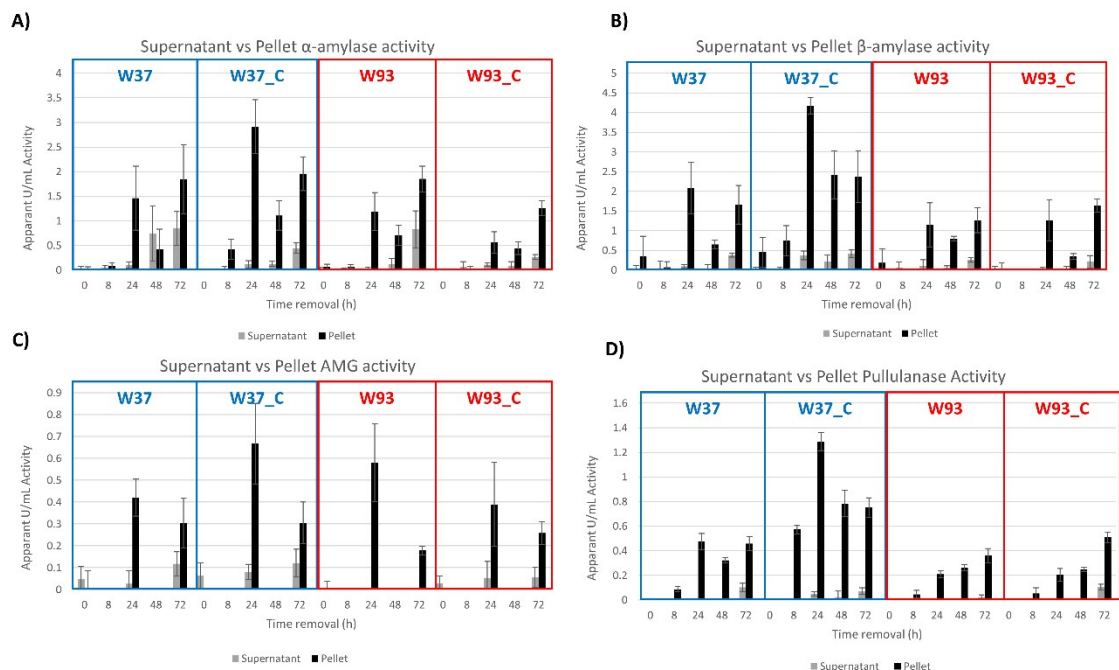


Fig. S2: Comparison of enzyme activity (U/mL) from A) α -amylase, B) β -amylase, C) amyloglucosidase (AMG), and D) pullulanase between the supernatant and bacterial pellet. Enzyme activities are from W37 and W93 along with their cooked counterparts over the 72 h fermentation. Absorbance values from the medium + inoculum control have been subtracted from enzyme activity values to generate the apparent activity.

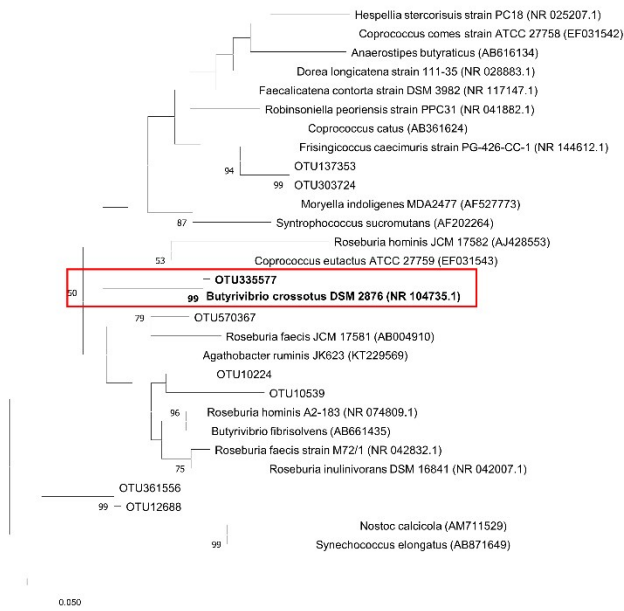


Fig. S3 Phylogenetic analysis of 16S rRNA unclassified Lachnospiraceae to identify closest taxonomic assignment. Red box highlights the most abundant unclassified Lachnospiraceae present in this study. Only bootstrap values >50% are shown and the scale bar represents 5% sequence divergence, with *N. calcicola* and *S. elongatus* used as the outgroups.