

**Online supplementary figures to**

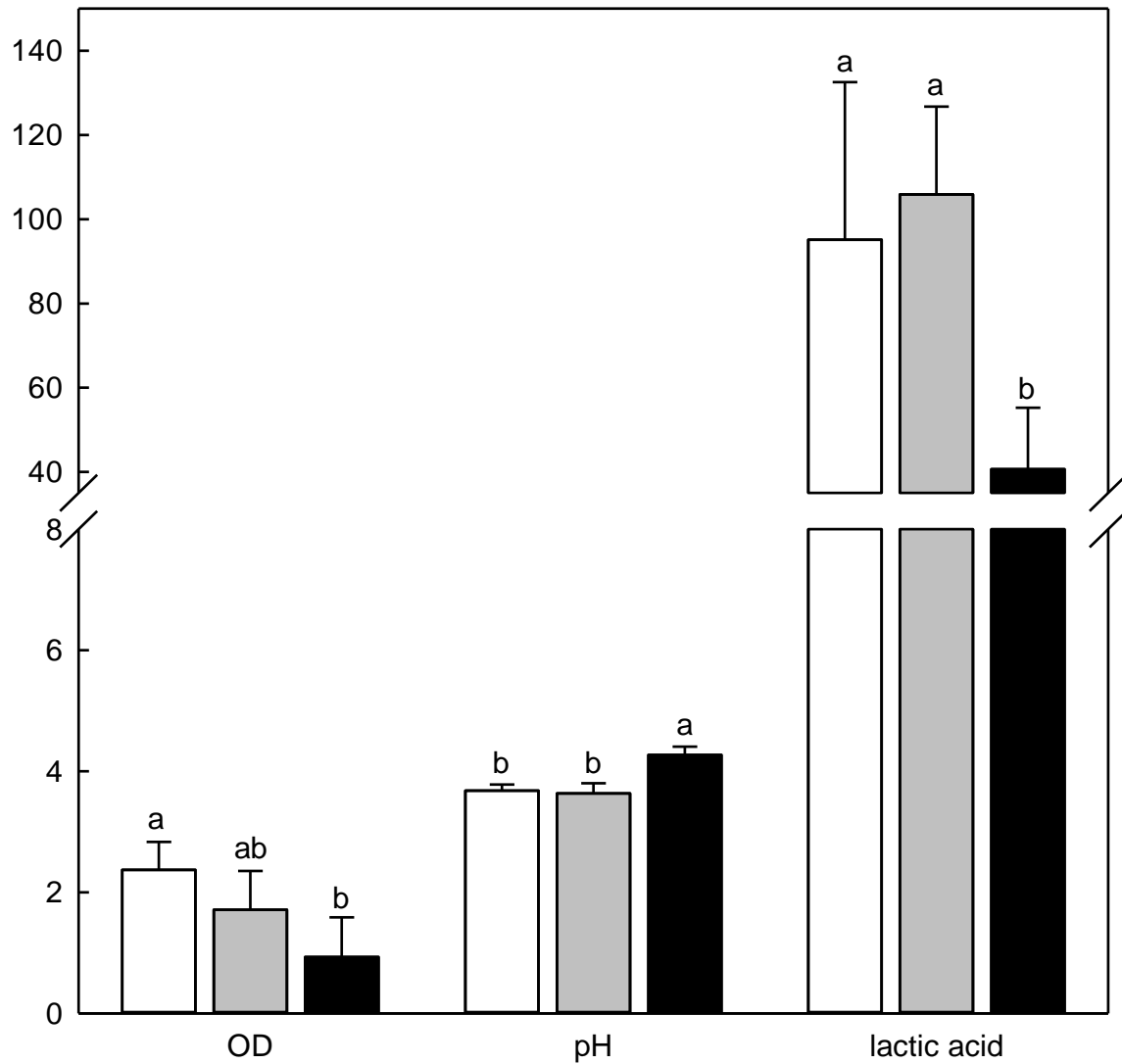
**Characterization of the extracellular fructanase FruA in *Lactobacillus crispatus* and its contribution to fructan hydrolysis in breadmaking.**

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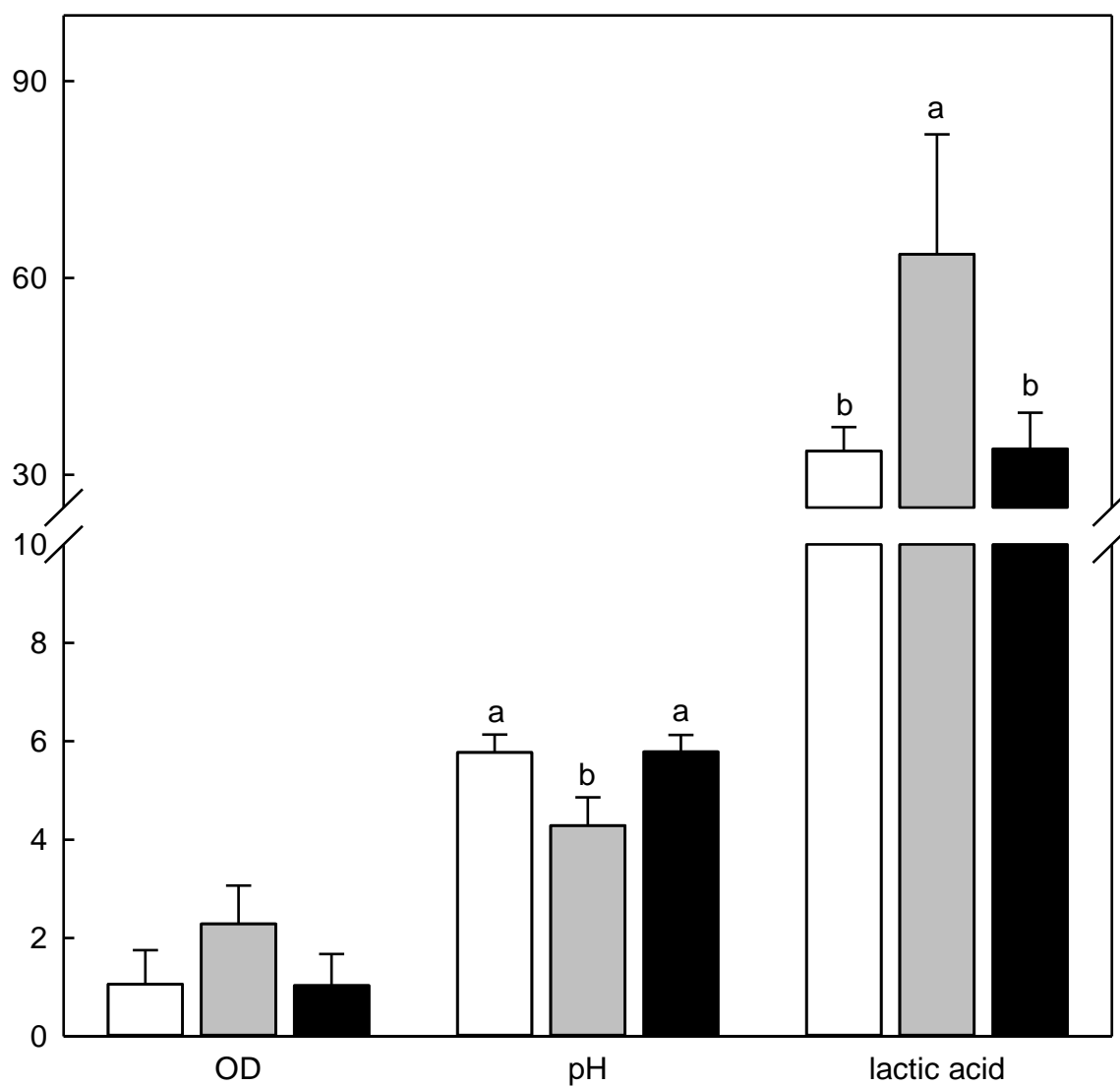
**Figure S1.** Growth of *L. crispatus* DSM29598 in mMRS with inulin (white bar), regular mMRS (gray bar) or mMRS base (black bar).

**Figure S2.** Growth of *Lm. frumenti* FUA3675 in mMRS with inulin (white bar), regular mMRS (gray bar) or mMRS base (black bar).

**Figure S3.** Operon structure of FruA in *L. crispatus* (Panel A) and homology to mobile element proteins upstream and downstream of FruA to transposases of lactobacilli (Panel B and Panel C).



**Figure S1.** Growth of *L. crispatus* DSM29598 in mMRS with inulin (white bar), regular mMRS (gray bar) or mMRS base (black bar). *L. crispatus* was incubated overnight in mMRS with 1% of inulin, regular mMRS or mMRS base broth, respectively. Lactic acid was expressed as mmol / kg. Significant differences ( $p < 0.05$ ) between different media are indicated by different letters.

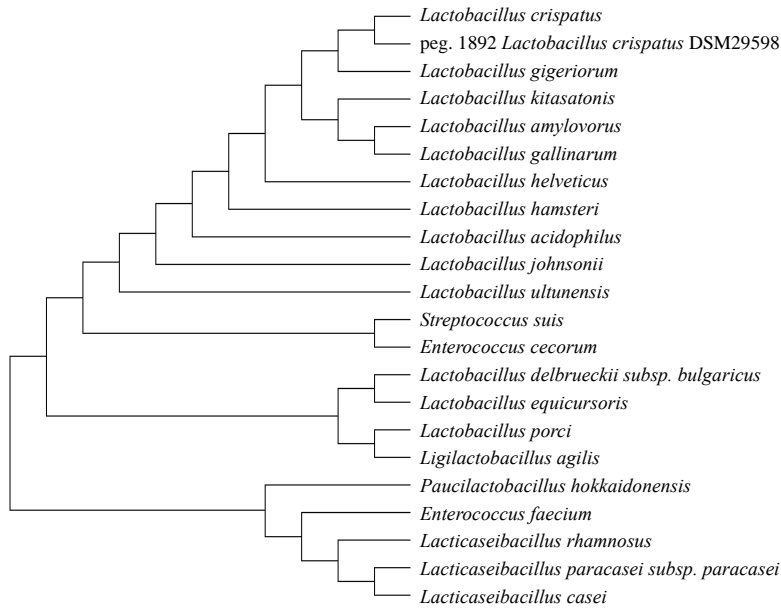


**Figure S2.** Growth of *Lm. frumenti* FUA3675 in mMRS with inulin (white bar), regular mMRS (gray bar) or mMRS base (black bar). *Lm. frumenti* FUA3675 was incubated overnight in mMRS with 1% of inulin, regular mMRS or mMRS base broth, respectively. Lactic acid was expressed as mmol / kg. Significant differences ( $p < 0.05$ ) between different media are indicated by different letters.

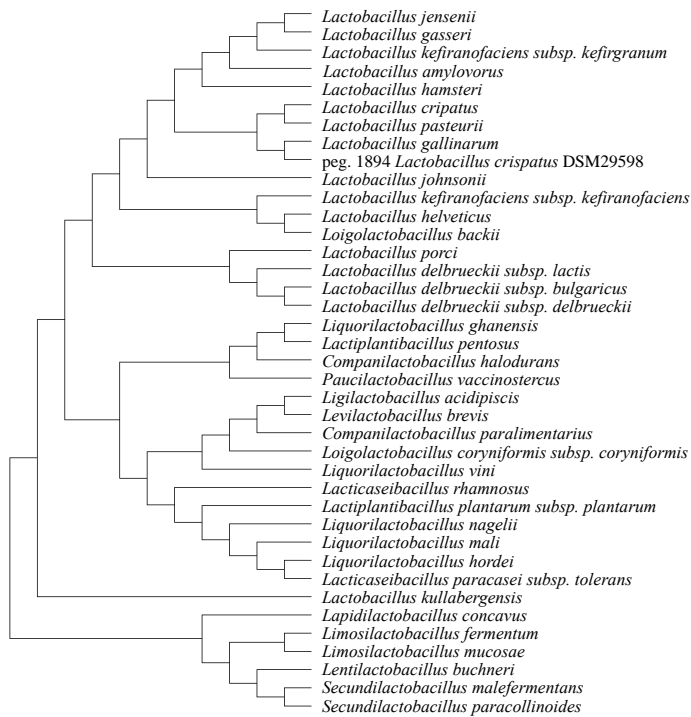
A



B



C



**Figure S3.** Operon structure of FruA in *L. crispatus* (Panel A) and homology to mobile element proteins upstream and downstream of FruA to transposases of lactobacilli (Panel B and Panel C). Panel A. From left to right: IS66 family transposase; hypothetical protein, mobile element protein, extracellular FruA, IS256 family transposase. Panel B and C. Sequences in all genomes were identified by BLASTp using peg.1892 (B) or peg.1894 (C) in *L. crispatus* DSM29598 as query sequences. Shown are representative sequences from every species of lactic acid bacteria in which the protein was identified with more than 50% coverage and more than 50% amino acid identity.