Enzymes as a tool to characterise cereal flavour and chemistry

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BACKGROUND

Whole grain cereal products are widely agreed to be health-beneficial, which is presumed to relate to their high level of bioactive phytochemicals and dietary fiber. However, consumers' food choices are mostly driven by taste, and the healthiness is perceived more as an extra positive element. In particular, certain intrinsic flavours of cereal whole grains are often not regarded attractive by consumers. For instance, the intensive and bitter flavour of rye, which is expected to be caused by specific phenolic compounds and small peptides, can form obstacles for its use[1].

The flavour of cereal foods can be modified by different bioprocessing methods[2,3]. Enzymes, such as lipases, proteases and amylases, are generally used as bioprocessing aids in breadmaking mainly for texture modification, but enzymes can also have impact on the perceived flavour (Table 1). Moreover, germination and sourdough fermentation can be used to adjust flavour and texture of whole grain cereal products[3]. Bioprocessing of flavour of whole grain cereals can be challenging, since, due to the complexity of grain structure, flavour attributes are not uniformly distributed in the kernel. In rye grain, the innermost endospermic part is considered mild-tasting, whereas the outermost bran fraction, which also contains significant amounts of bioactive compounds, is perceived as bitter[4].

Table 1 Possible enzyme classes, which could have potential for tailoring cereal flavour

Enzyme type	Enzyme class	Action / substrate	Hypothetical influence on flavour
Polymerising enzymes	Laccase, peroxidase, glucose oxidase, tyrosinase	Polymerisation of phenolic compounds	Decreased bitterness
	Transglutaminase, tyrosinase	Polymerisation of peptides and proteins	Decreased bitterness
Hydrolysing enzymes	Protease	Hydrolysis of proteins (or peptides)	Increased (or decreased) bitterness
	Lipase	Hydrolysis of lipids	Increased bitterness
	Xylanase, hemicellulase, cellulase	Hydrolysis of cell wall material	Increased bitterness

AIM

The aim of the study was to increase understanding of the correlations between the chemistry and the characteristics of perceived flavour of rye-derived foods, and to screen bioprocessing techniques for targeted flavour modification. The specific objective was to develop controlled enzymatic tools to tailor the perceived flavour of rye.

EXPERIMENTAL

Proteases and lipases (Table 2) were used to selectively modify protein- and lipid-derived non-volatile compounds of rye bran. Flour-water suspensions were prepared and treated with the enzymes (Fig. 1). Enzyme dosages of the proteases and lipases were 500 and 1000 nkat/g substrate, respectively, based on the content of proteins and lipids of the bran. After the enzymatic treatments, chemical analyses (free amino nitrogen content and lipid composition) and sensory descriptive profiling of the bran samples were performed. The perceived flavour of the enzyme-treated rye bran was assessed as a screening-type analysis using a 6-member trained sensory panel. Due to the small size of the sensory panel, the data was not analysed statistically.

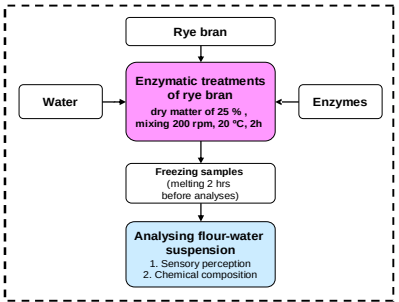

Figure 1 Process scheme for the treatments of rye fractions: preparation of rye supernatant and flour-water suspension.

Table 2 Proteases and lipases studied in the flavour modification of rye bran

Proteases	Supplier
Protease 1	Amano
Protease 2	Amano
Protease 3	Novozymes
Protease 4	Biocatalysts

Lipases	Supplier
Lipase 1	Biocatalysts
Lipase 2	Novozymes
Lipase 3	Novozymes
Lipase 4	Novozymes

RESULTS

Among the studied proteases, Protease 1 was observed to most effectively increase the bitterness and aftertaste intensity of rye, followed by Protease 2 and Protease 4 (Fig. 2). Protease 2 was detected to have a rather high xylanase side activity (data not shown), which may explain the influence of the enzyme preparation on the decreased viscosity. The bitterest rye bran sample was also the one with the highest content of free amino nitrogen (Fig. 3), suggesting that a higher degree of protein hydrolysis could lead to the more intense bitterness of rye bran.

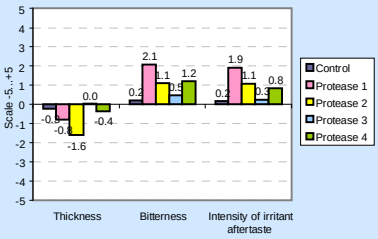

Figure 2 Sensory profiles of rye bran after protease treatments. The samples were evaluated as flour-water suspensions (n=6).

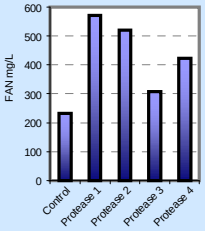

Figure 3 Free amino nitrogen content (descriptive for the degree of protein hydrolysis) of rye bran after protease treatments

Among the studied lipases, Lipase 3 increased most effectively the bitterness and aftertaste intensity of rye bran, followed by Lipase 2 (Fig. 4). The lipases had no impact on the viscosity of the rye samples. According to the lipid analyses, the Lipase 3 -treated rye bran had the highest content of free fatty acids (Fig. 5). The other lipases had clearly less effect on the rye lipids. The result suggests that the liberated fatty acids from the triglycerides may correlate with the bitterness and intense aftertaste of rye.

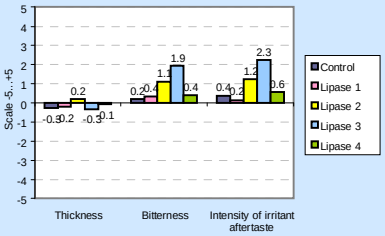

Figure 4 Sensory profiles of rye bran after lipase treatments. The samples were evaluated as flour-water suspensions (n=6).

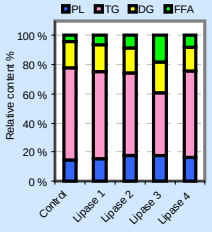

Figure 5 Lipid profiles of rye bran after lipase treatments (polar lipids = PL, triglyceride = TG, diglyceride = DG, free fatty acid = FFA).

CONCLUSIONS

- Enzymatic treatments with proteases and lipases enhanced the bitterness and flavour intensity of rye bran.
- Both peptides and lipid-derived compounds of rye bran can have a significant role in the formation of the rye flavour.
- The sensory results must be considered as suggestive due to the small size of the panel. Full-size assessments by a 10-member panel in two replicate sessions will be conducted in the next step to confirm the results obtained.
- Proteases and lipases with different substrate specificities showed potential in studying different flavour-active compounds of rye.

LITERATURE CITED

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