SELECTION OF LACTIC ACID BACTERIA FOR RYE BREAD SOURDOUGH

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Lactic acid bacteria are widely used to produce diverse type of fermented products. One of conventional applications for lactic acid bacteria is inclusion into sourdough for bread baking. These microorganisms play a key role in dough fermentation of rye flour or wheat and rye mixture since the yield of stable and well-leavened rye dough is possible only in acidic environment. Lately, despite the development of accelerated baking technologies and technological improvements, which in some cases eliminate the need for sourdough, interest in the tradition of making bread using sourdough as a source of flavoring, nutrient and health-enhancing compounds is constantly growing across the globe. It is natural therefore that focus of the researchers is centered on seeking new strains of lactic acid bacteria attractive as potential constituents of rye bread sourdough.

Screening of strains-candidates to be included in the consortia for rye flour fermentation was conducted among collection cultures (23 strains), isolates from rye flour samples (154 strains) and among craft rye dough cultures for spontaneous fermentation kindly provided by private households of Minsk, Turov, Zhitkovichi (21 strains).

Identification of lactic acid bacteria following examination of morphological, cultural, physiological and biochemical characteristics of the cultures and guided by the data of MALDI TOF mass spectrometry indicated that the compared microorganisms represented genera *Lactiplantibacillus*, *Limosilactobacillus*, *Pediococcus*, *Weissella*, *Lactococcus*. The majority of lactic acid bacteria isolated from rye flour samples belonged to genera *Lactiplantibacillus* and *Pediococcus*. Representatives of genera *Lactiplantibacillus* and *Levilactobacillus* prevailed among domestic variants of rye bread sourdoughs.

Evaluation of acidogenic capacity of analyzed cultures upon 16 h fermentation in water-flour suspension by Neumann technique and organoleptic assessment of the obtained solutions sorted out for further studies 10 strains of lactic acid bacteria referred to species *Levilactobacillus brevis* (4 strains) *Lactiplantibacillus plantarum* (3 strains) and singular strains of species *Lactiplantibacillus paraplantarum*, *Limosilactobacillus fermentum*, *Weissella cibaria*.

Glycosyl-hydrolases produced by lactic acid bacteria constituting starter cultures largely determine biochemical processes during fermentation of flour mixtures. Chromogenic substrates o-nitrophenyl-β-D-galactopyranoside, o-nitrophenyl-α-D-galactopyranoside, 4-nitrophenyl-β-D-glucopyranoside were used in 1 mmol concentration to assay activities of β-galactosidase, α-galactosidase, β-glucosidase, respectively. It was found that all tested bacteria of species *Levilactobacillus brevis* and *Limosilactobacillus fermentum* were characterized by synthesis of proteins with α-galactosidase and β-galactosidase activities in the course of growth on media with glucose and maltose. β-glucosidase activity was revealed in all representatives of species *Lactiplantibacillus plantarum*, *Levilactobacillus brevis* and *Lactiplantibacillus paraplantarum*. Amylolytic activity was detected in two *Lactiplantibacillus plantarum* strains, whereas bacteria of species *Weissella cibaria* displayed a weak β-glucosidase activity.

An important criterion to select microbial constituents for dough fermentation is antagonistic activity toward contaminating microbiota. Antagonistic response of lactic acid bacterial cultures to causal agents of bread spoilage was demonstrated, including epidemiologically significant fungi of genera *Fusarium*, *Aspergillus*, *Penicillium*, etc.

Analysis of obtained data has enabled to compose microbial consortia promising for further elaboration of technologies for producing active bread-making starter formulas with upgraded biotechnological properties and enhanced alimentary, nutritional and biological value.