

## PROMISING MICROORGANISMS FOR TREATMENT OF POULTRY PROCESSING WASTEWATER

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Massive volumes of effluents discharged by the poultry-processing plants contain elevated levels of pollutants (dissolved keratins, blood, lipids and proteins), and are distinguished by high BOD and COD values, as well as by large concentrations of suspended particles [1]. Therefore, there is an urgent need to develop effective and eco-safe methods protecting the environment from contamination. Among such methods the application of efficient microbial degraders of toxicants, possessing enhanced flocculating and decomposing activity, that can be introduced into the decontamination units to supplement the microbiota of the activated sludge at various stages of treatment, seems to be especially promising. Currently, biopreparations of microbial consortia intended for remediation of the environments exposed to organic pollutants are widely spread. The most common constituents of such consortia represent such genera as *Rhodococcus*, *Bacillus*, *Pseudomonas*, *Arthrobacter*, etc. [2].

Our study was focused on the microorganisms of the *Rhodococcus* and *Bacillus* genera, which are able to utilize the organic compounds in the poultry processing wastewater. There were selected 14 variants out of 145 screened strains that were either deposited in the laboratory of environmental biotechnologies, Institute of Microbiology, NAS of Belarus, or isolated from effluents of poultry-processing plants. They were tested for the COD degradation activity in poultry-processing wastewater, assayed for the proteolytic and lipolytic activities [3], and estimated for the biosurfactant forming potential [4].

The degradation activity of the selected microbial cultures was investigated using poultry-processing effluents with initial COD value of 1144 O<sub>2</sub>/dm<sup>3</sup>. It was found that the top COD reduction was by *B. subtilis* 6/2-APF1, *B. coagulans* 1710, *Bacillus* sp. FL-9MV, *Bacillus* sp. FL X-5, *Bacillus* sp. PF1, *R. ruber* 30P, *R. ruber* 200N, *R. ruber* 1NG – 52,3-71,6%. The maximum proteolytic activity toward milk proteins was observed for *B. coagulans* 1710, *B. subtilis* 6/2-APF1, *Bacillus* sp. FL-9MV, *Bacillus* sp. FL X-5. The lipolytic activity on the tributyrin-containing medium was detected in all 14 tested strains – *B. coagulans* 1710, *B. subtilis* 6/2-APF1, *Bacillus* sp. FL-9MV, *Bacillus* sp. FL X-5, *Bacillus* sp. PF1, *R. erythropolis* 7D, *R. erythropolis* 23F, *R. erythropolis* 70F, *R. ruber* 2B, *R. ruber* 1NG, *R. ruber* 30P, *Rhodococcus* sp. P1, *Rhodococcus* sp. G13, *R. ruber* 200N with the last two being especially active. The highest capacity to produce biosurfactants in the specific nutrient medium with methylene blue was displayed by *B. coagulans* 1710, *B. subtilis* 6/2-APF1, *Bacillus* sp. FL-9MV, *Bacillus* sp. FL X-5. In addition, the ability to produce surface active agents was observed for the bacterial cultures of *Bacillus* sp. PF1, *R. ruber* 2B, *Rhodococcus* sp. R1-3FN, *Rhodococcus* sp. G13 and *R. erythropolis* 7D.

Among the tested bacterial strains, the following cultures proved to be the most effective in decontamination of the poultry-processing wastewater: *B. coagulans* 1710, *B. subtilis* 6/2-APF1, *Bacillus* sp. FL-9MV, *Bacillus* sp. FL X-5, *Bacillus* sp. PF1. The above-listed microorganisms may act as promising components of the biopreparations promoting decontamination of the poultry-processing effluents.

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