

## METHODS OF MOLECULAR GENETIC DIAGNOSTICS OF FOOD SAFETY IN UKRAINE

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Standardized methods of diagnosing the safety of food and raw materials are classical methods of food microbiology, which are time-taking, based on the phenotypic characteristics of microorganisms and are not always able to diagnose their toxigenic properties. Analytical information on the inaccuracy of indication of bacillary food poisoning, the need for a preventive analysis of the risks that aerobic and facultative-anaerobic spore-forming microorganisms of the genus *Bacillus* bear, cause the urgency of their detection by accelerated modern methods. Such diagnostics will allow producing new competitive food of guaranteed quality and microbiological safety. The work was aimed at molecular-biological diagnostics of potential causative agents of food poisonings – the contaminants of the genus *Bacillus* – according to the genetic determinants of their toxicity.

Characteristics of 9 morphotypes of contaminants in 117 food samples were studied with standardized classical methods by phenotypic properties. Samples of food for PCR were prepared by the priority method developed by us. PCR was carried out with specific primers to detect toxicity in various kinds of bacilli genes: *nhe*, *hbl*, *cyt K*.

Among the bacillary contaminants of the samples, the *subtilis-licheniformis* group is the most numerous one (20 to 37% of total bacilli count), *Bacillus megaterium* was detected in the amount of 6 to 21%, *B. pumilis* – 4 to 13%, *B. circulans* – 2 to 7%, gas-forming *Paenibacillus polymyxa* and *P. macerans* – the causative agents of bombarding spoilage – 3 to 14% and 2 to 9%, respectively, the microorganisms of the *Bacillus cereus* group (in particular *B. cereus* and *B. thuringiensis*) – 10-31% and 4-13%, respectively. Molecular genetic diagnosis showed the specificity of the contaminants in Ukraine: the presence of the *nhe* gene was detected in 100% of *B. cereus* strains, *hbl* in 60% and *cyt K* in 40% of the strains studied. It should be noted that the presence of the toxicity gene *cyt K* was established for a typical saprophyte – the strain *B. licheniformis*.

Studies of food raw materials and products have confirmed the need to improve microbiological control of product safety by introducing accelerated specific diagnostics of contaminants by molecular genetic methods. Such studies should be continued, which will allow diagnosing both traditional and emergent pathogenic contaminants.