DIVERSITY OF THE SPECIES OF THERMOSTABLE MESOPHILIC BACTERIA FROM RAW VEGETABLE MATERIALS AND CANS WITH SIGNS OF DAMAGE

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The work presents the analysis of the microbiota of vegetable raw materials, zoned in Ukraine and grown in Odesa region (carrot, zucchini, eggplants) and mushroom preserves with signs of damage.

23 strains of heat-resistant spore forming bacteria were isolated. The study of morphological and physiological properties of thermostable mesophilic bacteria from raw vegetable materials and cans allowed to assign them to order *Bacillales* by using 10 edition of Bergey's Manual of Systematic Bacteriology and studied phenotypic properties of the investigated strains allowed to include them into certain genera and species. The species belonging of bacilli was confirmed by carrying out fatty acid analysis and comparing them with the known standards by using automated microbial identification system MIDI Sherlock based on the gas chromatograph Agilent 7890 with flame-ionization detector and capillary column ULTRA 2, with application of hydrogen as a carrier gas.

The predominance of branched fatty acids in fatty acid profile is a characteristic feature of bacteria of order *Bacillales.* According to the literature and to the results of our research the content of branched fatty acid of bacilli ranged from 54 to 85% of the total fatty acid pool of cells, including both saturated and unsaturated acids with predominance of iso-C15: 0 and C15-antiizo: 0. They were also characterized by a high content of antiizo-C 17: 0 and iso-C 17: 0 of fatty acids.

High similarity indices were obtained for the species under study, which allowed revealing the species identity for the studied strains. Thus, according to the results of identification of mesophilic spore-forming aerobic bacteria isolated from vegetable raw materials by installing the fatty acid composition of cells studied strains belonged to 5 families of the order *Bacillales: Bacillus, Lysinibacillus, Paenibacillus, Virgibacillus, Brevibacillus.*

The isolated strains of the genus *Bacillus* were identified to the species *Bacillus thuringiensis ssp.israelensis, B. subtilis, B.cereus GC subgroup A, B. pumilus GC subgroup B, B. atrophaeus* according to the results of fatty acid analyzing.

Isolated strains of the genus *Lysinibacillus* were related to the species *Lysinibacillus sphaericus GC subgroup E*, isolated strains of the family *Paenibacillus* were related to the species *Paenibacillus larvae ssp.pulvifaciens*, isolated strains of the family *Virgibacillus* were related to the species *Virgibacillus pantothenticus*, isolated strains of the family *Brevibacillus* were related to the species *Brevibacillus choshinensis.*