

SPECIES DIVERSITY OF THE MICROBIOTA OF SEA BUCKTHORN BERRIES

Natalia NETREBA^{1*}, ORCID: 0000-0003-4200-1303

Iuliana SANDU¹, ORCID: 0000-0003-1266-3154

Artur MACARI¹, ORCID: 0000-0003-4163-3771

Olga BOESTEAN¹, ORCID: 0000-0002-0390-3550

Alexei BAERLE¹, ORCID: 0000-0001-6392-9579

Irina DIANU¹, ORCID: 0000-0001-8632-8987

¹Technical University of Moldova, 168 Ștefan cel Mare Blvd., MD-2004, Chisinau, Moldova

*Correspondence author: Natalia Netreba, natalia.netreba@tpa.utm.md

Sea buckthorn has nutritional and medicinal value, which makes it an attractive object of study for scientists around the world. Sea buckthorn berries contain many sugars, organic acids, vitamins, amino acids, etc., which are a good breeding ground for microorganisms. A wide variety of microorganisms that can cause spoilage have been found on sea buckthorn berries. These are yeasts of various families, species and genera, bacteria, mold fungi. Due to the high demand for sea buckthorn fruits and the increased demand for non-thermal products, plant microflora plays an important role in assessing the impact of fruits on food quality and human health.

As objects of study, 8 varieties of sea buckthorn R1, R2, R4, R5, L1, C6, AGG, AGA at the stage of full ripeness were used [1]. Sampling for research was carried out in accordance with SM SR ISO 874:2006. The berries of the studied sea buckthorn are dry, no external signs of damage and disease were found. The isolation of microorganisms was carried out by successive re-plating on dense nutrient media. A stroke with the culture was applied in the form of a straight or zigzag strip to grow the crop, which was kept in a thermostat at a temperature of 25-28°C for 3-6 days. The grown colonies were subjected to diagnostic testing according to cultural and morphological characteristics, by which yeasts were identified, guided by determinants and reference books.

The results of the study of phytopathogenic microbiota (fungal and bacterial) of 8 varieties of sea buckthorn, collected in the phase of full ripeness, are the average values for 3 determinations for each variety. The percentage of detected microorganisms was calculated. The results of the study showed that the phytopathogenic microbiota identified on the studied sea buckthorn fruits formed the following percentage sequence: *Rhodotorula* (2.5%) > *Geotrichum* (2%) > *Pichia* (1.5%) > *Penicillium*, *Cladosporium*, *Mucor*, *Candida*, *Alternaria* (1%) > *Aspergillus niger* (0.5%).

Comparison of the obtained results showed that the composition of the microflora of sea buckthorn berries is diverse. Species *Rhodotorula*, *Geotrichum*, *Pichia* predominate on the surface of sea buckthorn fruits, the main share falls on *Rhodotorula* (2.5%). These microbial species are part of the specific microflora of sea buckthorn fruit and can be carried by insect vectors such as fruit flies, bees and wasps.

Keywords: sea buckthorn microbiota, yeast, nutrient medium, microbial spoilage.

References:

1. MACARI, A., NETREBA, N., BOEȘTEAN, O. et. al Proprietățile fizice și organoleptice ale fructelor de cătină albă *Hippophae rhamnoides* L. cultivată în Republica Moldova. In: *Știința agricolă nr. 1 (2021)*, pp. 51-55, CZU: 634.743:581.1.03(478)

Acknowledgments: The authors would like to thank the Moldova State Project no. **20.80009.5107.13**, “*Elaboration of the technology for the production of sea buckthorn in an ecological system and the processing of fruits and biomass*”, running at Technical University of Moldova.