

**PRELIMINARY ANALYSIS OF THE FATTY ACID CONTENT IN
ERWINIA AMYLOVORA AND ERWINIA 'HORTICOLA' STRAINS REVEALS THE DIFFERENCES
BETWEEN THE CLOSELY-RELATED SPECIES**

Minchuk Y¹, Shapoval S¹, Faidiuk Y^{1,2}, Kharkhota M², Moroz S², Tovkach F.²

¹Taras Shevchenko National University of Kyiv, ESC Institute of Biology and Medicine

²D.K. Zabolotny Institute of Microbiology and Virology of the NAS of Ukraine

e-mail: minchukyevheniia@gmail.com

A fact of *Erwinia amylovora* (*Eam*), a causative agent of the fire blight disease, being present on the territory of Ukraine is indisputable. A closely related pathogen causing similar symptoms in beech trees, *Erwinia "horticola"* (*Eho*), has also been isolated in far 60s of the 20th century, with its taxonomical position not established precisely yet. To reveal the distance between the species a comparative analysis of fatty acid (FA) content in *Eam* strains, isolated from tissues of affected quince, pear, as well as rowan-tree and pyracantha, against *Eho* collection strains has been performed.

Isolated *Eam* strains appeared to be a homogeneous group due to their FA content, which corresponded to that of collection strain *Eam* 9057. In contrast, *Eho* strains were shown to be a more heterogeneous group, with obvious differences vs *Eam*.

In both species the range of major acids includes 12:0, 14:0, 16:0; 16:1, 18:1 and 17:0cyc, while in *Eho* it also includes 17:0. Saturated even FA (SEFA) content is higher in *Eam*: 48.43±0.92% vs 39.30±1.36% in *Eho*. On the contrary, saturated odd FA (SOFA) content is higher in *Eho* strains: 5.25±1.7% vs 1.86±0.52% in *Eam*. While the content of unsaturated FA (UFA) is similar: 46.40±0.52% in *Eam* vs 45.37±0.03% in *Eho*. Thus, the ratio of SFA:UFA in both strains is close, being slightly higher in *Eam* 1.09±0.02% vs 0.99±0.05%. Similarly close is the content of hydroxy-FA (HFA), being slightly higher in *Eam* (0.21±0.04% vs 0.19±0.03%). The drastic difference in content can be seen in cyclic acids, being only 2.22±0.38% in *Eam* strains, while 9.19±2.40% in *Eho*, with the highest content of 13.33% in *Eho* 120 strain.

In addition to each set of strains, we have a species representatives suspected of being an R-variant that differed from the rest of the specific strains in their interaction with phages (collection strains *Eam* 8507 and *Eho* 60-3m). Their FA content reveals significant differences from the characteristic for the group. Namely, *Eam* 8507 deviates from other *Eam* strains in SEFA, as well in 12:0, 16:0, 18:1 and 17:0cyc content, being closer to *Eho* strains. While *Eho* 60-3m differs from species group in SEFA, SOFA, 16:0, 17:0, 16:1 and 17:0cyc content, being more similar to *Eam* in those values.

Thus, the FA analysis appeared to be a useful tool to differentiate *E. "horticola"* from *E. amylovora*. In combination with the phage typing, it provides the basis for revealing the differences among 2 closely-related species, despite their high identity in 16S rRNA gene sequence being reported by other authors.