

Abstract

Agrobacterium tumefaciens is a species of phytopathogenic Gram-negative bacteria with a very broad host spectrum. These bacteria cause the formation of callus (crown gall disease) at the site of injury to the plant. After infection, the pathogen transforms host cells, forcing them to divide excessively, which leads to the formation of cancer tissue. The transformation of plant cells results from the ability of *Agrobacteria* to transfer a fragment of their own DNA into plant cells and integrate it with the genetic material of the host.

One of the main factors determining the pathogenic interactions between *Agrobacterium* and plants is the composition and spatial structure of the outer membrane of these bacteria. The aim of the study was to determine the impact of changes in the architecture of the outer membrane of *A. tumefaciens* C58 (by depriving the lipopolysaccharide of long-chain fatty acids (VLCFA) and depriving the bacteria of the ability to synthesize the main membrane lipid - phosphatidylethanolamine (PE)) on the process of plant infection and possible migration inside the organism. host.

On the basis of experiments carried out on a model plant - tomato (*Solanum lycopersicum* L.), it was found that the virulence capacity of mutants in the *acpXL-msbB* gene cluster responsible for VLCFA synthesis and the mutant defective in PE synthesis (*pssA* gene, locus *Atu1062*) is much weaker compared to wild strain *A. tumefaciens* C58.

Chemical analyses of infected plant tissues (callus tissue and adjacent stem fragment) using mass spectrometry imaging (MALDI MSI) and spectroscopic imaging (FT-IR and Raman) showed changes in the spatial distribution of secondary metabolites from the group of antibacterial glycoalkaloids, as well as proteins and lipids including phospholipids. Different changes were observed after infection with the mutants compared to the wild type.

In addition, this work attempts to determine the effect of infection with *A. tumefaciens* C58 on the microbiome of the host plant. It has been shown that the infection causes quantitative and qualitative changes in the plant microbiome. The introduction of a phytopathogen contributes to the displacement of natural endophytes belonging mainly to the genus *Pseudomonas* and to colonization mainly by Gram-positive bacteria of the following genera: *Arthrobacter*, *Microbacterium* and *Micrococcus*.

Key words: *Agrobacterium tumefaciens*, membrane lipids, microbiome, mass spectrometry imaging, spectroscopic imaging

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