cel/mL with/without $CaCl_2$ (2% w/v) addition over pears *Packham's Triumph* (PT, n≈ 1800 per treatment) and *Beurrè d' Anjou* pear cultivars (*BA*, n≈ 400 per treatment). The natural incidence (NI) of *Penicillium expansum*, *Botrytis cinerea*, *Alternaria* sp. and *Cladosporium* sp. decays was evaluated after 120 and 180 days. Treatments were conserved postharvest in cold rooms (-1/0°C and 95% RH). On the other hand, the fresh biomass grown (CFU/cm^2) on pears with different treatment was compared. After 180 days of cold storage, using *BA* pear cultivars, the *V. victoriae* with $CaCl_2$ controlled 87% of *B. cinerea* decay and 72% of *P. expansum* decay; while reduced the incidence of *Alternaria* sp. and *Cladosporium* sp. decays only by 39% and 45%, respectively. On the other hand, the yeasts applied without $CaCl_2$, obtained a similar control percentage at 120 days of cold storage and minor percentage at 180 days for the same disease. During the same cold storage conservation, employed *PT* pears, *V. victoriae* with $CaCl_2$ significantly reduced the incidence of *P. expansum* decays by 55% and 34-38% of *Alternaria* sp., *B. cinerea* and *Cladosporium* sp. decay. Finally, in this variety pear *V. victoriae* without $CaCl_2$ not shows antagonistic activity, only 17% of control of *Cladosporium* sp. decay was observed. In this work, the addition of $CaCl_2$ improved the antagonist effect of *V. victoriae*. This combination revealed the most promising method to control pear decays by four fungal diseases, attaining 34%-87% biocontrol, which is consistent with $CaCl_2$ role as an inducer of fruit defence responses against several pathogens. The simple and easily accessible biomass production medium employed in this work (CWP) ensured the necessary amount of yeasts for scale-up biocontrol testing. The observed reduction in the rate of decay of two pears cultivar by several pathogens achieved by the selected BCA entail a considerable decrease in postharvest economic losses in organic pear production in the North Patagonian region.

MICROBIOLOGY – MICROBIAL PHYSIOLOGY

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DEGRADATION OF THE MYCOTOXIN FUSARIC ACID IN *Burkholderia ambifaria* T16: GENES AND METABOLIC PATHWAYS INVOLVED.

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Fusaric acid (FA, 5-butylpyridine, 2-carboxylic acid) is a secondary metabolite produced by several *Fusarium* species, which is toxic for bacteria, plants, animals and humans. This mycotoxin contributes to the virulence of phytopathogenic *Fusarium* in several crops, causing important economic losses. Moreover, FA reduces survival and competition abilities of bacterial species able to antagonize *Fusarium* spp. due to its negative effects on viability and production of antibiotics effective against these fungi. *Burkholderia ambifaria* T16 is a bacterial strain isolated from the rhizosphere of barley that showed the interesting ability to degrade FA and detoxify this mycotoxin from barley seedlings. The genes and metabolic pathways involved in FA degradation have not been identified so far in any bacterial species. By screening of a transposon insertion library and proteomic analysis we were able to identify genes and metabolic pathways that would be involved in FA degradation. A functional 2-methylcitrate cycle (2-MCC), a carbon anaplerotic pathway widely distributed among bacteria and fungi where propionyl-CoA is converted to pyruvate and succinate, was shown to be essential for the growth of *B. ambifaria* T16 in the presence of FA. Propionyl-CoA and its derived catabolites are lethally toxic to cells when accumulate. For that reason, besides providing succinate and pyruvate, the 2-MCC also has a very important role in the detoxification of propionyl-CoA and its catabolites. The comparison of the proteomic profile of *B. ambifaria* T16 growing with FA or citrate as sole carbon sources showed that more than 50 enzymes were significantly overexpressed during growth with FA, including 2-MCC enzymes and enzymes that convert butyryl-CoA to propanoyl-CoA, suggesting that propanoyl-CoA is produced during FA degradation. Moreover, several proteins, including an AraC-type transcriptional regulator, a FMN-dependent two-component luciferase like monooxygenase (LLM) system, an amidohydrolase, two enoyl-CoA hydratases and a long-chain fatty acid ligase, encoded in the same gene cluster, were highly over-expressed during growth with FA (>10 fold up-regulation). In the last years, two-component LLMs were shown to catalyze the pyridine-ring cleavage of several N-heterocyclic compounds, suggesting that the mentioned gene cluster is a good candidate to be involved in the initial steps of FA degradation in *B. ambifaria* T16.

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MODIFICATIONS OF *Burkholderia contaminans* LIPOPOLYSACCHARIDE IN ISOLATES RECOVERED DURING CHRONIC LUNG INFECTION OF PATIENTS WITH CYSTIC FIBROSIS

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Burkholderia contaminans is one of the most prevalent species of the *Burkholderia cepacia* complex (Bcc) recovered from patients with cystic fibrosis (CF) in Argentina. While infections by *B. contaminans* could be transient, in most cases it results in a chronic lung infection. Colonization with these bacteria is associated with a high difficult eradication, accelerated decline