



**8th Symposium
of the Mexican
Proteomics Society**

**3rd PanAmerican
-Human Proteome
Organization
(Pan-HUPO) Meeting**

**2nd Ibero-American
Symposium on Mass
Spectrometry**

October 20-23, 2019

Acapulco, Guerrero, Mexico
Grand Hotel Acapulco & Convention Center

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BOOK OF ABSTRACTS

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Proteomic analysis and physicochemical, antioxidant, and sensory characteristics of three wild and two commercial prickly pears fruits from Mexico

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Opuntia ficus-indica is the most domesticated plant species between the *Opuntia* genus. However, Mexico presents the highest richness of wild *Opuntia* species. In these areas, it represents an important food resource of arid and semiarid areas. Although several investigations have tried to elucidate the process of domestication of these species through the study of changes at the molecular level in the cladodes, it is still unknown what characteristics are favored in the fruits. To find additional comprehensions about these molecular changes, a proteomic analysis, as well as a study of physicochemical, antioxidant, and sensory characteristics of three wild prickly pears (*O. macrocentra*, *O. phaeacantha*, and *O. engelmannii*), and two commercial prickly pears (*O. ficus-indica*) fruits were carried out. Protein identification of pulp tissue determined by a gel-free shotgun (nanoLC-MS/MS) strategy showed a wide variation in the number of proteins identified in each species. Only 28 proteins were common among the five species, 39 proteins were unique and common to wild species, and 175 proteins to the commercial ones. Identified proteins were classified by the biological interest mainly in carbohydrate metabolism, stress responses, and transport. Pulp, peel, and the seed of fruits of wild prickly pears showed the lowest pH values, as also the highest titratable total acidity, antioxidant capacity, and total phenolic, flavonoid, protein, lipid, ash, carbohydrate, and fiber contents. Furthermore, *O. engelmannii* showed a tendency to present the highest betacyanins, betaxanthins, and betalains contents. Sensory profiles of wild species were characterized by higher color, smell, and an acidic taste compared with the commercial varieties. Therefore, fruits of wild prickly pears could be proposed as an important nutritional source with biological interest for the food and pharmaceutical industry.

This project was supported by the infrastructure of the Autonomous University of Ciudad Juárez.

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Whole proteome analysis of $\Delta pknG$ *Mycobacterium tuberculosis* reveals a role of PknG in bacterial adaptation to host environment.

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Mycobacterium tuberculosis, the etiological agent of tuberculosis, is a major global human health problem being the first cause of death due to a single infectious agent. The success of *M. tuberculosis* as human pathogen resides mostly in its ability to maintain a latent infection in the host. It has been demonstrated that the Ser/Thr-kinase PknG from *M. tuberculosis* regulates critical processes in bacterial physiology and pathogenesis by still poorly understood mechanisms.

To further characterize the role of PknG in mycobacteria, quantitative global changes in the proteome of *M. tuberculosis* WT and $\Delta pknG$ were analyzed by shotgun proteomic approach. We identified an average of 1700 proteins in each replicate of each strain, and more than one-hundred proteins were differentially detected between strains. Our results demonstrate that $\Delta pknG$ shows diminished abundance of a set of proteins, expressed in the WT, that are crucial for adaptation to host environment such as hypoxic conditions, redox stress and nutrient starvation. Also, we detected changes in the relative abundance of proteins involved in the biosynthesis of complex lipids from the outermost layer of mycobacterial cell wall involved in the crosstalk between the bacterium and the human host. To confirm these results, some proteins were selected to validate their differential abundance in WT *M. tuberculosis*.

Altogether our proteomic data suggest that the role of PknG in intracellular survival could be attributed to the regulation of essential bacterial pathways required for its fitness to environmental conditions found in the human host.