

“Functional genomics as a tool to unveil bioactives compounds in commercial and natives plants in Chile”



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UNIVERSIDAD DE CHILE

Date / Time : June 13th (Tue.), 2017 / 10:30-12:00

Venue : Seminar room No. E321

Chile is part of the Andean region, origin of several native fruit crops, providing it with a unique opportunity to investigate the underlining mechanisms by which fruits produce human health related compounds. Furthermore, the Chilean fruit industry has positioned itself as a key market for economic development. Fruits are rich in antioxidants, vitamins, minerals, carbohydrates and fiber. Moreover, many studies have associated fruit derived micronutrients, including carotenoids, flavonoids and minerals, with health promoting and disease preventive properties. Many of these compounds have been described in plants, indicating the evolutionary complexity of regulatory mechanisms and metabolic pathways that lead to their production and/or accumulation in different species. In order to begin to decipher these regulatory mechanisms, we are performing comparative nutritional genomic analyses among members of the Rosaceae family as well as indigenous species ancestrally cultivated in the Andes region. In order to achieve this goal two approaches are under way. A biochemical approach is being carried out to determine antioxidants activities as well as a nutritional characterization for these plants. Additionally, RNA seq analyses has been performed to identify regulatory genes that are involved in the metabolic pathways related to functional compounds. Our analyses have focused on the indigenous highland papaya and quinoa (a pseudocereal) as well as an introduced blood-flesh peach variety with high values of antioxidants. Furthermore, we are performing these analyses on Rosaceae crop species that are important for the Chilean fruit industry, such as plum, peach and sweet cherry.

Acknowledgments: CONICYT, FONDECYT/Regular N°1160600 and N°1150919