**Charla:** Identificación y caracterización de los genes de floración en quinoa (*Chenopodium quinoa* Willd)

**Proyecto:** Colaboración internacional proyecto Fondecyt de iniciación 1170226 The role of photoperiod flowering genes in the latitudinal adaptation of quinoa (*Chenopodium quinoa* Willd.).

**Investigador:** Agnieszka Golicz P.h.D, es especialista en genómica y bioinformática del “Plant Molecular Biology and Biotechnology Laboratory” de la Universidad de Melbourne, Australia. Este grupo de investigación reconocido a nivel internacional se dedica al estudio y desarrollo de cultivos de grano, forrajes y hortalizas a través del mejoramiento tradicional y el uso de herramientas biotecnológicas y computacionales.

**Abstract:** Quinoa (*Chenopodium quinoa* Willd.) is a grain crop grown in the Andes, receiving world-wide attention as a highly nutritious plant producing gluten free, low-glycaemic index seeds. Its unique tolerance to abiotic stresses such as drought, severe cold and high salinity allows quinoa to be grown even in the most adverse conditions. Crop improvement programs mainly aim to breed high yielding varieties for ensuring future food security. The yield of a crop plant is majorly governed by flowering process as it is the first step towards seed set formation. However, current knowledge of molecular basis of quinoa flowering is limited and the details of flowering genes and associated pathways in quinoa remain elusive. We have investigated flowering pathways in quinoa using computational biology approaches. We identified and analysed orthologues of known Arabidopsis thaliana genes involved in flowering as well as quinoa specific genes expressed in the flower and/or shoot apical meristem, with no know orthologues in other species. Together the genes identified provide a resource for further studies of flowering in quinoa and related species.