Avocado (*Persea americana*) and cherimoya (*Annona cherimola*) crop ontologies facilitate data interoperability among different descriptors in biological databases. 

Authors: Alicia Talavera¹, Hugo Pineda², J. Iñaki Hormaza¹, Antonio J. Matas¹²

Affiliations

1. Instituto de Hortofruticultura Subtropical y Mediterránea “La Mayora”, IHSM-UMA-CSIC. Algarrobo-Costa, Málaga, Spain.

2. Departamento de Biología Vegetal, Universidad de Málaga, Málaga, Spain.

Subtropical fruits, like avocado and cherimoya, are key crops for food security in a wide range of countries, with an increasing commercial importance worldwide. Even though their importance is starting to be recognized and high throughput sequencing approaches are currently being used to characterize genome-wide patterns from natural diversity populations and breeding stocks, currently ontological available information for these subtropical fruits crops is scarce and often not based in internationally standardized formats. Thus, the challenge to correlate the expanding molecular information data available with plant phenotype and crop traits remains an important issue in breeding programs for these crops. With the aim to facilitate future analyses we present a controlled vocabulary for harmonizing the annotation of phenotypic and genomic data for these crops. These new ontologies represent an extended ontology to fit avocado and cherimoya traits commonly used in variety descriptions, mainly established by Biodiversity International and the International Union for the Protection of New Varieties of Plants (UPOV), but also custom *ad hoc* descriptors. The developed ontology includes measurable or observable characteristics of plants as well as abiotic and biotic stress susceptibility. The resource is available in standard OBO formats ready to be used in GMOD and Tripal inspired biological databases to allow data sharing and reusability. The approach followed here can be of interest to other crops in which standardized ontologies are still missing.