BIOINFORMATIC ANALYSES OF OLIVE POLLEN TUBE AND SEED TRANSCRIPTOMES AND THEIR INTEGRATION IN AN INTERACTIVE OLIVE EXPRESSION ATLAS

<u>Amanda Bullones^{1,2}</u>, Noe Fernandez-Pozo¹, Elena Lima-Cabello³, Antonio Jesús Castro³, Juan de Dios Alché³, M. Gonzalo Claros^{1,2,4,5}

1. Institute for Mediterranean and Subtropical Horticulture "La Mayora" (IHSM-CSIC-UMA), Málaga, Spain

2. Department of Biochemistry and Molecular Biology, Universidad de Málaga (UMA), Málaga, Spain

3. Estación Experimental del Zaidín, Consejo Superior de Investigaciones Científicas (CSIC), Granada, Spain

4. CIBER de Enfermedades Raras (CIBERER), Málaga, Spain,

5. Institute of Biomedical Research in Malaga (IBIMA), IBIMA-RARE, Málaga, Spain

Presenter e-mail: amandabullones@uma.es

The olive tree (Olea europaea L.) is of great socioeconomic importance due to the production of oil and table olives, and the seed is also an emergent source of nutraceuticals (Jiménez-Ruiz et al., 2020) and feed supplements (Maestri et al., 2019). Spain is the world's leading producer and, of the 272 varieties present in our country, Picual is the most cultivated and the main source of olive oil. Despite its relevance, there are many unknown aspects in its biology. Here we study the development of the Picual pollen tube to discover the biological processes involved and its potential regulation. Highly relevant transcripts like those of two RING proteins and other two Zinc-finger containing proteins seem to indicate that they play a main role in the process of mitosis II, and its cross-talk with environmental and developmental clues. In addition, Picual orthologues of the 14 olive allergens known to date were determined and their expression in the pollen tube monitored. Allergens are consistently expressed during pollen tube development, most of them at a high level. Despite Ole e 1 being the first olive pollen allergen to be identified (Villalba et al., 1993), it is the second most abundant transcript, behind Ole e 14 which was only recently described (Oeo-Santos et al., 2018), with Ole e 15 being the last allergen identified (San Segundo-Acosta et al., 2019) and the one less expressed. We are characterizing the transcriptome of Picual seeds at different developmental stages, where the biological processes of the endosperm that nourish the embryo, and the establishment of embryonic polarity are particularly overrepresented. Finally, an interactive gene expression atlas for olive tree (OliveAtlas) where expression data were mapped to the Picual reference genome and its gene model annotation was created. This tool tries to ease the lack of bioinformatics and genomics resources and assists olive research and breeding. This research was founded by grants PID2020-113324GB-I00 (AEI), P18-RT-1577 (JA, excellent research), and UMA20-FEDERJA-029 (JA), all of them co-founded by ERDF/EU.