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Genome Wide Sequence-Based Association Studies for Dissection of Important Agronomic Traits in Apricot

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Room: Pacific Salon 3

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Worldwide, sharka disease significantly impacts the economics and productivity of *Prunus* fruit producing countries affecting a wide range of stakeholders from breeders to nurserymen and fruit producers. Natural resistance sources have been identified in few cultivated and wild species of Prunoideae, mostly in apricot (*Prunus armeniaca*).

Utilizing the current genomic resources available for peach as a reference, we have implemented a project to examine in detail the genome diversity of apricot germplasm as a foundational genome system for studying gene/trait associations and to describe the nature, extent and evolution of diversity within breeding and wild germplasm. Within the French ANR CHEX ABRWIG program (2012-2014), we have completed whole genome sequences of over 100 breeding accessions using NGS technologies. In this communication, we will present data on genome-wide association analyses for resistance to sharka disease.

This work was completed, in the frame of the FP7 Marie Curie STONE project (#246795, 2011-2014), by a search of the geographical origin and a world-wide genetic diversity analysis of resistance source(s) to sharka in apricot. We also sampled fourteen populations of wild apricot trees, covering five distinct eco-geographical zones. Among this material, 60 accessions

originating from wild, Central Asian germplasm were re-sequenced following the same procedure as for the cultivated germplasm. These sequences are being utilized to describe the diversity within the wild compartment and to examine how forces of breeding selection may have shaped genome diversity in this species.