

PAXAP

Project title: Development of tools to characterize the interaction *Xanthomonas arboricola* pv. Pruni / *Prunus armeniaca*

Acronym: PAXAP

Project duration: 24 months - Start date: 01/01/2019 End date: 31/12/2020

Key-words: wild compartment, centre of origin, *Xanthomonas*, apricot, detection, phenotyping

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Summary:

Xanthomonas arboricola pv. pruni (Xap) is responsible for the bacterial spot of *Prunus* spp., a disease in continuous expansion and with major economic impacts on stone and nut fruit tree production. It has been shown that the centre of origin of cultivated crops could play an important role in pathogen emergence. However, no information is available on the presence of *Xanthomonas* bacteria in the centres of origin of fruit trees. This “Starter” project aims at developing tools to explore the interaction between Xap and one of its host *Prunus armeniaca* (apricot tree). It is based on a synergistic collaboration between two INRA teams that have complementary skills and resources. In a first step, molecular detection tools will be developed thanks to genomics data of Emersys team, to explore the presence of *Xanthomonas* in lyophilized samples of wild apricot trees from Central Asia collected by partner2. Positive results would support the future setup of a sampling expedition in Central Asia to get bacterial isolates of *Xanthomonas*. In addition, protocols and detection tools setup in the frame of this project will be useful to search for the presence of Xap in herbarium. The second objective of this “starter” project is to setup a high throughput phenotypic test using detached leaves of apricot trees to assess on one hand bacterial strain aggressiveness and on the other hand host susceptibility. In future projects, this phenotypic test will allow us to compare the aggressiveness of strains isolated on natural populations in the centres of origin to the one of strains isolated in agroecosystems. These data are essential for the understanding of bacterial adaptation to their host. The phenotypic test will also allow to assess the susceptibility to Xap of wild apricot trees from Partner2 collection. The genome of 80 wild apricot trees has been sequenced; the implementation of this phenotypic test will allow to get data for a Genome Wide Association Study (GWAS) and to search for genetic resistance to Xap in *Prunus armeniaca*, similar to the GWAS already carried out for the sharka virus.