

*Agrobacterium tumefaciens*-mediated plant transformation is an indispensable tool for plant functional genomics, crop improvement, genome editing and synthetic biology (Hwang et al., 2015; Nester, 2015; Sainsbury and Lomonosoff, 2014; Xu et al., 2014). Although *A. tumefaciens* is routinely used in the transformation of model plant species (e.g., *Arabidopsis*, tobacco), several economically important plant species (e.g., members of legumes, cereals, biofuel crops, fruit trees, ornamental and medicinal plants) remain difficult to transform using this bacterium due to “plant recalcitrance”, a phenomenon not understood so far. Widespread occurrence of this phenomenon across the plant kingdom hinders the use of contemporary tools as CRISPR / Cas9 or RNAi in several plant species. Although the mechanism of plant recalcitrance is ambiguous, we evidenced that the incompatible interaction of *A. tumefaciens* with recalcitrant plants and successful activation of plant defense as the prevailing cause (Franklin et al 2008, 2009; Hou et al 2016). As a continuation of this pioneering discovery, we propose to elucidate the relevance of pathogenesis-related defense mechanisms on plant recalcitrance against *A. tumefaciens* infection using cutting edge molecular biology tools. The results to be obtained in this project would help scientist to understand the basic mechanisms of plant recalcitrance and to devise transformation strategies for important plant species that remain recalcitrant today. On the other hand, our results also would provide novel means of neoplastic diseases (crown gall and hairy root) control in the near future for economically important plant species that are prone to these diseases (apple, pear, cherry, apricot, almond, walnut, roses, grapevines, raspberries, cotton, sugar beets, tomatoes, beans, alfalfa etc.) at present. Thus, execution of this project would be of great interest to the scientific community and to other stakeholders.