Molecular Ecology of Geminivirus C2 protein over the viral insect vector *Bemisia tabaci*

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Plant-pathogen-vector systems are characterized by a complex array of direct and indirect interactions, usually not well understood. The whitefly *Bemisia tabaci* is responsible for extensive losses mainly through the transmission of plant pathogenic viruses, primarily begomoviruses. Begomovirus (*Fam. Geminiviridae*) genomes encode 6 to 8 small multifunctional proteins. One of these is C2 (also known as TrAP, AC2 or AL2), a small multifunctional protein of about 15 kDa in molecular weight that is mainly localized in the nucleus and may inactivate plant defence responses. Recently, we found that C2 suppresses jasmonate responses when expressed in *Arabidopsis thaliana* or *Nicotiana benthamiana* [1]. Jasmonates are essential signalling molecules modulating plant responses to both biotic and abiotic stresses and regulating plant development. It has been reported that nymph development of *B. tabaci* is slowed or disrupted by jasmonate-induced defences [2]. Thus, it would be possible that begomovirus-mediated suppression of the jasmonate response accelerates the whitefly reproduction efficiency, thereby enhancing virus dispersal. Additionally, the suppression of the jasmonate response could also prevent the synthesis of secondary metabolites interfering with the interaction between plant and insect. Remarkably, this indirect mutualism between *B. tabaci* and begomoviruses, which occurs via their host plants, has been reported [3]. Whether C2 is the viral protein responsible for this effect remains to be determined. The overall purpose of this work is to investigate if the begomoviral C2 protein exerts an indirect effect, via the host plant, on the viral insect vector, *B. tabaci*. We will show results of the performance analysis of *B. tabaci* on: (i) transgenic *Arabidopsis* lines expressing the begomoviral C2 protein (from different begomovirus species) and (ii) plants infected with the begomovirus *Tomato yellow curl virus* either wild-type or a mutant lacking C2. Results will help better understand the molecular mechanisms and the ecological implications of how viruses can manipulate plant defense systems to the benefit of their vectoring insects.

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References:

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