

In silico prediction of candidate gene targets for the management of African cassava whitefly (*Bemisia tabaci*, SSA1-SG1), a key vector of viruses causing cassava brown streak disease.

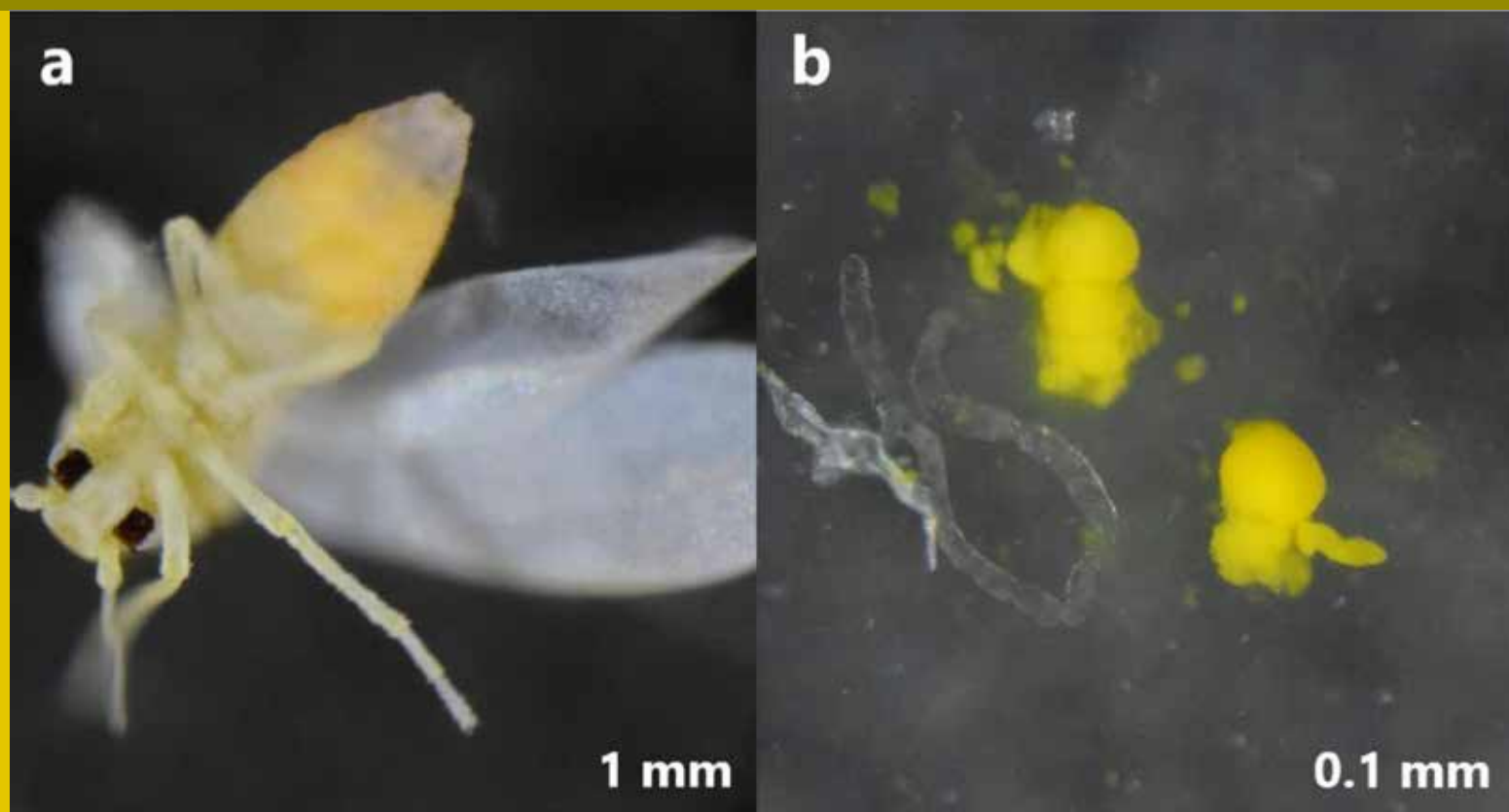
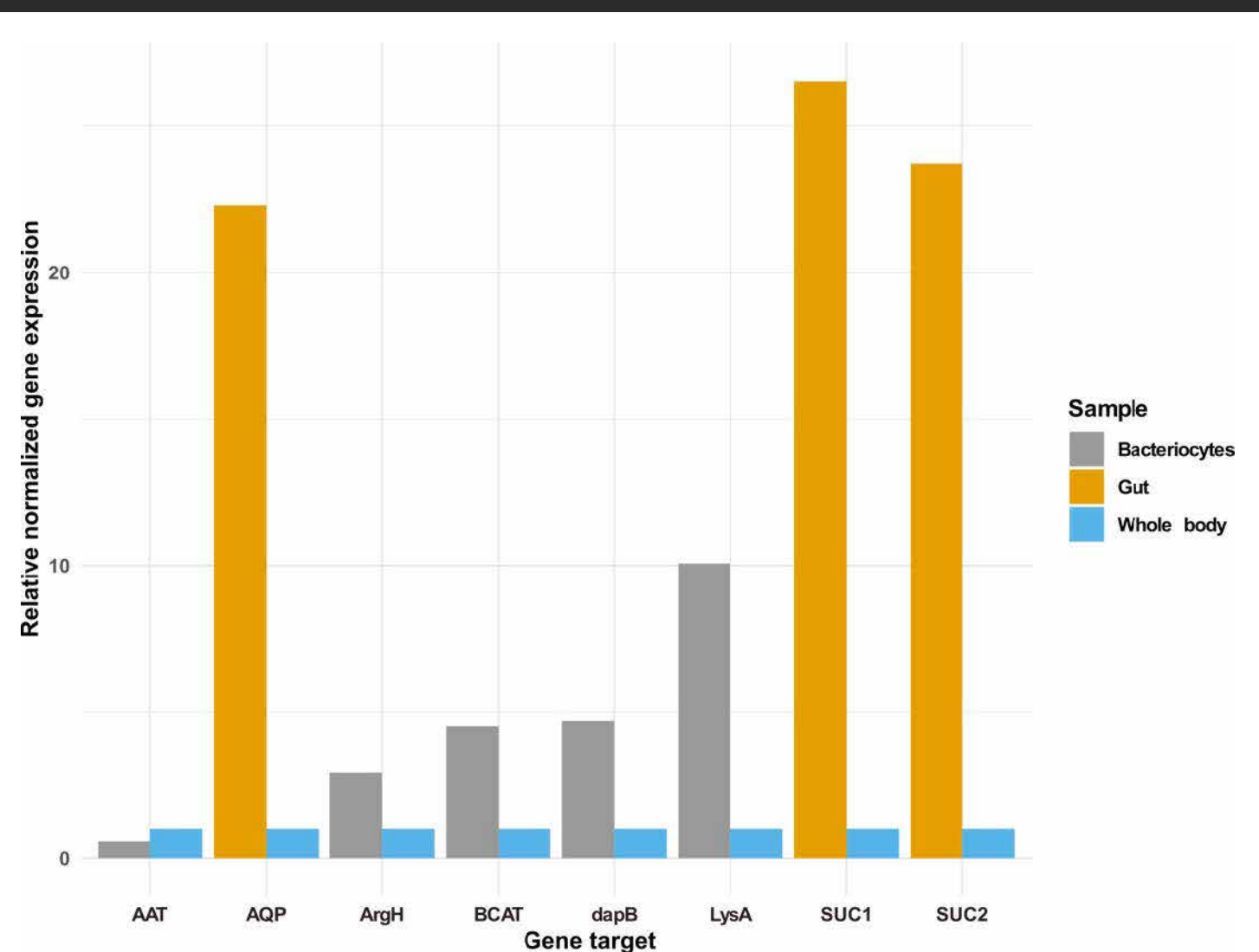


Figure 1. Bacteriocytes dissected from the abdomen of *Bemisia tabaci* (SSA1-SG1). **a)** shows the location of the bacteriocytes in the abdomen of the whitefly and **b)** dissected whitefly gut (translucent tubular organ) and bacteriocyte where osmoregulation and amino provisioning take place respectively.

Whitefly (*Bemisia tabaci*) affect crops directly as pests and as vectors of more than 300 plant viruses. This study focused mainly on the cassava whitefly that transmits the Cassava brown streak disease and Cassava mosaic disease to cassava, devastating a crop that provides food security to more than 800 peoples in Sub-Saharan Africa. We identified essential genes within the cassava whitefly that can be used to develop highly effective management strategies like RNA interference.



Gene expression of selected gene targets in whitefly gut or bacteriocyte compared to whole body



Cassava root affected by cassava brown streak disease symptoms



We used a system biology approach to study how the whitefly survives on impoverished diet (phloem sap) containing high sugars and lacking essential amino acids. Two critical systems; osmoregulation and amino acid provisioning in the gut and bacteriocyte respectively provided key gene targets that, when silenced can lead to a reduction in growth, development and death.

A total of seven gene targets, three osmoregulation genes (aquaporin and sucrases) and four symbiosis genes (both of intrinsic origin and horizontally-transferred genes), with enriched expression in the gut and bacteriocyte, respectively, were identified and validated.