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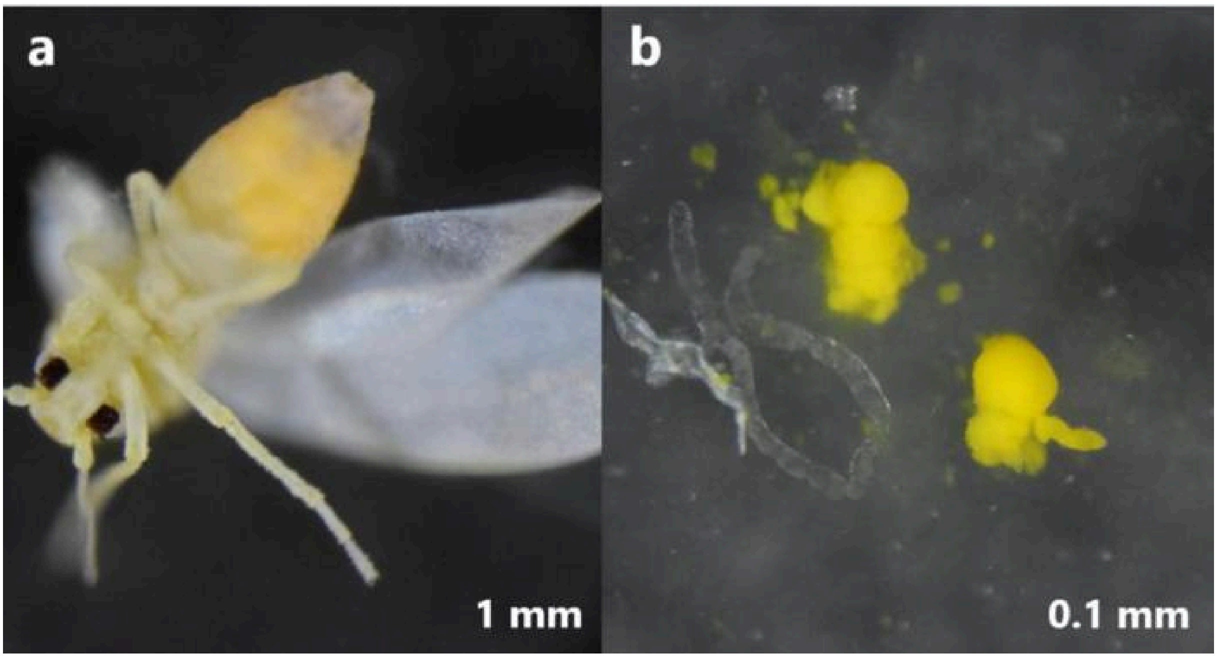
PRESS RELEASE

New study identifies potential gene targets for management of cassava whitefly, key vector of viral diseases threatening African food security



Bacteriocytes dissected from the abdomen of Bemisia tabaci (SSA1-SG1)

Whiteflies, particularly the African cassava whitefly (*Bemisia tabaci*, SSA1-SG1), pose a significant threat to agricultural productivity in Sub-Saharan Africa by transmitting viruses that cause cassava brown streak disease and cassava mosaic virus disease. In a new study published in *PeerJ Life & Environment*, Dr. Tadeo Kaweesi and his team at the National Agricultural Research Organization identify potential gene targets that could revolutionize the management of this devastating pest and prove vital for food security in the region.

In the article ("In silico prediction of candidate gene targets for the management of African cassava whitefly (*Bemisia tabaci*, SSA1-SG1)"), the researchers describe utilizing advanced computational methods to pinpoint genes crucial for osmoregulation and symbiosis within the gut and bacteriocytes of the cassava whitefly. By comparing gene expression profiles through RNAseq analysis and conducting phylogenetic and metabolic reconstruction analyses, the team identified seven critical gene targets with enriched expression in the target organs.

The study highlights three osmoregulation genes - *AQP1, SUC1*, and *SUC2* - involved in sucrose hydrolysis and water cycling, and four symbiosis genes *argH, lysA, BCAT*, and *dapB* - essential for amino acid biosynthesis pathways. These genes play key roles in regulating physiological processes vital for the survival of cassava whiteflies.

The identification of these gene targets opens up new avenues for the development of novel management strategies against cassava whiteflies. By targeting these genes, the aim is to not only reduce direct feeding damage but also mitigate the spread of viral diseases, ultimately safeguarding food security for millions in Sub-Saharan Africa.

The next steps involve further evaluation of the impact of targeting these genes, individually or in combination, on the development and survival of B. tabaci. The most effective gene or gene combination will be integrated into transgenic plants for use in comprehensive whitefly management programs in cassava-growing regions.

For more information about this research, the full article can be accessed at PeerJ.com

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Please see a video with the author https://www.youtube.com/watch?v=-IStv79KHYk

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