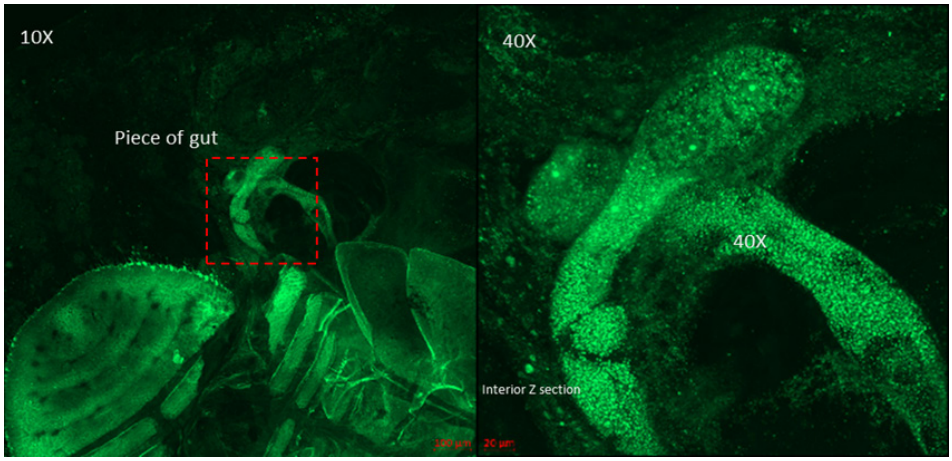
A Culturable *L. crescens* Model for Functional Genomics of *C*Las



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The primary reason for the lack of efficacious treatments to control HLB is likely due to lack of experimentally useful *C*Las cultures; at best only complex co-cultures can be obtained, containing such low *C*Las titers that they are detectable only by PCR. Potential *C*Las target genes necessary for psyllid acquisition, maintenance and transmission to citrus that might be useful to control *C*Las remain largely unknown and uninvestigated. All *C*Las strains lack key biosynthetic, metabolic and structural pathways that are found in *Liberibacter crescens* (Lcr), which is axenically cultured. Our recently published data indicates that wild-type *C*Las will never be axenically cultured without adding all 95 Lcr genes that are missing in all *C*Las strains and required for growth (Cai et. al. 2022). To help identify *C*Las targets, a practical alternative to culturing is step-wise additions to Lcr of small blocks of *C*Las "symbiosis" genes needed for psyllid acquisition, replication and citrus transmission. Lcr is missing only 23 genes implicated as being required by *C*Las for psyllid infection. Additional genes are published to be required to cause HLB in citrus. We have developed a functional genomics toolkit for practical manipulation of Lcr, including adding fluorescent markers (glowing Lcr are visualized inside psyllid gut 1 day after feeding by microscopy below) and *C*Las genes to Lcr. Our goal is to characterize *C*Las genes in Lcr that condition acquisition and transmission to citrus, but short of causing HLB. This will provide a platform for identifying critical gene targets for genetic and chemical controls.

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