



## Genetic deletions in *Ca. Liberibacter asiaticus* psy62: absences in the pathway of glycolysis.

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**Introduction.** The genus *Ca. Liberibacter*, is a Rhizobium member and is a bacterial limited to the phloem and correlated with the Citrus Huanglongbing disease (HLB) (1). Is considered the most serious disease in citrus, because is a destructive, progressive and there's not exist a effective treatment (2). The genome Asiatic strain has been sequenced using metagenomic techniques during the interaction with the vector *Diaphorina citri* (3). The genome is small (1.23Mb) and has important deletions reported in similar organisms like strict symbionts and parasites.

The analysis *in silico* of this genome has show important putative properties about this bacteria, like ABC transporters (4) and other pathogenic factors (5).

The knowledge of the bacteria could help in the design of control mechanism for the disease; by this the objective of this study was the interpretation of glycolysis pathway and the putative interaction in the host microniche.

**Methods.** Annotation of the genome of *Ca. Liberibacter asiaticus* psy62 (NC\_012985) was done using the PATRIC platform (6),

and are necessary for the conversion of glucose to Glyceraldehyde-6P. The bacteria needs to import intermediaries of the pathway probably Glyceraldehyde-6P to introduce in the pathway for bioconversion.

An important difference between this bacteria and others rhizobials that can be cultivate, is that they have their full pathway, like shows in Fig. 2.



**Fig. 2** Comparative analysis of the Glycolysis/Gluconeogenesis pathway between *Ca. Liberibacter asiaticus* psy62 and other Rhizobials members.

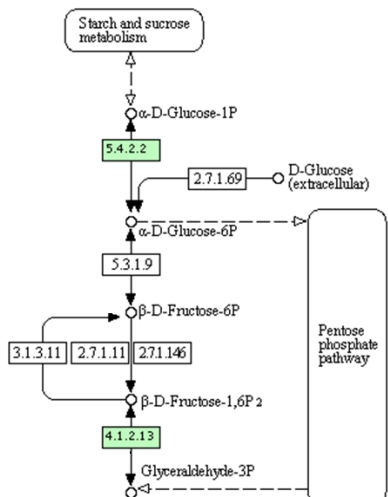
### Conclusions.

This absences in the genome of *Ca Liberibacter asiaticus* psy62 make them strict endobiota, and could be molecular targets for bacterial control using genetic engineering.

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**Fig.1** Glycolysis pathway showing in green the gens presented in the genome of *Ca Liberibacter asiaticus* psy62.

**Results.** The Glycolysis/Gluconeogenesis COG's pathway in the bacteria shows 1109 total ORF's and 15 associated to this pathway. Using the comparative tools we added some rhizobials genomes, with only one chromosome and shows important absences in critical steps of the Glycolysis pathway (Fig. 1). This absences are really controversial because this enzymes are over regulated