

Reconstruction of metabolic pathways of *Klebsiella* spp. bacteria for improve the biologic control of Mediterranean fly (*Ceratitis capitata*).

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Abstract

Pests are known to cause significant damage to crops and affect agriculture productivity. Mediterranean fruit fly (*Ceratitis capitata*) is a serious horticultural pest, it attacks a range of cultivated fruits and vegetables. Several findings show that bacteria are present in the Mediterranean fruit fly microbiota and one of the most important bacteria is *Klebsiella* spp. Nowadays, scientists develop multiple methods to control pests as the Sterile Insect Technique (SIT) to release infertile males produced by irradiation. There are some metabolic pathways in *Klebsiella* spp. that can improve the behavior of the irradiated Mediterranean fruit fly males at the moment of liberation. The possible relationship between these organisms produces multiple quantities of biological data, to explain it, is necessary the use of mathematical models and computational scientific techniques. Processing these data in an efficient way facilitates its interpretation and scientific application. The objective of the present work is to reconstruct metabolic pathways of three strains of *Klebsiella* spp., from genome scale and choose one strain that can improve the biological control of *C. capitata*. Two approaches were used; 1) Stoichiometric reconstructions of pathways and 2) Directed graphs to analyze and evaluate the pathway analysis of the metabolic pathway generated with Elementary Modes (EM) analysis. From genome scale the sequences of the three bacteria were used to find possible metabolic pathways metabolites present in the nitrogen metabolism at these sequences using BLAST tool, those genes are related with symbiotic interaction between bacteria *Klebsiella* spp and *C. capitata*. The metabolites in the sequence indicated a possible metabolic pathway in the organism. Using KEGG database with the possible metabolic pathways involved we generate a directed graph and with it, then we produce a stoichiometric matrix with rows representing the metabolites that participate in reactions and columns with the number of molecules of metabolites involved (stoichiometric coefficients) in one reaction. Based on this information we analyzed and evaluate the pathway analysis with EM. The above-discussed considerations suggest that we can identify possible metabolic pathways involved in the process of symbiosis between *Klebsiella* sp. and *C. capitata* and we can generate a strategie to improve the production of infertile males of *C. Capitata* for the liberation and population control.

Funding: