

# A genome-scale metabolic model of the compatible interaction between *Solanum tuberosum* and *Phytophthora infestans*

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## Introduction

*Phytophthora infestans* is a Oomycete Phytopathogen that causes late blight, one of the most destructive diseases in potatoes and other vegetables hosts[1,2]. Despite the importance of this disease, the main molecular mechanisms involved in the pathosystem are poorly understood[3]. In recent years have been integrated genomic data and biochemical knowledge within genome scale metabolic reconstruction [4] that allow to study molecular aspects of different metabolic processes. A computational metabolic model of the compatible interaction between *P. infestans* and *Solanum tuberosum* was generated to predict the molecular mechanisms underlying the disease.

## Methodology

### Automatic metabolic reconstruction

Two automatic reconstructions were built using the RAVEN and Subliminal Softwares. Subsequently, a consensus was performed by the sum of the common and unique reactions obtained from each reconstruction. This consensus was taken as a basis for further analysis.

### Manual and automatic Refinement Reconstruction

- Gap find and Gap fill:
  - Manual refinement with KEGG Pathways and Plant Metabolic Network for *S. tuberosum*
  - Automatic refinement whit R package G2F specific-organism
- Manually refines all the energetic and of carbohydrates metabolism through biochemical data bases and scientific literature
- The anabolic/catabolic directionality and reversibility was corrected:
  - Manually whit KEGG pathways maps
  - Thermodynamically through of the standard  $\Delta$  Gibbs free energy for reactions obtained of MetaCyc and eQuilibrator data bases.
- Exchange reactions reported in other plant metabolic reconstructions were included.

Manual and automatic Refinement Reconstruction				
New. rxn	New. Met	New. Sub.	Sub. Com	Rxn. Inter
794	478	6	31	13

### Metabolic Model generation and Flux balance analysis

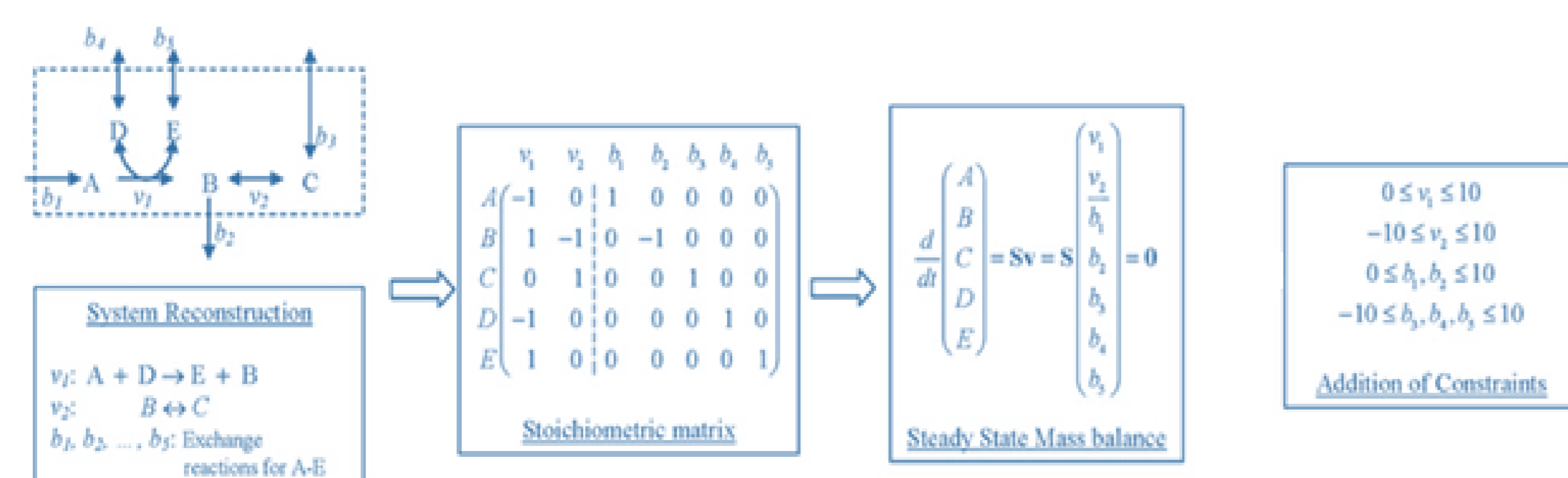


Fig 1. Initial steps to get the metabolic model [5].

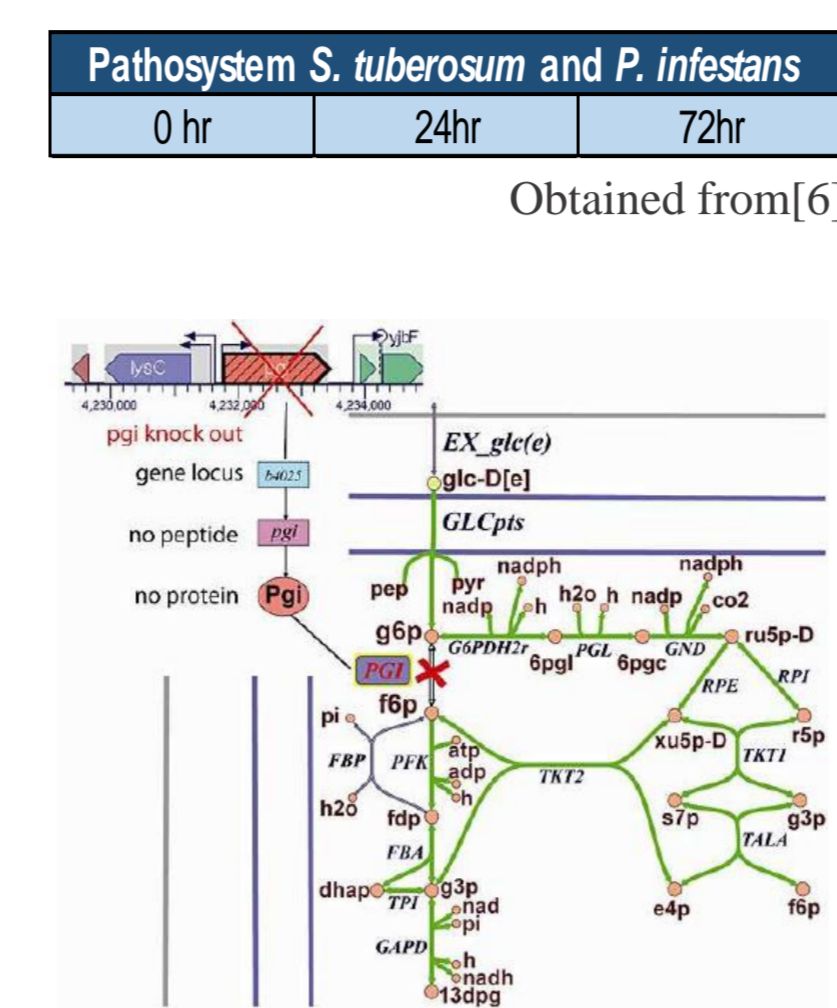


Fig 2. Integration gene expression data into metabolic model [7].

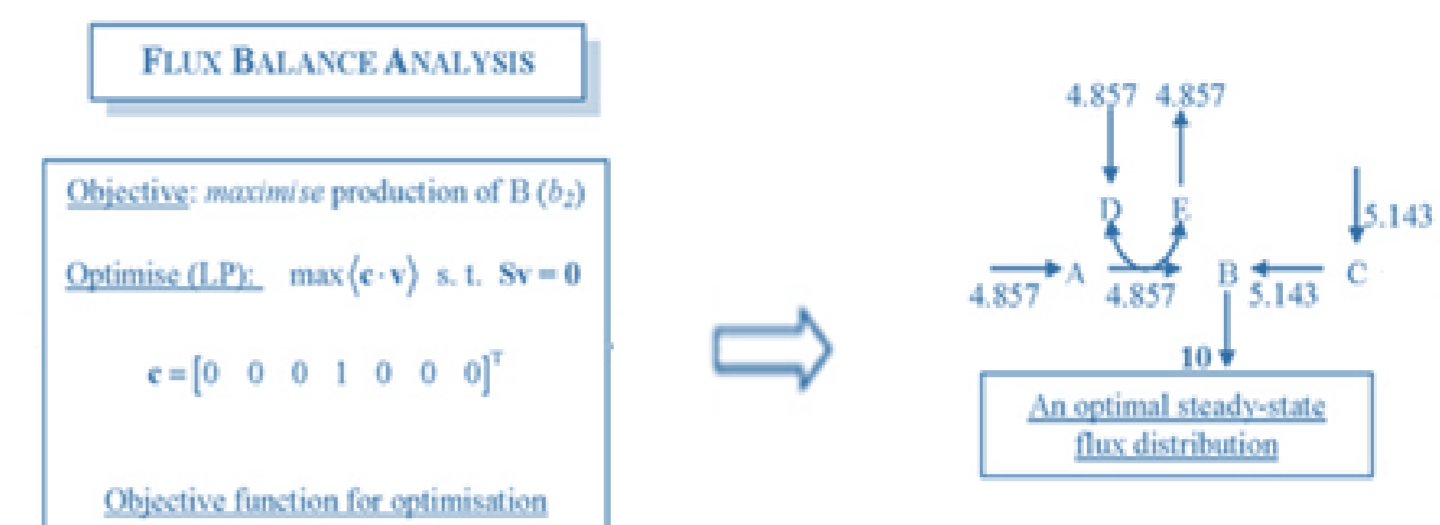


Fig 3. Flux balance analysis [5].

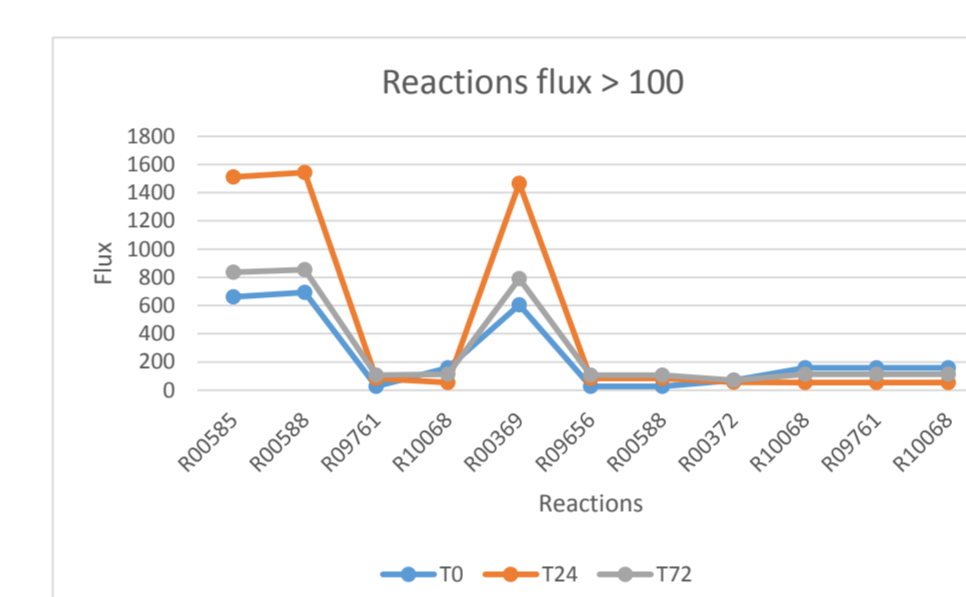
Objective function: Biomass synthesis (Leaf) [8].

## Results

### General feature of the metabolic model generated

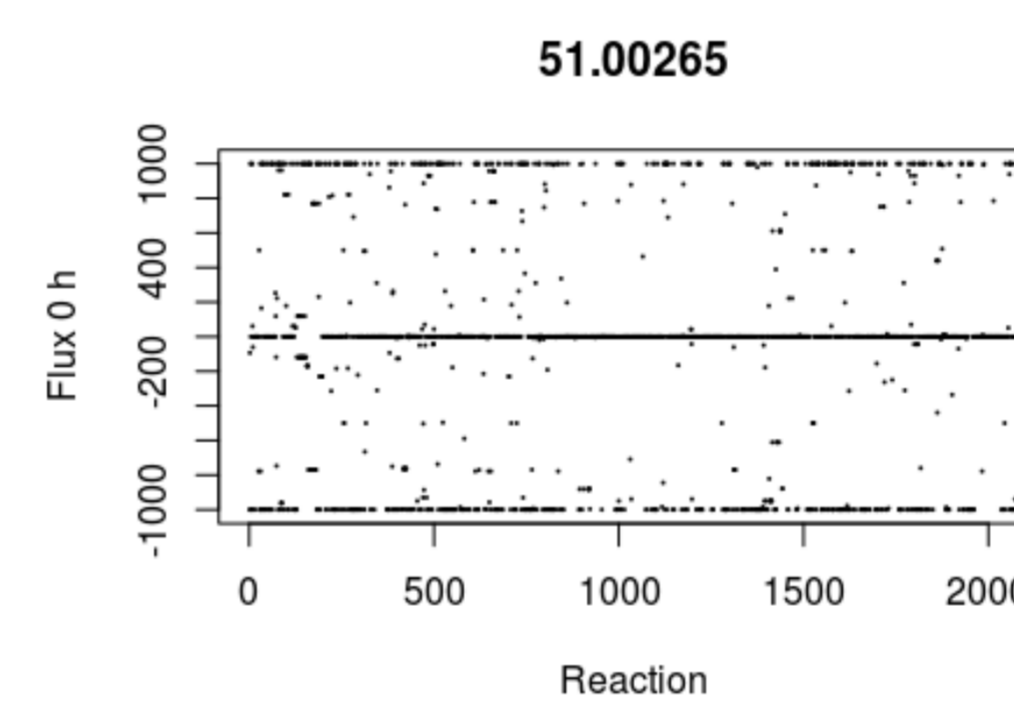
Metabolic model	
Reactions	2082
Metabolites	1970
Metabólic Function	1117
Genes	2292
Pathways	101

### Flux balance Analysis

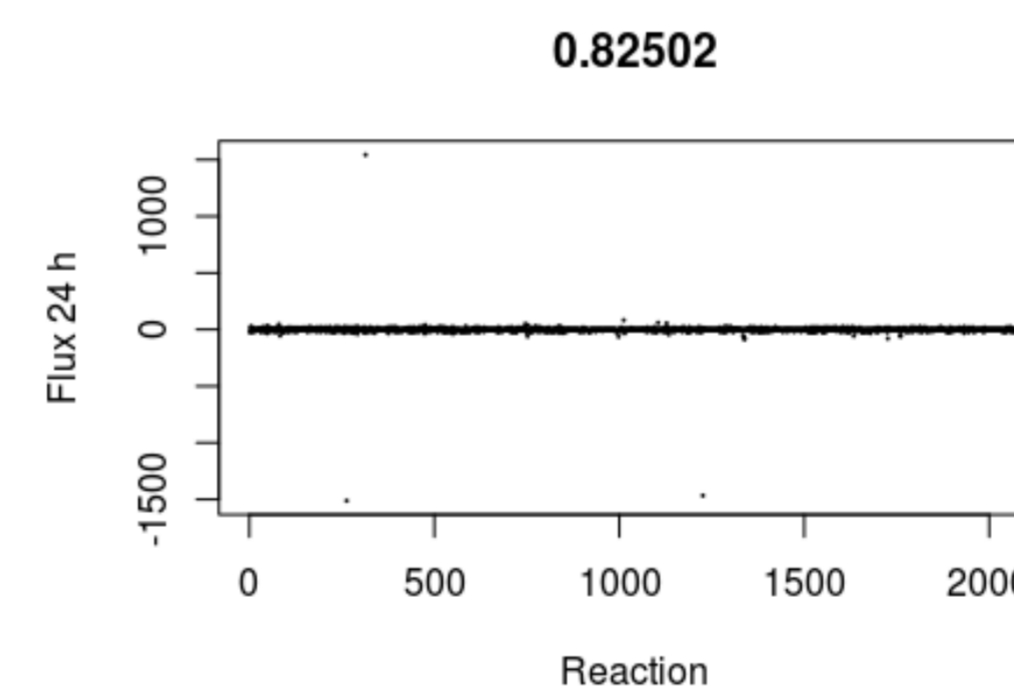


Linear Programming solutions showed that all biomass precursors could be synthesized.

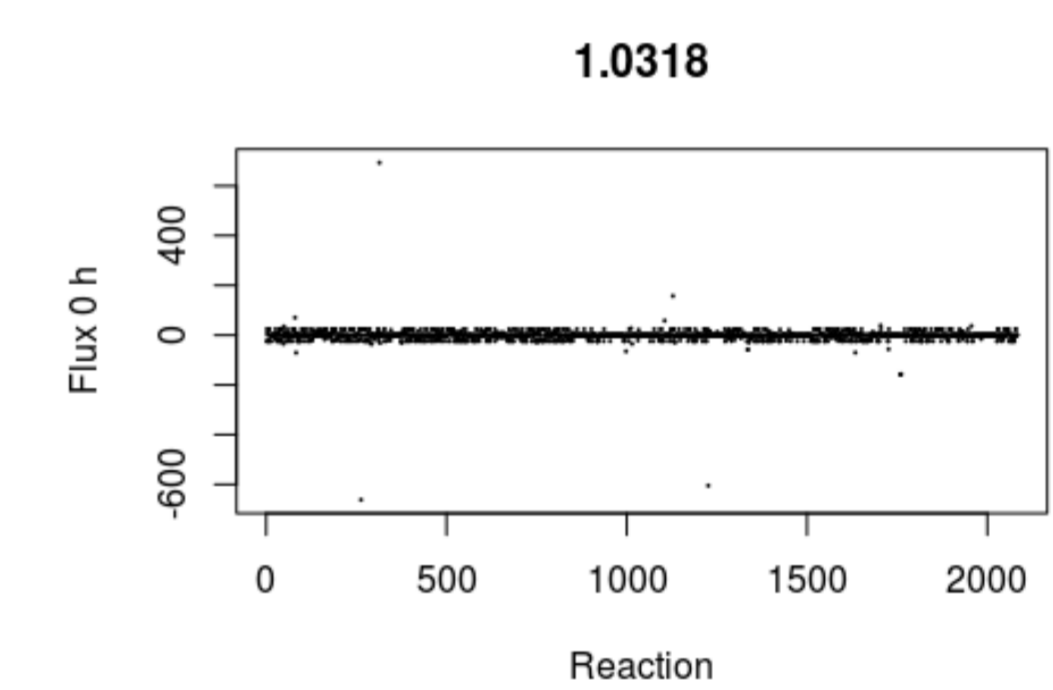
### *S. Tuberosum* model



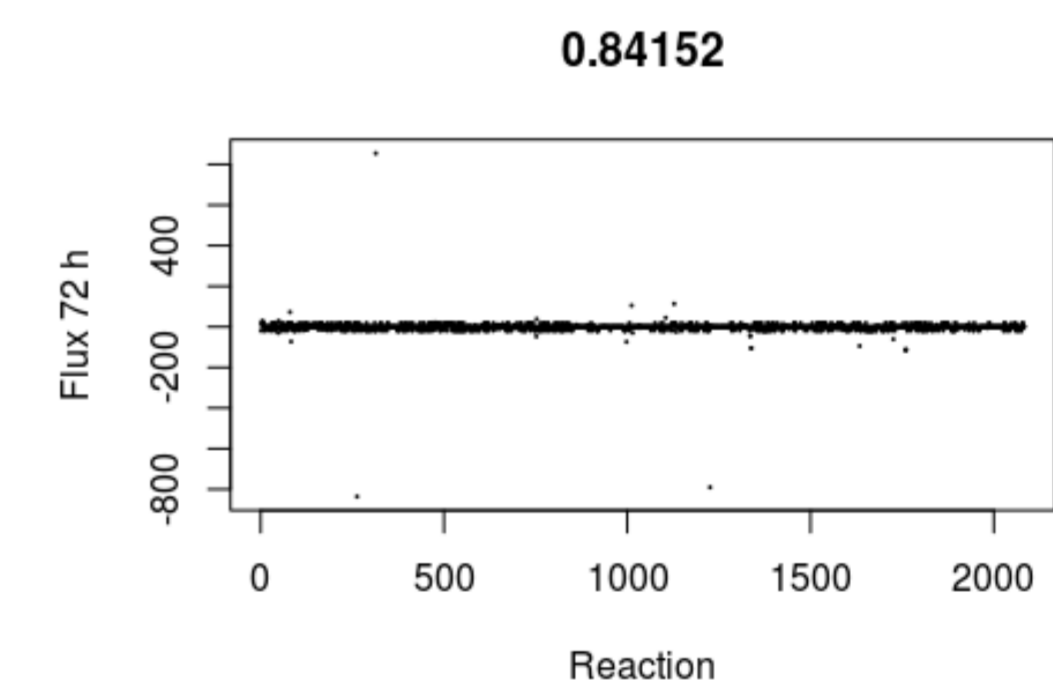
### Pathosystem model



### Pathosystem model



### Pathosystem model



## Conclusion

We report the first genome scale metabolic reconstruction of *S. tuberosum* and the first genome escale metabolic model of a interaction plan-pathogen. Compatible interaction *P. infestans* in *S. tuberosum* affects biomass synthesis in plant leaf.

## References

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