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## Studies of evolution and genetics of metabolic functions by high-throughput methods in bacteria and their hosts

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High-throughput molecular and bioinformatics techniques developed in the past decade have ushered in a new era for the study of currently difficult, or impossible, to cultivate organisms. Among these are most of the endosymbiotic bacteria harbored by eukaryotes. Here, the focus will be on the betaproteobacterial endosymbionts of insect-infecting trypanosomatid parasites, namely *Candidatus Kinetoplastibacterium* spp. (Betaproteobacteria, Alcaligenaceae). Until recently, studying the genomes of these bacteria was not feasible, since they do not grow outside of their eukaryotic host – any molecular data was restricted to genes amplified by PCR using universal primers, mainly the ribosomal RNA genes. Thus, the genetic bases for the characterized aspects of their interactions, determined through decades of biochemical experiments, remained completely unknown. High-throughput sequencing and efficient sequence assembly algorithms allowed us to determine the genomes of host and bacterial endosymbiont at the same time, yielding data that both uncovered the genetic bases for the close collaboration between these organisms as well as revealed other new and interesting aspects of the evolution of their lineages and genomes. *Ca. Kinetoplastibacterium* occurs inside insect-infecting trypanosomatids of the genera *Angomonas* and *Strigomonas*. Each eukaryotic cell contains only one bacterial cell in its cytoplasm, with binary division of the two organisms occurring in synchrony. They collaborate in the synthesis of numerous essential compounds, including amino acids, vitamins, heme, and lipids. Their interaction is so close that the bacterium changes the host cell's surface composition and aspects of the trypanosomatid-insect interaction. Not surprisingly, these endosymbionts are considered a model of organellar evolution.

### Biography

J M P Alves has a PhD from University of Sao Paulo (USP) and Postdoctoral studies from Virginia Commonwealth University. He is currently a visiting Researcher at the Dept. of Parasitology (USP), and his main research interests include evolution, genomics, and their intersection, in the study of protozoans and their endosymbionts.

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