The Acinetobacter pan-plasmidome

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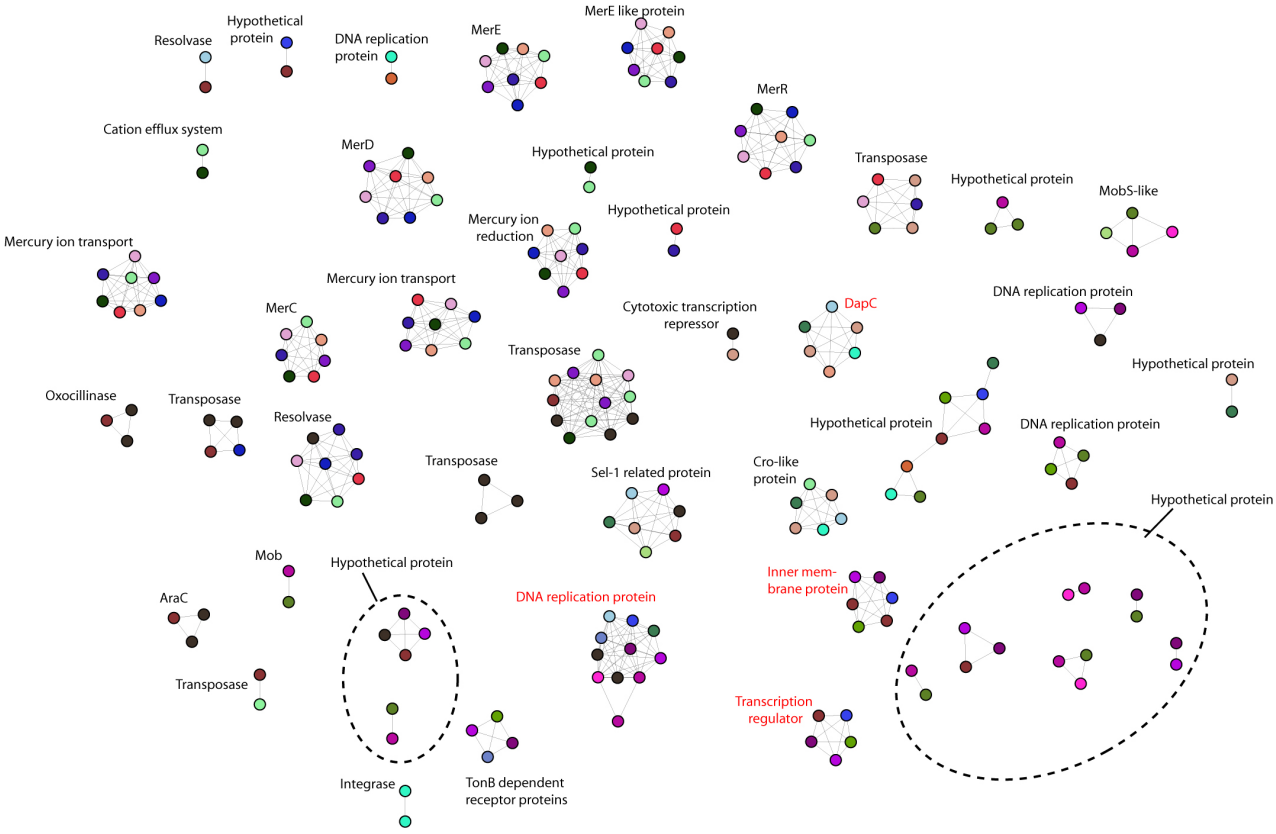
Motivation

Plasmids have a large impact on the metabolic functions of host cells, providing traits that sum up to the functions encoded by the chromosome(s). Moreover, plasmids can provide a basis for genome rearrangements via homologous recombination facilitating the loss or acquisition of genes during transposition and/or horizontal gene transfer (HGT) events . For the roles they play in nature, plasmids are gaining increasing interest, and the recent adoption of whole plasmid genome sequencing as a routine analytical technique has provided the basis for developing computational approaches for comparative studies. One possible strategy is to focus on a group of organisms using the most recent plasmid and chromosome sequence data available to characterize relationships existing between the proteins they encode for. In this context the Acinetobacter genus has several interesting features because it comprises species isolated from many different sources, some of which are human pathogens and others are interesting from a bioengineering perspective (e:g. for bioremediation). In GenBank there are 29 plasmids and 7 chromosomes belonging to the this genus, and we characterize them in terms of encoded functions and evolutionary relationships using a recently published approach.

Methods

Blast2Network (B2N) is a recently published software that allows the immediate visualization and evaluation of evolutionary relationships existing among a large dataset of aminoacid and/or nucleotide sequences, through the building up of similarity networks, where proteins are the nodes, and the similarities between them are the links, in Figure). Starting from the all-against-all similarity search, B2N computes phylogenetic profiles of the molecules under analysis and use them to calculate distance matrices in two different dimension, namely the protein cluster and the DNA molecule dimensions that are then encoded as Neighbor Joining dendrograms. In the first case the algorithm allows to identify proteins with the most similar occurrence pattern in the different source molecules (plasmids and/or chromosomes), helping the identification of proteins belonging to the same cellular process . In the second case, the algorithm describe the relationships existing between the molecules used for the analysis by quantifying the similarities in terms of shared gene content.



Results

Data obtained revealed interesting clues on the evolution of Acinetobacter plasmids, and facilitated the identification of those evolutionary steps through which plasmids have been assembled and shaped from the available families of modular plasmid components. Moreover, we evaluated the interrelationships existing between plasmids and chromosomes and identified several events of horizontal gene transfer that have occurred in the course of evolution among plasmids and leading, for example, to the appearance of mercury resistance in A. baumannii AYE. Finally, our analysis, based on a phylogenetic profiling approach, permitted to assign a putative function to previously uncharacterized proteins. It is worth of noticing that, following this strategy, we found co-occurrences among previously uncharacterized proteins and the pathogenic lifestyle of those cells harbouring them, suggesting that they might be responsible for unexplored traits in the pathogenic mechanisms of these bacteria. In conclusion, the whole body of data presented in this work underlines the importance of an in silico approach in the comparative studies of genes and genomes that, although cannot substitute for molecular and biochemical experiments, may serve as a basis for generating hypotheses for future research and experimental validations.

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