Poster

AnABlast: a useful tool to analyse the Caenorhabditis elegans genome sequence

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ABSTRACT

Motivation: During the last decade, genomes analysis has experienced great advances. However, genomes still hide mysteries to be decoded. There are many computer programs that can assist us to better understand genomes and to their annotation. AnABlast (Ancestral-patterns search though A BLAST-based strategy) was developed to detect small and complex hidden coding sequences. It generates profiles of alignaments on query amino acid sequences using lo-stringency BLAST strategy. Three years ago, AnABlast was tested in a genome-wide search for coding sequences in Schizosaccharomyces pombre and several new genes and ancient coding sequences were efficiently identified in the fission yeast genome. Due to this huge success, this strategy is now being applied to Caenorhabditis elegans. In this work, we have used AnABlast to search the C. elegans genome for new, uncharacterized putative coding sequences. As a fuctional assay we have performed, RNA interference (RNAi) against these sequences to check if a visible phenotype could be observed. Upon genome analysis AnABlast hits show up as the alignments along query sequences accumulation peaks in possible coding regions. Although, the genome of C. elegans is well annotated it could still be challenging because AnABlast has discovered several peaks that could probably be new genes or undescribed exons from previously of annotated genes.

Methods: The methodology consists in two main processes. First, we searched for possible new coding sequences by AnABlast. Second, we are constructing a library to perform RNAi experiments against all possible sequences chosen. In order to do that, primers were generated to amplify each selected sequence. The resulting framents are cloned on the RNAi producing plasmid L4440 and transformed into the Escherichia Coli HT115 strain, resulting in individual bacterial strans, each designed to produce RNAi aganinst a single C elengas predicted peak. These E. coli expressing the dsRNA are then used to perform separate RNAi experiments to individually analyze the possible phenotype of each selected nucleotides sequences.

Conclusions: With this, we will have a very potent RNAi library of possible new genes that could be very useful in the future. Moreover, we are demostrating that AnABlast is a potent tool to uncover new genes, and it may applicable to the "in silico" analysis of others organism sequences genome.

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