A COMPARATIVE STUDY OF TWO ORTHOLOGOUS GENE IDENTIFICATION METHODS ON SYNTENY BLOCK INFERENCE

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A Comparative Study of Two Orthologous Gene Identification Methods On Synteny Block Inference (“this Work”):

Field of Study: Bioinformatics, Synteny, Orthologs, Inparalogs

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ABSTRACT

A synteny block is a set of orthologous genes that share the same relative ordering on the chromosomes of two species. Synteny analysis at the genome scale is a powerful means of identifying orthologs in a set of genomes of interest for downstream phylogenetic studies. OrthoCluster is a data mining tool for inferring synteny blocks among multiple genomes. Before using OrthoCluster to infer synteny blocks, orthologous gene relationships between the species of interest have to be identified first. In this study, we evaluated the effects of two different orthologous gene identification methods: InParanoid and ad hoc BLAST, on the number, size and content of synteny blocks returned by OrthoCluster using the genomes of *Oryza sativa* and *Arabidopsis thaliana*.

Results show that InParanoid identified 22,124 orthologous relationships while ad hoc BLAST identified 14,928. Subsequently, OrthoCluster identified 942 conserved synteny blocks that contain no mismatches using input from InParanoid. These synteny blocks cover 1234 genes (5.97 Mb) in *O. sativa* and 1403 genes (2.76 Mb) in *A. thaliana*, respectively. With input from ad hoc BLAST, OrthoCluster detected just 314 conserved synteny blocks, which cover 427 genes (2.3 Mb) in *O. sativa* and 435 genes (1.1 Mb) in *A. thaliana*. Allowing mismatches within a synteny block, OrthoCluster identified 1510 non-conserved synteny blocks from InParanoid input, which cover 3509 genes (25.1 Mb) in *O. sativa* and 3648 genes (9.06 Mb) in *A. thaliana*. Only 589 non-conserved synteny blocks were detected using ad hoc BLAST input, with 1335 genes (8.22 Mb) in *O. sativa* and 1257 genes (3.32 Mb) in *A. thaliana*. 
InParanoid identified about 50% more orthologous genes compared to ad hoc BLAST. This subsequently led to OrthoCluster detecting at least 2 times more synteny blocks (conserved / non-conserved), and about 3 times more genes. This result suggests that synteny blocks inferred by OrthoCluster are highly dependent on the method and parameters used for identifying orthologous gene relationships.
ABSTRAK


Hasil menunjukkan InParanoid mengenal pasti 22 124 hubungan ortolog manakala ad hoc BLAST mengenal pasti 14 928 hubungan ortolog. Seterusnya, OrthoCluster mengenal pasti 942 blok sinteni abadi yang tidak mengandungi ketakpadanan dengan menggunakan input daripada InParanoid. Blok sinteni yang dikenalpasti masing-masing mengandungi 1234 gen (5.97 Mb) pada O. sativa dan 1403 gen (2.76 Mb) pada A. thaliana. Dengan input daripada ad hoc BLAST, OrthoCluster mengesan hanya 314 blok sinteni abadi yang masing-masing mengandungi 427 gen (2.3 Mb) pada O. sativa dan 435 gen (1.1 Mb) pada A. thaliana. Dengan membenarkan ketakpadanan dalam blok sinteni, OrthoCluster mengenal pasti 1510 blok sinteni tak abadi daripada InParanoid, meliputi 3509 gen (25.1 Mb) pada O. sativa dan 3648 gen (9.06 Mb) pada A. thaliana. Hanya 589 blok sinteni tak abadi dikesan dengan menggunakan input daripada ad hoc BLAST, meliputi 1335 gen (8.22 Mb) pada O. sativa dan 1257 gen (3.32 Mb) pada A. thaliana.
*InParanoid* mengenal pasti kira-kira 50% lebih gen ortolog berbanding dengan *ad hoc* BLAST. Dengan demikian, *OrthoCluster* mengesan sekurang-kurangnya 2 kali lebih banyak blok sinteni (abadi / tak abadi), dan kira-kira 3 kali lebih banyak gen. Keputusan ini menunjukkan bahawa blok sinteni yang dikenalpasti oleh *OrthoCluster* sangat bergantung kepada kaedah dan parameter yang digunakan untuk mengenal pasti hubungan gen ortolog.
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<tr>
<td>AL</td>
<td>aligned length</td>
</tr>
<tr>
<td>BBH</td>
<td>bidirectional best-hit</td>
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<tr>
<td>BLAST</td>
<td>Basic Local Alignment Search Tool</td>
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<tr>
<td>CALIP</td>
<td>cumulative alignment length identity percentage</td>
</tr>
<tr>
<td>CALP</td>
<td>cumulative alignment length percentage</td>
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<tr>
<td>COG</td>
<td>Cluster of Orthologous Group</td>
</tr>
<tr>
<td>eggNOG</td>
<td>evolutionary genealogy of genes: Non-supervised Orthologous Groups</td>
</tr>
<tr>
<td>HSP</td>
<td>high-scoring segment pairs</td>
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