

Analysis of *Dictyostelium discoideum* cDNA Obtained from Multicellular and Unicellular Stages

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1 Introduction

The cellular slime mold *Dictyostelium discoideum* has both multicellular and unicellular characteristics in its life cycle and hence it is considered as a powerful system for studying development, differentiation, and inter- or intra-cellular signaling. We have analyzed cDNA sequences of *Dictyostelium discoideum* in the Dicty_cDB [2] database developed by Tsukuba University. The database contains cDNA sequences obtained from various stages of its life cycle, especially slug (multicellular) and vegetative (unicellular) stages.

The analysis is expected to uncover differences and similarities of the sets of gene that are expressed in the two stages, to allow comparison with other eukaryotes, and to give insights into the characteristics of multicellular and unicellular organisms. We here report preliminary results of our analysis.

2 Material and Method

We obtained 5,783 contigs (partial cDNA sequences), which had been assembled by PHRAP from EST sequences of the two stages in Dicty_cDB. They were classified according to the expression stages (slug or vegetative) of the original ESTs, and 3,102 contigs were from the slug stage, 1,596 from the vegetative stage, and 1,085 from both.

For functional prediction of each contig, we performed homology search (SSEARCH) to the amino acid sequences of selected eukaryotes, *D. melanogaster*, *C. elegans*, *A. thaliana*, *S. cerevisiae*, and *S. pombe*, obtained from KEGG/GENES [3]. Then we annotated *Dictyostelium* contigs based on the description of Gene Ontology [1] assignments to homologous genes. These annotations are used for functional classification of genes expressed at each stage.

The five eukaryotes mentioned above and human (from the Ensemble database [4]) were classified into three major groups, animal, plant, and fungi, and the distribution of *Dictyostelium* homologs were investigated.

We used BioRuby [5] to extract information from KEGG/GENES.

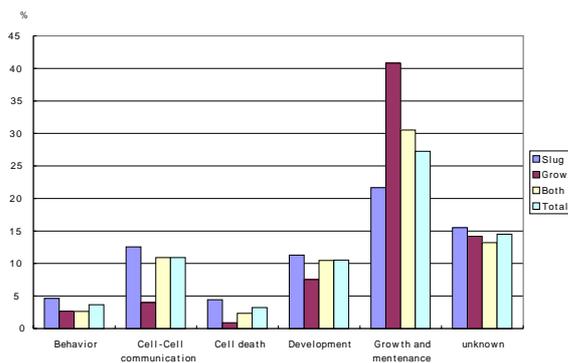


Figure 1: The functional classification of cDNA .

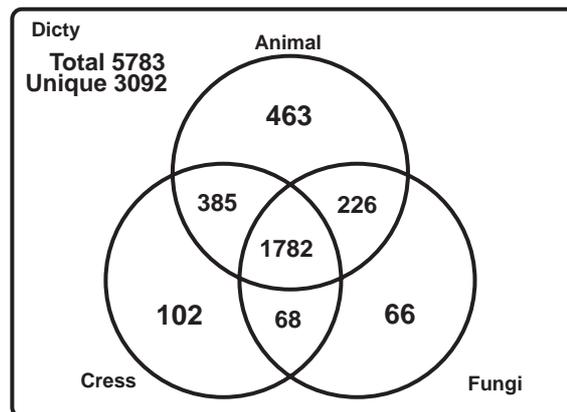


Figure 2: The distribution of cDNA homologs.

3 Result and Discussion

The distribution of expressed genes at each stage is shown in Figure 1, together with their functional classification according to the category of biological process in Gene Ontology. The ratio of genes classified in cell-cell communication, which include signaling and adhesion related genes, are higher at the slug stage than the vegetative stage. The difference indicates multicellular and unicellular characteristics of slug and vegetative stages, respectively.

Figure 2 shows the distribution of cDNA homologs to the three major eukaryotic groups. First of all, the majority of *Dictyostelium* genes are unique, i.e. there are no homologs to these eukaryotes. Second, about 65 % of the genes with homologs have homology to all the three groups. The functions of these genes are basic functions such as intermediary metabolism and translation and transcription machineries.

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- [4] <http://www.ensembl.org/>
- [5] <http://BioRuby.org/>