

Quantitative and computational phenotype analysis of early *C. elegans* RNAi embryos

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Abstract

An embryo is a spatially and temporally dynamic system. To understand basic principle of such multi-cellular systems, we are conducting a computational phenotype analysis of *C. elegans* RNAi embryos. Because previous RNAi phenotype analyses were conducted using manual phenotype detection, the objectivity and sensitivity of these analyses was limited. Our computer system [1,2] automatically measures cell division pattern of *C. elegans* embryo from four-dimensional DIC microscope image of an embryo by using image processing and object tracking; this quantitative cell division pattern includes the xyz positions and outlines of nuclear regions of every 40 sec and their lineage. This system enables a highly objective and sensitive phenotype analysis.

In this presentation, we report RNAi phenotype analysis of very early stage of embryogenesis (from one- to eight-cell stage) of all 97 genes on chromosome III that give 100% embryonic lethal phenotype by RNAi. We obtained quantitative cell division patterns of RNAi embryos for 77 genes; RNAi embryos for the remaining 20 genes did not show cell division. By mathematically defining 246 quantitative phenotype signatures and statistically comparing these signatures between wild-type and RNAi embryos, we detected 2179 phenotypes in the cell division patterns of these RNAi embryos. Most of these phenotypes (2156/2179) were not reported in the previous large-scale phenotype analyses whereas all 23 cell division pattern phenotypes in this very early stage embryogenesis reported in the previous large-scale analyses were detected by our computational analysis. Based on these results, we are predicting gene regulatory network for this very early stage of embryogenesis. The progress of this gene regulatory network study will be presented. We will also present our new software for quantitative cell division pattern analysis that is applicable to public movies and images.

References

1. Hamahashi et al., *BMC Bioinformatics* **6**, 125 (2005).
2. Hamahashi et al., *Systems Comput. JPN* **38(11)**, 12-24 (2007).