QBiC CDB JOINT SEMINAR

Speaker

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Program in Systems Biology, University of Massachusetts Medical School

Date & Location

Thursday, July 24, 2014 16:00 - 17:00

Kobe CDB A7F Seminar Room
(2-2-3 Minatojima-minamimachi, Chuo-ku, Kobe)
*There will be a video broadcast in OLABB 1F Lounge

Title

Genetically speaking, BIG ≠ FAT

Abstract

According to World Health Organization, > 35% of adults worldwide are overweight. Being overweight drastically increases the risk factors for many diseases such as hypertension, type 2 diabetes, and obesity. Large-scale screenings using nematode and fly models have previously identified genes contributing to fat storage. However, obesity is a multifactoral disorder with complex traits. These traits are influenced by both metabolism and developmental processes, which are closely linked and often indistinguishable between their similar phenotypes (e.g. bigger animals contain more fat because of the size). Despite this intertwined complexity, previous experimental strategies have been limitedly applied to decipher gene functions regulating each of those processes. Therefore, identification of genes involved in the regulations of each phenotype remains elusive both in quality and quantity.

We studied *Caenorhabditis elegans* to comprehensively identify transcription factors (TF) purely contributing to a single phenotype (i.e. fat storage, body size) in a complex phenotype. We achieved precise quantifications for targeted phenotypes by developing a de novo image processing platform, IPPOME (Image Processing for Precise and Objective MEasurement). This platform enables automatic detection of an individual object from high-magnification images in a high-throughput manner with greater sensitivity and accuracy than currently available tools. By using RNA interference, we systematically screened the contributions of each of ~1,000 TFs to body size and/or fat storage which was visualized by Oil-Red-O staining. We recapitulated the known phenotypes caused by knock-down in fat storage and/or body size control and found many other TFs are involved in the these regulations. Interestingly, we also found that a large number of TFs regulate either fat content or body size suggesting that these phenotypes might be controlled by overlapping yet independent gene regulatory mechanisms.

Host

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