Institut Européen de Chimie et Biologie

I E C B

Why sometimes a bit more is too much (gene dosage) and tools for genetics in worms.

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My talk will be comprised of two main parts. First, I shall discuss our published work regarding genes that are deleterious to growth when overexpressed. Starting with publicly available data sets of yeast genome wide screens for genes yielding a poor growth phenotype when their dosage is increased or decreased, we investigated potential mechanisms of action. Contrary to a commonly held view, we found no evidence to suggest that genes with overexpression phenotypes affect growth by the disruption of protein complex formation due to imbalance between complex subunits. Instead we found that the presence of short, information-poor linear motifs and 'disordered regions' are important predictors of whether a gene will have an overexpression phenotype.
In the second part of my talk I will describe the puromycin drug selection system we developed in worms and in particular I will focus on how we are using drug selection to implement the bulk segregant analysis method in worms for mapping quantitative trait loci (QTL). Although still in development, this method could provide high resolution mapping of genes involved in complex traits with considerably less effort than currently used methods involving recombinant inbred lines.