E335 Developmentally regulated putative cell-cell adhesion molecule in *Dictyostelium discoideum*

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A cDNA encoding putative cell-cell adhesion molecule (DdCAD-2) has been identified from *Dictyostelium discoideum* by reverse transcriptase polymerase chain reaction. The amino acid sequences of DdCAD-2 have similarity to DdCAD-1, a Ca^{2+}-dependent cell-cell adhesion molecule from *Dictyostelium discoideum*. The open reading frame of DdCAD-2 cDNA consists of 603 base pairs and predicted polypeptide contains 201 amino acids, with a calculated molecular mass of 22,516 Da. DdCAD-2 mRNA was not detected at vetetative amoeba. However, DdCAD-2 mRNA accumulated during the first 8 hours of development and then rapidly decreased between 8 hours and 12 hours. After 16 hours, DdCAD-2 mRNA was not detected like vegetative amoeba. Also, change of DdCAD-2 protein level is similar to that of mRNA except that protein level remains constant after accumulation. DdCAD-2 expression pattern is different from DdCAD-1 in that DdCAD-1 is constitutively expressed during development.

E336 Pheromone Induction of *Schizosaccharomyces pombe*: Factors Affecting Induction and Isolation of Pheromone Induction Mutants

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The mating pheromones of *Schizosaccharomyces pombe* are induced by nutritional starvation. However, this nutritional signaling pathway is largely unknown. For a complete understanding of pheromone induction, we examined the environmental factors affecting the induction after cells were transferred to nitrogen starvation medium. It appeared that the induction of *mfm2* transcription was affected by the general environmental stress including incubation time, incubation temperature, and the growth phase of the cells. We identified 7 pheromone induction mutants by screening temperature sensitive mutant bank. Three of these mutants showed elongated cell shapes and one mutant exhibited swollen cell morphology in permissive culture, suggesting that their cell cycles were also impaired. Characterization of the pheromone induction mutants may elucidate the components required in nutritional signaling pathway leading to pheromone induction.