

Identification of differentially expressed genes during fruiting body development of the aggregative ciliate *Sorogena stoianovitchae*

Hiroki SUGIMOTO (Div. of Life Sci., Grad. Sch. of Natural Sci. & Technol., Kanazawa Univ)

*Sorogena stoianovitchae* is the only ciliate that undergoes fruiting body development. When *Sorogena* are mildly starved, a number of cells aggregate beneath the water surface, and then the aggregate develops into the aerial fruiting body. Essential requirements for fruiting body development are high cell density, light-dark cycle, and a consecutive dark period of more than 8 hours. Previously we demonstrated that the developmental process is divided into five distinct stages: 1) aggregation; 2) compact aggregation; 3) secretion of mucous matrix; 4) stalk elongation; and 5) completion of the fruiting body. In addition, the initial aggregation begins during the night, and then light stimulation at sunrise triggers subsequent development. To elucidate genes involved in development, differential display RT-PCR was carried out against cells before and after development. Forty-four sequences with stage-specific expression patterns were cloned and partially sequenced. A BLASTX search revealed that some sequences with high identity for extracellular proteins (mucin, proteophosphoglycan) or membrane proteins (surface protein, TM9SF) are likely candidates for aggregation material, mucous matrix, and stalk material. Other sequences showed similarities with proteins such as casein kinase and cysteine protease, suggesting that they are involved in signaling pathways for fruiting body development.