

Life cycle specific secondary metabolites in the model eukaryotic microbe, *Dictyostelium*

The social amoeba *Dictyostelium discoideum* is an environmental eukaryote that detects and engulfs bacteria and yeast as a food source. Its life cycle progresses from unicellular to multicellular stages, with cAMP as the chemoattractant and the signal controlling the developmental programme. Chemosensing and signalling, cell-type differentiation, the similar gene content to higher animals, and its phagocytosis of other microbes have all led to *Dictyostelium* becoming a useful biomedical and cell-biology model organism. Its secondary metabolism is less explored, although interest is increasing. The amoeba encodes genes involved in quite diverse biosynthetic pathways, through to those encoding the proteins carrying out final transport mechanisms. Two multidrug and efflux (MATE) transporters are encoded, orthologues of which are notable for sequestering flavonoids in plant vacuoles, among other functions. Having demonstrated the ability of *Dictyostelium* MATE proteins to efflux specific polyphenolic substrates, genes were identified in the amoeba that are similar to those for synthesis of plant polyphenolics. These enabled targeted analysis of 'plant' compounds in the amoeba. Life cycle analysis reveals peaks of genetic expression and chemical content at specific stages in development, augmenting the currently limited knowledge of the physical roles of *Dictyostelium* secondary metabolites.