

Identifying the molecular basis of functions in the transcriptome of the social amoeba *Dictyostelium discoideum*

T.J. Whitney^{1,2*}, D.G. Gardner^{1*}, M.L. Mott^{1,3} and M. Brandon^{1,4}

¹Department of Biological Sciences,
Idaho State University, Pocatello, ID, USA

²Current address: Department of Pathology,
University of Utah, Salt Lake City, UT, USA

³Current address: Pritzker School of Medicine,
University of Chicago, Chicago, IL, USA

⁴Current address: Fort Lewis College,
School of Natural and Behavioral Sciences, Durango, CO, USA

*These authors contributed equally to this study.

Corresponding author: M. Brandon

E-mail: Brandon_m@fortlewis.edu

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ABSTRACT. The unusual life cycle of *Dictyostelium discoideum*, in which an extra-cellular stressor such as starvation induces the development of a multicellular fruiting body consisting of stalk cells and spores from a culture of identical amoebae, provides an excellent model for investigating the molecular control of differentiation and the transition from single- to multi-cellular life, a key transition in development. We utilized serial analysis of gene expression (SAGE), a molecular method that is unbiased by dependence on previously identified genes, to obtain a transcriptome from a high-density culture of amoebae, in order to examine the transition to multi-cellular development. The SAGE method pro-

vides relative expression levels, which allows us to rank order the expressed genes. We found that a large number of ribosomal proteins were expressed at high levels, while various components of the proteasome were expressed at low levels. The only identifiable transmembrane signaling system components expressed in amoebae are related to quorum sensing, and their expression levels were relatively low. The most highly expressed gene in the amoeba transcriptome, *dutA* untranslated RNA, is a molecule with unknown function that may serve as an inhibitor of translation. These results suggest that high-density amoebae have not initiated development, and they also suggest a mechanism by which the transition into the development program is controlled.

Key words: *Dictyostelium discoideum*; Amoebae; Transcriptome; SAGE