

Highlight: Origins of Multicellularity Revealed by Single-Celled Amoebae

Casey McGrath*

Ithaca, New York

*Corresponding author: E-mail: mcgrath.casey@gmail.com.

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The transition from a unicellular to a multicellular lifestyle has occurred multiple times—most notably in the lineages leading to plants, animals, and fungi. How this transition is made, however, has remained a major question among biologists, and new evidence may come from an unlikely quarter: The study of single-celled amoebae.

In plants, animals, and fungi, dividing cells remain attached to each other, forming multicellular organisms. In many protist lineages, however, multicellularity involves the coming together of dispersed cells under starvation conditions to form a structure known as a fruiting body, which produces airborne spores (fig. 1). These spores are the organism's way of playing the evolutionary lottery; the hope is that some of these spores find their way to better living conditions, thus perpetuating the lineage. It appears that this particular form of multicellularity has evolved multiple times, including in the model organism *Dictyostelium discoideum* and its relatives in the Amoebozoa. A study of *Dictyostelium* genes by Gernot Glöckner and colleagues in 2016 revealed the presence of several unique membrane or secreted proteins that may have enabled the evolution of multicellularity in this lineage (Glöckner et al. 2016). For Glöckner, a professor at the University of Cologne, the natural next question was: where did these genes come from?

To answer this question, Glöckner looked to protosteloid amoebae, single-celled relatives of *Dictyostelium*. Protosteloid fruiting bodies are composed of one or a few spores on the end of a stalk, but unlike in *Dictyostelium*, the entire fruiting body is derived from a single cell. In a recent article in *Genome Biology and Evolution* (Hillmann et al. 2018), Glöckner, along with Falk Hillmann of the Hans Knöll Institute and other colleagues, compared the gene repertoires and expression patterns of the protosteloid amoebae *Protostelium aurantium* and *Protostelium mycophagum* with those of the distantly related multicellular *Dictyostelium*. In doing so, they hoped

to distinguish genes related to fruiting body development, a process shared by *Dictyostelium* and *Protostelium*, from those related to multicellularity, found only in *Dictyostelium*.

Among the genes used for fruiting body development in *Dictyostelium*, Glöckner et al. were able to identify orthologs involved in the same process in the two *Protostelium* species. "It was exciting to see that developmental signaling is conserved from simple to multicellular systems," says Glöckner. However, they noticed that the regulation of these genes was often in opposite directions in *Protostelium* and *Dictyostelium*. For example, the gene *statA* is upregulated during fruiting body development in *Dictyostelium*, where it plays a major role in chemical sensing and the formation of the fruiting body stalk. In contrast, its ortholog in *P. aurantium* is downregulated during fruiting body development. This was a surprise according to Glöckner, as it indicates that "the genes involved in fruiting body formation were most likely independently recruited to this task in different lineages of Amoebozoa."

Also unexpected, according to Pauline Schaap, co-author of the study, was the exceptional number of genes involved in signaling and environmental sensing in the protosteloid amoebae. These genes are necessary for finding prey, evading predators, and adapting to environmental change, and it was somewhat surprising to find more of these genes in the unicellular *Protostelium* than in *Dictyostelium* with its complex multicellular life cycle. Glöckner and colleagues note that such a large collection of signaling genes likely reflects the ability of the Amoebozoa to adapt to various environmental conditions, and they speculate that these signaling molecules provided the building blocks for cell–cell communication in early multicellular forms. Adds Schaap, "This suggests that their interactions with each other and with other organisms in their habitat are much more complex than is generally thought."

For Glöckner, these results offer a new paradigm for thinking about the evolution of complex traits like fruiting body formation and multicellularity. "Some researchers currently

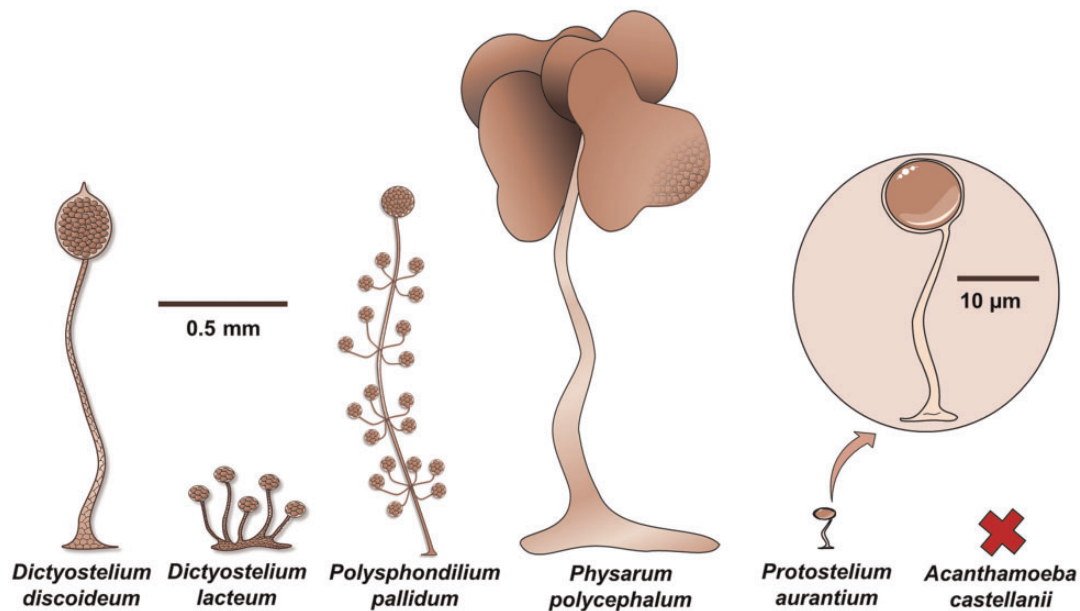


Fig. 1.—Amoebozoa fruiting bodies. Schematic view of the different “fruiting bodies” in the Amoebozoa. Depicted are only species where a genome sequence is available including the here presented *Protostelium* spp. genomes. The fruiting bodies are drawn to scale, the inset shows an enlargement of the tiny *Protostelium* fruiting body. No fruiting body is known for *Acanthamoeba castellanii*, indicated by a cross. However, other Acanthamoebae do form sporocarps, as was recently discovered for *A. pyriformis* (Tice et al. 2016).

believe that complex programs like fruiting body formation could have evolved only once in a certain lineage.” For example, in a 2017 paper in *Molecular Biology and Evolution*, Matthew Brown, a professor at Mississippi State University, and colleagues suggested that the protosteloid type of fruiting body may have been present in the common ancestor of all Amoebozoa (Kang et al. 2017). This hypothesis is based on the fact that protosteloid amoebae do not represent a single group, but rather appear in at least two deep lineages within the Amoebozoa. However, Glöckner believes that their new data “show that the same outcome (a fruiting body) might evolve independently from the same [genetic] toolbox, thus thwarting this belief.”

In future studies, Glöckner and colleagues will continue investigating the molecular mechanisms that drive the life cycles of these eukaryotic microbes, as well as their interactions with each other and the environment. This may not be straightforward, however, as Glöckner notes that “the developmental program seems to be redundant with overlapping functions and therefore robust against disturbance. This redundancy hinders us from obtaining a clear picture about the basic requirements for the setup of such a program.” Moreover, as Schaap points out, “very few [protists] can yet

be genetically transformed, which severely hinders identification of the function of known genes and the discovery of novel genes with important roles in the organism’s physiology and development.”

In overcoming these challenges, future studies promise to reveal the origins of the signaling genes that may have enabled the evolution of multicellularity in *Dictyostelium*. In addition, analyses of other independent instances of multicellularity should shed light on whether similar mechanisms apply to other unicellular to multicellular transitions.

Literature Cited

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