Preface

Protozoan parasites, especially the ones which cause disease, are of tremendous interest to biologists. The reason is that these 'lower eukaryotes' are able to successfully encroach, occupy and not only live-off a 'higher eukaryote', they also cause terrible misery to their unknowing hosts. One such human pathogen is Entamoeba histolytica. It invades this special issue of Journal of Biosciences at our invitation, unlike its usual modus operandi, when it drops in uninvited along with lunch!

These unicellular organisms were referred to as 'primitive eukaryotes' in text books and journals alike, since they (supposedly) lacked 'typical eukaryotic subcellular organelles'. It was commonly believed that they were ancestral to higher eukaryotes which appeared later in evolution. They were also thought to divide by a process of asexual reproduction called 'amitosis' which was not seen in eukaryotes. In the last 15 years, molecular biology has eradicated many of these myths and established that parasitic protozoa are not primitive - but are actually very complex, often exhibiting 'atypical' characteristics when compared to other eukaryotes.

Samuelson's review in this issue effectively argues against the idea that these protests represent ancient, transitional forms. This review shows how amoeba and giardia contain proteins and structures similar to higher eukaryotes, suggesting that they could well serve as models for the common ancestral form. He points to lateral gene transfer as a means whereby parasitic eukaryotes acquired prokaryotic genes. He also raises the intriguing possibility of convergent evolution while comparing amoebic cyst wall lectins with plant and insect lectins. All hint at the innate complexity of parasitic protists.

The signals and molecular events controlling differentiation to cyst are poorly understood but happen to be extremely important for disease management. Eichinger unveils a complex model involving the al/GalNAc lectin, G-protein coupled receptors and biogenic amines. The rediscovery of biogenic amines and their receptors may lead to the discovery of unexplored signalling pathways in amoeba in the near future.

With the completion of the genome sequencing projects by The Institute of Genome Research and the Sanger Centre in sight, we are at the threshold of identifying novel gene products and DNA sequences which may explain the elusive behaviour of this organism. The use of microarrays is still in its infancy but promises to become a potent tool for the study of this organism soon as described by Singh and Shah. Lastly, although E. histolytica does not affect an alarming number of humans, unlike HIV or the malaria parasite, molecular and cellular information from this organism promises to yield many of biology's well kept secrets which may be important in understanding human response to disease and survival strategies in adversity.

Undersigned is confident enough that this work will prove its worth what it has been created for.

— Author