

## Analysis of expressed genes of apicomplexan parasites using full-length cDNA libraries

Junichi WATANABE<sup>1</sup>, Yutaka SUZUKI<sup>2</sup>, Hiroyuki WAKAGURI<sup>2</sup> (<sup>1</sup>Institute of Medical Science,  
<sup>2</sup>Graduate School of Frontier Sciences, The University of Tokyo)

Apicomplexan protozoa are obligatory parasites that cause various diseases including malaria. Recent studies revealed that they belong to the superkingdom Alveolata which also contains Ciliata and Dinoflagellata. Using oligo-capping methods, we have produced full-length cDNA libraries from various apicomplexa, including *Plasmodium falciparum*, *P. vivax*, *P. yoelii*, *P. berghei*, *Toxoplasma gondii* and *Cryptosporidium parvum*. Large scale determination of 5'-end one-pass sequences and comparisons with the genome sequences revealed that 80–90% contain the entire ORF (open reading frame) and these were considered to represent full length clones. The database, Full-malaria, was produced and published on the internet (<http://fullmal.ims.u-tokyo.ac.jp>). Determination of the entire sequences of these clones should elucidate the exact gene structures and transcriptional start sites. The latter defines the regions that control gene expression upstream. Comparative analysis of these libraries will help elucidate the process of evolution of apicomplexan parasites. Similar studies involving Ciliata and Dinoflagellata are expected to unravel the mechanisms behind the parasitism. The clones will also be used for various experiments.